# Advanced 3D Cell Culturing and Monitoring System 

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## Zusammenfassung

Die vorgelegte Doktorarbeit stellt ein 3D-Zellkultursystem mit einem vollautomatisierten analytischen, biochemischen Assay und vollautomatisierter Kultivierung mit Mediumwechsel vor. Dieses integrierte Kultivierungs- und Analysesystem wurde in dieser Arbeit mit 3D-Hepatozytenkulturen in Polycarbonat-MatriGrid®-Gerüsten für das 3D-Wachstum von Zellkulturen prototypisiert. Das System perfundiert MatriGridKulturen kontinuierlich mit Wirkstoff-ergänztem Medium und führt bei Bedarf eine Bewertung der Wirkstofftoxizität durch Beobachtung und Messung der Konzentration eines Indikators, des Biomarkers Albumin, durch. Das System kann die MatriGrid-Kultur mit unterschiedlichen Flussraten perfundieren, automatisierte Medienwechsel durchführen und mit dem mitgelieferten ELISA-Modul Proben des zu analysierenden Kulturmediums nach Bedarf untersuchen. Das System unterstützt die parallele Kultivierung von Zellen in mehreren Bioreaktoren. Das Fluidnetzwerk wurde aus Materialien konstruiert, die wenig Proteine und kleine Moleküle binden, absorbieren oder adsorbieren, um seine Anwendung für niedrige Biomarkerkonzentrationen und Langzeitexperimente zu erweitern. Die Doktorarbeit beschreibt das Systemdesign, den Aufbau, das Testen und die Verifikation unter Verwendung von 3D-gewachsenen HepaRG-Zellkulturen. Die zeitabhängige Wirkung von APAP auf die Albuminsekretion wurde über 96 h untersucht, wobei sowohl mit dem neu entwickelten System als auch konventionell in Mikrotiterplatten, gemessen wurde. Es zeigte sich, dass die Ergebnisse vergleichbar sind. Dieses Resultat belegt die Verwendung des Systems als eigenständiges Gerät, das in Echtzeit arbeitet und in der Lage ist, gleichzeitig Zellkultur- und Mediumanalyse in mehreren Bioreaktoren durchzuführen, mit erhöhter Zuverlässigkeit der 3D-Kultivierung, in einfacher Handhabung und Messung. Auf diese Weise soll das neu entwickelte 3D-Zellkultivierungs- und Analysesystem 3DZellkultivierungstechniken und -experimente für weitere Forschungsgruppen bekannt machen.


#### Abstract

This thesis presents a 3D cell culturing system with a fully automated analytic biochemistry assay and fully automated culturing with medium change. This integrated culturing and analytic system was prototyped in this work with 3D hepatocyte cultures in polycarbonate MatriGrid ${ }^{\circledR}$ scaffolds for 3D growth of cell cultures. The system continuously perfuses MatriGrid cultures with drug supplemented medium and performs, on demand, drug toxicity evaluation by observing and measuring the amount of an indicator, the biomarker albumin. The system can perfuse the MatriGrid cultures using different flow rates, performs automated medium changes and can make on-demand samples of the culture medium to be analyzed with the included ELISA module. The system supports parallel culturing of cells in multiple bioreactors. The fluidic network was constructed from low protein and small molecules binding, absorbing or adsorbing materials to extend its application for low biomarker concentration and long-term experiments. The thesis describes the system design, construction, testing, and verification using 3D-grown HepaRG cell cultures. The time-dependent effect of APAP on albumin secretion over 96 h , measured with newly developed system and conventional microtitre plates was measured and the results are comparable. These results confirm the use the system as a standalone device that works in real time and is capable of simultaneous cell culture and medium analysis in multiple bioreactors, with increased reliability of 3D-culturing, ease of handling and measurement. This way the newly developed 3D cell culturing and analysis system is aimed to promote 3D cell culturing techniques and experimentation to more research groups.


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## Abbreviations and acronyms

| 1D | one-dimensional |
| :--- | :--- |
| 2D | two-dimensional |
| 3D | three-dimensional |
| 3D-ACAD | automatic 3D-culturing and analysis device |
| ABTS | 2,2'-azino-di [3-ethylbenzthiazoline] sulfonate |
| AC | alternating current |
| ADC | analog to digital converter |
| ADHP | 10-Acetyl-3,7-dihydroxyphenoxazine |
| ALF | acute liver failure |
| ANSI | American National Standards Institute |
| APAP | N-acetyl-para-aminophenol |
| ARM | advanced RISC machines |
| BSA | bovine serum albumin |
| BW | bandwidth |
| CAN | controller area network |
| CDT | C/C++ development tooling |
| CFA | cyst fluid antigens |
| CK-MB | creatine kinase myocardial band |
| CMOS | complementary metal-oxide-semiconductor |
| CPU | central processor unit |
| CYP | cytochrome P450 family |
| DC | direct current |
| DI | de-ionized |
| DMSO | dimethyl sulfoxide |
| DPSS | diode-pumped solid state |
| EC50 | half maximal effective concentration |
| ECM | extracellular matrix |
| EEPROM | electrically erasable programmable read-only memory |
| ELISA | enzyme-linked immunosorbent assay |
| EMA | European Medicines Agency |
| EMI | electromagnetic interference |
| AD |  |


| FBS | fetal bovine serum |
| :---: | :---: |
| FCS | fetal calf serum |
| FDA | Food and Drug Administration |
| FEP | poly-(tetrafluoroethylene-co-hexafluoropropylene) |
| FMIA | flow-through membrane immunoassay |
| FTA | flow-through assay |
| GBW | gain-bandwidth product |
| GDB | GNU debugger |
| GNU | extensive collection of free software |
| GSH | glutathione |
| GST- $\alpha$ | glutathione-S-transferase alpha |
| Heparg | immortalized human hepatic cell line |
| HepG2 | human hepatocyte carcinoma cell line |
| HPA | hydroxyphenylacetic acid |
| HPLC | high-performance liquid chromatography |
| HPPA | 3-p-hydroxyphenylproprionic acid |
| HRP | horseradish peroxidase |
| $\mathrm{I}^{2} \mathrm{C}$ | inter-integrated circuit |
| IDE | integrated development environment |
| iPSC-CM | induced pluripotent stem cell-derived cardiomyocytes |
| JTAG | Joint Test Action Group |
| KTP | potassium titanyl phosphate |
| LDH | lactate dehydrogenase |
| LED | light-emitting diode |
| LQFP | low profile quad flat package |
| LSB | least significant bit |
| MIT | Massachusetts Institute of Technology |
| MTP | microtiter plate |
| Na: $\mathrm{YVO}_{4}$ | neodymium-doped yttrium orthovanadate |
| NAPQI | N -acetyl-p-benzoquinone imine |
| NEMA | National Electrical Manufacturers Association |
| OEM | original equipment manufacturer |
| OPD | o-phenylenediamine |


| PBS | phosphate-buffered saline |
| :--- | :--- |
| PC | polycarbonate |
| PC | personal computer |
| PCB | printed circuit board |
| PDMS | polydimethylsiloxane |
| PEEK | polyether ether ketone |
| PEG | polyethylene glycol |
| PMT | photomultiplier tube |
| POF | plastic optical fiber |
| PS | polystyrene |
| PVA | polyvinyl alcohol |
| PVC | polyvinyl chloride |
| R\&D | research and development |
| RISC | reduced instruction set computer |
| RMS | root mean square |
| RTC | real time clock |
| SD | secure digital |
| SDS | sodium dodecyl sulfate |
| SMD | surface-mount device |
| SPI | serial peripheral interface |
| TFT | thin-film transistor |
| TIA | transimpedance amplifier |
| TMB | $3,3 ', 5,5 '$ tetramethylbenzidine |
| TRIS | tris(hydroxymethyl)aminomethane |
| UART | universal asynchronous receiver-transmitter |
| USB | universal serial bus |
| WCA | whole cyst antigens |
| WME | Williams' medium E |

## 1 Introduction

YOU, WHO are blessed with shade as well as light, you, who are gifted with two eyes, endowed with a knowledge of perspective, and charmed with the enjoyment of various colours, you, who can actually see an angle, and contemplate the complete circumference of a Circle in the happy region of the Three Dimensions.
(Edwin Abbott, Flatland, 1884)

### 1.1 Motivation

2D cell culture schemes grow cells on flat surfaces. Such surfaces are coated with material to promote the adherence of cells, growth, and the spread of the culture. Having been used successfully for decades in labs, 2D culturing remains the primary method used in most cell culturing applications. Certainly, the technology and techniques involved in 2D culturing are straight-forward and comparatively inexpensive, and the long-standing use of 2D cultures has generated a wealth of available literature. However, the strongest argument in favor of 2D systems is the ease with which cells can be observed and measured. 2D cell schemes are characteristically simpler to evaluate compared to the widely varying and non-standard 3D cell culture systems which are currently available.

This latter point, the ease of observation and measurement, is the primary issue. The advantages of 3D culturing are certainly numerous and can be listed in extraordinary detail, but this does not change the fact that the observation and measurement of cells in the majority of new 3D culturing systems is more complex, requiring more intricate 3Dspecific culturing laboratories. This, regrettably, inhibits the use of 3D culturing systems for many laboratories which would require a complete retooling of equipment and training for staff to be specific to the new 3D system. The ideal situation would therefore be a 3D culturing system, which is reproducible and simple to use for interested laboratories, and which increase the ease of observation and measurement, using the
automation and system integration techniques. The importance of development of new scientific techniques was also recognized by Nobel Prize laureate Sydney Brenner: "Progress in science depends on new techniques, new discoveries and new ideas, probably in that order." ${ }^{[1]}$

### 1.2 Thesis Aims and Objectives

At first glance, an extensive study of commercially or otherwise available automated systems for cell culture management and analysis revealed a wide range of possibilities. What until now is not available, however, is a device platform that combines these two claims. In the case of 3D cell culture, such a link is necessary, since the inherent properties of 3D cell culture make it necessary in the most cases for analysis to interrupt the experiment. From this point of view, a combined solution of automatic cell culture management and directly linked analytics is of great scientific interest. This is exactly what in this thesis should be done.

The aim of this thesis is therefore to develop a new cell culturing system suitable for 3D cell cultures which would be easy to work with and encourage more research laboratories to transition towards 3D cell cultures. The new culturing tool must be robust, easy to handle and provide high reliability of culturing. Additionally, reliable way of monitoring the cell culture state by measuring the concentration of selected biomarkers should be provided. This analysis should be performed in an automated way and on-demand to support the concept of easy-to-use tools. The 3D culturing part and the analytical part should be compatible and create an integral 3D culturing and analytical system. Further objective is to design whole system in a compact and portable form, which could be used anywhere needed. Such 3D culturing system could be advantageously in routine preparation of 3D cell cultures or to perform toxicity assessment of various drugs towards the 3D cultured cells. It is known that 3D cultures resemble more closely in-vivo environment and thus toxicity tests performed on 3D cultures provide more relevant results [2, 3]. It is obvious that both scientific aspects from the life sciences field and engineering considerations play a role in answering such a question and play a role in the construction of such a device platform.

The functionality of the developed system should be verified on real 3D cell culture and the analytical measurement results should be verified by comparing with the results measured by conventional analytical methods.

The prototype of culturing device should preferably support the micro-bioreactor and MatriGrid® polycarbonate scaffolds - the tools previously developed at Ilmenau University of Technology [4].

The automated analytic part of the system should be preferably based on the enzymelinked immunosorbent assay (ELISA). ELISA is a method which uses optical readout and antibodies to detect a molecule of interest in, for example, the cell medium. More specifically, ELISA is based on the detection of this molecule of interest in a liquid environment by way of a liquid reagent, a reagent which creates a series of biochemical reactions and yields a final indicator, an indicator which can be easily observed and measured to give the amount of this molecule of interest in the liquid environment.

The problem posed for this thesis should be therefore approached from two sides, with the life science question taking the lead and the engineering side working as an assistant for the problems to be solved.

### 1.3 Thesis layout

Chapter 2, which follows this introduction reviews available 3D culturing systems with respect to the possibility of biomarker level measurements and degree of automation. Second part of this chapter reviews existing automated ELISA systems. Chapter 3 lies out the concept of the analytical module, discuss the selection of its building components and describes the assay protocol in detail. This is followed by the detailed description of the readout system and its integration to the analytical module. The last part of chapter 3 is dedicated to the control unit design and functional explanation of underlying electronics. Short description of associated software and corresponding software development tools is also included. The 3D culturing unit prototype design is described in the Chapter 4. The topology and functionality of its fluidic network is explained in detail. This chapter also include description of the MatriGrid ${ }_{\circledR}$ scaffolds and the microbioreactor tools. The initial testing and functional evaluation of the 3D culturing and
analytical modules are described in the Chapter 5. This includes the testing of the culturing unit fluidics, the analytical module fluidics and readout performance evaluation. Finally, the complete albumin ELISA was conducted by the analytical module. Few problems were identified, which required design adjustment. Chapter 6 describes the identification of the functionality flaws pointed out in the previous chapter and their solving. This include the cleaning procedure improvement and the fluidic manifold redesign. The performance improvement is demonstrated by the standard curve measurement in the low concentration range, as well as by comparing the measurements results with the conventional ELISA method results. The usability of the complete 3D culturing and analytical system is demonstrated in Chapter 7. The toxicity of APAP on the 3D grown and perfused HepaRG cell culture was evaluated over 96 hours. Again, the results provided by the prototype system were compared to conventional ELISA protocol. Chapter 8 discuss the drawbacks of the newly developed system and proposes possibilities for improvement during the further development. Additionally, finished and tested extension of the 3D culturing system, which allows parallel operation of 8 units is described. In the Chapter 9, potential applications of the culturing and analytic systems are discussed. The last part of the thesis is the conclusion provided in Chapter 10.

## 2 State of the art

### 2.1 Cell culturing systems

In general, although simpler for observation and measurement, 2D cell cultures are not demonstrative of the real situation of cells in real 3D in-vivo environment. Mounting cells on a flat surface is certainly a fast method to visualize growth and differentiation, however the resulting biological system is perhaps not the most optimal to comprehend function in the human body. For simple experiments to answer simple questions, the complexity of 3D cultures is likely unwarranted, but it is very clear that cells in 3D behave quite differently compared to cells which are surrounded by other cells in 3D.

This latter point is important in the context of predictivity. 2D cell systems are currently used in numerous drug and therapy screening applications but if the system is not demonstrative of the real situation, can the system be trusted to always be predictive? By slightly increasing the complexity of the technology and system into 3D, in the long-term this could decrease the price and failure-rate in clinical trials for novel drug discovery (which succeeded in and pre-clinical study at the 2D level). Indeed, large pharma companies devote extraordinary monetary resources each year for trials of novel drug therapies, with the majority of such trials ending in failure. 3D culture systems could provide a greater degree of predictivity at the pre-clinical level.

At the experimental level, a typical result of cell growth and differentiation is that cells consume molecules form the cell media and correspondingly release waste. This media must necessarily be changed, in almost all cases manually by the user. This disrupts the cell culture, the hermeticity, and, due to the manual nature of the process makes largescale testing of the culture (for example in screening or therapeutic applications) an impossibility. This means, a culture should be 3D to increase predictivity, but the culturing should be automated to increase through-put and applicability to large-scale pre-clinical testing.

Following the previous sentence in detail, there are numerous 3D cell culture and culturing products available on the market today. However, the automation of culturing in these products is still in its infancy. In Table 2.1, essentially all relevant 3D culturing
technologies, commercially or semi-commercially available, are summarized. In the context of "Fully Automated Culturing", this means that the cells of interest can be seeded and the device will provide all necessary interim steps without manual user intervention. In the context of "Fully Automated Measurement", this means that the molecule or molecules of interest for measurement can be sampled by the system without manual user intervention. There is not a single instance of a system meeting both these requirements. In extreme contrast, as will be presented in this text, the 3D-Automated Culturing and Analysis Device (3D-ACAD) does meet both requirements.

Table 2.1 Overview of 3D culturing systems and their automation capabilities.

| Company | 3D area of expertise | Fully <br> Automated <br> Culturing | Fully <br> Automated <br> Measurement |
| :--- | :--- | :--- | :--- |
| 3D Biomatrix | (2010, spin-off, U. of Michigan) Hanging drop plates <br> for the generation of 3D spheroids. | No | No |
| 3D Biotek | (2007) Inserts of various materials designed to turn <br> 2D culture plates into 3D culture environments. Also, <br> 3D inserts for bioreactors. | No | No |
| Biontex Laboratories | (1998) 3D cell cultures on solid substrates, optimized <br> for hydrogel substrates. | No | No |
| CellASIC | (2005, 2012 acquired by Merck) MiCA (Microfluidic <br> Cell Array) for 3D culture, a perfused plate for <br> hepatocytes. | No | No |


|  | culture of several cell types under controlled media <br> flow |  |  |
| :--- | :--- | :--- | :--- |
| Kiyatec | (2005, U. of Clemson) 3D co-culture. 3DKUBE <br> configurations: independent chambers, segregated <br> co-culture, cell migration. | Yes | No |
| MatTek Corporation | (1985, MIT) Produces in vitro human cell-derived <br> tissue equivalents for use in product <br> development/efficacy. EpiDerm-FT, a full thickness <br> skin model, EpiVaginal, an ectocervico-vaginal model, <br> and EpiOral, an oral (buccal) model. | No | No |

In contrast to many 3D culturing systems listed in Table 2.1, the 3D-ACAD design strictly avoids the use of hydrogels or construction materials based on PDMS. Hydrogels based on natural or synthetic polymers are commonly used in commercial 3D culturing systems as the support matrix for cell culture. (Biontex Labotatories, Cellendes, Irisbiosciences, Stemmaters, etc.) However, the use of hydrogel in general slows down the diffusion (or even traps) of the biomarkers and other molecules from cells to the medium [5]. Moreover, PDMS-based technology strongly interferes with the detection of soluble protein metabolites or markers due to absorption and adsorption [6]. To avoid these problems, the 3D-ACAD system uses the scaffold mediated 3D culture.

### 2.2 Automated ELISA systems

The enzyme-linked immunosorbent assay (ELISA) is an analytical measurement method which has existed in various forms for more than 40 years. During that time, iterations on the method have developed ELISA into the immunoassay with the highest sensitivity and highest specificity, leaving ELISA the clear and obvious choice to measure molecules of interest, in particular in complex liquid environments with numerous other molecules. As such, ELISA was the obvious choice for an automated system analyzing cell medium from 3D cultures. The work presented in this text demonstrates the full automation of the ELISA method, taking cures from classic automated flow systems developed previously by Lund University in Sweden [7].

In the previous work of Lund, a fully automated immunoassay was developed by joining flow-injection analysis with ELISA resulting in a fast flow-ELISA system. The system utilized competitive binding between antibodies, antigens, and fixed amounts of enzymelabelled antigens, all in the liquid environment. Although novel for the time, the method unfortunately relies on antibodies to be immobilized to a solid support and then to be placed in a small column of the flow system. This does not allow for multiple assays and multiple concentrations as the solid support is necessarily manually replaced by the user leaving the system essentially dedicated to a single assay. Although protein interactions were used instead of real immunochemical interactions, the system did at least show that flow-ELISA could be suitable for on-line monitoring of biological macromolecules.

In the classic follow-up from Lund process integration using fermentation was studied with on-line process monitoring of the molecule of interest, alpha-Amylase [8]. A column of crosslinked starch was used to adsorb the a-amylase before and after specific fermentation steps so that the concentration of a-amylase could be continuously monitored using flow-injection and immunochemical measurement. This system, although not technically more advanced than their previous system, did show that flowELISA could be suitable for living cells (being from the fermentation process). However, due to the industrial nature of the fermenter, only simple measurements of the concentration were performed. Multiple parameters were not investigated and modified.

In contrast to the work of Lund, two key papers have recently claimed to have fluidic methods which outperform ELISA and therefore both of these papers deserve a brief comment. In the first such study, the flow-through membrane immunoassay (FMIA) platform was utilized as an alternative to ELISA in fast high-throughput scheme [9]. However, the FMIA utilizes a 96-well vacuum plate in which the molecule of interest and other reagents are drawn through a fixed nitrocellulose membrane. This already limits the design of the system as the nitrocellulose the membrane must necessarily be covered in advance with the capture molecules (concentrations therefore remain invariable). Additionally, the capture molecules in this study are gold nanoparticle-labeled antibodies which are then utilized for the visible assay signals. Gold-nanoparticles are toxic to cells/cultures [10], immediately limiting the technology as the possibility of contamination, in particular with complex (3D) cultures is too great to risk using metal nanoparticles. On the positive side, the FMIA does provide rapid results ( $<30 \mathrm{~min}$ ), but the authors further claim to require fewer user steps than ELISA which is simply not true if the individual steps of the FMIA are counted. Finally, the final three arguments for FMIA over ELISA are that FMIA: 1) "provides multiple assay results (including controls) for each sample", and 2) "uses reagents that can be stored in stable dry form", and "generates visible spots that can be quantified by a camera or a flatbed scanner". Standard ELISA meets these criteria, and the system presented in this thesis exceeds the FMIA parameters in all aspects.

In the second such study, a flow through assay (FTA) was developed on cellulose acetate membranes for the cysticercosis, a parasitic tissue infection caused by larval cysts of the tapeworm [11]. FTA was claimed to be as good as ELISA in such a situation. Trying both
cyst fluid antigens (CFA) and whole cyst antigens (WCA) in the FTA, the assay consisted of (very similar to the previous alternative method) an antigen coated onto a membrane and then the membrane being mounted on a flow-through device. The membrane is again the assay capture matrix, with the criticisms from the previous paragraph still valid in this case. Although not as toxic as nano-particles, a colloidal gold conjugate was used as the antigen-antibody reagent for detection - again, possibly not ideal for cell cultures. The authors showed that between CFA and WCA, that results in the FTA were better with CFA ( $96.0 \%$ sensitivity; $96.0 \%$ specificity) compared to WCA ( $92.0 \%$ sensitivity; $96.0 \%$ specificity). These results were then compared to tests performed using ELISA. The ELISA showed 96 per cent sensitivity with both the antigens. This demonstrates that FTA is not superior to ELISA, the FTA simply has a sensitivity and specificity which agrees closely with the results of the ELISA, and only under certain conditions. Indeed, as the authors say, "The highest diagnostic accuracy (96\%) was obtained with CFA-FTA and CFA-ELISA". However, the FTA is by no means fully automated as the work presented here.

More recently, four proof of concept studies were published, using the electrochemical sensor as the means of readout. Lebogang at all (2017) uses the Separose ${ }^{\mathrm{TM}}$ beads filled into micro column for the quantification of microcystin-LR [12]. The setup is based on flow-ELISA with amperometric sensor and 2,2'-azinobis-(3-ethylbenzothiazolinesulfonic acid) (ABTS) as the substrate. The run time of automated sequential flow assay is 20 min . The setup does not provide means for parallel measurements and it can be regarded as single channel system. The amperometric sensor is connected to laboratory potentiostat and can perform up to 6 measurements without significant accuracy degradation. The setup is based on standard laboratory equipment and it is not portable.

Riahi at all (2016) uses flow-ELISA in combination with PDMS microfluidic chips to measure transferrin and albumin levels in hepatocyte culture medium [13]. Disposable magnetic beads are used as the solid phase and electrochemical amperometric sensor connected to the potentiostat as the detector. The system comprises microfluidic bioreactor for perfusing 2D hepatocyte culture. Similarly, to previously described system, the setup was designed as single channel quantitation tool. The supporting equipment is not integrated with the fluidic part.

The works presented by Shin at all (2017) and Zhang at all (2017) use the same electrochemical sensor design with functionalized surface by antibodies to achieve specific selectivity for detection of desired biomarkers [14, 15]. The sensor uses the electrochemical impedance measurement as the means of detection. Other common features are automated flow-ELISA architecture and the use of microfluidic chips based on PDMS material. The system presented by Shin was designed to measure the concentration of albumin and glutathione-S-transferase-alpha (GST- $\alpha$ ) in samples from hepatic culture bioreactor. The multiparameter sensing capability was extended in work presented by Zhang, where additional measurement of cardiac biomarker creatine kinase MB (CK-MB) was included, together with three environmental sensors (temperature, pH and dissolved $\mathrm{O}_{2}$ ). Separate, gel-based 3D hepatocyte HepG2 culture and cardiomyocyte culture (iPSC-CMs) were grown in micro bioreactors and perfused in one common loop. The functionalized immunosensors saturate after several measurements and require invasive in-situ regeneration process where the thin layer surface of gold electrode is etched out. As the consequence, the sensor lifetime (number of regeneration cycles) is reduced. However, it was demonstrated that 25 regeneration cycles cause no significant loss of functionality. Both systems, despite being capable of multiparameter sensing, provide no more than single channel, meaning no support for parallel sample measurement. The complexity and handling requirements of those systems are extensive.

The use of PDMS material is not optimal for cell culture systems due to problems associated with adsorption and absorption of hydrophobic small molecules and drugs [6, $15,16]$. This becomes the limiting factor during long experiments and low biomarker concentrations. For long term 3D cell culture experiments, a reliable and robust culture and analysis platform is needed, which is hard to achieve using PDMS technology. Moreover, contamination is a major problem that arises in most modern culture and analysis devices due to complex handling of units during cell seeding/harvesting, medium exchange and sale collection [17]. The immuno-electrochemical sensors technology, despite the excellent sensitivity they provide, is not matured and the stability of those sensors is not sufficient for use in measurement equipment where the reliability and robustness is the priority. The principal disadvantage of single channel system is the lack of concurrent calibration. The sensor must be calibrated prior to sample measurement and recalibrated in regular intervals to avoid the loose of accuracy. This becomes even more important for sensors with reduced stability.

In summary, the presented work here aimed to develop a fully automated and robust device (the 3D-ACAD) which combines 3D cell culture with a fully automated perfusion, medium change, ability for repeated drug applications, sampling, and followed by an automated flow-ELISA for detection of cell-derived albumin for the assessment of hepatotoxicity. In comparison to other works, this device was focused on developing a scaffold-based 3D-culture-and analysis system which allows good accessibility of the drug to the cells, minimizing adsorption and absorption of small molecules, drugs, and biomolecules inside the closed system. Additionally, the readout system is based on robust optical sensing principle designed for multi-channel operation, with inherent calibration. In contrast to some of the problems and methods discussed above, the ELISA analyzer module in this work has been designed in such a way that almost any commercially available ELISA assay kit can be used with this system and therefore made available to a wide range of users rather than using custom membranes and custom assays.

## 3 Designing the prototype of the ELISA analytical device

### 3.1 Introduction

This chapter describes the development and design of the prototype of the automated ELISA analytical device, including the associated electronic control unit. The purpose of the prototype device is to verify the possibility of automated ELISA assay in a flowthrough configuration. The prototype device was preferentially built from commercially available components, rather than custom components, allowing for rapid improvements and modifications in trial versions of the system. The following text describes the design of the fluidic part along with the sandwich ELISA details and the design of the integrated fluorimeter as the means of readout. The associated control unit schematics, layout and the embedded software are also briefly described.

### 3.2 Fluidics

The design of the fluidics must support all fluidic operations required by the typical ELISA procedure. This includes sequential transfer of the capture antibody, the analyte, the labeled antibody, and the substrate into the reaction chamber. Thorough washing of the fluidic paths is very important. The fluidic designs must enable efficient washing to prevent cross contamination of the fluidic paths by different regents.

### 3.2.1 Selected Elisa Assay

For the detection of albumin in the cell culture medium the commercial Human Albumin Quantitation Set (Bethyl, E80-129) was selected. The analyzer device is supposed to replicate the protocol recommended by the manufacturer. It is based on the sandwich ELISA assay (Figure 3.1) using the Goat anti-Human Albumin Coating Antibody, human reference serum and the HRP labelled Goat anti-Human Albumin Detection Antibody. Useful quantitation range lies inside the concentration interval from $6,25 \mathrm{ng} / \mathrm{ml}$ to 400 $\mathrm{ng} / \mathrm{ml}$ of albumin.


Figure 3.1 Sandwich ELISA principle.

The assay protocol as recommended by the manufacturer comprises the following steps:

1. Coat the plate using the primary (capture) antibody
2. Incubate the plate at room temperature 1 hour
3. Wash the plate five times
4. Coat the plate using the blocking solution
5. Incubate 30 min at room temperature
6. Wash the plate five times
7. Add samples and standards to plate wells
8. Incubate 1 hour at room temperature
9. Wash the plate five times
10. Add HRP conjugated (detection) antibody to the plate wells
11. Incubate 1 hour at room temperature
12. Wash the plate five times
13. Add the substrate solution to the plate wells
14. Develop the plate 15 min
15. Stop the reaction adding the stop solution to the plate wells
16. Measure the absorbance or fluorescence (depending on the used substrate) using plate reader.

This protocol uses MTP as the solid phase reaction carrier assuming the fluid operations are performed by the pipetting operations. The protocol needs to be adapted for the flowthrough configuration to address the different means of liquid handling. On the other side, the fluidic components should be selected with regard to assay protocol requirements.

In order to automate the assay, one could choose to use pipetting robots, complex machines optimized for using MTPs and automated pipetting. However, pipetting robots tend to be large in size and quite expensive, and trained personnel are necessary to operate such robots. Furthermore, many biological experiments simply require the monitoring of some metabolic indicator in the cell culture medium at regular intervals and for such a trivial task, the use of pipetting robots would be a unnecessarily expensive investment and not economically justified. Therefore, there is a need for a smaller, simpler device which could provide repeated and automated analysis using e.g. ELISA as the analysis method. One way to achieve this goal is to utilize a flow-through configuration. The pipetting operations are eliminated this way and replaced by the pumps and valves as the means of liquid handling according to required protocol. This configuration is rarely utilized because it creates new challenges - e.g. to avoid cross contamination of the commonly used fluidic paths or cleaning the fluidics after the end of essay. Careful choice of the fluidics material, components and washing procedures is very important to successfully implement of selected assay in the flow-through configuration analytic device.

### 3.2.2 Selection of the fluidic components

In the first step of the ELISA protocol, the capture antibody needs to be bound to a solid surface (also referred to as solid phase). Various materials have been used for this purpose - polystyrene (PS) and polyvinyl chloride (PVC) are among the most commonly used [18]. For the implemented flow-through configuration the $20 \mu \mathrm{l}$ size PVC capillary (SCSanguia Counting, Type 100024) was chosen as the solid phase component. PVC and PS are reported to have a high protein binding capacity. The selected volume is sufficiently high to enable the measurement by the optical readout device, but reasonably small to save expensive reagents. The selected PVC capillary had internal diameter of 0.96 mm , outside diameter 1.8 mm and are approximately 28 mm long.

### 3.2.2.1 Tubing selection

The appropriate tubing material for this application needs to have a low protein binding capacity. The ELISA protocols usually use highly diluted antibody solutions. It is therefore important that binding of antibodies to the tubing walls be minimized to prevent
the depletion of reagent solution and also to prevent unwanted reactions inside the tubing. The tubing material should be also chemically inert to withstand cleaning and protein desorption operations. Optimal material properties for this application has the flexible polymer with a trade name C-Flex manufactured by the Saint Gobain Performance plastics [19]. This polymeric compound is based on hydrogenated styrene/isoprenebutadiene/styrene block copolymer and belongs to the thermoplastic elastomers group. It is highly biocompatible, has low protein binding capacity, and sufficient chemical resistance. Moreover, it is also compatible with the selected pinch solenoid valves of the system designed here. Another material used in the manifold construction is the Teflon FEP. It is characterized by excellent chemical resistance, high temperature processability and low protein binding capacity compared to other standard materials. The tubing internal diameter should be small to minimize dead volume on one side, but of sufficient size to prevent clogging by eventual precipitates. The internal diameter of 0.58 mm seemed to be a good compromise and was therefore chosen for this application.

### 3.2.2.2 Active fluidic components

An analytical flow-through device is expected to use a rather higher number of fluidic paths. The switching between different fluidic paths as required by the ELISA protocol is realized by use of two-way and three-way valves. For practical reasons, only solenoid (electromechanically operated) isolation valves were considered. Important requirements for our selected valves were low dead volume and biocompatibility of all the wetted parts. A low footprint area and a low power operation are of secondary importance. The use of pinch valves over traditional seat or membrane valves is preferred for truly zero dead volume and very simple washing and maintenance. The pinch valves manufactured by Bio-Chem Fluidics Inc. perfectly fit all these requirements. The 19 mm diameter valves optimized for 0.5 mm internal diameter C-Flex tubing were selected: the type $075 \mathrm{P} 2 \mathrm{NC} 12-23 \mathrm{~B}$ is normally closed two-way valve and the type $075 \mathrm{P} 3 \mathrm{MP} 12-23 \mathrm{~B}$ is the three-way valve (Figure 3.2). The valves require $12 \mathrm{~V} / 240 \mathrm{~mA}$ ( 2.9 W ) for switching, after that the power can be reduced to $5 \mathrm{~V} / 100 \mathrm{~mA}(0.5 \mathrm{~W})$ to hold the valve in the switched position. The tubing can be easily inserted to or removed from the valve head.


Figure 3.2 Selected types of the 2-way (left) and 3-way (right) solenoid valves

The pump selection is primarily dictated by the flexibility. It is required to operate in a wide flow-rate range ( $10 \mu \mathrm{l} / \mathrm{min}$ to $1000 \mu \mathrm{l} / \mathrm{min}$ ), the precise (accuracy $10 \%$ of pumped volume is sufficient) and predictable dosing must be possible and reverse operation is also required. Similarly, as in the case of the valves, all wetted parts must be biocompatible and have sufficient chemical resistance. The low protein binding property is not required for the pump. The syringe pumps and the peristaltic pump are principally suitable for this application, however the peristaltic pump is preferred over the syringe pump because the pumped volume can be unlimited and does not depend on the syringe size. Syringe pumps are more precise and have more uniform flow-rate compared to peristaltic pumps, which makes the very suitable for segmented flow and microfluidic applications. The pumping accuracy of the peristaltic pump is mainly dependent on the accuracy of controlling its rotor speed and position. For that reason, peristaltic pumps using a DC motor or asynchronous AC motor are not suitable. The preferred motor for controlling the peristaltic pump suitable for the ELISA analyzer is a DC stepper motor, because a stepper motor is synchronous, the rotor position depends only on the number of step pulses issued by the motor controlled and is independent of the mechanical load (to a certain maximum limit). Suitable stepper motor controlled peristaltic pump heads are manufactured by the company Boxer GmbH and the type 61131.000 was selected for use in the analyzer (Figure 3.3). It is powered by NEMA23 size stepper motors with 200 steps per revolution. The pump head uses the pharmed tubing with internal diameter of 0.5 mm arranged in four independent channels. The measured pumped volume is $12.5 \mu \mathrm{l}$ per revolution. The calculated motor speed for the flow-rate $10 \mu \mathrm{l} / \mathrm{min}$ is 0.8 rpm or 160
steps $/ \mathrm{min}$ and the calculated motor speed for the maximum flow-rate $1000 \mu \mathrm{l} / \mathrm{min}$ is 80 rpm or 16000 steps/min.


Figure 3.3 Selected stepper motor driven peristaltic pump

### 3.2.3 Fluidic Topology

Figure 3.4 shows schematically the complete fluidic topology of the prototype analyzer device. It accomplishes all steps of the sandwich ELISA protocol for seven samples and/or analyte standards. Special attention was paid to the design of the washing and cleaning operations. The whole fluidic subsystem is composed of the following components:

- Two peristaltic pumps (type 61131.0000, Boxer GmbH)
- 19 two-way normally closed solenoid pinch valves (075P2NC12-23B, Bio-Chem Fluidics Inc.)
- One three-way solenoid pinch valve (075P3MP12-23B, Bio-Chem Fluidics Inc.)
- Four nine-port manifolds (P-191, IDEX Health \& Science)
- Two 50 ml polypropylene containers - one for the washing buffer and one for the waste.
- Eleven 2 ml polypropylene containers - seven for the samples or analyte standards and four for sandwich ELISA reagents.
- Eight replaceable $20 \mu \mathrm{l}$ PVC capillaries (Type 100024, SC-Sanguia Counting)
- C-Flex tubing, internal diameter 0.58 mm (type $10025-23 B$, Bio-Chem Fluidics Inc.)


Figure 3.4 The fluidic topology of the analyzer based on the ELISA protocol

The operation of this fluidic network is relatively simple. The valves V17 to V20 select which reagent will be transferred to the selected capillary. The valves V1 to V7 select which sample or analyte standard will be transferred to the selected capillary. Normally, only one valve from the groups V1 to V7 and V17 to V20 will be open at the same time. The valves V9 to V16 select the destination capillary into which the fluid will be pumped. The main Pump is the pump used for the transfer of selected sample or reagent into selected capillary. The washing pump is stopped during this operation. The washing pump is used to wash all the fluidic paths and capillaries using the washing buffer. When some capillary needs to be washed, one of the valves V9 to V16 corresponding to selected capillary will be opened and both the main pump and the washing pump will be started at the same speed. By opening the valve V21 during the washing procedure, it is possible to empty the whole fluidic network. Capillary 8 has a special purpose as it is used as the fluidic bypass during the washing operations - in case capillaries 1 to 7 are filled with reagents according to the protocol and in case it is also necessary to wash the manifold common fluidic paths. Then capillary 8 is used to drain the washing solution to the waste. This way the washing of the common fluidic paths can be realized without disturbing the content of the other capillaries.

For example, if the protocol requires to pump a conjugated antibody into capillary 2 , the following sequence will be executed: V19 will be open to connect the conjugate antibody to the fluidic network, V10 will be also open to enable the flow through the capillary 2 and the Main Pump will be instructed to pump a calculated amount of reagent so that capillary 2 will be filled with it. All remaining valves are in the closed position and the washing pump is stopped.

Because this prototype analyzer version contains only seven capillaries available for the measurement, it is possible to measure only seven points in one run. Those seven points comprise the actual samples as well as the concentration standards. A typical configuration is to use the 5 capillaries to measure points of the standard curve and the remaining two capillaries can be used to measure samples automatically taken from the two culturing units (described in the Chapter 4)

The following section describes the complete sandwich ELISA protocol optimized for this flow-through configuration in detail. The specific flow-rates and volumes used in the protocol are dependent on the fluidic network physical size, taking into account the dead volume of the fluidic paths, and preventing a significant pressure drop over the fluidic network.

### 3.2.4 Flow-through optimized sandwich ELISA protocol

### 3.2.4.1 Step 1 - Coating the capillaries with the capture antibody.

The first step of the human albumin ELISA protocol coats the walls of capillaries (solid phase) with the capture antibody. The capture antibody as purchased (A80-129A-11, Bethyl Inc.) was diluted with the coating buffer in the ratio 1:100. The coating buffer has the following composition:

Coating Buffer:

- $50 \mathrm{mM} \mathrm{Na} 2 \mathrm{CO}_{3}$
- pH adjusted to 9.6 using HCl or NaOH

During step 1 the diluted capture antibody is pumped to capillaries 1 to 7 using the following sequence:

- Valves V16 and V17 will open, all other valves remain closed (unpowered)
- The main pump will be activated to pump $300 \mu \mathrm{l}$ at the speed of $350 \mu \mathrm{l} / \mathrm{min}$ of diluted capture antibody solution through the reagent and capillary manifolds to capillary 8 . The purpose is to fill the fluidic paths and manifolds with the reagent.
- The valve V16 will be closed again and the valve V9 will open
- The main pump will be activated to pump $50 \mu \mathrm{l}$ at the speed of $100 \mu \mathrm{l} / \mathrm{min}$ of diluted capture antibody solution to capillary 1 . The pumping speed is reduced to prevent turbulent flow through the capillary
- The previous step will be repeated six more times to fill the capillaries 2 to 7 in the serial sequence. The corresponding valves V10 to V15 will be used instead of the valve V9.

The flow path of step 1 for filling capillary 1 is illustrated in Figure 3.5. During this step all the capillaries are filled with the capture antibody solution. The total duration of step 1 is 4 minutes and 28 seconds. $700 \mu \mathrm{l}$ of the capture antibody reagent is consumed in the first step.


Figure 3.5 Flow path for filling capillary 1 with the capture antibody during step 1. Capillaries 2 to 7 are subsequently filled using the valves V10 to V15 instead of V9.

### 3.2.4.2 Step 2 - Incubation of the capture antibody.

During step 2, the dissolved capture antibodies in the capillaries are adsorbed on the surface of the PVC capillaries. The incubation period is 15 min and takes place at room temperature. The schematic picture of the ELISA after step 2 is shown in Figure 3.6.


Figure 3.6 The first step of sandwich ELISA - the capture antibody was attached to the solid phase.

The incubation time remains constant for all capillaries despite the serial way of filling the capillaries and the non-negligible pumping time. This is achieved by keeping the capillary filling speed the same for the steps before and after the incubation period. The incubation period is only slightly extended by the time required to fill the manifold and drain capillary 8 of the liquid, which is the duration of the first part of the sequence following the incubation (usually 75 seconds). The incubation time can be easily corrected for this increase if needed. The timing of the first three steps of the ELISE sequence: the coating with capture antibody, the incubation and the washing is shown in Figure 3.7. The same principle is used also in the following parts of the ELISA sequence.


Figure 3.7 The beginning of the ELISA sequence - capture antibody coating (blue), incubation period (green) and the first part of the washing (orange). The time between the start of coating and the capillary with antibody to the washing of the same capillary is constant for all channels.

### 3.2.4.3 Step 3 - Washing

After the capture antibody was attached to the solid phase, the fluidic paths and the capillaries need to be washed to remove all residuals of the capture antibody reagent. The cleaning is performed using the washing buffer of the following composition:

## Washing Buffer:

- 50 mM Tris(hydroxymethyl)aminomethane (TRIS)
- 140 mM NaCl
- pH adjusted to 8.0 using HCl or NaOH

During this washing step the washing buffer is pumped to all capillaries using the following sequence:

- The valve V16 will open and the valve V21 will switch to the washing container fluidic path, all other valves remain closed (unpowered)
- The main pump and the washing pump will be simultaneously activated to pump $500 \mu \mathrm{l}$ at the same speed of $400 \mu \mathrm{l} / \mathrm{min}$. This will wash the sample manifold, the reagent manifold and the capillary manifold. The washing buffer will be pumped through capillary 8.
- The valve V16 will be closed again and the valve V9 will open
- The main pump and the washing pump will be simultaneously activated to pump $50 \mu 1$ at the same speed of $100 \mu 1 / \mathrm{min}$. This will wash capillary 1 at low speed to not desorb the attached antibodies.
- The previous step will be repeated six more times to wash capillaries 2 to 7 in the serial sequence. The corresponding valves V10 to V15 will be used instead of the valve V9.

This washing procedure is repeated two times during the step 3 . The total time required to complete step 3 is 9 minutes and 42 seconds. $1700 \mu 1$ of washing buffer is consumed during this time. The Figure 3.8 shows the washing flow path.


Figure 3.8 Flow path used for washing the capillary 1. Capillaries 2 to 7 are washed in the same manner using the valves V10 to V15 instead of V9.

### 3.2.4.4 Step 4 - Blocking the capillaries with the bovine serum albumin (BSA)

The coverage of the solid phase with the capture antibody performed in the steps 1 and 2 leaves a lot of binding sites on the surface free. The purpose of blocking step is to saturate those free sites with the BSA which is inactive in the assay. This greatly reduces the
interference and lowers the background reading. The blocking solution has the following composition:

Blocking buffer:

- 50 mM Tris(hydroxymethyl)aminomethane (TRIS)
- 150 mM NaCl
- $1 \%$ Bovine serum albumin (BSA)
- pH adjusted to 8,0 using HCl or NaOH

The fluidic operation to complete step 4 is very similar to the first step. It differs in using the blocking reagent instead of the capture antibody reagent. The exact sequence of the step 4 is following:

- Valves V16 and V18 will open, all other valves remain closed (unpowered)
- The main pump will be activated to pump $300 \mu \mathrm{l}$ at the speed of $350 \mu \mathrm{l} / \mathrm{min}$ of the blocking buffer through the reagent and capillary manifolds to the capillary 8 .
- The valve V16 will be closed again and the valve V9 will open
- The main pump will be activated to pump $50 \mu \mathrm{l}$ at the speed of $100 \mu \mathrm{l} / \mathrm{min}$ of the buffer solution to the capillary 1.
- The previous step will be repeated six more times to fill the capillaries 2 to 7 in the serial sequence. The corresponding valves V10 to V15 will be used instead of the valve V9.

The step 4 flow path for filling the capillary 1 is illustrated on the Figure 3.9. During this step all the capillaries are filled with the blocking buffer solution. The total duration of step 1 is 4 minutes and 28 seconds. $700 \mu 1$ of the blocking reagent is consumed in the step 4.


Figure 3.9 Flow path for filling the capillary 1 with the blocking buffer. Capillaries 2 to 7 are subsequently filled using the valves V10 to V15 instead of V9.

### 3.2.4.5 Step 5 - Blocking Incubation

During incubation time the BSA will saturate the surface of the solid phase and it will block all free binding places not occupied by the capture antibody. The blocking incubation time is 30 min and the operation is also made at room temperature. The schematic picture of the ELISA after step 5 is shown on the Figure 3.10.


Figure 3.10 Situation at the capillary surface after blocking step. No free place is left on the surface for binding more proteins.

### 3.2.4.6 Step 6 - Washing

After the completion of the blocking step, the washing is needed again to clean the fluidic paths and to remove the blocking solution from the capillaries. This washing step is exactly the same as the washing described in the step 3. Again, it requires 9 minutes and 42 seconds and $1700 \mu$ l of washing buffer to complete.

### 3.2.4.7 Step 7 - Filling the capillaries with human serum albumin samples

During this step the analyte samples held in the containers 1 to 7 will be transferred one by one to respective capillaries 1 to 7 . Until now the procedure was the same for all 7 capillaries. Starting from this step each capillary will have different protein compositions on the surface, depending on the analyte composition.

The fluidic topology as designed contains 8 capillary channels. The capillary 8 is not used for the measurement and serves as the draining the fluid through manifolds while not affecting the capillaries 1 to 7 , which are the actual measurement channels. The typical ELISA procedure includes the standard curve measurement along with the samples containing unknown concentration of the analyte. The standard curve serves as way of concentration calibration. The standards curve is created by measurement of a series of standards with different but known concentration of analyte. The seven available channels of the proposed device can be allocated either to the sample or standard measurement. The configurations providing reasonable measurement accuracy are: 6 standards +1 sample, 5 standards +2 samples or 4 standards +3 samples.

## The sample source

There are two ways in which the sample solution can be interfaced to this analytic device: The sample can be place in a small container directly in the device. This is the way the concentration standards are connected to the device. Alternatively, and preferably the fluidic connection is used to interface the culturing unit (see the Chapter 4) with the selected sample valve (V1 to V7). This will enable the automated sample feeding from the culturing unit to the analytic device. In this case the volume of pumped sample is increased to compensate for the dead volume of the inter-module fluidic connection.

The step 7 will start with the transfer of the sample 1 to capillary 1 according this sequence (Figure 3.11):

- Valves V1 and V16 will open, all other valves remain closed (unpowered)
- The main pump will be activated to pump $300 \mu \mathrm{l}$ at the speed of $350 \mu \mathrm{l} / \mathrm{min}$ of the first sample solution through the reagent and capillary manifolds to the capillary 8.
- The valve V16 will be closed again and the valve V9 will open
- The main pump will be activated to pump $50 \mu 1$ of the sample 1 solution at the speed of $100 \mu \mathrm{l} / \mathrm{min}$ of to the capillary 1 .
- Valve V9 will close


Figure 3.11 Fluidic path for transferring the sample 1 into the corresponding capillary 1
After the sample 1 has been transferred to the capillary 1 and before the transfer of sample 2 to corresponding capillary 2 the fluidic paths must be washed to avoid the cross contamination of the samples. This "washing after sample" procedure is performed after each sample transfer and has the following sequence:

- The valve V16 remains open after the previous sample transfer. All other valves stay closed.
- The main pump and the washing pump will be simultaneously activated to pump $350 \mu \mathrm{l}$ at the same speed of $350 \mu \mathrm{l} / \mathrm{min}$. This will empty the fluidic path inside the sample manifold, reagent manifold and capillary manifold. The liquid will be drained through the capillary 8 .
- The valve V16 will close and the valve V9 will open
- The washing pump will be activated to pump $3 \mu \mathrm{l}$ at the speed of $100 \mu \mathrm{l} / \mathrm{min}$. This will make small air gap inside the capillary manifold from the common fluidic path towards the fluidic path of the capillary 1.
- The valve V9 will close and the valve V1 will open
- The washing pump will be activated to pump $50 \mu \mathrm{l}$ at the speed of $100 \mu \mathrm{l} / \mathrm{min}$. This will make small air gap inside the sample manifold from the common fluidic path towards the fluidic path of the sample 1.
- The valve V1 will close and the valves V16 and V21 will open
- The main pump and the washing pump will be simultaneously activated to pump $500 \mu \mathrm{l}$ at the same speed of $350 \mu \mathrm{l} / \mathrm{min}$. This will wash the sample manifold, the reagent manifold and the capillary manifold common fluidic paths. The washing buffer will be pumped through the capillary 8 .
- The valve V21 will close

In this moment the transfer of the sample 1 to the capillary 1 has been finished and the fluidic paths were washed and transfer of the sample 2 to the capillary 2 can take place. The sequence of emptying the flow path is depicted on Figure 3.12.


Figure 3.12 After the sample 1 has been transferred to the corresponding capillary 1 , the fluidic path will be emptied in three steps: $1^{\text {st }}$ - the fluid is pumped out of all manifolds through the capillary 8 , $2^{\text {nd }}$ - the side arm of the capillary manifold is emptied by introducing a small air gap, $3^{\text {rd }}$ - the side arm of the sample manifold is also emptied. Subsequent washing of the common fluidic path (marked as red " 1 " on the figure) completes the "washing after sample" sequence.

The step 7 then continues with transferring of sample 2 to the capillary 2 followed by the "washing after sample" sequence again. This scheme is repeated until all seven samples are transferred to their corresponding capillaries. The step 7 consumes $350 \mu \mathrm{l}$ of each sample and $3500 \mu \mathrm{l}$ of washing buffer. The total time required for completion of this sequence step is 30 minutes and 55 seconds.

### 3.2.4.8 Step 8 - Sample Incubation

During this incubation time the human serum albumin contained in the sample bonds to the capture antibody. The number of the antibody-albumin pairs will be different in each
capillary depending on the albumin concentration in the samples. The samples must be sufficiently diluted so that even for the maximum sample albumin concentration the antibody binding capacity will be not exceeded at the end of the incubation time, which is set to 15 minutes. The incubation takes place at room temperature. The schematic picture of the ELISA after step 8 is shown on the Figure 3.13.


Figure 3.13 Situation at the capillary surface at the end of sample incubation time. The human serum albumin is selectively bonded to the capture antibody. Ideally there is no other possibility for the albumin to bond.

### 3.2.4.9 Step 9 - Washing

The sample incubation is followed by washing again. This washing uses the sequence described the step 3 . This washing step requires 9 minutes and 42 seconds and $1700 \mu 1$ of washing buffer to complete - same values are used in the step 3 .

### 3.2.4.10 Step 10 - Filling the capillaries with enzyme labeled secondary antibody.

The secondary antibody binds specifically to the human serum albumin. The amount of bonded antibody will be therefore directly proportional to the amount of human serum albumin already bonded to the capture antibody. If the sample contained no human serum albumin, no secondary antibody will be bonded and it will be washed away in the following steps. This secondary antibody has covalently bonded HRP enzyme which later allows substrate conversion to a colored dye. The secondary antibody as purchased (A80-129P-30, Bethyl Inc.) was diluted with the blocking buffer (described in the step 4) in the ratio $1: 10^{5}$.

During step 10 the diluted secondary antibody is pumped to capillaries 1 to 7 using the following sequence:

- Valves V16 and V19 will open, all other valves remain closed (unpowered)
- The main pump will be activated to pump $300 \mu 1$ at the speed of $350 \mu 1 / \mathrm{min}$ of diluted secondary antibody solution through the reagent and capillary manifolds to the capillary 8 .
- The valve V16 will be closed again and the valve V9 will open
- The main pump will be activated to pump $50 \mu \mathrm{l}$ at the speed of $100 \mu \mathrm{l} / \mathrm{min}$ of diluted capture antibody solution to the capillary 1 . Low pumping speed prevents disturbing the surface layer.
- The previous step will be repeated six more times to fill the capillaries 2 to 7 in the serial sequence. The corresponding valves V10 to V15 will be used instead of the valve V9.

The step 10 flow path for filling the capillary 1 is illustrated on the Figure 3.14. During this step all the capillaries are filled with the secondary antibody solution. The total duration of step 10 is 4 minutes and 28 seconds. $700 \mu \mathrm{l}$ of the secondary antibody reagent is consumed.


Figure 3.14 Flow path for filling the capillary 1 with the secondary antibody solution. Capillaries 2 to 7 are subsequently filled using the valves V10 to V15 instead of V9.

The secondary antibody is covalently bonded to the HRP enzyme, which converts the substrate to colored compound. This reaction is supposed to take place inside capillary where the enzyme is attached to the capillary walls as a part of the sandwich ELISA stack. Even traces of HRP enzyme inside the fluidic paths preceding the capillary start the substrate conversion prematurely and result in the increased signal background. It is therefore very important to carefully clean the common fluidic paths to remove traces of

HRP enzyme before substrate enters the flow paths. For that reason, a special cleanup sequence is executed at the end of the step 10 .

This cleanup sequence comprises following operations:

- The valve V16 will open while all the other valves remain closed.
- The main pump and the washing pump will be simultaneously activated to pump $350 \mu \mathrm{l}$ at the same speed of $350 \mu \mathrm{l} / \mathrm{min}$. This will empty the fluidic path inside the sample manifold, reagent manifold and capillary manifold. The liquid will be drained through the capillary 8.
- The valve V16 will close and the valve V17 will open
- The washing pump will be activated to pump $50 \mu \mathrm{l}$ at the speed of $100 \mu \mathrm{l} / \mathrm{min}$. This will remove the fluid still remained in the coating reagent side flow path of the reagent manifold.
- The previous operation will be repeated two more times to remove fluid remaining in the blocking and conjugated flow paths of the regent manifold. The valves V18 and V19 will be used instead of the valve V17.
- The valves V16 and V20 will open while all the other valves remain closed.
- The main pump will be activated to pump $25 \mu \mathrm{l}$ at the speed of $200 \mu \mathrm{l} / \mathrm{min}$. This will extract any secondary antibody solution possibly present in the substrate side flow path of the reagent manifold.
- The valves V20 will close and the valves V16 and V21 will open
- The main pump and the washing pump will be simultaneously activated to pump $500 \mu \mathrm{l}$ at the same speed of $350 \mu \mathrm{l} / \mathrm{min}$. This will wash the sample manifold, the reagent manifold and the capillary manifold common fluidic paths. The washing buffer will be pumped through the capillary 8 .
- The valves V16 will close and the valves V17 will open
- The washing pump will be activated to pump $50 \mu \mathrm{l}$ at the speed of $350 \mu \mathrm{l} / \mathrm{min}$. This will pump the washing buffer into the coating reagent side flow path of the reagent manifold.
- The previous operation will be repeated two more times to pump the washing buffer into the blocking and conjugated flow paths of the regent manifold. The valves V18 and V19 will be used instead of the valve V17.

This special reagent manifold cleanup requires 4 minutes, 38 seconds and $650 \mu \mathrm{l}$ of washing buffer to complete.

### 3.2.4.11 Step 11 - Incubation of the secondary antibody

This incubation time provides sufficient time for the conjugated secondary antibody to bind to the human serum albumin which was possibly (depending on the albumin content of the sample) present on the capillary surface layer. The secondary antibody contains covalently attached label which later convert the substrate to detectable substance. The amount of the enzyme attached to the protein stack during the incubation period is directly proportional to amount of immobilized albumin on the capillary surface. The incubation time is set to 15 minutes. The operation is performed at room temperature. The schematic picture of the ELISA after step 11 is shown on the Figure 3.15.


Figure 3.15 The complete sandwich ELISA stack at the end of step 11. If the sample contained human serum albumin, the HRP conjugated secondary antibody will be attached to it.

### 3.2.4.12 Step 12 - Washing

A regular washing procedure is introduced at the end of the incubation time. The sequence already described in the step 3 is repeated three times to address increased requirements for cleanliness before the substrate pumping step. This step requires 14 minutes and 33 seconds to complete. Additionally $2550 \mu$ l of washing buffer is consumed.

### 3.2.4.13 Step 13 - Transferring substrate to the capillaries

The substrate is generally colorless solution which can be converted by the action of enzyme to colored, fluorescent or chemiluminescent compound depending on the substrate type. The concentration of resulting compound can be measured by suitable optical detector. The substrate chosen for this albumin assay is QuantaRed ${ }^{\text {TM }}$ Enhanced Chemifluorescent HRP Substrate (Number 15159, Thermo Scientific). For more details see the Chapter 3.3.

The substrate solution is prepared according to manufacturer instructions and has the following composition:

- 50 parts of QuantaRed ${ }^{\text {TM }}$ Stable Peroxide Solution
- 50 parts of QuantaRed ${ }^{\text {TM }}$ Enhancer Solution
- 1 part of QuantaRed ${ }^{\text {TM }}$ ADHP Concentrate

This substrate solution is pumped to capillaries 1 to 7 using the following sequence:

- Valves V16 and V20 will open, all other valves remain closed (unpowered)
- The main pump will be activated to pump $300 \mu \mathrm{l}$ at the speed of $350 \mu \mathrm{l} / \mathrm{min}$ of the substrate solution through the reagent and capillary manifolds to the capillary 8 .
- The valve V16 will be closed again and the valve V9 will open
- The main pump will be activated to pump $50 \mu \mathrm{l}$ at the speed of $100 \mu \mathrm{l} / \mathrm{min}$ of the substrate solution to the capillary 1 .
- The previous step will be repeated six more times to fill the capillaries 2 to 7 in the serial sequence. The corresponding valves V10 to V15 will be used instead of the valve V9.

The corresponding flow path for filling the capillary 1 is illustrated on the Figure 3.16. During this step all the capillaries are filled with the substrate solution. The total duration of step 13 is 4 minutes and 28 seconds. $700 \mu \mathrm{l}$ of the substrate reagent is consumed.


Figure 3.16 Flow path for filling the capillary 1 with the substrate solution. Capillaries 2 to 7 are subsequently filled using the valves V10 to V15 instead of V9.

### 3.2.4.14 Step 14 - Substrate incubation and readout

Immediately after the substrate solution enters the capillary, the immobilized enzyme starts to convert the optically inactive substrate into a detectable compound. In this specific case the non-fluorescent ADHP substrate is converted in the presence of hydrogen peroxide into resorufin - a highly fluorescent compound (Figure 3.19). The fluorescence of the substrate solution is measured by the integrated fluorimeter after exactly measured incubation time (same incubation time is used for each capillary). More details about the readout system can be found in the Chapter 3.3. The situation inside the capillary during this phase is depicted on the figure Figure 3.17.


Figure 3.17 Conversion of the non-fluorescent ADHP substrate to fluorescent resorufin dye by the action of immobilized HRP enzyme during the step 14.

The fluorescence measurement is performed at fixed time points of 7, 14, and 21 minutes for each capillary to provide possibility to measure reaction kinetics. The duration of this step is 21 minutes and 26 seconds.

Step 14 completes the whole ELISA protocol with the total execution time of 3 hours, 13 minutes and 26 seconds.

### 3.3 Readout system

The selection of the readout system is based on the used enzyme label. The horseradish peroxidase (HRP) is widely used because the molecule is relatively small, does not cause hindrance problems, and is robust and inexpensive. A variety of substrates are available for HRP and they can be divided into the following categories:

- Colorimetric substrates
- Fluorescent substrates
- Luminescent substrates

Colorimetric substrates provide directly visible colored product which absorbs light in the visible range. The absorbance is proportional to the analyte concentration and it is measured photometrically. The usual dynamic range is about two orders of magnitude. The representative example of colorimetric substrate is TMB (3,3',5,5' tetramethylbenzidine), which produces a blue dye which can be measured at a wavelength of 650 nm . Other colorimetric substrates compatible with HRP are ABTS ( $2,2^{\prime}$-azino-di [3-ethylbenzthiazoline] sulfonate), and OPD (o-phenylenediamine).

In the fluorimetric assay a non-fluorescent substrate is converted to fluorescent dye by the action of the enzyme. The produced dye fluoresces when excited by the light of suitable wavelength. The intensity of the fluorescence is proportional to the analyte concentration. Compared to the colorimetric substrates, the fluorescent substrates benefit from higher sensitivity and broader dynamic range. On the other side the instrumentation is more complicated than for the absorbance measurement. Commonly used fluorimetric substrates include Amplex Red ${ }^{\text {TM }}$, HPA (hydroxyphenylacetic acid) and HPPA (3-phydroxyphenylproprionic acid).

In a luminescent assay the enzyme converts the substrate to a chemical compound which emits photons of visible light instead of producing a colored product. Enhanced luminescent assays provide the highest sensitivity and dynamic range. The intensity of the produced light is proportional to the analyte concentration. The drawback is the stability of the luminescent light emission which is transient in its nature. The produced light must be intense, since it is not accumulated over time like in the case of color or fluorescence. Examples of luminescent substrates suitable for HRP comprise the luminol, luciferin, and some polyphenols.

The choice of the fluorimetric substrate for this prototype device is preferred over the other options. It provides the advantage of the higher dynamic range over the photometric assay (four orders of magnitude required) and the stability of the output signal. After reviewing the markets substrates for HRP, the use of QuantaRed ${ }^{\text {TM }}$ Enhanced Chemifluorescent substrate (15159, Thermo Fisher Scientific) was selected as the most suitable for this application. The kit contains the ADHP (10-Acetyl-3,7dihydroxyphenoxazine) non-fluorescent compound which is converted by the action of HRP in the presence of hydrogen peroxide to highly fluorescent dye resorufin (Figure 3.19). The sensitivity of this enhanced substrate is comparable with luminescent substrates. The development of the colored resorufin allows also the colorimetric measurement if needed.

The fluorimeter creates an integral part of the analyzer system. Its mechanical, optical, and electrical properties should be specifically designed to support the resorufin spectral properties. This will provide the advantage or easier automation and optimal price to performance ratio.

The design of the optics is driven by the properties of the fluorophore and the physical size of the measurement cell. The fluorophore used in the selected albumin assay is resorufin (Figure 3.18), which is created by the deacetylation and oxidation of the QuantaRed ${ }^{\mathrm{TM}}$ substrate catalyzed by HRP enzyme.


Figure 3.18 The chemical structure of the resorufin fluorescent dye

Resorufin has the peak excitation wavelength 571 nm and the peak emission wavelength 585 nm . Figure 3.20 shows the corresponding spectra. The Stokes shift is about 14 nm and the corresponding spectra partly overlap. For accurate fluorescence measurements it is therefore necessary to use optical filters with an optical density of 5 or higher to prevent even traces of the excitation light to reach the detector. Otherwise the sensitivity and the dynamic range of the fluorimeter would be decreased.


Figure 3.19 ADHP substrate reaction. Non-fluorescent ADHP compound is converted by the action of HRP enzyme in the presence of $\mathbf{H 2 O 2}$ into highly fluorescent resorufin dye.

In a typical configuration the short pass excitation filter is used to block the higher wavelength part of the excitation light, which would otherwise pass through the emission filter and reach the detector. Similarly, the emission filter blocks the filtered excitation light to reach the detector. Obviously, the excitation filter cut-off wavelength should be lower than the emission filter cut-off wavelength. Ideally the excitation light source should have maximum radiation energy close to the 571 nm and the emission filter allows as much as possible of the emission light to reach the detector.

### 3.3.1 Excitation light source selection

During the initial testing both the Green LED (SSL-LX5093SGC/B, Lumex) and green DPSS laser (DJ532-10, Thorlabs) were evaluated as the possible excitation sources for the resorufin. Green high intensity LEDs with peak wavelengths between 525 nm to 565 nm are available on the market. Typical spectral width for these LEDs is about 40 nm to 50 nm , which requires use of the excitation filter to limit the excitation spectrum at the upper end.


Figure 3.20 The excitation and emission spectrum of resorufin fluorescent dye with overlaid emission filter passband (blue area) and excitation laser line (green line)

During the initial test it was found very problematic to focus the LED generated beam precisely without significant loss of intensity. The tested packages were T-1 $1 / 4.4 \mathrm{~mm}$ diameter through-hole LED) with standard hemispherical ends and also with the flat end. The other advantages of the LED source are low price, simple driver circuit, longer lifetime, and good temperature stability.

The other option was to use a green diode-pumped solid state (DPSS) laser. With a 532 nm spectral line the absorption by the fluorophore is only $56 \%$ of the maximum. This disadvantage is more than compensated by the very intense light compared to LED. Also, thanks to very narrow spectrum and higher distance from the emission spectra, the use of the excitation filter is not necessary. On the other side laser source is more expensive, requires precise driver, and has a relatively narrow operating temperature range.

After considering the advantages and disadvantages for both the LED and laser solutions, the 10 mW green DPSS laser (DJ532-10, Thorlabs) was selected as the excitation light source for the fluorimeter design.

### 3.3.2 Detector selection

Many fluorimeters use the photomultiplier tube (PMT) or the photodiode as the detector. PMTs are special sort of vacuum tubes with high internal gain (up to several millions). Photomultiplier tubes are used in application which require high sensitivity and low noise
operation. Single photon counting mode can be used if required. PMTs are not affected by the Johnson (thermal) noise, which is another great advantage. The operation of PMTs requires using of high voltages (low KV range), they are generally sensitive to electrostatic and magnetic fields. Long term stability is affected by the diffusion of the helium from the surrounding atmosphere into the tube through the glass walls. The price is relatively high (hundreds to thousands $€$ ).

Photodiodes have generally lower sensitivity compared to PMTs, they have no internal gain (with the exception of avalanche photodiodes) and are affected by thermal noise. Photodiodes are low voltage devices, small physical size and insensitivity to electromagnetic interference makes them easy to integrate into portable devices. The photodiodes are very cheap when compared to prices of photomultiplier tubes.

Because the volume of the measured sample is relatively high (about $10 \mu \mathrm{l}$ ) and the concentration of the resorufin in a typical assay sample is also reasonably high (nM to $\mu \mathrm{M}$ range) the selection of the photomultiplier tube as the detector for this application is not justified. The use of difficult to integrate, environmentally sensitive and expensive device is not outweighed by the requirement for higher sensitivity.

Use of the silicon photodiode has proven to be satisfactory for this application during the initial tests. The preferred type should have radiant sensitive area of several square millimeters, high quantum yield, low capacitance, low noise equivalent power and metal housing. After reviewing datasheets of several potentially suitable photodiodes (S1223, OSD5-5T, BPX61, BPW21R) the BPX61 and S1223 types have very low capacitance, dark current and good noise performance. The BPX61 type (OSRAM) was selected as the fluorimeter detector because of better pricing and availability while the performance is similar to the S1223 type.

The traditional way ELISA reactions take place in the wells of a microtiter plate. For a flow-through setup a kind of "flow cell" is needed. In this application the transparent PVC capillary tubes ( $20 \mu$ l, SC-Sanguia Counting 100024) normally used for the blood sampling. The capillary has the outer diameter 1.8 mm , the inner diameter 0.9 mm and length approximately 27 mm . It is inside this capillary where the resorufin fluorophore will be produced by the oxidation of ADHP catalyzed by HRP enzyme. The fluorimeter should be therefore adapted to excite and sense the emission light from this cylindrical shaped space.

### 3.3.3 Fluorimeter configuration

Fluorimeters are usually constructed is such way that the emission sensing axis is at the right angle with the excitation beam axis. This minimizes the amount of excitation light entering the sensing path thus improving the signal to noise ratio. The fluorimeter of the ELISA analyzer uses the same configuration. The cross section of the fluorimeter with the depicted excitation and emission optical pathways is shown on the Figure 3.21. The fluorimeter uses construction components of the $1 / 2$ inch lens tube system marketed by Thorlabs.


Figure 3.21 Cross section of the fluorimeter showing the excitation beam (green) and emission pathway (yellow)

### 3.3.4 Excitation optical path description

The DJ532-10 laser output beam diameter is approximately $50-60 \mu \mathrm{~m}$. The beam is first expanded using the sapphire ball lens (diameter 0.5 mm , type 46117, Edmund Optics) and collimated into parallel beam using the plano-convex lens (LA1540, Thorlabs). The beam is then passed through the 50:50 beam splitter (BS010, Thorlabs) which diverts the portion of the beam to the feedback photodiode (BPW34, Vishay) of the laser driver circuit. The other portion of the excitation beam is focused by the cylindrical lens (type 46194, Edmund Optics) to the center of the modified cage cube (SC6W, Thorlabs) where the capillary will be positioned by the rotary capillary holder. The rotary holder is a motor powered double disc which has eight capillaries mounted on its circumference. The cylindrical surface (with the diameter equal to the diameter of the rotary capillary holder) was milled at the diagonal plane of the cube cage, which allows the capillary to be aligned
with the center of the cube and the focal line of the excitation beam (Figure 3.22). The length of the capillary interior which is illuminated by the excitation beam is about 8 mm .


Figure 3.22 The Fluirimeter assembly including the rotary holder with capillaries (blue color)

### 3.3.5 Emission optical path description

A portion of the resorufin emitted light is collimated into a parallel beam using the cylindrical lens (type 46194, Edmund Optics), which is passed through the suitable optical filter (type 67020, Edmund Optics). The filter is a bandpass filter with center line 591.5 nm , bandwidth of 43 nm and OD $>6$ blocking in the stopband. Although the use of longpass filter would allow emission light with longer wavelengths to reach the detector and slightly increase the sensitivity, the bandpass filter provides better signal to noise ratio by filtering out the stray light with longer wavelengths. The transmission profile of the filter is shown on the Figure 3.23. The filtered light is focused by the plano-convex lens (LA1540, Thorlabs) to the radiant sensitive area of the photodiode (BPX61).


Figure 3.23 Transmission profile of the bandpass filter, type 67020 (Edmund Optics, center wavelength $591,5 \mathrm{~nm}$, bandwidth 43 nm )

### 3.3.6 DPSS Laser driver circuit

It is important to keep the excitation light optical power constant in order to provide stable, reproducible measurements. If the required dynamic range of the fluorimeter is four orders of magnitude, the excitation power density must not fluctuate more than $0.01 \%$. Used DPSS laser contains the monitoring photodiode. This photodiode senses the optical power of the 808 nm pumping laser diode and not the power of the 532 nm output beam produced by the Nd: $\mathrm{YVO}_{4}$ and KTP crystals. The performance of those crystals is temperature dependent. Stabilizing the pumping diode optical power therefore does not provide stable output power of the green light. The heat dissipated by the pumping diode heats the crystals and the output power will have significant drift. It was necessary to use a separate photodiode sensing the portion of the excitation beam to stabilize the output optical power.
The diver circuit is based on a dedicated integrated circuit (iC-WKN, iC-Haus). The functional schematic is shown on the Figure 3.24. iC-WKN is designed to drive laser diodes in the continuous mode. It contains multiple protection circuits for the laser diode and requires only a few external components to operate. The adjustable resistor RP1 serves for adjusting the laser output power (up to 10 mW ). The laser beam intensity is sensed by the PD1 photodiode ad is fed back to the driver U2. All capacitors in this circuit work like bypass or filtration capacitors. The input voltage in the range 3 to 5 V is
connected to XC5. The current consumption is in the range 120 to 200 mA depending on the adjusted optical output power.


Figure 3.24 Laser diode driving circuit schematic

### 3.3.7 The photodiode front end amplifier

The fluorimeter photodiode usually needs to measure very low light intensities. It requires an amplifier with the gain of several millions to provide voltage suitable to interface to analog to digital converter (ADC). The photodiode BPX61 works in photovoltaic mode and it is connected to the transimpedance amplifier, which provides many performance advantages. The schematic of the photodiode amplifier is shown on Figure 3.25. The zero bias means no dark current, the internal diode capacitance stays at constant (zero) potential, therefore its influence on the detector speed is minimal. The $\mathbf{R 2}$ defines the gain of the transimpedance amplifier, which is $10^{7}$ in this case. $\mathbf{C 1}$ limits the bandwidth of the detector to reduce the noise. Another noise reduction occurs at the output filter R1 C2. The corner frequency is set to 1.59 KHz . Operational amplifier U1 (LTC6244, Linear Technology) is a low noise CMOS type with low input bias current. The reference voltage is set to 2.5 V and it is generated by the $\mathbf{U 3}$.

The voltage output vs. incident light characteristic has negative slope. The output voltage is highest at 2.5 V in the dark (no light reaching the photodiode) and it is decreasing with the increasing light level. The minimum output voltage (maximum light reaching the photodiode) is defined by the low saturation voltage of the $\mathbf{U 1}$, which is about 25 mV . This negative slope was necessary to use in order to interface to the ADC in the environment with the unsymmetrical power supply.


Figure 3.25 The functional schematic of the photodiode amplifier

### 3.3.8 The Analog to Digital (ADC) interface

The functional schematic of the ADC part is shown in Figure 3.26. The AD7794 AD converter is configured in the differential input mode, internal gain set to unity and update rate to maximum $(470 \mathrm{~Hz})$. According to AD7794 datasheet, the converter has effective noise free resolution 16 bits in this configuration. Using only one half of the input differential range $(+2.5 \mathrm{~V}$ down to 0 V$)$ the final noise free resolution is 15 bits. And the ADC input voltage resolution will be:

$$
\begin{equation*}
V_{1 L S B}=\frac{V_{r e f}}{2^{15}}=76.3 \mu \mathrm{~V} \tag{3.1}
\end{equation*}
$$

Where:
$\boldsymbol{V}_{\text {ref }}$ is the ADC reference voltage

The maximum photodiode current for the full-scale ADC reading is given by the following equation:

$$
\begin{equation*}
I_{P D \max }=\frac{V_{r e f}}{R_{f}}=250 \mathrm{nA} \tag{3.2}
\end{equation*}
$$

Where:
$V_{r e f}$ is the ADC reference voltage,
$\boldsymbol{R}_{f}$ is the transimpedance amplifier feedback resistance

On the other side, the minimum photodiode current needed for ADC reading of one (1LSB) will be calculated as follows:

$$
\begin{equation*}
I_{P D \min }=\frac{V_{r e f}}{R_{f} \cdot 2^{15}}=7.63 p \mathrm{~A} \tag{3.3}
\end{equation*}
$$

Where:
$\boldsymbol{V}_{\text {ref }}$ is the ADC reference voltage,
$\boldsymbol{R}_{f}$ is the transimpedance amplifier feedback resistance


Figure 3.26 The functional schematic of the fluorimeter ADC converter

In order to maintain the noise free resolution of 15 bits, the photodiode and transimpedance amplifier total peak-to-peak noise must be kept below $76.3 \mu \mathrm{~V}$. Typically noise calcullations use the root-mean-square noise (RMS). The conversion between the peak-to-peak noise and RMS noise uses the fact that both thermal noise and shot noise have the Gaussian probability distribution. By specifiing the noise amplitude interval normalized to the standard deviation $\sigma$ it is possible to estimate the probability of occurrence of the amplitude. Using the Gauss error function for the $6.6 \sigma$ interval provides the $99.9 \%$ probability of occurrence [20]. In this way the $76.3 \mu \mathrm{~V}$ peak to peak noise corresponds to the $11.56 \mu \mathrm{~V}$ RMS noise using the factor 6.6. The following part the electrical noise background of the fluorimeter will be investigated.

### 3.3.9 The fluorimeter detector and amplifier noise estimation

The photodiode noise is calculated as the sum of three components: the thermal (Johnson) noise $\boldsymbol{i}_{\boldsymbol{t} \boldsymbol{h}}$ of the photodiode internal shunt resistor $\boldsymbol{R}_{\boldsymbol{s} \boldsymbol{h}}$, the dark current shot noise $\boldsymbol{i}_{\boldsymbol{s} \boldsymbol{d}}$ and the photocurrent shot noise $\boldsymbol{i}_{\boldsymbol{s l}}$ [21]. The internal shunt resistor $\boldsymbol{R}_{\boldsymbol{s} h}$ of the BPX61 photodiode was calculated to be $2 \mathrm{G} \Omega$ using the dark current and the reverse bias voltage values provided in the datasheet. Because the photodiode works in the photovoltaic mode, the bias voltage is zero (see Figure 3.25), the dark current is also zero and the dark current
shot noise will not contribute to the total photodiode noise. In the following noise calculations the temperature of 300 K is assumed. The thermal noise density of the photodiode is calculated as follows:

$$
\begin{equation*}
i_{t h}=\sqrt{\frac{4 K_{b} T}{R_{s h}}}=2.88 \mathrm{fAHz}^{-1 / 2} \tag{3.4}
\end{equation*}
$$

Where:
$\boldsymbol{K}_{\boldsymbol{b}}$ is the Boltzmann constant,
$\boldsymbol{R}_{s h}$ is the photodiode shunt resistance,
$\boldsymbol{T}$ is the temperature in K

The noise density due to photocurrent shot noise is calculated according to equation (3.5). It is calculated for the minimum photocurrent because this case will be affected the most by noise and the signal to noise ratio (SNR) will be the worst.

$$
\begin{equation*}
i_{s l}=\sqrt{2 q I_{P D \min }}=1.56 \mathrm{fAHz}^{-1 / 2} \tag{3.5}
\end{equation*}
$$

Where:
$\boldsymbol{q}$ is the elementary electric charge,
$I_{P D \min }$ is the photocurrent corresponding to the one quantization step of the ADC

Total RMS noise at the output of the TIA amplifier originating from the photodiode only and contained within defined bandwith $\boldsymbol{B} \boldsymbol{W}$ is calculated using the following formula:

$$
\begin{equation*}
V_{p d}=R_{f} \sqrt{\left(i_{t h}^{2}+i_{s d}^{2}+i_{s l}^{2}\right) \cdot B W}=1.64 \mu V \tag{3.6}
\end{equation*}
$$

Where:
$\boldsymbol{i}_{\boldsymbol{t} h}$ is the thermal photodiode noise density,
$\boldsymbol{I}_{\boldsymbol{s} \boldsymbol{d}}$ is the photodiode noise density originating from the dark current
$\boldsymbol{I}_{s l}$ is the photodiode noise density originating from the photocurrent
$\boldsymbol{R}_{f}$ is the transimpedance amplifier feedback resistance
$\boldsymbol{B} \boldsymbol{W}$ is the noise bandwidth

The corresponding bandwidth is defined as the brick-wall equivalent of the TIA low pass filter and it is calculated as follows:

$$
\begin{equation*}
B W=\frac{1}{4 R_{f} C_{f}}=2500 \mathrm{~Hz} \tag{3.7}
\end{equation*}
$$

Where:
$\boldsymbol{R}_{f}$ is the transimpedance amplifier feedback resistance $\boldsymbol{C}_{\boldsymbol{f}}$ is the transimpedance amplifier feedback capacitance

This way, the total noise voltage originating from the photodiode is estimated to be 1.64 $\mu \mathrm{V}$ (RMS value). TIA limits the photodiode noise bandwidth to 2.5 KHz .

The TIA noise must be also evaluated. Usually its noise contribution is the most significant. The Amplifier noise can be separated into three components: the thermal noise of the feedback resistor $\boldsymbol{R}_{f}$, the input voltage noise of the operational amplifier and the input current noise of the operational amplifier [22]. The photodiode internal capacitance $\mathbf{C i}$ ( 72 pF for BPX61 and zero bias) at in input of the amplifier causes the amplifier noise gain peaking at higher frequencies which has negative impact on the noise performance of the detector. The noise gain begins to increase at the $\boldsymbol{F}_{\boldsymbol{z}}$ frequency:

$$
\begin{equation*}
F_{z}=\frac{1}{2 \pi R_{f}\left(C_{i}+C_{f}\right)}=194 \mathrm{~Hz} \tag{3.8}
\end{equation*}
$$

Where:
$\boldsymbol{R}_{f}$ is the transimpedance amplifier feedback resistance
$\boldsymbol{C}_{\boldsymbol{f}}$ is the transimpedance amplifier feedback capacitance
$\boldsymbol{C}_{\boldsymbol{i}}$ is the photodiode internal capacitance

The thermal noise originating from $\boldsymbol{R}_{\boldsymbol{f}}$ has limited bandwidth with corner frequency $\boldsymbol{F}_{\boldsymbol{p}}$ :

$$
\begin{equation*}
F_{p}=\frac{1}{2 \pi R_{f} C_{f}}=1.59 \mathrm{KHz} \tag{3.9}
\end{equation*}
$$

Where:
$\boldsymbol{R}_{f}$ is the transimpedance amplifier feedback resistance
$\boldsymbol{C}_{\boldsymbol{f}}$ is the transimpedance amplifier feedback capacitance

The total thermal noise contained within this bandwith will be:

$$
\begin{equation*}
V_{t h}=\sqrt{4 K_{b} T R_{f} \frac{\pi \cdot G B W}{2} \cdot \frac{F_{p}}{F_{p}+G B W}}=20.35 \mu V \tag{3.10}
\end{equation*}
$$

Where:
$\boldsymbol{K}_{\boldsymbol{b}}$ is the Boltzmann constant,
$\boldsymbol{R}_{f}$ is the transimpedance amplifier feedback resistance,
$\boldsymbol{T}$ is the temperature in K ,
$\boldsymbol{G B} \boldsymbol{W}$ is the gain bandwidth product of used operational amplifier ( 50 MHz for LTC6244)

The noise contribution by the operational amplifier input current noise is calculated according the following formula:

$$
\begin{equation*}
V_{i n}=i_{n} R_{f} \sqrt{\frac{\pi \cdot G B W}{2} \cdot \frac{F_{p}}{F_{p}+G B W}}=0.28 \mu V \tag{3.11}
\end{equation*}
$$

Where:
$\boldsymbol{i}_{\boldsymbol{n}}$ is the input noise current density of used operational amplifier $(0.56 \mathrm{fA} / \sqrt{ } \mathrm{Hz}$ for LTC6244),
$\boldsymbol{R}_{f}$ is the transimpedance amplifier feedback resistance,
$\boldsymbol{G B} \boldsymbol{W}$ is the gain bandwidth product of used operational amplifier ( 50 MHz for LTC6244)

The noise contribution by the operational amplifier input voltage noise is calculated according the following formula:

$$
\begin{equation*}
V_{e n}=e_{n} \sqrt{\frac{\pi \cdot G B W}{2} \cdot \frac{F_{p}\left(G B W+F_{z}\right)}{F_{z}\left(G B W+F_{p}\right)}}=202.92 \mu V \tag{3.12}
\end{equation*}
$$

Where:
$\boldsymbol{e}_{\boldsymbol{n}}$ is the input noise voltage density of used operational amplifier ( $8 \mathrm{nV} / \sqrt{ } \mathrm{Hz}$ for LTC6244),
$\boldsymbol{R}_{f}$ is the transimpedance amplifier feedback resistance,
$\boldsymbol{G B} \boldsymbol{W}$ is the gain bandwidth product of used operational amplifier ( 50 MHz for LTC6244)

It can be seen that this last noise contribution alone is one order of magnitude higher than other noise sources. This is caused by high bandwidth of the LTC6244 amplifier. To reduce this noise contribution, a simple RC low pass filter needs to be connected to the output of the transimpedance amplifier. This filter is represented on the Figure 3.25 by the components $\mathbf{R 1}$ and $\mathbf{C 2}$. The corner frequency of this filter will be:

$$
\begin{equation*}
F_{l p}=\frac{1}{2 \pi R_{1} C_{2}}=15.9 \mathrm{KHz} \tag{3.13}
\end{equation*}
$$

The noise contribution by the operational amplifier input voltage noise after the low pass filter is calculated according the following formula:

$$
\begin{equation*}
V_{e n f}=e_{n} \sqrt{\frac{1}{4 R_{1} C_{2}}}=1.26 \mu \mathrm{~V} \tag{3.14}
\end{equation*}
$$

Where:
$\boldsymbol{e}_{\boldsymbol{n}}$ is the input noise voltage density of used operational amplifier ( $8 \mathrm{nV} / \sqrt{\mathrm{Hz}}$ for LTC6244),

The Vin and Vth noise component contributions will be unaffected by the filter, because their bandwidth is within the passband of the output filter. The total noise of the transimpedance amplifier will be calculates as a square root of the sum of squared components:

$$
\begin{equation*}
V_{a m p}=\sqrt{V_{e n f}^{2}+V_{i n}^{2}+V_{t h}^{2}}=20.39 \mu \mathrm{~V} \tag{3.15}
\end{equation*}
$$

This calculation does not include the flicker noise of the operational amplifier and the thermal noise of the otput filter resistor R1. Their contribution is neglible. The Figure 3.27 shows the PSPICE noise simulation of the TIA with and without the output filter. The total noise density and integrated noise are shown. The simulated total noise of the TIA is $22.14 \mu \mathrm{~V}$, which is in good agreement with the previous calculations.


Figure 3.27 The simulated noise density and integrated noise of the transimpedance amplifier

The ADC quantization noise also significantly contributes to the overall noise performance. It is calculated according the following equation [23]:

$$
\begin{equation*}
V_{n A D C}=\frac{V_{1 L S B}}{\sqrt{12}}=22.03 \mu V \tag{3.16}
\end{equation*}
$$

The resulting noise is calculated by combining the total photodiode noise $\boldsymbol{V}_{\boldsymbol{p} \boldsymbol{d}}$, the total amplifier noise $\boldsymbol{V}_{\boldsymbol{a m p}}$ and the ADC quantization noise $\boldsymbol{V}_{\boldsymbol{n} A D C}$ together:

$$
\begin{equation*}
V_{n}=\sqrt{V_{a m p}^{2}+V_{p d}^{2}+V_{n A D C}^{2}}=30.06 \mu V \tag{3.17}
\end{equation*}
$$

The total noise is still higher than required RMS maximum $11.56 \mu \mathrm{~V}$ for the flicker-free ADC conversion. A further possibility to decrease noise is to use signal processing in the digital domain. Provided that the signal is almost stationary and the noise is not correlated to the signal the averaging of $\boldsymbol{N}$ ADC samples will reduce the noise by factor $\sqrt{ } \boldsymbol{N}$, while the signal remains unaffected [23, 24]. In this case the averaging of 16 samples is used to decrease the noise four times:

$$
\begin{equation*}
\bar{V}_{n}=\frac{V_{n}}{\sqrt{N}}=7.52 \mu V \tag{3.18}
\end{equation*}
$$

Where $N$ is the number of averages

This resulting RMS noise $7.52 \mu \mathrm{~V}$ should provide the flicker-free digital representation of the photodiode detected emission light intensity.

### 3.4 Control Unit

There is an obvious need to electrically drive all the active fluidic components of the analyzer and culturing unit in a specific preprogrammed way to enable its proper functionality. During the early testing phase, it is likely that some changes or adjustments in the fluidics and its active components will be made. The control unit should therefore provide sufficient flexibility to support the varying count of the active fluidic components (valves, pumps) or ability to interface sensors with various interfaces. Widely used approach to control such systems is to use a commercially available modular system (e.g. LabVIEW) using the personal computer (PC) as the central control element. Although this may be practical approach for many laboratory experimental setups, the control unit for the analyzer and culturing modules described in this work benefits from the advantages which provides the customized embedded technology. Among the most important is the real-time operation and high degree of integration which provides the
timing precision and reliability required by this application. The additional benefits are independence on the control PC, low power consumption, portability and cost effectiveness. The control unit described here has the ability to control six stepper motors in microstepping mode, 32 solenoid valves and two constant current sources capable of driving low power laser diodes. Additionally, the control unit provides direct interfaces for various sensors (spectrometer head, fluorimetric and photometric sensors, pressure sensor, capacitive sensors, analog voltage inputs and others). The core of the control unit makes use of the 32-bit microcontroller STM32F103ZET [25] which is based on the ARM CORTEX-M3 architecture. Interfacing to potential host system is possible through the USB or serial interfaces. Graphical LCD display and two rotary encoders serve as the user interface. The corresponding printed circuit board (PCB) was designed using four electrical layers and has the size $160 \times 200 \mathrm{~mm}$. The whole system is powered by single 12 V source. The schematic and layout design were made using the Altium Designer software [26], version 10.391.

### 3.4.1 Control unit schematics

This section describes the function of important schematic parts of the control unit in more detail. The complete schematics can be found in the Appendix 1.

### 3.4.1.1 Microcontroller and communication interfaces

The central element of the control unit is the 32-bit microcontroller STM32F103ZET [25] (STMicroelectronics, U6) in the 144-pin LQFP package which offers sufficient I/O ports to interface all used peripherals. The controlling program is stored in the internal 512 KB nonvolatile memory. The schematic part covering the microcontroller and related system and interface circuitry is shown on the Figure 3.28. The system clock is generated by internal oscillator stabilized by the 8 MHz crystal $\mathbf{X 2}$. The microcontroller core is clocked by the 72 MHz clock signal internally multiplied and derived from the 8 MHz oscillator. A low frequency oscillator synchronized by $\mathbf{X 1}$ serves as the clock source for internal real-time-clock (RTC). A small lithium battery BT1 keeps the RTC running during the time the control unit is unpowered. The microcontroller is powered by single supply voltage VCC (3.3V). Capacitors C13-C23, C31, C37, C47, C50 and C51 serve as power supply decoupling. In the normal state the jumpers $\mathbf{J} \mathbf{1}$ and $\mathbf{J} \mathbf{2}$ are switched to ground, so
the microcontroller always boots from the internal flash memory. The control unit contains two USB interfaces. Both are configured as the "USB Device" and support the standard USB2.0 Full Speed. The connection USB1 (XC2) serves for sending control commands by the host system, while the USB2 connection (XC1) is intended for hi-speed debugging. The control unit also provides two serial interfaces without hardware handshake function supporting maximum transfer rate 115200 Baud. These allow connection of various slave integrated sensors or modules. Alternatively, it can be used for low-speed debugging. CAN bus interface (XC4) allows direct interfacing of the CETONI neMESYS [27] syringe pumps.


Figure 3.28 Schematic of the microcontroller part and communication interfaces

Additionally, the powered connector with $\mathrm{I}^{2} \mathrm{C}$ bus is available for connecting low-speed OEM sensor modules. The JTAG interface (JP2) allows programming of the internal
memory of the microcontroller and the low-level debugging. The address decoder (U7) provides chip select signal demultiplexing for all peripheral chips controlled by the SPI bus.


Figure 3.29 Schematic of the human interaction interfaces

### 3.4.1.2 Human control interfaces

For the interaction with user, the control unit contains a graphical display (U8) with resolution of $64 \times 128$ pixels and resistive touchscreen connected through the connector XC8. Display is controlled over a serial SPI bus. The touchscreen is connected directly to the microcontroller and is read using the internal AD converters. Additionally, two rotary encoders ( $\mathbf{S 6}, \mathbf{S} 7$ ) simplify the numerical input by the user. Quadrature signals are internally decoded by the microcontroller. Acoustic signalization is provided by small piezo transducer B1. Eight directly controlled LEDs (D2-D9) and four pushbuttons (S2 - S5) are intended for software debugging purposes. The schematic of the human control interface part is shown on the Figure 3.29.

### 3.4.1.3 External memory interface

The control unit of the standalone system should have the possibility to store the system configuration and the measurement results on the internal or removable media. For this purpose, the control unit has one Secure Digital (SD) memory card interface and one internal ferroelectric random-access memory (F-RAM, U5) for storing up to 32 KB of configuration data (Figure 3.30). Both devices can communicate with the microcontroller over the SPI bus. The SD card interface additionally supports faster 4-bit data bus mode.


Figure 3.30 Schematic of the memory interfaces

### 3.4.1.4 Power supply

The control unit is powered by the single DC source of 12 V with maximum current 3 A . However, typical current consumption is much lower -1 A to $1,5 \mathrm{~A}$ so the whole system could be powered by larger accumulator if needed. The schematic of the power supply circuitry is shown on the Figure 3.31. Connector XC30 serves as the 12V power supply input. The fuse F3 serves as the overcurrent protection, while the diodes D56 and D59 provide overvoltage and reverse polarity protection. The 12 V power supply for stepper motor drivers 12VMOT is derived from the main power over the EMI filter (L3, C174, C176, C183 and C185). Powering of the solenoid valves comprises two phases: during the active switching phase the voltage is set to 12 V , while during the standby phase (the solenoid valve is in the steady ON state) the driving voltage is lowered to approximately 5 V . During the active phase the solenoid power supply $\mathbf{1 2 V S O L}$ is connected to the main power supply node VIN through the EMI filter (L2, C172, C173, C182 and C184) and transistor Q11. The signal EN12V controls switching of the Q11. When the Q11 is switched off, the $\mathbf{1 2 V S O L}$ node is powered from the $\mathbf{+ 6 V}$ source through decoupling diode D62. This way the power needed to keep the solenoid valve in the switched-on position is reduced from 240 mW to 100 mW . In the situation where multiple solenoids are switched on, the power saving is significant. The power supply for all the digital circuitry is provided by the switching step-down regulator U38, providing stable voltage output of 3.3 V at the node VCC. Most of the analog circuitry requires stable +5 V power supply with low ripple voltage. This is derived from the main 12 V supply using the two-stage regulator. The first stage is switched step down regulator generating output voltage $\mathbf{+ 6 V}$. To remove the switching ripple a second linear low-drop regulator U37 downregulates
the $+\mathbf{6 V}$ input voltage to the required ripple-free +5 V output AVCC5. The switching regulators operate with high efficiency of $70-90 \%$ which helps to save power and reduce thermal losses at higher load currents.


Figure 3.31 Schematic of the control unit power supplies

### 3.4.1.5 Spectrophotometer and combined photometric/fluorimetric sensor interfaces

The control unit was designed to accommodate a commercial spectrophotometer head based on the Hamamatsu S8378 CMOS linear sensor chip (U40, Figure 3.32)[28]. The spectral range is 316 nm to 1210 nm with a spectral resolution of $3,5 \mathrm{~nm} /$ pixel. Optical input is provided via SMA connector attached optical cable. After the light exposure the pixels values are sequentially clocked out of the chip to the video output. Because the sensor chip works with 5 V level signals, a voltage level converter (U36) is necessary to interface to the 3.3 V signal level of the microcontroller. The analog pixel voltage is digitized using the 16-bit imaging signal processor (U35). The signal processor has three analog input channels. Only one channel is used by the spectrometer part. Additionally, two four-channel combined photometric/fluorimetric sensors can be connected to the control unit. Each channel of the sensor comprises one excitation LED and two photodiodes with integrated preamplifiers. The amplified signals provided by the
photometric channels are connected to the inputs S1A - S8A of the multiplexer U41. Similarly, amplified signals of the fluorimetric channels are connected to the inputs S1B - S8B of the same integrated circuit. The outputs of the multiplexer are connected to the remaining two channels of the signal processor $\mathbf{U 3 5}$ where they are digitized and read by the microcontroller. The LED diodes of the sensor are driven by the adjustable constant current source created by operational amplifiers U32, U33. Those are connected as the differential amplifiers regulating the voltage drop across the output $50 \Omega$ resistor according to the input voltage provided by the $\mathrm{D} / \mathrm{A}$ converter $\mathbf{U 4 2}$.


Figure 3.32 Schematic of the spectrometer interface and photometric/fluorimetric sensors interface

The differential amplifier has internal gain of $1 / 2$. Therefore, for the input voltage of 1 V , voltage drop of 0.5 V across the output $50 \Omega$ resistor will be created, which means 10 mA LED current. The A/D converter U42 has internal gain 2 and using the reference voltage of 1.25 V the maximum output voltage will be 2.5 V and the maximum LED current will
be 25 mA . Figure 3.32 shows the constant current sources for the first sensor only. The identical constant current sources for the second sensor are connected to the respective outputs VOUTE - VOUTH of the D/A converter U42.

### 3.4.1.6 Solenoid valve drivers

The control unit allows connection up to 32 solenoid valves. Each valve is directly switched by the Darlington transistor inside the integrated circuit U11, U12. The maximum driver output current is 500 mA . The drivers U11 and U12 contain integrated free-wheeling diodes, therefore are capable of switching inductive loads. The Darlington drivers are controlled by the I/O extension circuit $\mathbf{U} 9$ controlled by the SPI bus. The power source $\mathbf{1 2 V S O L}$ is set to 12 V during the switching period, after which it is decreased to 5 V to reduce power consumption.


Figure 3.33 Schematic of the solenoid valves driver

This switching is realized using the signal EN12V as described in the power supply section. The indication LED diodes are connected in parallel to the solenoid valves. The driver circuitry for the first 16 valves is shown on the Figure 3.33. The remaining valve drivers are of identical design.

### 3.4.1.7 Stepper motor drives

The control unit can independently operate up to six two-phase bipolar stepper motors in the microstepping mode. The driver circuitry is based on the integrated stepper motor driver L6208 (STMicroelectronics)[29]. Figure 3.34 shows the driving circuitry for one stepper motor. The I/O expanders U19, U20 and the D/A converters U21, U22 are shared by several stepper motor drivers L6208 (U24 - U29). The L6208 driver has built in pulse width modulated (PWM) output stages with adjustable current limit. L6208 does not natively support microstepping operation. However, by varying the maximum phase current limit for both phases independently the microstepping can be realized. The software implements the microstepping operation with up to 32 microsteps for smooth motor operation. The dynamic current limit setting is provided by the D/A converter U22. The decay mode, direction of operation, driver enable signal and stepping mode control signal are controlled by the I/O extension chip U20.


Figure 3.34 Schematic of the stepper motor driver

The stepping clock input is routed directly to the timer module of the microcontroller. The maximum phase current, which is possible to set by the $\mathrm{D} / \mathrm{A}$ converter is 5 A , however the peristaltic pump motors operate with the phase current 3 A or less, depending on the motor speed. The maximum supported motor speed is 160 rpm , which corresponds to stepping frequency of 17066 microsteps per second using the 32 microstepping mode.

### 3.4.1.8 Pressure sensor and capacitive sensors

The integrated differential pressure sensor with the maximum pressure range of 1000 KPa (U18, MPXV5100DP, NXP Semiconductors)[30] was added to the design of the control unit to help diagnose possible problems in the fluidic part of the system by measuring pressure profiles during fluidic operations. The sensor has linear analog output in the range $0.2-4.7 \mathrm{~V}$ with a slope of $4.5 \mathrm{mV} / \mathrm{KPa}$. The sensor is connected to the input of 24bit A/D converter U17. For the correct operation with the sensor, the reference inputs 2 are selected by the software (REFIN2+, REFIN2- inputs of the U17). The reference voltage source $\mathbf{U 1 5}$ is connected to the primary reference inputs of the U17 (REFIN1+, REFIN1-) and is needed for the fluorimeter readout, as the A/D converter U17 is also shared with this peripheral. The schematic part relevant to the pressure sensor and the capacitive sensors is shown on the Figure 3.35.


Figure 3.35 Schematic of the pressure sensor and capacitive sensors

The capacitive sensors are intended to be used for detection of a fluid inside the tubing. Total of twelve sensors are supported and the interface uses the capacitance-to-digital
converter chip AD7147 (U16, Analog Devices)[31]. The AD7147 chip contains all necessary circuitry for the intended functionality, so the corresponding schematic part contains minimum of external components. The chip communicates with the microcontroller using the SPI bus.

### 3.4.2 Printed circuit board (PCB) design for the control unit

Design of the PCB is of crucial importance for good overall performance of the control unit. Sensitive analog circuitry intended for measuring of low-level signals are combined with the high-speed digital integrated circuits on the same board. The layout was designed with focus to physically and electrically decouple those parts using proper shielding techniques. Together with the effort to keep the board size as small as possible, the layout design resulted in a four-layer PCB with the dimensions of $200 \mathrm{~mm} \times 160 \mathrm{~mm}$ and standard thickness of 1.6 mm . The layer stack details can be found in the Table 3.1. The layout was designed with the minimum track width 0.2 mm and minimum clearance between different tracks 0.2 mm . The minimum plated through-hole diameter is 0.4 mm . The top and bottom layers were protected by the green solder mask. The assembly is combined using mostly surface mounted devices (SMD), but some through-hole components are also used. The prototype board contains 783 components in total, with 566 components assembled on the top side and 217 components on the bottom side. The prototype board was assembled manually. The assembly plan and layout of all layers can be found in the Appendix 2 and Appendix 3. Figure 3.36 shows assembled control unit PCB.

Table 3.1 The layer arrangement of the control unit printed circuit board

| Layer | Layer designator | Copper Thickness | Purpose |
| :--- | :---: | :---: | :--- |
| Top Layer | L 1 | $35 \mu \mathrm{~m}$ | top signal layer |
| Internal Layer 1 | L 2 | $35 \mu \mathrm{~m}$ | ground plane |
| Internal Layer 2 | L 3 | $35 \mu \mathrm{~m}$ | power supply plane |
| Bottom Layer | L 4 | $35 \mu \mathrm{~m}$ | bottom signal layer |



Figure 3.36 Assembled top side of the control unit PCB including the spectrometer module

### 3.4.3 Control unit embedded code overview

The code for the control unit was written in ANSI C programming language and it was compiled for the ARM CORTEX-M3 architecture. The latest source code version v1.09 contains approximately 10 thousand lines of code excluding used libraries. Additionally, the open source bootloader OpenBLT [32] was used to simplify the firmware update procedure. The embedded code makes use of two external libraries provided by the microcontroller manufacturer: STM32F10x Standard peripheral library v3.5.0 and STM32F10x USB-FS-Device Driver v3.3.0. Additionally a ported code for formatted output (printf.c) is also used [33]. Table 3.2 lists the shortly described source code files. The hierarchical order of the embedded code modules is shown on the Figure 3.37.


Figure 3.37 the hierarchical order of the control unit code modules

The control unit embedded code in the recent version allows the user to control whole system using a host computer. The communication between the computer and control unit is realized over the USB bus. The control unit behaves as the USB device class with implemented virtual serial communication interface. The host computer uses arbitrary terminal program to facilitate the serial communication. The control unit has implemented a set of commands for controlling and debugging all analyzer and culturing unit functions. Table 3.3 lists the implemented command set including the command parameter description.

## Bootloader implementation

The OpenBLT bootloader simplifies the embedded code updating. The bootloader is located at the beginning of the embedded flash memory of the microcontroller. After the microcontroller system reset the bootloader is always executes as the first. The bootloader checks if a valid application code is present in the flash memory using the checksum mechanism. If valid application has been found, the bootloader exits and the application
code starts to execute. Otherwise the bootloader will wait for connection with the host computer in order to program new application code into the flash memory.

Table 3.2 The list of embedded code files with corresponding description

| File name |  |
| :--- | :--- |
| elisa.c | High-level routines for the sandwich ELISA protocol and culturing unit |
| main.c | Low-lever routines for the peripheral chips and sensors |
| commands.c | Definition of host control and debug commands |
| Touchscreen.c | Touchscreen driver code |
| glcd.c | Graphical LCD driver code |
| st7565.c | High-level routines for graphical LCD |
| sm_cntr.c | Stepper motor driver code |
| printf.c | High-level formatted output routines |
| startup.c | System initialization code, interrupt vectors definition |
| stm32f10x_it.c | Interrupt handler routines |
| system_stm32f10x.c | System routines, system clock management |
| virtual_com.c | Virtual communication port high-level routines |
| usb_desc.c | USB descriptor definition |
| usb_endp.c | USB endpoint routines |
| usb_istr.c | USB interrupt routines |
| usb_prop.c | Virtual communication port low-level routines |
| usb_pwr.c | USB power handling routines |
| global.h | I/O port definitions, peripheral chip registers definitions |
| elisa.h | Header file for elisa.c, definition of parameters for fluidics |
| main.h | Header file for main.c |
| commands.h | Header file for commands.c |
| Touchscreen.h | Header file for Touchscreen.c, configuration parameters for the touchscreen |
| glcd.h | Header file for glcd.c |
| st7565.h | Header file for glcd.c, configuration parameters for LCD |
| sm_cntr.h | Header file for sm_cntr.c, configuration parameters for stepper motors |
| printf.h | Header file for printf.c |
| font5x7.h | Small font definition for LCD |
| fontgr.h | Large font definition for LCD |
| mnlogo.h | Definition of MN logo for LCD |
| stm32f10x_it.h | Header file for stm32f10x_it.c |
| stm32f10x_conf.h | STM32F10x Peripheral library configuration file |
| virtual_com.h | Header file for virtual_com.c, configuration parameters for USB |
| usb_desc.h | Header file for usb_desc.c, configuration parameters for USB |
| us__conf.h | USB endpoint configuration file |
| usb_istr.h | Header file for usb_istr.c |
| usb_prop.h | Header file for usb_prop.c |
| usb_pwr.h | Header file for usb_pwr.c |
|  |  |

The uploading utility named "MicroBoot" is part of the OpenBLT project [32], and communicates with the microcontroller over a USB interface. The complied code to be uploaded should be in the Motorola S-record format (*.srec).


Figure 3.38 the microcontroller flash memory map

The application code must be compiled with starting address of $0 x 08004000$. The microcontroller flash memory map is shown on the Figure 3.38. The 4KB area at the top of the flash is reserved for emulation of EEPROM memory to store the application configuration data. The bootloader can be called directly from the application code using the command "callbootloader".

## Software development tools

For developing the embedded code, the open source development tools were used exclusively. The compiler, debugger and integrated development environment (IDE) was running on personal computer using Windows as the operating system. The compiler was based on the YAGARTO GNU ARM toolchain, version v2.22 [34]. Eclipse was used as the IDE, version 4.2.1 [35]. Additional C/C++ Development Tooling (CDT) plugin was installed into Eclipse IDE. The JTAG interface was used for code debugging. The used OpenOCD debugger tool consists from the software part and the hardware debugging tool [36]. The software part (used version v0.9.0) enables the remote debugging and communicates with the GNU GDB tool. The hardware part (JTAG adapter) is of own design and it is based on the original OpenOCD FTDI2232 interface [37]. The schematic and layout of this JTAG interface can be found in the Appendix 8 and Appendix 9.

Table 3.3 the list of the control commands for the control unit including the syntax and description.
The commands are marked in blue and the command parameters are marked in red.

| Main menu commands | Parameter: (valid range) - parameter description | Command description |
| :--- | :--- | :--- |


| ELISA menu commands |  |  |
| :---: | :---: | :---: |
| exit |  | exit ELISA menu and return back to the main menu |
| sequence start starting_step | starting_step: (1-250) - selects the starting point of the sequence | start execution of the ELISA sequence |
| sequence stop |  | immediately stop executing the ELISA sequence |
| sequence pause |  | pause the ELISA sequence execution, but finish the current step |
| sequence continue |  | resumes the execution of the ELISA sequence |
| current incubation time new_time | new_time: (0-30000) - new incubation time in seconds | change the recently running incubation time |
| substrate time new_time | new_time: (0-3000) - new incubation time in seconds | change the substrate incubation time |
| global incubation time new_time | new_time: (0-30000) - new incubation time in seconds | change the all incubation periods in the sequence except the current time and the substrate time |
| measurements repeats | repeats: (1-10) - number of measurement repeats for each channel | set the measurement repeating for each channel, the interval between successive measurements is defined by substrate time command |
| dosing speed speed | speed: (1-1000) - new pumping speed to be set | set the pumping speed when pumping liquid to the capillary |
| sample mode mode | mode: (br1 \\| prepared) - select one of two sampling modes | configure the sampling mode: br1 take sample directly from the culturing device, prepared - take the sample from the sample container |
| shortcut start end | start: (1-255) - the shortcut starting point (as the protocol step) - will be not executed | allows to skip certain steps in the ELISA |
| shortut star | end: (1-255) - the shortcut end point (as the protocol step) - will be executed | sequence |
| manifold speed speed | speed: (1-1000) - new pumping speed to be set | set the pumping speed when pumping liquid to the manifolds |
| wash manifold speed speed | speed: (1-1000) - new pumping speed to be set | set the pumping speed when pumping liquid to the manifolds during washing operations |
| wash dosing speed speed | speed: (1-1000) - new pumping speed to be set | set the pumping speed when pumping liquid to the capillary during the washing operations |
| wash manifold volume volume | volume: (1-10000) - new washing volume to be set | set the volume for washing the manifold fluidic paths |
| wash dosing volume volume | volume: (1-10000) - new washing volume to be set | set the volume for washing the capillary fluidic paths |
| wash repeat repeats | repeats: (1-10) - number of washing steps | set the number of washing repeats between the ELISA protocol steps |
| Bioreactor related commands |  |  |
| br control new_state | new_state: (0 1 ) - turn ON (1) or OFF (0) the perfusion | control the culturing unit bioreactor perfusion |
| br change medium volume speed | volume: (-10000-10000) - pumped volume in $\mu \mathrm{l}$, negative number means opposite direction | change the medium inside the bioreactor |
|  | speed: (1-5000) - pumping speed in $\mu \mathrm{l} / \mathrm{min}$ |  |
| br sample volume speed | volume: (0-10000) - pumped volume in $\mu \mathrm{l}$ | sample the bioreactor medium of defined volume with defined speed |
|  | speed: (1-5000) - pumping speed in $\mu \mathrm{l} / \mathrm{min}$ |  |
| br mix | volume: ( $0-30000$ ) - pumped volume of air in $\mu \mathrm{l}$ | mix the sampled bioreactor medium using stream of air |
|  | speed: (1-5000) - pumping speed in $\mu \mathrm{l} / \mathrm{min}$ |  |
| br prepare sample |  | start the bioreactor sample preparation - comprise sampling and mixing operations |
| br set speed speed | speed: (1-500) - perfusion speed in $\mu \mathrm{l} / \mathrm{min}$ | set new bioreactor perfusion speed |


| br stop |  | reset all ongoing bioreactor operations |
| :---: | :---: | :---: |
| Cleaner related commands |  |  |
| cleaner start starting_step | starting_step: (1-250) - selects the starting point of the sequence | start the cleaning of the fluidics from defined step |
| cleaner stop |  | immediatelly stop the clening procedure |
| cleaner pause |  | pause the cleaning sequence execution, but finish the current step |
| cleaner continue |  | resumes the execution of the cleaning sequence |
| cleaner shortcut start end | start: (1-255) - the shortcut start point (as the protocol step) - will be not executed | allows to skip certain steps in the cleaning sequence |
|  | end: (1-255) - the shortcut end point (as the protocol step) - will be executed |  |

### 3.5 Intermediate summary

As can be seen, the development of the proof of the concept analytical device for the automated flow-through human albumin sandwich ELISA was relatively complex. The performance in the terms of sensitivity and assay time will can be potentially improved to the standard MTP ELISA procedure. This was evaluated during the testing phase and it is described in the later chapters. As with every prototype device some optimization was necessary to reach the required performance level. Figure 3.39 and Figure 3.40 show the finished ELISA analytical unit and the control unit respectively.


Figure 3.39 The automated flow-through ELISA module prototype


Figure 3.40 The control unit prototype

## 4 Designing the prototype of automated 3D cell culture device

### 4.1 Introduction

The use of 3D cell cultures, especially when perfused, are more closely related to in vivo conditions, making them potentially a more relevant model than 2D cultures [2]. Recently, two new tools, micro bioreactors and MatriGrid® porous polycarbonate (PC) scaffolds, were developed at Ilmenau University of Technology for 3D culturing of cell [4]. The culture device described here serves as an extension of these two tools to create an incubator environment compatible with a platform having integrated active perfusion and automated medium change. This chapter first briefly describes the MatriGrid® and micro bioreactor devices, following by the design and functionality description of the automated culture unit.

### 4.2 Required functionality definition of the culture unit

The intended purpose of the culture unit within the automated system is to automate the 3D cell culturing process and provide the fluidic interface for transferring medium samples to the analytical module for further analysis. The basic functionality of the culture unit comprises:

- Compatibility with the existing micro bioreactor and MatriGrid® devices
- Active perfusion of the cell culture
- Automated medium change
- Sampling of the culture medium for the purpose of analysis with the optional possibility of dilution

Aside from the main functionality, some additional properties are also required: The culture unit should be compatible with the incubator environment, it should allow easy handling and maintenance. The culture unit size should be therefore compact. The prototype device may be constructed from commercially available fluidic components to verify the design concept and required functionality.

### 4.3 The culture platform: Micro Bioreactor and MatriGrid ${ }^{\circledR}$

The porous polycarbonate scaffolds termed MatriGrid ${ }^{\circledR}$ (Figure 4.1, left side) were previously developed at Ilmenau University of Technology for 3D cell culturing [4]. The scaffold contains up to 187 microcavities in which the cells are cultured. In contrast to 2D cultures, cells grow 3-dimensionally due to the limited space inside these microcavities. The scaffold consists of a rectangular $50 \mu \mathrm{~m}$ thick biocompatible polycarbonate piece with a microstructured seeding area of $5 \mathrm{x} 5 \mathrm{~mm}^{2}$. Porous polycarbonate foils are structured to achieve pore sizes that are necessary for the nutrient supply in active perfusion of 3D cultured cells during bioreactor culture.


Figure 4.1 The MatriGrid® scaffold (left) and the micro bioreactor (right)

The externally perfused micro bioreactor (Figure 4.1, right side) used for 3D organotypic cell culture has a total fluid volume of $1350 \mu 1$ and outer dimensions of $41 \times 43 \times 40 \mathrm{~mm}$ (W x D x H) [4]. The housing consists of heat-resistant biocompatible PC components and is therefore autoclavable. Within the bioreactor, two fluid chambers are located above and below the inserted 3D cell carrier MatriGrid ${ }^{\circledR}$ which are connected to an in- and outflow channel to facilitate medium exchange and sample extraction. The inlet and outlet of the micro bioreactor are connected to medium containing tubes via 1/4-28 UNF flangeless tube connectors (Upchurch Scientific, IDEX Health \& Science LLC, USA). De-aeration of the fluid cycle is via an infusion port (B. Braun Melsungen AG, Germany).

### 4.4 Fluidics design

Based on the requirements defined before the prototype version of the fluidics for the culture unit has been designed (Figure 4.2). It contains five active fluidic components: one peristaltic pump (type 61131.000, Boxer GmbH), one two-way solenoid valve ( $075 \mathrm{P} 2 \mathrm{NC} 12-23 \mathrm{~B}$, Bio-Chem Fluidics Inc.) and three three-way solenoid valves (075P3MP12-23B, Bio-Chem Fluidics Inc.). The use of the components of the same type as in the case of the analytical module is advantageous, because this allows using the control unit also for driving the culture unit components. The control unit has sufficient hardware resources to control one analytical unit and two culture units simultaneously. Two kinds of tubing were used for the culture unit: The C-Flex ${ }^{\circledR}$ with internal diameter of 0.58 mm (type 10025-23B, Bio-Chem Fluidics Inc.) and the PharMed ${ }^{\circledR}$ BPT tubing with internal diameter of 0.51 mm (type SC0339, Cole-Parmer GmbH). Additionally, three 15 ml Eppendorf tubes serve as the reservoirs for the fresh medium, sample and waste containers.


Figure 4.2 Fluidic diagram of the culture unit

The fluidic network is divided into two parts. The circulation loop including the bioreactor and the fresh medium reservoir must work under sterile conditions. Therefore, this part was designed as removable (Figure 4.2, lower part). The cell culture supported on the MatriGrid $®$ can be inserted into the bioreactor and the whole circulation loop can
be filled with culture medium under the clean bench. Once completed, the circulation loop can be mounted on the culture unit outside the clean bench. The PharMed ${ }^{\circledR}$ material was selected for circulation loop tubing, because in contrast to the C-Flex ${ }^{\circledR}$ material it can withstand the autoclaving cycle. The second part of the fluidic network (Figure 4.2, upper part) is designed to handle sample or the waste medium from the bioreactor and the sterility or autoclaving operation is not required. The C-Flex tubing is therefore used for this second fluidic part.

The culture unit functionality will be described in more detail in the following paragraphs separately for each operating mode.

### 4.4.1 Culture unit during the active perfusion of the cell culture

Most of the time the culture unit perfuses the cell culture located in the micro bioreactor. The peristaltic pump maintains the circulation. The medium flow path is shown on the Figure 4.3. The valve V2 stays closed and V1 is also powered off, which means the V1NO part remains open and the V1-NC part remains closed. This way the cell culture medium circulates in the loop and the atmospheric oxygen diffuses through the tubing walls and facilitates the medium oxygenation. The entire culture unit may be placed into incubator with controlled temperature and atmosphere. For that reason, the culture unit does not contain any electronics, which could cause problems with the heat management and moreover the electronics would need to be protected from the humid incubator atmosphere as well. The solenoid valve and peristaltic pump drivers are located inside the control unit. The perfusion speed should be selected sufficiently low that the cells are not loaded with excessive shear stress. At the other hand too low perfusion can limit the oxygen supply to the cells. The typical perfusion speed is in the low tens of microliters per minute. The culture unit allows setting the perfusion speed in the range from $1 \mu 1 / \mathrm{min}$ to $500 \mu \mathrm{l} / \mathrm{min}$. The direction of the perfusion can be also changed if needed. The second channel of the peristaltic pump is not used in this mode. The circulation loop dead volume is about $250 \mu \mathrm{l}$ including the pump. The total internal volume including the micro bioreactor is $1600 \mu$ l. For a perfusion speed of $25 \mu \mathrm{l} / \mathrm{min}$ the time for one complete medium cycle will be 64 minutes.


Figure 4.3 Culture unit active perfusion flow path

### 4.4.2 Automated medium change

The regular refreshment of the cell culture medium is essential in the cell culturing experiments. It is always connected with the risk of microbial contamination, so it must be carried out under aseptic conditions. The cell culture unit was designed to automate the medium change process and minimize the risk of contamination. This is achieved by keeping the fluidic system closed during the medium change operation. The whole procedure consists of two phases. During the first phase the fresh medium is pumped into the bioreactor while the old medium is pumped out of the bioreactor to the waste container. The second phase empties the fluidic paths. The respective flow paths are shown on the Figure 4.4 and Figure 4.5. During the Phase I the solenoid valves V1 and V2 are powered on, while the valves V3 and V3 stay powered off. The circulation loop is opened and the pump delivers now the fresh medium to the bottom end of the bioreactor.


Figure 4.4 The culture unit flow path during the medium change or sampling, phase I


Figure 4.5 The culture unit flow path during the medium change phase II

The old medium is continuously displaced from the top part of the bioreactor through the valve V2 and the calibrated volume fluidic part (which plays no role in this mode of operation) to the waste container. By keeping the flow inside the bioreactor laminar (which is always the case for the relevant perfusion speed range) the mixing between old and new medium is limited to the diffusion. The user has the freedom to select the medium
change volume and speed. Partial or full medium exchange can be achieved by varying the exchange volume. The exchange speed is usually the same like the perfusion speed, but it can be also increased for speeding up the medium change process if the cultured cells can handle such perfusion rate increase. At the end of phase I the valves V1 and V2 switch off again, which will restore the circulation loop and the cell culture continues to be perfused with the refreshed medium. The fluidic paths behind the valve V2 are filled with the old medium, which needs to be removed. This is the purpose of the phase II in which the valve V3 switches on and the old medium in the tubing behind the valve V2 will be displaced by the air pumped by the second channel of the peristaltic pump. At the end of phase II, the valve V3 will be switched off. The cell culture perfusion is not affected during the phase II. The volume of the fresh medium container $(15 \mathrm{ml})$ together with the medium exchange volume sets the limit how many times the medium exchange can be performed without refilling it and thus opening the aseptic part. Another limitation is the stability of the medium at the incubator temperature.

### 4.4.3 Automated sampling of the cell culture medium

The basic feature of the integrated culture and analytic system is the possibility of automated online medium sampling and subsequent analysis. The culture medium can be supplemented with vehicle control or test chemical as needed. The sampling procedure is similar to the medium change and consists of two phases as well. During the first phase the solenoid valves V1 and V2 are powered on. The medium being sampled flows out from the top side of the bioreactor through the valve V2 and the calibrated fluidic part to the waste container. The fresh medium flows through the valve V1 to the bottom side of the bioreactor. The situation is shown on the Figure 4.4. However, the volume displaced during the phase I is chosen so that it will fill the fluidic paths until the point of valve V4. The required volume will be slightly more than the calibrated value if $200 \mu$. The difference accounts for the dead volume of the tubing connecting the calibrated part with the valves V2 and V4. The medium stored in the calibrated part is displaced into the sample container during the phase II (Figure 4.6). This way the volume delivered to the sample container will be always known and constant. This approach was preferred over the simple metering by peristaltic pump. Although the stepper motor can rotate for exact angle, the pumped volume depends also on the exact position of the tubing inside the peristaltic head or the degree of tubing wearing. During the sampling phase II the valves

V3 and V4 are powered on, while the valves V1 and V2 remain powered off. The circulation loop is closed and the cell culture remains to be perfused.


Figure 4.6 The culture unit flow path during the medium sampling phase II

The optional sample dilution can be reached by filling the required amount of diluent into the sampling container prior to sampling. The amount of sample is known so the amount of diluent can be calculated for required dilution factor. Once the sample was displaced into the diluent there is possibility to mix the resulting solution by the stream of air. In this case the pumped volume during the phase II is increased several times, so after the sample was flushed into the diluent the air continues to be further pumped to the solution. The sample container tubing must end at the bottom of the container. At the end of phase II, the sample ready for the analysis is present in the sample container. The additional tubing provides the fluidic connection between the culture unit sample container and the analytical module. Alternatively, the sample can be cryopreserved and analyzed later.

### 4.5 Intermediate summary

The culture unit described in this chapter together with the analytical module and the control unit presents a new tool for cell culturing with high degree of automation and system integration. The possibility of automated medium change while keeping the
fluidic system closed minimizes risk of cell culture contamination. The prototype of the culture unit shows Figure 4.7. The evaluation of this culturing system will be described in the following chapters.


Figure 4.7 The culture unit prototype

## 5 Evaluation of the prototype system

### 5.1 Introduction

This chapter describes initial testing of the culturing and analytical system after the hardware and software development has been finished as described in the previous two chapters. First the basic functionality of the fluidic components was verified. Next the flow rates were optimized for the culturing part and the analytical part. The measurement of standard curves for ELISA protocols was performed to confirm the assay validity after its adaptation to the flow-through topology. During this testing phase some problems were discovered, which required some design changes and protocol optimizations. Those changes are discussed in detail in the following chapter.

### 5.2 Fluidics evaluation

The initial fluidic testing of the analyzer unit was performed with water as the working fluid. The complete flow-through ELISA sequence was executed and the proper function of active fluidic components (peristaltic pumps and solenoid valves) was visually inspected. No leaks were detected. Furthermore, the pumping speed was optimized. It is desirable to use the highest possible pumping speed to shorten the assay time. The upper limit of the pumping speed is $2000 \mu 1 / \mathrm{min}$ (software limitation). However, pumping speeds above $500 \mu 1 / \mathrm{min}$ caused significant increases in the liquid pressure, which together with the tubing elasticity caused inconsistency in the pumped volume. Experimental testing showed that it is necessary to keep the pumping speed bellow 500 $\mu 1 / \mathrm{min}$ in order to maintain the pumped volume accuracy. The pumping speed needed to be further reduced for pumping liquids to the capillaries to prevent the desorption of antibodies and to not affect the assay accuracy. Pumping volumes were determined according to dead volume of the respective fluidic paths and increased by $15-25 \%$ to compensate for priming phase and peristaltic tubing wearing. The satisfactory pumping parameters for various assay fluidic operations are listed in the Table 5.1.

Similarly, the fluidic system of the culture unit was inspected for proper functionality. Since its fluidic system is much simpler compared to the analytical unit and the pumping
speed used for perfusing cell culture are typically in the range of tens of $\mu \mathrm{l} / \mathrm{min}$, no additional optimization of the fluidic network was necessary during the initial testing phase. One minor problem however, was occasionally observed. The MatriGrid ${ }^{\circledR}$ mounting in the Bioreactor proved to be critical. If the MatriGrid® was nor perfectly aligned with its support, the O-rings sealing of the bioreactor was leaky and the loop circulation in this case failed.

Table 5.1 Optimized fluidic parameters for flow-through ELISA assay

|  | Fluidic operation | Pumped volume <br> $[\mu \mathrm{l}]$ | Pumping speed <br> $[\mu \mathrm{l} / \mathrm{min}]$ |
| :---: | :--- | :---: | :---: |
| 1 | Filling manifolds with a reagent | 300 | 350 |
| 2 | Filling capillary with a reagent | 50 | 100 |
| 3 | Filling manifolds with washing buffer | 500 | 350 |
| 4 | Filling capillary with washing buffer | 50 | 100 |
| 5 | Filling manifolds with a sample | 300 | 350 |
| 6 | Filling capillary with a sample | 50 | 100 |
| 7 | Removing reagent or sample from manifolds | 350 | 350 |
| 8 | Removing sample from sample manifold | 50 | 100 |
| 9 | Removing reagent from reagent manifold | 50 | 100 |
| 10 | Washing after sample | 500 | 350 |
| 11 | Washing reagent manifold | 50 | 350 |

### 5.3 Readout system evaluation

Functionality of the fluorimeter as the readout subsystem was evaluated first by measuring the noise level in the dark. The transfer curve - the dependence of measured fluorescence on the resorufin concentration was measured and the limit of detection was determined. The fluorimeter was also tested in cooperation with the sample changer to evaluate the "autofocusing" algorithm for proper sample alignment.

The fluorescence measurement sequence begins with the ADC sampling in the dark, i.e. with the excitation laser turned off. This ADC reading includes the transconductance amplifier offset and it is used as a baseline for the final fluorescence calculation. Those dark ADC readings can be also used for the fluorimeter electrical noise evaluation. The dark ADC readings obtained during the 48 florescence measurements of the resorufin standards were used to estimate the noise level. Out of the 48 readings, the ADC generated the output number 32828-21 times and the number 3282927 times. No other codes were
generated. Obviously, the peak-to-peak noise is 1 LSB and the design goal in the terms of noise performance was met.

Because the transconductance amplifier transfer function has a negative slope, the actual fluorescence reading is calculated by subtracting the measured value from the dark (baseline) value. This way the fluorescence reading is proportional to the fluorophore concentration and blank solution provide the reading of 0 . The sensitivity of the fluorimeter was evaluated by measuring a series of concentration standards of resorufin sodium salt (R3257-5G, Sigma Aldrich). The measured dependence is shown on the Figure 5.1.


Figure 5.1 Dependence of the fluorimeter reading on the resorufin concentration. Blank, 10nM and $\mathbf{2 0 n M}$ solution of resorufin was not detected (reading of 0 ). Lower limit of detection is 50 nM of resorufin.

It can be seen that blank solutions resulted in consistent zero readings. This proves we had the appropriate optical filter selection, because no excitation light caused false readings. The resorufin concentration of 10 nM and 20 nM was too low and was not detected by the fluorimeter. The lower limit of detection was found to be 50 nM of
resorufin. This limit is more than adequate for adapted assay, as will be shown later by measuring the standard curve.

The fluorimeter was designed to work together with the rotary sample changer. The rotary sample changer is formed by a double disk and contains eight capillaries equally spaced around its circumference. The implemented algorithm eliminates problems with the sample alignment with the focal line of the fluorimeter. During the actual measurement the capillary is positioned at some angular distance before the focal line. The sample changer then rotates through the focal line while continuously measuring the fluorescence. The extent of rotation is adjustable, but the value of 100 microsteps was found to be satisfactory. The sample changer stepper motor is configured to make 6400 microsteps per one revolution, so 100 microsteps corresponds to the angle of $5.625^{\circ}$. The Figure 5.2 shows the fluorescence dependence on the angular distance (number of microsteps) for $10 \mu \mathrm{M}$ resorufin solution. It can be seen that the area near the maximum is relatively flat, implying that the fluorescence is not very sensitive to the angular position.


Figure 5.2 Dependence of the fluorescence on the capillary angular position during the sample holder rotation. The $x$-axis span shown ( 100 microsteps) corresponds to angular distance $5.625^{\circ}$. The capillary was filled with $10 \mu \mathrm{M}$ resorufin solution.

### 5.4 Albumin assay evaluation

To fully evaluate the analyzer functionality, complete human albumin assay was run on the analyzer module as described in the Chapter 7. A series of human albumin solutions with known concentration was used to measure the standard curve. The actual concentrations were selected according to quantitation kit manufacturer recommendations (Bethyl, E80-129): 0, 6.25, 12.5, 25, 50, 100 and $200 \mathrm{ng} / \mathrm{ml}$ of albumin. According to used QuantaRed ${ }^{\text {TM }}$ substrate manufacturer instructions (15159, Thermo Fisher Scientific), the enzymatic color reaction needs to be stopped using the stop solution, following the fluorescence measurement in the MTP reader. In contrast to that, in a flow-through protocol there is no need to use the stop solution, because the fluorimeter creates an integral part of the analyzer and the fluorescence of each capillary is measured after exactly the same incubation time. This way, no manipulation with the capillaries is required and all related errors are thus eliminated. Moreover, this approach allows fluorescence measurement in multiple time points which allows internal quality control and the measurement of reaction kinetics, if required. For this reason, all fluorescence data measured by the analyzer module was taken for at least three time points. Table 5.2 shows the fluorescence data for the standard curve test. The measurement at three substrate incubation times: $370 \mathrm{~s}, 740 \mathrm{~s}$ and 1110 s .

Table 5.2 Standard curve test - measured fluorescence

| Albumin conc. [ng/ml] | Fluorescence [arb. units] |  |  |
| :---: | :---: | :---: | :---: |
|  | 370s | 740s | 1110s |
| 0 | 172 | 281 | 401 |
| 6.25 | 363 | 642 | 849 |
| 12.5 | 492 | 881 | 1318 |
| 25 | 1013 | 1863 | 2593 |
| 50 | 1529 | 2649 | 3890 |
| 100 | 2923 | 4846 | 6926 |
| 200 | 3463 | 5722 | 8154 |

The shape of dose-dependent curves of the sandwich immunological assay has sigmoidal shape [38] and the four-parameter logistic model is considered the most suitable for nonlinear regression of such assays [39]. The four-parameter model is based on the following equation:

$$
\begin{equation*}
y=d+\frac{a-d}{1+\left(\frac{x}{c}\right)^{b}} \tag{5.1}
\end{equation*}
$$

The parameters $a, b, c$ and $d$ have following meaning:
$a$ - corresponds to response ( $y$ ) at zero analyte concentration ( $x$ )
$b$ - represents the slope of the sigmoid curve
$c$ - represents the sigmoid curve inflexion point
$d$ - represents expected response $(y)$ for infinitely high analyte concentration $(x)$

The equation x is typically solved numerically using various iterative algorithms (e.g. Gauss-Newton algorithm), to find model parameters for a given concentrations and measured fluorescence [38]. Initial parameter setting is needed as starting point, and following procedure was used for this purpose:
$a$ - use the minimal value of the response $y$
$b$ - use the slope defined by minimal and maximal response $y$
$c$ - use the response value $y$ which is closest to the middle point between minimum and maximum
$d$ - use the maximal value of the response $y$

The regression algorithm uses residual sum of squares (RSS) as the assessment criteria for the quality of curve fit. The RSS is calculated according the following equation:

$$
\begin{equation*}
R S S=\sum_{i=1}^{l} w_{i}\left[Y_{i}-\left(Y_{c}\right)_{i}\right]^{2} \tag{5.2}
\end{equation*}
$$

Where $Y$ is the observed response and $Y_{c}$ is calculated response. The $w_{i}$ is weighting factor for $i$-th data point. The use of weighting factor greatly improves the accuracy of curve fit, because the error tends to be proportional to the signal (Y) magnitude [40, 41].

The curve fitting in the frame of this work was done using an automated MS Excel sheet [42], which implements weighted logistic model and Solver add-in tool to calculate model parameters. The estimated model parameters for the standard curve measurement contained in Table 5.2 are shown in the Table 5.3, and corresponding curves are shown in Figure 5.3.

Table 5.3 Estimated model parameters for standard curve for three different incubation times

|  | 370s | 740s | 1110s |
| :---: | ---: | ---: | ---: |
| $\mathbf{a}$ | 4789 | 7824.23 | 10726.3 |
| $\mathbf{b}$ | -1.26769 | -1.21539 | -1.25709 |
| $\mathbf{c}$ | 89.07887 | 84.08654 | 76.5626 |
| $\mathbf{d}$ | 176.9873 | 286.172 | 404.1411 |
| $\mathbf{R}^{\mathbf{2}}$ | 0.9959 | 0.9965 | 0.9978 |

Once the model parameters are known; any sample analyte concentration $X$ can be calculated from the corresponding fluorescence $Y$ using the following equation:

$$
\begin{equation*}
X=c\left(\frac{a-d}{Y-d}-1\right)^{\frac{1}{b}} \tag{5.3}
\end{equation*}
$$



Figure 5.3 Standard curve fitting of data shown in Table 5.2. Quality of fit: $\mathbf{R}^{\mathbf{2}=0.9959 \text { for } \mathbf{3 7 0 s}, ~}$


The measured standard curve shown on Figure 5.3 confirm that the analyzer unit is functional and the adaptation of standard MTP based ELISA protocol was successfully modified to a flow-through version. However, the fluorescence data is not ideal. The recorded fluorescence for blank standard is approximately 10x higher than expected. This
high background signal decreases overall dynamic range of the assay and indicates problems with contamination of fluidic paths or insufficient cleaning procedure. To find the concrete source of the problem, additional testing was necessary, which is described in the following chapter.

### 5.5 Intermediate summary

The initial hardware and software testing of the whole system described in this chapter successfully verified basic functionality of the whole culturing and analytical system and proves its suitability for intended purpose - that is an automated cell culturing and automated cell culture analysis utilizing the sandwich ELISA assay. During this testing phase, minor problems were identified. By solving those problems, the accuracy and dynamic range of the immunoassay could be increased on the side of analytical module, as well as the manipulation reliability on the side of culturing unit.

## 6 Optimizing the performance of analytical module

### 6.1 Introduction

This chapter describes the analyzer unit modifications to solve some assay accuracy problems as described in the previous chapter. The analyzer performance after those modifications made the measurement of standard curves in low concentration ranges possible, allowing the measurement of values lower than recommended by the substrate kit manufacturer. The accuracy of the assay was verified by comparing with standard microtiter plate assay and the results are presented.

### 6.2 Analyzer unit cleaning procedure

Cleaning of all the fluidic pathways before the start of new assays is of critical importance. A proper cleaning procedure removes all chemically active residuals which remain after the previous assay, such as the adsorbed proteins on the tubing and manifold walls. The extent of removal must be sufficient to not influence or distort the results of the following assay. The assay interference caused by insufficient cleaning can be observed as increased background fluorescence or the incoherent standard curve.

The initial cleaning procedure involved the emptying of all fluidic paths and washing it with $70 \%$ ethanol, followed by washing with deionized (DI) water. Although it is known that $70 \%$ ethanol denatures proteins and it is an efficient disinfectant, this cleaning procedure did not provide a satisfactory result. The background fluorescence was significantly higher after each assay, which indicated insufficient desorption and / or denaturation of proteins. The cleaning procedure was therefore extended, and as the first step a desorption solution of the following composition was used: $70 \%$ ethanol, $2 \%$ citric acid and $0.5 \%$ sodium dodecyl sulfate (SDS). In the second step, washing with $70 \%$ ethanol was used, followed by final washing with DI water. All three components of the desorption solution cause protein denaturation by various mechanisms. The ethanol disrupts the hydrophobic interactions of the protein core, the citric acid at concentration of 100 mM lowers pH to approximately 2 , which causes negative charge neutralization of the protein amino acid residues. SDS is a well-known detergent and causes protein
unfolding by binding of the SDS hydrophobic part to the protein amino acids [43]. Moreover, disrupting hydrophobic interaction between the protein and fluidic channel surface helps to desorb and remove the proteins. The use of above described three stage cleaning procedure proved to be satisfactory and allows running multiple assays without replacing the C-Flex ${ }^{\mathrm{TM}}$ tubing. The only part required to be replaced for each assay run are the capillaries which are considered to be critical component, because they serve as the assay's solid phase. The cleaning procedure is automated and it is part of the control unit firmware.

### 6.2.1 Extension of the cleaning procedure

During later tests using the optimized FEP manifolds it was found that occasionally, those manifolds become clogged by precipitated proteins. The cleaning procedure was therefore extended for additional washing by 1 M sodium hydroxide solution. It is known that proteins, including BSA, can be desorbed and solubilized by NaOH at high pH values [44, 45]. All used fluidic component materials are chemically compatible with 1 M NaOH solution: PharMed ${ }^{\text {TM }}$, C-Flex ${ }^{\text {TM }}$, PVC, FEP and PEEK. The sodium hydroxide washing was selected as the first step in the cleaning sequence to dissolve and remove most of the proteins, which prevents formation of the protein precipitates in the following steps. The citric acid in the second cleaning step helps to neutralize rests of the alkaline solution trapped in the fluidic network. At the end of the last cleaning step (DI water), a pH measurement confirmed the neutral reaction of the effluent. The final version of the cleaning procedure is listed in the Table 6.1.

Table 6.1 The final cleaning sequence of the analyzer fluidic network

| Cleaning <br> sequence <br> step | Description |
| :---: | :--- |
| 1 | Empty the fluidic network |
| 2 | Wash the network with 1M NaOH solution |
| 3 | Empty the fluidic network |
| 4 | Wash the network with desorption solution |
| 5 | Empty the fluidic network |
| 6 | Wash the network with 70\% Ethanol |
| 7 | Empty the fluidic network |
| 8 | Wash the network with DI water |
| 9 | Empty the fluidic network |

### 6.3 The cause of decreased assay performance

Looking at the fluorescence data listed in the Table 5.2, two problems can be identified: the relatively high background fluorescence of the blank standard, and additionally slightly decreased accuracy which can be seen on the Figure 5.3, where the measured points do not coincide closely with the standard curve (i.e. it was not possible to make curve fittings with a smaller error). This may be caused by several reasons, such as improper washing, instability of the substrate, contamination of the substrate by secondary antibody or various assay protocol problems. To diagnose the origin of this inaccuracy, a series of tests were conducted and evaluated.

The stability of the substrate was tested for stability as the first step. The substrate mix consists of the non-fluorescent ADHP dye, the enhancer and stabilized hydrogen peroxide solution. This mix should be used within 30 minutes according the manufacturer instructions. The presence of traces of HRP enzyme or possibly other interfering compounds may result in resorufin dye development. The flow-through ELISA sequence was used for this test as described in the Chapter 3.2.4 with one modification: it was started from the step 13 (Introducing the substrate to the capillaries). Also, new capillaries were used for this test and the whole fluidic system was washed using previously described three-step cleaning procedure. Recorded fluorescence is shown in the Table 6.2. Ideally, fluorescence values of zero or close to zero should be recorded for all 7 channels. It can be seen that the fluorescence after 5 minutes is zero for all channels except the channels 3 and 7, where minimal fluorescence was recorded.

Table 6.2 Substrate stability test - measured fluorescence

| Channel | Fluorescence [arb. units] |  |  |
| :---: | :---: | :---: | :---: |
|  | $\mathbf{5} \mathbf{~ m i n}$ | $\mathbf{1 0} \mathbf{~ m i n}$ | $\mathbf{1 5} \mathbf{~ m i n}$ |
| 1 | 0 | 10 | 15 |
| 2 | 0 | 9 | 15 |
| 3 | 5 | 13 | 18 |
| 4 | 0 | 9 | 14 |
| 5 | 0 | 3 | 6 |
| 6 | 0 | 12 | 16 |
| 7 | 4 | 9 | 10 |

The fluorescence in all channels slowly increased with time and after 15 minutes the fluorescence remained below 18 units. Those values are more than 20 times lower than the values for channel 0 (blank) listed in the Table 5.2. It may be therefore assumed that the substrate is sufficiently stable and does not contribute to problems with assay accuracy.

Logically, the next test should involve the conjugated secondary antibody. This test was aimed to evaluate substrate contamination by the conjugated antibody. Ideally, the conjugated antibody is pumped to all capillaries, followed by a washing step using the washing buffer and finally the substrate solution will be pumped to the capillaries. If the fluidic system will be completely washed of the conjugated antibody, the fluorescence reading should stay close to the levels listed in Table 6.2. The whole fluidic system must be previously blocked by BSA blocking buffer, to prevent non-specific binding of conjugate antibody to the surface of capillaries and fluidic pathways. Again, an incomplete flow-through ELISA sequence was used for this test, starting from the step 4 (pumping the BSA blocking buffer to the capillaries). The blocking incubation time was extended to 1 hour to allow for sufficient surface blocking. The steps 7,8 and 9 were skipped as no standards were using in this test and the sequence continued by the step 10 (pumping the conjugate antibody to the system). The fluorescence levels measured in the last step (14) are listed in the Table 6.3.

Table 6.3 Conjugated antibody contamination test - fluorescence data

| Channel | Fluorescence [arb. units] |  |  |
| :---: | :---: | :---: | :---: |
|  | $\mathbf{5} \mathbf{~ m i n}$ | $\mathbf{1 0} \mathbf{~ m i n}$ | $\mathbf{1 5} \mathbf{~ m i n}$ |
| 1 | 467 | 928 | 1365 |
| 2 | 426 | 708 | 1085 |
| 3 | 432 | 834 | 1125 |
| 4 | 400 | 770 | 1055 |
| 5 | 265 | 490 | 666 |
| 6 | 349 | 685 | 949 |
| 7 | 325 | 558 | 798 |

The result of the test shows high fluorescence values, implying substrate contamination by the enzyme conjugated antibody. However, it is not clear whether this contamination originates from cross-contamination of fluidic pathways or there might be some conjugated antibody adsorbed on the capillary walls caused by possible insufficient
blocking. To investigate this possibility, the test was repeated with one important modification: at the end of step 13, when the conjugate antibody was pumped to the capillaries and washed afterwards, all capillaries were replaced for new ones and the sequence then continued with the step 14 (pumping the substrate). This way, it was guaranteed that no conjugated antibody was present in new capillaries and eventual substrate color reaction must be inevitably caused by conjugated antibody remained in the fluidic system. The fluorescence data as the result of this experiment is presented in the Table 6.4.

Table 6.4 Conjugated antibody contamination test with replaced capillaries - fluorescence data

| Channel | Fluorescence [arb. units] |  |  |
| :---: | :---: | :---: | :---: |
|  | $\mathbf{5} \mathbf{~ m i n}$ | $\mathbf{1 0} \mathbf{~ m i n}$ | $\mathbf{1 5} \mathbf{~ m i n}$ |
| 1 | 84 | 158 | 234 |
| 2 | 155 | 259 | 351 |
| 3 | 225 | 441 | 651 |
| 4 | 164 | 258 | 390 |
| 5 | 394 | 717 | 945 |
| 6 | 494 | 955 | 1291 |
| 7 | 25 | 39 | 47 |

Comparing the fluorescence data with the previous test it can be concluded that the contamination was reduced but not significantly. Moreover, the fluorescence between the channels differs significantly! This fact implies various degree of contamination for various channels. This cannot be attributed to improper washing directly, because the washing cycle in the step 12 is repeated 3 times with exactly same pumping volumes and timing for all capillaries. It is obvious that, despite intense washing cycle, traces of conjugate antibody solution remain in the fluidic system. Logically, the most probable place in the fluidic system where the washing could be problematic are the places with highest topologic complexity, more specific - the manifolds. The analyzer unit used during those tests the commercial 9-port manifolds with the "star" topology (P-191, IDEX Health \& Science, Figure 6.1 - left).

It is difficult to prevent the contamination of adjacent channels in the star joint. A small portion of solution always diffuses to all channels connected to the center point. Also, the washing procedure sequenced as switching of one arm only at same time, will not result in perfect cleaning for the same reason.


Figure 6.1 The 9-port manifold with "star" fluidic topology (left), and its internal fluidic channels (right)

This idea led to change of the manifold topology, which would allow more efficient reagent separation and cleaning. The topology of nine port manifold was therefore changed from the star configuration to series of 7 "tee" joints. This way, no joint has more than three branches: one inlet, one outlet and one side arm. Also, the problem with diffusion will be limited to one side arm, and the sequencing algorithm can easily correct this effect. The Figure 6.2 shows redesigned 9-port manifold.


Figure 6.2 The fluidic topology of 9-port manifold composed from series of " $T$ " joints

Three out of four manifolds were replaced with the new version (see Figure 3.4): the sample manifold, the reagent manifold and the capillary manifold. Only the waste manifold was kept unchanged, because it is located in the waste stream and is therefore
irrelevant for the assay accuracy. New manifolds were built by hot-air welding of pieces of FEP tubing (VICI JR-T-6802, $1 / 16$ " $\times 0.5 \mathrm{~mm}$ ). The capillary manifold is located at the top of the circular sample changer and it is therefore required to have a circular shape. A dedicated manifold holder was therefore manufactured to support the FEP tubing (see Figure 6.3).


Figure 6.3 The circular holder of the capillary manifold (left), and corresponding FEP tubing manifold (right)

After the manifolds replacement, the analyzer was tested with full sequence to evaluate possible improvements in the background fluorescence and cross-channel contamination. The result of the are listed in the Table 6.5.

Table 6.5 Full sequence test with redesigned manifolds - fluorescence data

| Albumin <br> conc. <br> [ng/ml] | Fluorescence [arb. units] |  |  |
| ---: | ---: | ---: | ---: |
|  | $\mathbf{7} \mathbf{~ m i n}$ | $\mathbf{1 4} \mathbf{~ m i n}$ | $\mathbf{2 1} \mathbf{~ m i n}$ |
| 0 | 61 | 104 | 150 |
| 6.25 | 172 | 319 | 474 |
| 12.5 | 405 | 773 | 1126 |
| 25 | 828 | 1573 | 2211 |
| 50 | 2000 | 3689 | 5135 |
| 100 | 4922 | 8370 | 9903 |
| 200 | 6148 | 9903 | 9903 |

The fluorescence data of the assay test after the replacement of the manifolds show significant improvement in the background fluorescence for blank standards. Additionally, the florescence values for monotonically increasing albumin concentrations in standards are also monotonically increasing in uniform steps, which is presumably caused by reduced cross-channel contamination. The fluorescence values of 9903 units
for the high albumin concentrations and longer times ( 14 min and 21 min ) represents the maximum readout value under the fluorimeter amplifier saturation. This value is not constant for every assay and may slightly vary, depending on the offset calibration, which is performed at the beginning of each fluorimeter operation.

### 6.4 Standard curve measurement in low concentration range

According to Human Albumin Quantitation Set (Bethyl, E80-129) manufacturer instructions, recommended standard concentrations cover the albumin concentration range from $6.25 \mathrm{ng} / \mathrm{ml}$ to $400 \mathrm{ng} / \mathrm{ml}$. Given the improved analyzer performance with optimized manifolds and improved cleaning procedure, a trial test was conducted to investigate the analyzer performance with the albumin concentrations below $6.25 \mathrm{ng} / \mathrm{ml}$. Result of this test represents the standard curve in low albumin concentration range and corresponding fluorescence data are listed in the Table 6.6, the 4-parameter logistic model fit parameters are listed in the Table 6.7, and the standard curve is plotted on the Figure 6.4.

Table 6.6 Fluorescence data of standard curve in low albumin concentration range.

| Albumin <br> conc. <br> [ng/ml] | Fluorescence [arb. units] |  |  |
| ---: | ---: | ---: | ---: |
|  | 7 min | $\mathbf{1 4} \mathbf{~ m i n}$ | $\mathbf{2 1} \mathbf{~ m i n}$ |
| 0 | 40 | 60 | 60 |
| 0.78 | 43 | 64 | 84 |
| 1.5 | 51 | 85 | 121 |
| 3.13 | 90 | 164 | 234 |
| 6.25 | 172 | 295 | 425 |
| 12.5 | 414 | 788 | 1141 |
| 25 | 906 | 1677 | 2523 |

Table 6.7 Estimated model parameters for standard curve in low concentration range

|  | $\mathbf{~ m i n}$ | $\mathbf{1 4} \mathbf{~ m i n}$ | $\mathbf{~ m i n}$ |
| :---: | ---: | ---: | ---: |
| $\mathbf{a}$ | 2360.463 | 4427.98 | 19753.53 |
| $\mathbf{b}$ | -1.62841 | -1.61524 | -1.39027 |
| $\mathbf{c}$ | 34.35895 | 34.56781 | 100.74 |
| $\mathbf{d}$ | 38.7509 | 57.90703 | 60.86779 |
| $\mathbf{R}^{\mathbf{2}}$ | 0.995 | 0.9959 | 0.9973 |



Figure 6.4 Measured standard curve in the low albumin concentration range.

The background fluorescence value was 40 units after 7 minutes, which is completely acceptable. Table 6.6 also shows that even the albumin concentration as low as $0.78 \mathrm{ng} / \mathrm{ml}$ can be clearly distinguished from the background and it is above the detection limit. For such low albumin concentration, longer substrate incubation times provide steeper curves, as can be seen on Figure 6.4. The measured points coincide more closely with the standard curve, compared to situation on Figure 5.3, despite the albumin concentration levels are 8 x lower.

### 6.5 Accuracy verification of the flow-through ELISA

The final verification step of the analyzer functional assessment is the comparison of an albumin standard measurement by the analyzer unit utilizing the flow-through protocol, with the measurements of the same standard by standard laboratory ELISA protocols. Two albumin solutions with concentration of $9 \mathrm{ng} / \mathrm{ml}$ and $18 \mathrm{ng} / \mathrm{ml}$ were prepared and
used for testing by both protocols. Both solutions were measured as triplicates, allowing the evaluation of measurement error. Both protocols used same human albumin quantitation set (Bethyl, E80-129), but different substrates. The QuantaRed ${ }^{\text {TM }}$ Enhanced Chemifluorescent substrate (15159, Thermo Fisher Scientific) was used for flow-through ELISA, while the TMB substrate was used for the MTP ELISA (Immunochemistry Technologies, \#6275). The Spectramax ${ }^{\circledR}$ M5 reader was used to measure samples optical density when using the MTP ELISA. The substrate incubation time for flow-through ELISA was 7 minutes. The comparison of the measured albumin levels is shown on Figure 6.5 and the statistical assessment of the measurement error is listed in Table 6.8.


Figure 6.5 Comparison of albumin measurement with two different ELISA protocols. The error bars represent the standard error of mean (SEM)

According to current regulatory guidelines from the U.S. Food and Drug Administration (FDA) and the European Medicines Agency (EMA), a validated assay to quantify the antibody should demonstrate an accuracy with $\pm 20 \%$ of the known antibody concentration and precision of less than $20 \%$ coefficient of variance [40]. The results in the Table 6.8 shows that the accuracy of the analyzer unit implementing the optimized flow-through ELISA protocol is significantly better than the required $20 \%$. The MTP ELISA protocols provided slightly lower results then the flow-through protocol (11.88\% lower result for $9 \mathrm{ng} / \mathrm{ml}$ standard and $6.35 \%$ lower result for $18 \mathrm{ng} / \mathrm{ml}$ standard). There
may be various reasons for that, such as variation of surrounding temperature, or the use of different substrate and different readout method (colorimetric vs. fluorimetric). Diagnosing the source of this error is beyond the scope of this work and it was not carried out.

Table 6.8 Statistical evaluation of measurement accuracy for both ELISA protocols.

| Flow - through ELISA |  |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: |
| Albumin standard [ng/ml] | Measured values [ng/ml] | Mean value [ng/ml] | Standard deviation [ng/ml] | Measurement error [\%] | Coefficient of variation [\%] |
| 9 | 9.60 | 9.34 | 0.29 | 3.73 | 3.07 |
|  | 9.03 |  |  |  |  |
|  | 9.38 |  |  |  |  |
| 18 | 16.11 | 16.99 | 0.82 | -5.59 | 4.85 |
|  | 17.13 |  |  |  |  |
|  | 17.74 |  |  |  |  |
| MTP ELISA |  |  |  |  |  |
| Albumin standard [ng/ml] | Measured values [ng/ml] | Mean value [ng/ml] | Standard deviation [ng/ml] | Measurement error [\%] | Coefficient of variation [\%] |
| 9 | 7.93 | 8.23 | 0.26 | -8.60 | 3.18 |
|  | 8.42 |  |  |  |  |
|  | 8.34 |  |  |  |  |
| 18 | 15.81 | 15.91 | 0.26 | -11.59 | 1.65 |
|  | 15.72 |  |  |  |  |
|  | 16.21 |  |  |  |  |

### 6.6 Intermediate summary

The issues identified and described in the Chapter $\mathbf{5}$ served as a starting point for the analyzer unit improvement. Two key modifications - the redesign of the manifolds and improvement of the cleaning procedure leaded to desired level of assay accuracy, as was confirmed at the end of this chapter. The ability of standard curve measurement at concentration levels $8 x$ below the recommended level was demonstrated. Additionally, the assay accuracy was compared to standard MTP ELISA protocol and it was confirmed that it fulfills recent international standards for validation of antibody quantitation assays. At this point, the analyzer unit is considered fully functional and ready to be used in connection with cell culturing units for on-line albumin level measurement in cell culture medium.

## 7 Evaluation of the prototype system

### 7.1 Introduction

The applicability of the automated compact device in online-kinetics measurement of albumin secretion was verified as a proof-of-concept using 3D HepaRG cultures perfused with acetaminophen (APAP) over a period of 96 h . This chapter demonstrates how this integrated in vitro system can be used for drug toxicity tests and show the potential for adaptation of online-monitoring to measure other secreted proteins, such as hormones and signaling molecules from 3D mono- and co-cultures. The APAP toxicity is discussed first, followed by the experimental part in which the APAP induced $\mathrm{EC}_{50}$ values were determined for HepaRG cell culture in various formats. To provide additional evidence of APAP metabolism in cell culture, the APAP consumption was measured by HPLC methods. Albumin measurements in the perfused 3D HepaRG culture with and without APAP supplemented medium using the integrated culturing and analytical system are described and the results are compared with conventional MTP ELISA.

### 7.2 APAP toxicity in 2D and 3D hepatocyte cultures

APAP is a well-known representative method for dose-related intrinsic liver toxicity [46, 47], making it an ideal test compound to use in these proof-of-concept studies. While predominantly phase II reactions account for the major metabolites of APAP, namely the APAP-sulfonate and APAP-glucuronide conjugates, toxic doses of APAP result in reactive metabolite formation ( N -acetyl-p-benzoquinoneimine (NAPQI), Figure 7.1) via phase I enzymes, namely CYP3A4, CYP1A2 and CYP2E1 [48-50]. At lower concentrations, NAPQI is detoxified by reduced glutathione (GSH) but once GSH is depleted, NAPQI covalently binds to cellular proteins, e.g. from mitochondria [50-52]. The resulting mitochondrial dysfunction leads to a number of forms of toxicity which initiate pathways ultimately leading to acute liver failure (ALF) [53]. These pathways include the impairment of hepatocyte mitochondrial respiration, ATP depletion and formation of reactive oxygen species ([54-56] (such as NO and superoxides resulting from mitochondrial permeability transition (MPT) [57]).


Figure 7.1 Metabolic conversion of acetaminophen (APAP) to toxic $\mathbf{N}$-acetyl-p-benzoquinoneimine (NAPQI)

For individual experiments, HepaRG cells (BIOPREDIC International, Saint Grégoire) were seeded at a density of 50.000 cells per well either in collagen pre-coated ( $5 \mu \mathrm{~g} / \mathrm{cm}^{2}$ ) 24 -well plates (monolayer) or collagen pre-coated scaffolds (3D organotypic cell culture) in 24-well plates. Cells were seeded in the scaffolds in a small volume ( $25 \mu \mathrm{l}$ ) to ensure selective growth in the microcavities. Subsequently, cells were allowed to adhere for 2 h before adding the remaining culture medium into the wells. After seeding, cells were cultured for 2 weeks in the maintenance medium in a cell incubator at $37^{\circ} \mathrm{C}, 95 \%$ relative humidity and $5 \% \mathrm{CO}_{2}$. Thereafter, cells were either cultured in the maintenance medium for another 2 weeks or shifted to a differentiation medium on day 14 (supplemented with $1 \%$ DMSO). For perfused 3D cell cultures, the MatriGrid ${ }^{\circledR}$ scaffolds were inserted in the supporting bioreactor and mounted on the culturing unit of the automated system. The culture medium was renewed every 2 days in all experiments.

APAP toxicity was measured by the determination of metabolic activity and albumin secretion. Metabolic activity of HepaRG cells was analyzed using the commercially available Alamar Blue ${ }^{\circledR}$ kit (BIO-RAD, BUF012A). Albumin levels in the culture supernatants were analyzed using the Albumin-ELISA Quantitation kit (Bethyl, E80-129) with TMB substrate (Immunochemistry Technologies, \#6275). After 4 weeks of differentiation, HepaRG cells grown either in monolayer or scaffolds were incubated with increasing concentrations of $\operatorname{APAP}(0,1,5,10,15,20,40,80 \mathrm{mM})$ in Williams medium $\mathrm{E}(\mathrm{WME})+0.1 \% \mathrm{FBS}$ in wells or in perfused micro-bioreactors for 24 h . Cells grown in monolayer culture (2D) or in scaffolds (3D) were treated with trypsin to return cells to suspension and the total cell number was determined. After centrifugation for 5 min at 515 g cells were incubated with resazurin for 2 h at $37^{\circ} \mathrm{C}$ in the incubator. The
fluorescence of the metabolite, resorufin, was measured at 560 nm excitation and 590 nm emission with a Spectramax ${ }^{\circledR}$ M5 microplate reader. Albumin levels were measured in the culture supernatants according to kit manufacturer instructions. The absorbance of the TMB oxidation product was measured by Spectramax ${ }^{\circledR}$ M5 microplate reader at 450 nm . Metabolic activity and albumin level values were normalized to the total cell number (per million cells), and values of APAP-treated samples were normalized against the control values (i.e. without APAP), which was set to $100 \%$.

To assess whether the culture format affects APAP-induced toxicity and the effect of APAP on secretion of hepatic albumin, DMSO differentiated HepaRG cells grown under 2 D and static (i.e., not perfused) 3D conditions were treated with increasing concentrations of APAP either statically (2D, 3D) or under perfusion (bioreactor "3D BR"). After 24 h of incubation, the concentration dependent toxicity of APAP was measured using two different readout parameters: resazurin metabolism and albumin secretion. As illustrated in Figure 7.2, 3D static cultures of HepaRG cells were more sensitive to APAP than 2D cultures according to resazurin metabolism ( $\mathrm{EC}_{50}$ 3D: 21.0 $\mathrm{mM}, \mathrm{EC}_{50} 2 \mathrm{D}: 27.1 \mathrm{mM}$ ). This could be due to the more highly differentiated state of the cells under 3D conditions, especially with respect to the presence of the bioactivating CYPs. Continuous perfusion of 3D cultures in a bioreactor ("3D BR") significantly enhanced the sensitivity of HepaRG cells to APAP, with an EC50 value of 9.7 mM , which is due to the increased accessibility of the hepatocytes for the drug.


Figure 7.2 Effect of APAP on resazurin metabolism (left) and albumin secretion (right) in HepaRG cells cultured under different conditions. The fluorescence of resorufin, the product of the resazurin assay, was measured with a SpectraMax M5 microplate reader. Each experiment was replicated 3 times ( $\mathrm{n}=3$ per concentration, mean $\pm$ SEM).

In comparison to the resazurin assay, inhibition of albumin secretion by APAP occurred at lower concentrations of APAP. The lowest concentration of APAP that inhibited albumin synthesis was detected in perfused 3D cultures ( $\mathrm{EC}_{50} 3 \mathrm{D}$ perfused: 2.8 mM ). The $\mathrm{EC}_{50}$ value for statically cultured 3D cultures was 3.9 mM , while 2D cultures were the least sensitive to albumin inhibition by APAP ( $\mathrm{EC}_{50} 2 \mathrm{D}: 7.0 \mathrm{mM}$ ). The results are consistent with those of others and show that in addition to the impairment of mitochondrial function, the secretion of albumin is also affected by APAP [15, 58-60].

To investigate whether the higher sensitivity of 3D HepaRG cultures to APAP are due to an increased metabolism of APAP (to NAPQI), we measured APAP consumption during the incubations. Differentiated 2D and 3D HepaRG cells were incubated with 20 mM APAP in Williams medium E with $0.1 \%$ FBS for 1 h in wells or under perfusion in the micro bioreactor. After incubation, culture supernatant was immediately frozen at $-80^{\circ} \mathrm{C}$ and the total cell number was determined. Before analyzing the samples by HPLC, the supernatant was processed by solid phase extraction using Sephadex ${ }^{\circledR}$ G-50, according to the manufacturer's instructions. A volume of $0.5 \mu 1$ sample was injected onto the HPLC system for analysis. The depletion of APAP was calculated by comparing the amount of APAP in each sample using the area under the chromatogram peak with the peak area of 20 mM APAP and normalized to the total number of cells.


Figure 7.3 Consumption of APAP by HepaRG cells cultured in different formats (2D, 3D and 3D BR). The consumption of APAP in the medium was calculated by HPLC analysis before and after culture with the cells. Each experiment was replicated at least 3 times (mean $\pm$ SEM).

In comparison to 2D cultures, APAP consumption was significantly increased in static and perfused 3D cultures (Figure 7.3; 3D vs 2D: 4.8 -fold; 3D BR vs 2D: 5.9 -fold, respectively). These data correlate well with the observed higher toxicity of APAP in static and perfused 3D HepaRG cultures. Based on these results, it can be concluded that 3D cell cultures show enhanced metabolic activity compared to 2D cell cultures, which is in keeping with other reports that 3D cell culture provides an in vivo-like realistic extracellular microenvironment that modulates differentiation and cellular functionality [61]. The extracellular matrix conditions in our MatriGrid® helps to maintain CYP2E1 and CYP3A4 activities, which in turn enhance the metabolism of APAP.

### 7.3 Online flow ELISA with APAP

The influence of APAP on albumin secretion was measured using online flow ELISA and also by conventional MTP, and the results were compared. After 4 weeks of static culturing, differentiated HepaRG cells in scaffolds were inserted into the micro bioreactor either filled with Williams Medium E with $0.1 \%$ FCS, $5 \mu \mathrm{~g} / \mathrm{ml}$ insulin, $5 \times 10^{-5} \mathrm{M}$ hydrocortisone hemisuccinate, 2 mM glutamine, $100 \mathrm{U} / \mathrm{ml}$ penicillin and $100 \mu \mathrm{~g} / \mathrm{ml}$ streptomycin (vehicle) or the same medium supplemented with APAP in a final concentration of 5 mM . Micro bioreactors were mounted on the culturing unit and continuously perfused with aforementioned media using an integrated peristaltic pump using the flowrate of $25 \mu \mathrm{l} / \mathrm{min}$ over 96 h . To measure the initial albumin levels, cells were continuously perfused with control cell culture medium for the first 24 h . After the first automatic medium change and sampling run was completed, the cell culture was supplemented with 5 mM APAP for another 72 h . Automatic medium change and sampling was carried out every 24 h .

Albumin secretion increased in vehicle-treated HepaRG cells over 72 h (by more than $150 \%$ of the initial level, Figure 7.4). By contrast, albumin secretion in APAP-treated HepaRG cells decreased to approx. $50 \%$ of the initial value within the first 24 h and was further decreased to $24 \%$ after 72 h . The $50 \%$ decrease of albumin levels in the first 24 h correlated well with the APAP EC 50 value of 2.8 mM after 24 h incubation with perfused HepaRG cells and measured using MTP ELISA (Figure 7.2, right).


Figure 7.4 Albumin secretion measurement by automated culturing and analysis system with and without administration of 5 mM APAP over the period of 96 h . Values are from at least $\mathbf{3}$ experiments (mean $\pm$ SEM).

The albumin concentrations of the online samples were also measured using traditional MTP ELISA and confirmed the accuracy of the adapted flow-through ELISA (i.e. the values were not significantly different, as can be seen on Figure 7.5).

### 7.4 Intermediate summary

According to both measurements of toxicity, 3D cell cultures were more sensitive to APAP than 2D cultures, which is in line with the findings of others [2, 62]. The use of 3D cell cultures, especially when perfused, are more closely related to in vivo conditions, making them potentially a more relevant model than 2D cultures [2]. The functionality of the automated culturing and analysis device with polycarbonate-scaffold cultured HepaRG organoids was demonstrated. Their excellent hepatofunctional properties can be used with advantage in spheroid culture toxicity assays. The use of this robust 3D cell culturing tool provides advantages of automated medium change, minimal contamination risk, and additional labor-saving benefit especially in long-term experiments.


Figure 7.5 Validation of measured albumin levels by automated system with conventional MTP ELISA. Albumin secretion increased in vehicle-treated HepaRG cells (top) and decreased in APAPtreated HepaRG cells (bottom). Values are from at least 3 experiments (mean $\pm$ SEM).

## 8 Culturing and analytic system extensions

### 8.1 Introduction

The automated system as described in previous chapters was built as a prototype device to verify the automation possibilities of 3D cell culturing with on-demand automated analysis based on ELISA. This functionality was achieved after several design improvements (Chapter 6) and demonstrated by the APAP toxicity evaluation in 3D hepatocyte culture (Chapter 7). However, the development of this system should not stop at this point. This chapter addresses the most important parts of the automated system, which would further improve the assay accuracy, long term culturing reliability or the analysis throughput. Some of those ideas has been realized, but majority serve as the basis for further development of this automated system.

### 8.2 Parallelization of the culturing units

During the experiments described in the previous chapter, it was realized that the possibility of conducting the automated culturing in more than one bioreactor would accelerate the experimental work. In a typical toxicity study, one needs to perform cell culturing in the presence of the active compound as well as in the control culture. In both cases, the culturing should be replicated at least three times to provide statistical relevance. Because the control unit of the automated system does not support more than two culturing units, a way for efficient controlling of six or more culturing unit was needed.

A concept of "the smart driver" was chosen, where each culturing unit would be controlled by a separate driver module. The driver module should be able to directly control the peristaltic pump and solenoid valves of corresponding culturing unit. It should be equipped with suitable microcontroller, programmed to manage the complete functionality of the culturing unit in an autonomous way. This covers the culture perfusion, automated medium change and also medium sampling. This driver should be controlled by a host system via high level commands and it should provide culturing unit status information on demand. Six or more culturing units with corresponding drivers
should be controlled by one common controller module, which would also serve as the user interface (Figure 8.1).

This parallel culturing system was realized as described in the two following subchapters and it was found to be extremely useful for conducting long term cell culturing in multiple bioreactors. The automated medium change significantly reduces the risk of culture contamination and additionally provides labor saving benefit. This second aspect becomes significant in long term experiments requiring operation of six or more bioreactors.


Figure 8.1 Block diagram of parallel operation of multiple culturing units.

### 8.2.1 Driver design for culturing unit

In contrast to the automated culturing and analysis system control unit, where the main objective was universality, the driver was designed with focus on simplicity and covers the culturing unit control requirements with little additional functionality. The driver is based on the 8 -bit ATmega32 microcontroller with more than adequate CPU speed. It provides the following functionality:

- One stepper motor driver with microstepping support
- Eight solenoid valve drivers
- Two galvanically isolated digital inputs
- Two analog inputs
- Asynchronous serial interface (UART)
- $I^{2} \mathrm{C}$ serial interface

The communication between driver units and the controller is accomplished via $\mathrm{I}^{2} \mathrm{C}$ serial interface. It is two-wire bi-directional serial interface with addressing. All drivers are connected to this interface in parallel and each driver must have assigned a unique address. The asynchronous serial interface serves for debugging purposes. The driver PCB was designed as two layers board with dimensions of $100 \times 65 \mathrm{~mm}$. The driver board is placed in aluminum housing and it is physically separated from the culturing unit. The main reason for that is incompatibility of power electronics with humid incubator environment. Figure 8.2 shows the assembled driver board without housing. The driver schematic can be found in the Appendix 6 and the corresponding printed circuit board layout in the Appendix 7.


Figure 8.2 The assembled culturing unit driver module.

Similar to the automated system control unit, the driver code comprises two parts - the bootloader and the driver application, and the source code was written in C programming language. The bootloader simplifies the application upgrade procedure, as no special tool is necessary and the upgrade is made via the UART interface. The recent application version is v 1.1 and it contains more than 2000 lines of code (excluding the bootloader).

The driver source code is listed in the Appendix 10. The implemented command set for communicating with the control unit is listed in Table 8.1.

Table 8.1 Implemented command set of the culturing unit driver module ( $\mathrm{I}^{2} \mathrm{C}$ interface)

| Command name | $\begin{array}{c}\text { Command } \\ \text { code } \\ \text { (Hex) }\end{array}$ | $\begin{array}{c}\text { Number of } \\ \text { parameter } \\ \text { bytes }\end{array}$ | $\begin{array}{c}\text { Parameter: (valid range) - parameter } \\ \text { description }\end{array}$ | Command description |
| :--- | :---: | :---: | :---: | :--- |$]$| Toggles red LED |
| :--- |
| COM_TEST |
| COM_BRCONTROL |
| COM_BRSTOP |
| $0 \times 31$ |

### 8.2.2 The common control module for culturing units

The control module provides a convenient way for a user to interact with multiple culturing units. It works in real time, supports simultaneous controlling up to 8 culturing units with corresponding drivers, and allows medium change scheduling in regular intervals independently for each culturing unit. In addition, it allows manual control of all solenoid valves and the pump of any connected culturing unit, as well as the manual (i.e. immediate or non-scheduled) medium change. The control unit periodically monitors the state of all culturing units and displays corresponding information or the medium change progress for all connected modules (see Figure 8.3). The graphic TFT display with resolution of $800 \times 480$ pixels and associated resistive touchscreen provides a convenient user interface. The internal real time clock (RTC) module allows user to program multiple medium change events on specific dates or hours.

The control unit was built using commercially available electronic modules as it did not require any special or precise functionality. The construction is based on the Arduino ${ }^{\circledR}$ Mega 2560 board and 5 -inch TFT display module with resolution of $800 \times 480$ pixels and integrated touchscreen. The ITDB02 Arduino MEGA Shield v2.0 is needed to interface the display module to Arduino board. Additional RTC module based on the DS3231 chip is connected directly to Arduino board via the $\mathrm{I}^{2} \mathrm{C}$ interface.


Figure 8.3 The control unit displaying status information from 8 culturing unit, showing the perfusion in progress with perfusion speed $15 \mu \mathrm{l} / \mathrm{min}$.

The whole assembly is mounted to aluminum housing for convenient handling. The control unit was programmed using the Arduino integrated development environment (IDE). The recent version of the source code is v1.2 and contains approximately 1500 lines of code. This source code is listed in Appendix 11.

### 8.3 Increasing throughput of the analyzer module

The analyzer module has 7 measurement channels which can be used either for standard curve or the bioreactor sample measurement. The reliable standard curve measurement requires a minimum of 5 points (including the blank), which leaves 2 channels for bioreactor samples. This configuration was sufficient to operate whole automated system with two culturing units connected to it. However, after the extension of the culturing
system to support up to 8 culturing units with corresponding bioreactors, a possibility of measuring all 8 samples in one run would save significand amount of time, and simultaneously increase the accuracy of sample comparison as all of them would be referenced to same standard curve. Additionally, each point of standard curve could be measured in triplicates, which would also improve standard curve precision. That way, a minimum of $23(8+15)$ channels would be required to be analyzed in a single run.

The simplest way to increase the analyzer throughput would be to keep the operation principle and construction same but extend the number of capillary channels. This approach is straightforward, requiring the extension of the capillary and waste manifold for more branches, the addition of more capillaries to the sample holder, the addition of one more solenoid valve for every new capillary, and the appropriate adjustment of the control unit software. This way of system extension has its limits mainly for two reasons: firstly - a limited number of capillaries will fit to the rotary sample changer, and secondly - as the number of channel increases, the time needed to sequentially fill all capillaries increases proportionally. This second point would mean significant increase of total assay time. For those reason the practical upper limit for channel number increase without conceptual change of the analyzer architecture is approximately 16 channels.

To increase the number of channels beyond this limit, preferably to 24,36 , or even more, the analyzer working principle must be changed to extensively use parallel operation where possible. The following list contains some key points for the design of such analyzer:

- Filling of capillary with reagent, sample or washing buffer should be done in parallel for all channels
- Readout should be done for all channels in parallel. This implies to use one readout device per channel. For this reason, the readout design should be kept as simple as possible, interfacing of optical sensors to capillaries should preferably use the optical fibers. Additionally, all readout devices will need to be calibrated.
- Use preferably modular design. Each module may contain 2 to 6 channels (capillaries) with associated readout devices and isolation valves. Each module should be provided with sample fluidic input or container. The modules should be connected to common manifold distributing the reagents.
- The capillaries are disposable, therefore the design should allow quick and easy replacement of used capillaries for new ones.

It is obvious that the design of such modular analyzer for 24 channels will be challenging. Nevertheless, the experience gained during the development of the prototype analyzer unit will make this task easier.

### 8.4 Other future system improvements

### 8.4.1 Adding sensorics to the culturing unit

Continuous monitoring of the environmental conditions of the cell culture in the bioreactor will certainly increase culturing reliability. A simple flow sensor inserted to the perfusion loop would provide valuable and early information about any failure of the perfusion. High accuracy sensors are not needed for this purpose. A simple mass flow sensor based on the thermal principle would be fully adequate.

Another useful environmental parameter is the monitoring of the oxygen saturation of the cell culture medium. A trial experiments were conducted using the OXY-4 mini device (PreSens, Precision Sensing GmbH), which based on the noninvasive fluorescence quenching measurement principle. Two SP-PSt3-NAU sensor spots were placed inside the bioreactor, one of the sensors was located in the bioreactor reservoir compartment near the perfusion inlet, while the other sensor was located on near the fluidic outlet. That way, the oxygen concentration difference representing cell culture oxygen consumption can be measured. The oxygen levels were measured during the 72h long culturing period of HepaRG cell with automated medium change every 24 h (Figure 8.4). The oxygen consumption can serve as indirect indicator of cell culture metabolic activity.

Additionally, the acidity $(\mathrm{pH})$ of the cell culture medium can be monitored either to prove correct culturing conditions or to provide early warning signals to generate medium change requests. The sensing principle can be used either using the pH sensor spots (e.g. SP-LG1-SA, PreSens), or spectrophotometrically if the culture medium is supplemented with pH indicator (e.g. phenol red). Both approaches are non-invasive.


Figure 8.4 The oxygen levels measured in the 3D HepaRG cell culture located in the bioreactor. Automated medium change was performed every 24 h and is visible as negative glitch on the consumption curve (red).

### 8.4.2 Temperature management of the analyzer unit

Keeping the temperature constant is important for consistent measurements. The prototype analyzer unit does not have the capability of thermostating the assay. This is usually not a problem as far as the measurement is conducted in the laboratory with controlled temperature. However, keeping the reagents and capillaries during the assay at constant temperature would increase the measurement accuracy and analyzer robustness.

Another improvement, especially for long term experiments, would be embedding the reagents cooling option to the analyzer. Most of the reagents have limited shelf-life at room temperature, so keeping them in a cooled state (e.g. $4^{\circ} \mathrm{C}$ ) would enable multiple runs without the need to replace the reagents.

### 8.4.3 Analyzer unit - on-site substrate preparation

The shelf-life of ADHP substrates is 30 minutes at room temperature. Because the assay run duration is approximately 3 hours, the substrate must be prepared fresh and placed to the analyzer shortly before it will be consumed (protocol step 13, see Chapter 3.2.4). A simple way of mixing 3 substrate components in pre-measured quantities would further
increase the comfort of analyzer operation. The components should be preferably stored in cooled state and brought to the reaction temperature after mixing.

### 8.4.4 Analyzer unit - further optimization of cleaning protocol

The recent analyzer cleaning procedure which must be conducted after each assay was optimized with respect to cleaning efficiency. However, this cleaning procedure takes approximately three hours to complete, so further optimization with respect to the cleaning duration would shorten the minimal time between two successive assays.

### 8.4.5 Control unit - implementation of curve fitting algorithms

The curve fitting was done using the external software tools (MATLAB or MS Excel). However, extending the control unit software to include four- or five- parameter logistic regression algorithms should be straightforward. The ARM CORTEX M3 architecturebased microcontroller used in the control unit provides sufficient computational power to allow this option.

### 8.4.6 Analyzer unit - extending the readout system for absorbance measurement possibility

The current readout configuration allows using fluorescent or luminescent substrates. However, the colorimetric substrates are very common and extending the readout system to support those substrates would increase the range of assays the analyzer unit would support. The conceptual layout of combined fluorometric and absorbance sensor is shown on Figure 8.5. The redesign of the readout system will be required for extending the analyzer to more than 16 channels, and utilization of plastic optical fibers (POF) will make such miniaturized and combined sensor design feasible.


Figure 8.5 The layout of combined fluorescence and absorbance sensor. The excitation LED is on the left side, the light passes through the excitation filter and is focused on the fluidic channel. The emission light passes at $\mathbf{9 0}^{\circ}$ angle through the emission filter and is detected by photodiode (bottom side). The absorbance is measured by photodiode aligned with the fluidic channel and emission light source (right side).

### 8.4.7 Miniaturization of the analyzer unit

One of the design goal of the whole automated system was to make the whole system portable. Miniaturization of the analyzer unit is generally required. The current design of the analyzer prototype represents by no means the limit in down-scaling. It is not based on microfluidic chip technology, which might be seen as obvious step towards miniaturization. While it is true that using the microfluidic chip technology would decrease the dead volume of the fluidic network, most of the space will remain to be occupied by valves. The use of on-chip integrated pneumatic valves does not provide overall space advantage, because switching of individual pressurized lines must be provided by another set of some off-chip solenoid valves. Additionally, handling and connecting of delicate microfluidic chips is more difficult, which may result in handling discomfort for analyzer operator. The key factor to scale down in this case will be the replacement of active fluidic components such as the peristaltic pumps and solenoid valves. The current analyzer design uses two peristaltic pumps, which are larger than required for this application. Similarly, more than 20 solenoid valves with the diameter 19 mm were used. Replacement of those valves with types with smaller footprint will save considerable amount of space. If the decision will be made to use microfluidic chip technology, care must be taken to use compatible materials with respect to low-protein binding properties or the compatibility with cleaning agents. Materials based on PDMS should be avoided because of the problems with the analyte adsorption on the surface and associated cleaning difficulties.

## 9 Application possibilities of the culturing and analytical system

In this chapter, application possibilities of the 3D-culturing and analytical system are described. The overview is not exhaustive and covers main areas of use. The system is very universal and it can be adapted to many other specific tasks. The applications are described in a general way and references to specific examples are provided if related experimental work was performed.

### 9.1 Applications of the Cell culturing systems

### 9.1.1 Drug toxicity tests

The combination of the automated culturing unit and the analytic unit provides many benefits for conducting short- and long-term toxicity assays with 3D cultures. This was demonstrated in acetaminophen toxicity study on 3D HepaRG cell culture [63]. In the study the culturing was performed in actively perfused bioreactor with automated medium exchange every 24 hours. The concentration of hepatocyte metabolite albumin was repeatedly determined by analytical module using the flow-through ELISA. High sensitivity of the assay combined with low protein binding materials for fluidics allowed to measure albumin concentrations as low as one nanogram per milliliter.

Presented tool can be used in variety of other toxicology studies such as screening of anticancer therapeutics using the 3D cell cultures or assessing of toxicity of various nanoparticles or toxic substance on 3D cell culture. The ease of parallelization and automation of the drug application to the cell culture makes this system ideal for toxicity assays.

### 9.1.2 Microenvironments testing

The cellular behavior of organoid in 3D cell culture is influenced by particular geometrical and biochemical boundaries of the growth microenvironment [64]. In the case of scaffold-based 3D cell cultures, the properties of cultured cells are influenced by physical and chemical properties of supporting scaffold. Therefore, another broad field of application of this novel culturing system is to evaluate various scaffold morphologies,
materials and its chemical modifications on cell proliferation, viability or differentiation. Possible applications include cell co-culturing, including organ-on-a-chip operation. Moreover, connecting multiple bioreactors in serial manner enables more complex body-on-a-chip experiments. In a previous work, human neuroblastoma cell lines (BE(2)-C, IMR-32) were grown on MatriGrid® scaffolds in the form of spheroids [65]. Although generally it is known that 3D-cultures are difficult to handle, the use of 3D-culturing units reduces and simplifies the handling operations and improves the consistency of the experiment results.

### 9.1.3 Influence of the fluidic shear stress in the cell culture

The fluid flow can directly influence cell proliferation [66] by means of mechanical actions such as compression, shear stress or pressure. These are important factors for organ development and function [67]. Advanced cell culture techniques such as previously mentioned organ-on-chips offer the possibility to control some of these factors. Therefore, advanced culturing techniques are suitable for studying biological phenomena that depend on tissue microarchitecture and perfusion [68]. The ability of the culture unit to precisely control of the perfusion flow rate in a time dependent manner allows it to be used for advanced cell culturing applications. Previous work with cooperation with the Jena University Hospital on the placenta explants revealed that the placenta tissue in the explants is very sensitive to fluidic shear stress. In order to increase the cell viability in the explant, a new adapted scaffold named TissGrid® was developed, which incorporated a protective cylinder made of porous film [69]. The explant was inserted inside the cylinder, where it was protected from excessive fluidic shear stress, but thanks to the porous scaffold material, the explant remained supplied with nutrients.

### 9.1.4 Cell line maintenance

One of the frequent operations in the biological laboratory is the cell line maintenance and passaging. The culturing unit can be used with advantage to maintain sensitive cell lines requiring perfusion with oxygenated medium. Continuous perfusion prevents consumptive oxygen depletion in cultures sensitive to hypoxia such as hepatocytes [70]. Automated medium change provides additional benefits of reducing the risk of contamination and simultaneously reducing the manual labor.

### 9.2 Applications of the analytical module

The analytical module was optimized for flow-through albumin florescence assay. The choice of Amplex ${ }^{\text {TM }}$ Red (ADHP) as the fluorescence substrate was based on its desirable properties, such as chemical and thermal stability, low background and increased dynamic range and fluorescence emission outside the range of compound autofluorescence. Because of these advantaged the substrate, it is used in many commercially available assays. A few examples of fluorescent assays using the ADHP as substrate are listed here:

- Glucose / Glucose oxidase assay (A22189, ThermoFischer)
- Cholesterol assay (A12216, ThermoFischer)
- Catalase assay (A22180, ThermoFischer)
- Hydrogen peroxide / Peroxidase assay (A22188, ThermoFischer)
- Acetylcholine / Acetylcholinesterase assay (A12217, ThermoFischer)
- Galactose / Galactose oxidase assay (A22179, ThermoFischer)
- Glutamic acid / Glutamate oxidase assay (A12221, ThermoFischer)
- Monoamine oxidase assay (A12214, ThermoFischer)
- Neuraminidase assay (A22178, ThermoFischer)
- Phospholipase D assay (A12219, ThermoFischer)
- Phosphate assay (P22061, ThermoFischer)
- Pyrophosphate assay (P22062, ThermoFischer)
- Sphingomyelinase assay (A12220, ThermoFischer)
- Uric acid / Uricase assay (A22181, ThermoFischer)
- Xanthine / Xanthine oxidase assay (A22182, ThermoFischer)

Additionally, LDH assay using ADHP related substrate resazurin (C20302, ThermoFischer) is also available as commercial product. Because all these assays are based on the same fluorescent molecule (resorufin) as the albumin assay which the analytical unit was designed for, no change on the readout part (fluorimeter) would be required if the analytical unit should be adapted for one of these assays. The fluidic part is flexible in design and it would not require extensive modifications to support these assays. Obviously, the software of the control unit would require extensions in order to support any additional assay.

Other fluorophores than resorufin can be supported if the fluorimeter would be appropriately modified. For example, to adapt the fluorimeter for one other common fluorophore - fluorescein, the excitation laser wavelength would need to be changed to 450 nm or 488 nm (e.g. L450P1600MM or L488P60, Thorlabs) and the emission filter would also need to be replaced to a suitable bandpass type (e.g. 513-556 nm, \#67-017, Edmund Optics). Thus, by replacing two components, the fluorimeter can be adapted to an assay using different fluorophore.

## 10 Summary

"Genes are effectively one-dimensional. If you write down the sequence of $A, C, G$ and $T$, that's kind of what you need to know about that gene. But proteins are threedimensional. They have to be because we are threedimensional, and we're made of those proteins. Otherwise we'd all sort of be linear, unimaginably weird creatures"
(Francis Collins, led the Human Genome Project, director of the National Institutes of Health in Bethesda, Maryland, United States, 2001)

The observation made by Francis Collins, namely that humans are three-dimensional, and not linear, unimaginably weird creatures, is amusing. Similarly, this thesis was started with an amusing quote from the book Flatland, in which a series of characters interact in a purely two-dimensional world, but a three-dimensional world is later discovered. These quotes, which juxtapose 1D and 2D environments with 3D environments, are amusing because the nature of our 3D environment is so self-evidently obvious to us. Here, it would be a poor transition to now simply say, "so stop using 2D cultures, because 3D is..., etc". A more relevant transition would be to say, "although our 3D environment is so self-evidently obvious, is there a justification for reducing the dimensionality?". The answer is certainly yes. There are many benefits of 2D systems (cost, ease of observation, ease of measurement) and these benefits have been discussed in the context of cell culturing in this text. For simpler systems, and simpler questions, the complexity of a 3D environment (and the inclusion of automation) is not always necessary.

However, at the clinical level, humans are three-dimensional, and the issue is the following. Although unautomated cell culturing systems in 2D can be used for some preclinical questions, it is without question that cells act in much different manner when surrounded by other cells in 3D. Therefore, the problem is predictivity. By introducing a 3D system more representative of the clinical environment with a more complex technology, this may reduce both the monetary cost and the degree of failures of drugs and therapies at the level clinical trials which previously passed 2D screening systems.

Certainly, pharmaceutical companies dedicate astonishing amounts of money to R\&D each year for pre-clinical drug trials, with the majority of such trials ending in failure once transferred to the clinical level. The introduction of 3D systems may give a better degree of predictivity in trails at the pre-clinical level. Essentially, as stated in the introduction, a culture should be 3D to increase predictivity, but the culturing should be automated to increase through-put and applicability to large-scale pre-clinical testing.

Indeed, there is currently a genuine renaissance in attempts to include forms of automation, or at least so-called online measurement, which allows the testing of certain parameters of the biological system without actually opening or disturbing the system. "New generation" organ-on-a-chip systems are equipped with biosensors or bioimaging that enable the online monitoring of pH and oxygen [71, 72], the cellular metabolic state [73, 74] and the detection of cell-derived analytes in the culture medium by microfluidic enzyme linked immunosorbent assay (ELISA) [13-15]. Thus, cells do not need to be removed from the perfused culture systems to define drug toxicity and cellular health. In particular, quantitative analysis of cell-secreted proteins by microfluidic ELISA provides a novel method of measuring non-invasively the toxicity of drugs to cells in complex culture systems [63] where the removal of cells or the opening/exposure of the system could compromise long-term experiments.

In the presented study of this text, a fully-automated and robust culturing system was developed, which combined 3D cell culturing with automated perfusion, medium change, and sampling, followed by an automated flow-ELISA for detection of cellderived albumin for the assessment of hepatotoxicity. The focus was on developing a scaffold-based 3D culture and analysis system which allowed excellent exposure of the cells to the applied drug and minimized adsorption and absorption of small molecules, drugs, and biomolecules by the system. The ELISA analyzer module was designed in such a way that almost any commercially available ELISA assay kit can be used with this system and therefore made available to a wide range of users.

The presented study describes the development and operation of an automated 3D culture system with a non-invasive online analysis system and its relevance compared to routinely-performed standard sandwich ELISA protocols. It was demonstrated that 3D cultures of HepaRG cells differ from 2D monolayer cultures in sensitivity to toxic
compounds, making them appropriate for online toxicity studies. Finally, the proper system functionality was verified using the applicability of the device in online-kinetics measurement of albumin secretion as a proof-of-concept using 3D HepaRG cultures perfused with APAP over a period of 96 hours. This study demonstrates how this highly integrated in vitro system can be used for drug toxicity tests and shows the potential for adaptation of the online-detection to include other secreted proteins, such as hormones and signaling molecules from 3D mono- and co-cultures.

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#### Abstract

Subsequent washing of the common fluidic path (marked as red "1" on the figure) completes the "washing after sample" sequence


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## Appendix 1 - Control unit schematics



Figure A-1 Control unit schematic - the microcontroller part


Figure A-2 Control unit schematic - solenoid valve drivers, constant current sources, capacitive sensors and $A / D$ converter.


Figure A-3 Control unit schematic - stepper motor drivers and optical sensors.


Figure A-4 Control unit schematic - power supply, spectrometer interface and combined optical sensors interface.

## Appendix 2 - Control unit PCB assembly drawing



Figure A-5 Control unit PCB assembly - top side.


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Figure A-8 Control unit PCB layout - ground layer (layer2).


Figure A-9 Control unit layout - power plane layer (layer 3).


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## Appendix 3 - Fluorimeter amplifier module schematic



Figure A-11 Fluorimeter front-end amplifier and laser driver schematic.

## Appendix 4 - Fluorimeter amplifier PCB layout



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Figure A-13 Fluorimeter amplifier PCB top layer (left) and bottom layer (right).

## Appendix 5 - Culturing module driver schematic



Figure A-14 Culturing module smart driver schematic.

## Appendix 6 - Culturing unit driver PCB assembly plan



Figure A-15 Assembly of the driver unit - top side (top) and bottom side (bottom).

## Appendix 7 - Culturing unit driver PCB layout



Figure A-16 Culturing unit smart driver PCB layout - top layer (top) and bottom layer (bottom).

## Appendix 8 - Schematics of the OpenOCD debugger hardware



Figure A-17 The schematic of the OpenOCD debugger

## Appendix 9 - The assembly plan and layout of the OpenOCD

 debugger PCB

Figure A-18 The assembly of the OpenOCD debugger - top layer


Figure A-19 The layout of the OpenOCD debugger, top layer (left) and bottom layer (right)

## Appendix 10 - Culturing unit driver source code listing



```
#define COM_PREPSAMPLE 0x34 //no parameters
#define COM_BRCHANGEMED 0x35 //4 parameter bytes: VolumeMSB, VolumeLSB,
    //SpeedMSB, SpeedLSB, volume limits: <-10000;10000> ul,
    //speed limits: <1;500> ul/min
//#define COM BRSAMPLE 0x36 //4 parameter bytes: VolumeMSB, VolumeLSB, SpeedMSB,
    //SpeedLSB, volume limits: <1;100000> ul,
    //speed limits: <1;500> ul/min
    //4 parameter bytes: VolumeMSB, VolumeLSB,
    //SpeedMSB, SpeedLSB, volume limits: <1;30000> ul,
    //speed limits: <1;500> ul/min
    define COM VALVE 0x38 // 2 parameters: Vavlve Number: <1;8>, new state: 0 or 1
#define COM STARTPUMP 0x39 //4 parameter bytes: VolumeMSB, VolumeLSB,
    //SpeedLSB, volume limits: <1;30000> ul, Seedmb
    //SpeedLSB, volume limits: <1;30000> ul
    /speed limits: <1;500> ul/min, speed=0 means STOP
#define COM_BRSTATUS 0x41 // no parameters
#define AIN1_ADC_CH 6
#define AIN2_ADC_CH
#define RXBUF
#define LEDR_OFF
    (PORTB&=~0\times01)
(PORTB|=0x01)
#define LEDR_TOGGLE (PORTB^=0x01)
#define LEDG_ON (PORTB&=~0x02)
#define LEDG_OFF (PORTB|=0x02)
#define LEDG_TOGGLE (PORTB^=0x02)
#define DACS_0 (PORTB&=~0\times10)
#define DACS - }1\mathrm{ (PORTB|=0x10)
#define DACSB_0 (PORTB&=~0x10)
#define DACSB_1 (PORTB|=0x10)
#define DACSA_0 (PORTB&=~0\times02)
#define DACSA_1 (PORTB|=0x02)
#define SM CLK 0 (PORTD&=~0x20)
#define SM_CLK_1 (PORTD|=0x20)
#define SM DISABLE (PORTD&=~0\times40)
#define SM ENABLE (PORTD|=0\times40)
#define SM_RESET (PORTD&=~0\times80)
#define SM_UNRESET (PORTDI=0x80)
#define SM_DIR_CCW (PORTB&=~0\times04)
#define SM_DIR_CW (PORTB|=0x04)
#define SM_STEP_FULL (PORTB&=~0x08)
#define SM_STEP_HALF (PORTB|=0x08)
#define VALVE1
#define VALVE2 2
#define VALVE3 3
#define VALVE4 4
#define VALVE5 5
#define VALVE6 6
#define VALVE8 8
#define SOL_SET_5V (PORTD&=~0x04)
#define SOL_-SET_12V (PORTD|=0x04)
#define OFF
O
#define DAC CHAN A 0
#define DAC_CHAN_B 1
// Speed ramp states
#define STOP states
Hdefine STOP
Mderne ACCEL
#define RUN
#define STOPPED
#define NONE
#define SPEEDUP
#define SLOWDOWN
#define SLOWSTOP
#define TRUE
#define FALSE 0
#define CW 
#define CCW
//#define HALFSTEPS
#define FULLSTEPS
//#define SLOWDECAY
#define FASTDECAY
// Timer/Counter 1 running on 16MHz / 64 = 0.25MHz (4uS). (T1-FREQ 250000)
#define T1_FREQ 250000
```

//! Number of (full)steps per round on stepper motor in use.


```
volatile unsigned char tim min;
volatile unsigned int tim hrs;
volatile unsigned char tim_ena=0;
volatile uint16_t solenoid_pwr_timer;//1ms interval
unsigned char baudrate;
char rxbuf[RXBUFSIZE];
volatile unsigned char rx ptr;
volatile unsigned char rx_overflow=0
//unsigned char read_ptr;
volatile unsigned char new_msg=0;
// i2c variables
unsigned char i2c_rxbuf[I2C_RXBUFSIZE]; //i2c RX buffer
unsigned char i2c-txbuf[I2C_TXBUFSIZE]; //i2c TX buffer
volatile unsigned int i2c_rxptr_top=1;
volatile unsigned int i2c_rxptr_bot=0;
volatile unsigned char i2\overline{c}_txpt\overline{r}_top=1;
volatile unsigned char i2c_txptr__bot=0;
volatile unsigned char i2c_rxbuf_err=0; //buffer owerflow flag
volatile unsigned char i2c_txbuf_err=0;
volatile unsigned char i2c_buserror=0;
volatile unsigned char i2c_newmsg=0;
volatile unsigned char last_command=0;
volatile unsigned char last_txbyte=1;
volatile unsigned char i2c_status=0;
volatile unsigned char error=0;
unsigned char disp_blink_period=0; //8ms per LSB, defined display on and off time,
                                    // range 8ms - 2s, 0=blink disabled
unsigned char cmd_valid=0;
signed int acceleration; // Accelration to use.
signed int deceleration; // Deceleration to use.
signed int steps; // Number of steps to move
signed int speed; // current Speed to use.
signed int last_speed; // current Speed to use.
uint8_t br1_perfusion=0;
uint8_t br1_make_sample=0;
uint8_t br1_changing_medium=0;
int16 t medium_change_vol=5;
uint1\overline{6}_t medium_change__speed=25;
uint16_t br1_pump_spee\overline{d}=25;
volatile uint16_t delay_timer_br; //10ms interval
speedRampData srd_sm1;
#define MICROSTEPS_TABSIZE 32
const unsigned char microstep_tab[2][MICROSTEPS_TABSIZE]={
    {0,5,10,15,20,24,29,34,38,43,47,51,56,60,63,67,71,74,
    77,80,83,86,88,90,92,94,96,97,98,99,100,100},
    {100,100,99,99,98,97,96,94,92,90,88,86,83,80,77,74,71,
    67,63,60,56,51,47,43,38,34,29,24,20,15,10,5}};
uint8 t progress[8]={0,0,0,0, 0,0,0,0}c;
void speed_cntr_Init_Timer1(void);
unsigned int min}(uns\overline{i}gned int x, unsigned int y)
void speed_cntr_Move(int32_t step, uint16_t accel, uint16_t decel, uint16_t speed)
void sm se\overline{t}}\mathrm{ iphase(uint16 }\overline{t}\mathrm{ iphasea, uint16 t iphaseb);
void sm set istandby(spee\overline{dRampData *srd motorx, int16 t istandby);}
void sm_motor_init(speedRampData *srd_motorx, uint8_t microsteps,
    uint16 t max_iphase, uint16_t standby_iphase);
void sm_motor_deinit(speedRampDā̄a *srd_motorx);
void i2c_send_byte(void);
void i2c_recv_byte(void);
void parse_i2\overline{c}_command(void);
void stop_pump(void);
uint8_t br1_init(void)
void \overline{br_status(void);}
void control_solenoid(uint8_t solenoid_id, unsigned char state);
void start_pump(int16_t volume, uint16_t speed);
const char cmd_valve[]
const char cmd startpump[]
const char cmd_stoppump[]
const char cmd pumpstatus[]
const char cmd_stats[]
const char cmd_callboot[]
const char cmd_seti2caddr[]
//bioreactor commands
const char cmdb_control[]
const char cmdb_changemed[]
const char cmdb_sample[]
const char cmdb_mix[]
```

PROGMEM="valve";
PROGMEM="start pump"
ROGMEM="stop pump";
PROGMEM="ps";
ROGMEM="stats";
PROGMEM="CALL BOOT";

PROGMEM="br control";
PROGMEM="br change medium";
PROGMEM="br sample";
PROGMEM="br mix";
PROGMEM="br mix";
PROGMFM="br prepar

```
404}\mathrm{ const char cmdb_setspeed[] }\quadl
406
407
409
410
413 uint64 t uint64 mul32 (uint64 t a, uint32_t b)
414 {uint64_t r = 0;
while (b) {
    if ((uint8_t)b & 1)
    a r<= += a;
    a<<= 1;
    b }>>= 1;
    return r;
}
uint64_t uint64_div32 (uint64_t a, uint32_t b)
{uint64_t r = 0;
    uint32_t h = 0;
    uint8_\overline{t c = 64, h2;}
    /* This looks much smoother in assembler (carry)... */
        while (c--) {
        h2 = (h & 0x80000000) ? 1 : 0;
    h<<= 1;
    if (a & 0x80000000000000000ULL)
        h l=1;
    a=(a<<< );
    if (h2 || h >= b) {
        h = = b;
        r I= 1;
        }
    return r;
}
static unsigned long sm_sqrt(unsigned long x)
{
    register unsigned long xr; // result register
    register unsigned long q2; // scan-bit register
    register unsigned char f; // flag (one bit)
    xr = 0; // clear result
    q2 = 0x40000000L; // higest possible result bit
    q2 =
    {
        if((xr + q2) <= x)
        {
            x == xr + q2;
            f = 1; // set flag
        }
        f = 0; // clear flag
        }
        xr >>=
        xr += q2; // test flag
        }
    } while(q2 >>= 2); // shift twice
        return xr +1; // add for rounding
    }
    else{
    }
}
unsigned int min(unsigned int x, unsigned int y)
if
    if(x<y) {
        return x;
    }
        return y;
    }
}
    void delay(unsigned int ticks) //oneskorenie asi 100ms
    {volatile unsigned char j,k;
    volatile unsigned int i;
    for(i=0;i<ticks;i++)
        for(j=0;j<255;j++)
    k++;
8 }
    void longdelay(char a)
    {while(a){a--;
        delay(1000);
    };
```

```
// --------------------------------------------------------------------------------
unsigned int SetDelay (unsigned int t)
return((tim_frac + t + 1)%1000)
}
char CheckDelay(unsigned int t)
{
    if(((signed int)t - (signed int)tim_frac)>0) return(0)
return(1);
}
// --------------------------
voi
unsigned int akt;
akt = SetDelay(w);
while (!CheckDelay(akt));
}
void ioinit(void) // init portov, watchdog
{// define inputs & outputs
    DDRA = 0x3F;
    DDRB = 0xBF;
    DDRC = 0xC0;
    DDRD = 0xE4;
    PORTA = 0x00;
    PORTB = 0\times13;
    PORTC = 0x00;
    PORTD = 0 <18;
}
void uartinit(unsigned char baud_rate)
{
    UBRRL = baud rate % 256;
    UBRRH = baud rate / 256;
    UCSRA = 0\times00-
    UCSRB = 0x98; //RXEN=1, TXEN=1, RXIE=1
    UCSRC = 0x86; // 8 bit, 1 stop bit, no parity, asynchro
rx_ptr=0;
// read_ptr=0;
    rx_overflow=0;
    new_msg=0;
}
void spi_init(void)
{
    SPCR=0x00; //SPI Disable
    SPCR=0x58; //Enable, Master, MSB first, SPI Mode 2, Cpuclk/4
}
void i2c_init(unsigned char i2c_baud)
{
    i2c_rxptr_top=1;
    i2c_rxptr_bot=0;
    i2c_txptr_top=1;
    i2c_txptr_bot=0;
    i2c_rxbuf_err=0;
    12c-txbuf-err=0;
    12c_txbuf_err=0;
    12C-buserror=0
    TWSR=0x0\overline{0}; //set prescaller to 1
    TWSR=0x00; (//set prescaller to 1
    lWAR=(eeprom_read_byte((uint8_t *)EE_I2C_ADDR)<<l);
}
void ad5601_write(unsigned char data, unsigned char channel)
void ad5601-write(
    tmp=(unsigned int) data<<6;
    if(channel==DAC_CHAN_A) DACSA_0; else DACSB_0;
    SPDR=tmp>>8;
    while(!(SPSR&0x80));
    SPDR=tmp&0xFF;
    while(!(SPSR&0x80));
    if(channel==DAC_CHAN_A) DACSA_1; else DACSB_1;
}
void ad5302 write(unsigned char data, unsigned char channel)
{unsigned int tmp;
tmp=(unsigned int)data<<4;
if(channel==DAC_CHAN_B) tmpl=0x8000;
    DACS_0;
    SPDR=tmp>>8;
    while(!(SPSR&0x80));
    SPDR=tmp&0xFF;
    while(!(SPSR&0x80));
    DACS 1;
```

```
608
610 int uartsend (char a, FILE *dummy)
612 while(!(U
614
615
617 void uart_SendByte(unsigned char data)
617 void uart_SendByte(u
619 子
void TO_start(void)
f
    TCNTO = 0x00; // set sampling frequency
    OCRO = 250;
    TIFR |= 0x02; // timerl overflow flag clear
    TCCRO = 0x0B; . // Timer mode CTC, / 64 prescalling
    TIMSK |= 0x02; // timer1 overflow interrupt enable
    tim_frac=0;
    tim_sec=0;
    tim_min=0;
    tim_hrs=0;
    tim_ena=0;
}
void adc_start(void)
ADMUX=0x40; //CH0, right adjust result, Vref=AVCC
ADCSRA=0x9E; //ADC enable, ADC start, prescaller = 64
    set_sleep_mode(SLEEP_MODE_ADC);
    adc_flag=\overline{0};
}
void set_adc_channel(unsigned char channel)
{
channel &=0\times07
ADMUX&=0xF8;
ADMUX|=channel;
7 }
unsigned int get_adc_sample(unsigned char channel)
{
    set_adc_channel(channel);
    ADCS}RA|=0\times40
    while(!adc_flag);
    //delay(1);
    ADCSRA|=0\times40;
    while(!adc_flag);
    adc_flag=0;
    return(adc_result);
}
SIGNAL(SIG_OUTPUT_COMPARE0) //TIMERO OCRO, serviced every 1ms
{
if(solenoid_pwr_timer) solenoid_pwr_timer--;
    if(solenoid_pwr_timer==1) SOL_SET_5V}; //set solenoid power to +5V
    if(tim_ena) tim_frac++;
    if(!(tim_frac%10)){
            if(delay_timer_br) delay_timer_br--;
            \) {
            tim_frac=0
            tim_sec++;
            if(\overline{tim_sec>59) {tim_sec=0;}
                    tim_min++;
                        if(tim_min>59) {tim_min=0;
                                    tim_hrs++;
                                    };
                            };
}
SIGNAL(SIG ADC) //ADC ISR
{static uns̄igned char i,j;
    j=ADCL;
    i=ADCH;
    adc_result=i<<8;
    adc_result+=j;
    adc_flag=1;
```

```
SIGNAL(SIG_UART_RECV) //UART receive ISR
    uart_SendByte(rxbuf[rx_ptr]); //echo character
    if(((rxbuf[rx_ptr]=='\r') || (rxbuf[rx_ptr]=='\n')) && rx_ptr) new_msg=1;
    if(rx_ptr<(RXBUFSIZE-1)) rx_ptr++; else rx_overflow=1;
}
ISR(TWI vect) //I2C ISR
ISR
//i2c_spy[spyptr]=TWSR;
    //if(spyptr<29) spyptr++;
/*
    //sendhex(TWSR);
    // MASTER TRANSMIT MODE
    if((TWSR&0\timesF8)==0x08){ //START SENT
                                    2c_send_byte();
                                    if(\overline{TWCR&\overline{0x80) I2C_CLRTWINT;}}\mathbf{}/2
    return;
    if ((TWSR&0\timesF8)==0\times10){ {
    i2c_send_byte();
    If(\overline{TWCR&\overline{0}\times80) I2C_CLRTWINT;}
    return;
    if((TWSR&0\timesF8)==0\times18){
                            //SLA+W SENT, ACK recv.
                            f(TWCR&0x80) I2C CLRTWINT;
    i2c_busy=0;
    retūrn;
    }
    //DATA SENT, ACK recv,
    12c send byte();
    if(\overline{TWCR&\overline{0}\times80) I2C_CLRTWINT;}
    return;
    if((TWSR&0xF8)==0x20){ //SLA+W SENT, NACK recv.
    I2C STOP;
    i2c_busy=1;
    return;
    \
    }
    I2C_STOP;
    return;
if((TWSR&0\timesF8)==0\times38){ //ARBITRATION LOST
    I2C_STOP;
    return;
    }
// MASTER RECIEVER MODE
    if((TWSR&0xF8)==0x40){ //SLA+R SENT, ACK recv.
    //if(TWCR&0x80) I2C_CLRTWINT;
    if((TWCR&0x80) && ack_gen) TWCR=I2C_CLRTWINT_ACK|i2c_int_ctrl;
    if((TWCR&0x80) && (!ack_gen)) TWCR=I2C_CLRTWINT_NACK|i2c_int_ctrl;
    return;
    }
    if((TWSR&0xF8)==0x48){ //SLA+R SENT, NACK recv.
    I2C_STOP;
    return;
    if((TWSR&0\timesF8)==0\times50){ //DATA RECIEVED, ACK sent.
    i2c recv byte();
    if((TWCR\overline{&}0\times80) && ack gen) TWCR=I2C CLRTWINT ACK|i2c int ctrl;
    if((TWCR&0x80) && (!ack_gen)) TWCR=İI2C_CLRTWINT_NACK|i2c_int_ctrl;
    return;
    }
    if((TWSR&0xF8)==0x58){ //DATA RECIEVED, NACK sent.
    i2c_recv_byte();
    2C_STOP;
    i2c-active=0;
    return;
    }
    */
// SLAVE RECEIVE MODE
    if((TWSR&0xF8)==0xA0) { //STOP OR REP. START RECV.
    // LEDR_OFF;
    if(TWCR-&0x80) I2C_CLRTWINT;
    return;
    }
    if((TWSR&0\timesF8)==0\times60){ //SLA+W RECV., ACK returned
    // LEDR_ON;
    if(TWC\overline{R}&0x80) I2C_CLRTWINT;
    return;
    }
    if((TWSR&0xF8)==0x68){ //ARBITRATION LOST, SLA+W RECV., ACK returned
        if(TWCR&0x80) I2C_CLRTWINT;
    return;
if((TWSR&0xF8)==0x70){ } //GENERAL CALL RECV., ACK returned
    if(TWCR&0x80) I2C_CLRTWINT;
    return;
    if((TWSR&0xF8)==0x78){ //ARBITRATION LOST,GENERAL CALL RECV., ACK returned
        if(TWCR&0x80) I2C_CLRTWINT;
    return;
```

```
if((TWSR&0xF8)==0\times80){ } //SLA+W RECV.,DATA recv., ACK returned
    i2c_recv_byte();
    //delay(1);
    if(TWCR&0x80) I2C_CLRTWINT;
    return;
if((TWSR&0xF8)==0x88) { //SLA+W RECV.,DATA recv., NACK returned
    i2c recv byte();
    if(TWCR&0\times80) I2C_CLRTWINT;
    return;
if((TWSR&0xF8)==0x90){ //GENERAL CALL RECV.,DATA recv., ACK returned
    i2c recv byte();
    if(TWCR&}0\times80) I2C_CLRTWINT
    return;
    }
if((TWSR&0xF8)==0\times98){ //GENERAL CALL RECV. RECV.,DATA recv., NACK returned
    i2c_recv_byte();
    if(TWCR&0x80) I2C_CLRTWINT;
    return;
    }
// SLAVE TRANSMITTER MODE
if((TWSR&0xF8)==0xA8){ //SLA+R RECV., ACK returned
    //LEDR_ON;
    //parse_i2c_command();
    12c_send_byte();
    if(TWCR&0x80) {
                            if(last_txbyte) TWCR=0x85;
                            else I2C_CLRTWINT;
        return;
    if ((TWSR&0xF8) ==0\timesB0) {
        } //ARBITRATION LOST, SLA+R RECV., ACK returned
        if(TWCR&0x80) I2C CLRTWINT;
        return;
    if ((TWSR&0xF8)==0xB8){ //DATA BYTE TRANSMITTED, ACK received
        i2c_send_byte()
            if(last_txbyte) TWCR=0x85;
                };
    return;
    }
        //DATA BYTE TRANSMITTED, NOT ACK received
        if(TWCR&0x80) I2C_CLRTWINT;
        return;
        }
            //LAST DATA BYTE TRANSMITTED, NOT ACK received
        if(TWCR&0x80) I2C_CLRTWINT;
        return;
    }
// I2C BUS ERROR
    if((TWSR&0xF8)==0x00){ //I2C BUS ERROR
        if(i2c buserror!=0xFF) i2c buserror++;
        if(TWCR&0x80) I2C_CLRTWINT;
        return;
        }
    //undefined state
    if(TWCR&0x80) {
        I2C_CLRTWINT;
}
vid i2c putchar(unsigned char byte)
}unsigne\overline{d char i}
i=i2c_txptr top;
    i2c_txbuf[i2c_txptr_top]=byte;
    i2c_txptr_top++
    if(\overline{i}2c_txptr_top==I2C_TXBUFSIZE) i2c_txptr_top=0;
    if(i2c_txptr_top==i2c_txptr_bot) {i2c_txbuf_err=1;
                i2c_txptr_top=i;
}
void i2c_send_byte(void)
{unsigned char i;
i=i2c_txptr_bot+1;
if(i>=I2C_TXBUFSIZE) i=0;
if(i==i2c_txptr_top) ,
    i2c_txptr_bot=i;
TWDR=i2c_txbuf[i2c_txptr_bot];
    last txbyte=0;
    i=i2\overline{c}_txptr_bot+1;
    if(i>=I2C_TXBUFSIZE) i=0;
    if(i==i2c- txptr top){ last txbyte=1;
                                    i2c_t\overline{xptr_top=1;}
                                    --**-
                                    2c_txptr_bot=0;
}
void i2c recv byte(void)
```

```
915
i=TWDR;
    i2c_rxbuf[i2c_rxptr_top]=i
    i2c rxptr top++
    if(i2c rxptr top>=I2C RXBUFSIZE) i2c rxptr top=0
    if(i2c_rxptr_top==i2c_rxptr_bot) {i2c__rxbuf_err=1;
    if(i=='\r' || i=='\n') i2c_newmsg=1;
}
    void i2c_txflush(void)
    {
    i2c_txptr_top=1
    i2c_txptr_bot=0
    i2c_-txbuf_err=0
3 }
unsigned char i2c_getchar(void)
    {unsigned int tmp;
    if(i2c_rxbuf_err) return(0);
    tmp=i2c_rxptr_bot
    i2c_rxptr_bot++;
    if(i2c_rxptr_bot>=I2C_RXBUFSIZE) i2c_rxptr_bot=0;
    if(i2c_rxptr_bot==i2c_rxptr_top) {i2c_rxptr_bot=tmp; return(0);};
    return(i2c_rxbuf[i2c_rxptr_bot])
    }
    void parse_i2c_command(void)
    {unsigned char i=0
    unsigned int tmp;
    signed int param1=0,param2=0
    i2c status=COM NOTVALID;
    i2c_newmsg=0;
    i=i2c getchar();
    if(i==COM_TEST){last_command=COM_TEST;
                        i2c status=NO_ERROR;
                            LED\overline{R} TOGGLE
    else if(i==C
BRCONTROL) {
i}\overline{2}\textrm{C
i=i\overline{2}c_getchar();
if(i==0 || i==1)\
                    br1_perfusion=i;
                    eeprom_write_byte((uint8_t *)EE_BR1_PERFUSION,br1_perfusion);
                    if(i==\overline{0}) stop_pump();
                l }
    else if(i==COM_BRSTOP){
                            i\overline{2}c_status=NO_ERROR;
                            brl_changing_medium=0
                            br1_make_sample=0;
                    eeprom_write_byte((uint8_t *)EE_BR1_MAKESAMPLE,br1_make_sample);
                    brl_init();
                    progress[0]=0;
                    progress[1]=0;
                    progress[2]=0;
                    progress[3]=0;
                    progress[4]=0;
                    stop_pump();
    =
    M BRSPEED) {
                            i2c status=NO ERROR;
                            tmp=i2c getchär();
            tmp=12c}-\mp@subsup{g}{}{\prime
            tmp+=i2c getchar();
            if(tmp<1 || tmp>500) i2c_status=COM_PARAM_ERR;
                    else{
                    br1_pump_speed=tmp;
                    eeprom_write_word((uint16_t *)EE_BR_SPEED,br1_pump_speed);
                    }
            }
    else if(i==COM PREPSAMPLE)
            i\overline{2c_status=NO_ERROR};
            br1_make_sampIe=1;
                            eep\overline{rom_write_byte((uint8_t *)EE_BR1_MAKESAMPLE,br1_make_sample);}
                        }
    else if(i==COM_BRCHANGEMED) {
        i2c_status=NO_ERROR
        tmp=i2c_getchar();
        tmp=tmp*256;
        tmp+=i2c_getchar();
        param1=(int16_t)tmp; //1st parameter - pumped volume
        if(param1<-10000 || param1>10000) i2c_status=COM_PARAM_ERR;
        tmp=i2c_getchar();
        tmp=tmp*256;
        tmp+=i2c getchar();
        param2=(int16_t)tmp; //2nd parameter - pump speed
        if(param2<1 |\ param2>500) i2c_status=COM_PARAM_ERR;
        if(i2c_status==NO_ERROR) {
            medium change vol=param1;
                                    medium change-speed=param2
                                    br1 changing medium=1;
            }
    else if(i==COM_VALVE)
    i2c status=NO ERROR;
```



```
119 void sm_set_istandby(speedRampData *srd_motorx, int16_t istandby)
1120 {
121 srd_motorx->standby_iphase = istandby
122
1123
1124
1126 // * \param imax phase Max phase current, in mA (range: 50 - 3000mA)
1127 void sm motor init(speedRampData *srd motorx, uint8 t microsteps,
1128
1129 {
130
if(microsteps && microsteps!=2 && microsteps!=4 &&
    microsteps!=8 && microsteps!=16 && microsteps!=32) microsteps=2;
    srd_motorx->run_state = STOPPED;
    srd_motorx->step_count = 0;
    srd_motorx->mstep_counter = 0;
    srd_motorx->rest = 0;
    srd_motorx->abs_position = 0
    //srd_motorx->driver_state=0;
    srd_motorx->microstep_inc=0;
    if(microsteps)srd_motorx->microstep_inc=MICROSTEPS_TABSIZE/microsteps;
    srd_motorx->mstep_counter = srd_motorx->microstep_inc; //initial state is
                                    // the first state after zero
srd_motorx->microsteps=microsteps;
srd_motorx->max_iphase = max iphase
srd_motorx->standby_iphase = standby iphase
srd_motorx->i_phaseb = (standby_iphase/100)*(microstep tab[0][srd motorx->microstep inc])
srd_motorx->i_phasea = (standby_iphase/100)*(microstep_tab[1][srd_motorx->microstep_inc]);
srd_motorx->driver_control=0x05; //enable on, Halfsteps
#ifdēf SLOWDECAY
srd_motorx->driver_control|=0x08; //additionaly set decay mode
#endif
1155
1 1 5 7 ~ s m \_ s e t \_ d r i v e r \_ c o n t r o l ( s r d \& m o t o r x - > d r i v e r \_ c o n t r o l ) ; ~
1159 //initial state - phase a current set to 0, phase b current set to standby
sm_set_iphase(srd_motorx->i_phasea, srd_motorx->i_phaseb);
61
}
// * disables motor driver and timer channel
void sm_motor_deinit(speedRampData *srd_motorx)
166 {
// Timer/Counter 1 Output Compare A Match Interrupt disable
    TIMSK & = ~(1<<OCIE1A);
    srd_motorx->run_state = STOP;
    srd_motorx->driver_control&=(~0x01); //enable OFF
sm_set_driver_control(srd_motorx->driver_control);
} }
177
1178 void sm_driver_gostandby(speedRampData *srd_motorx)
{ {int8_t next_xidx,next_yidx;
int1\overline{6}_t i_phasea,i_phaseb;
next_yidx=(0x66>>srd_motorx->driver_state) &0x01;
next_xidx=srd_motorx->mstep_counter;
i phaseb=(srd motorx->standby iphase/100)*(microstep tab[next yidx][next xidx]);
    i phasea=(srd_motorx->standby_iphase/100)*(microstep_tab[next_yidx^0x01][next_xidx]);
sm_set_iphase(i_phasea, i_phaseb);
void speed_cntr_Move(int32_t step, uint16_t accel, uint16_t decel, uint16_t speed)
{speedRampData *srd_motorx;
    int8 t next xidx,next_yidx;
    volatile uiñt64_t tmp;
    if(step==0) return;
    srd_motorx=&srd_sm1;
    //wait until previous movement will finish
    while(srd_motorx->run_state != STOPPED);
    srd_motorx->step_count = 0;
#ifdef SM_REVERSE_ROTATION
    step = -step;
#endif
    // Set direction from sign on step value.
    if(step < 0){
        srd_motorx->dir = CCW;
        step}=-step
        srd_motorx->driver_control&=(~0x02);
        if(\overline{srd_motorx->micrrostep_inc>0) srd_motorx->microstep_inc = -srd_motorx->microstep_inc;}
    }
    else{
        srd_motorx->dir = CW;
        srd motorx->driver control|=0x02; //change direction
        if(srd_motorx->microstep_inc<0) srd_motorx->microstep_inc = -srd_motorx->microstep_inc;
```

```
    sm_set_driver_control(srd_motorx->driver_control);
    // calculate phase currents for the next step
    next_yidx=srd_motorx->driver_state;
    if(next_yidx==0 | | next_yidx==7 || next_yidx==3 || next_yidx==4) next_yidx=0;
        else next yidx=1;
    next xidx=srd motorx->mstep counter+srd motorx->microstep inc
    if(next_xidx>=
                                    next_yidx=(~next_yidx)&0x01;
    if(next xidx<0){ next_xidx+=MICROSTEPS_TABSIZE
                next_\overline{y idx^=0x01;}
                }
    srd motorx->i phaseb=
            (srd_motorx->max_iphase/100)*(microstep_tab[next_yidx][next_xidx])
    srd_motorx->\overline{i}_phasea=
        (srd_motorx->max_iphase/100)*(microstep_tab[(~next_yidx) &0x01] [next_xidx]);
    // If moving only 1 step.
        if(step == 1)
        // Move one step..
        srd_motorx->accel_count = -1
        // ...in DECEL state.
        srd_motorx->run_state = DECEL;
        // Just a short delay so main() can act on 'running'.
        srd_motorx->step_delay = 1000;
        // OCR1A=100;
        }
    // Only move if number of steps to move is not zero.
    else if(step != 0)
    // Refer to documentation for detailed information about these calculations.
    // Set max speed limit, by calc min delay to use in timer.
    // min delay = (alpha / tt)/ w
    srd_mōtorx->min_delay = A_T_x1000 / (speed*srd_motorx->microsteps);
    // Set accelration by calc the first (c0) step delay .
    // step_delay = 1/tt * sqrt(2*alpha/accel)
    // step-delay =
    //( tfreqq*0.676/100 )*100 * sqrt( (2*alpha*10000000000) / (accel*100) )/10000
    srd motorx->step delay =
                (T1_FREQ_148 * sm_sqrt(A_SQ / (accel*srd_motorx->microsteps)))/100
    // Find out after how many steps does the speed hit the max speed limit
    // max_s_lim = speed^2 / (2*alpha*accel)
    srd_motorrx->>max_s_lim = (int32_t) speed*speed/
                (int32_t)(\overline{((int32_t)A_x20000*accel*100)/(100*srd_motorx->microsteps));}
    // If we hit max speed limit before 0,5 step it will round to 0.
    // But in practice we need to move atleast 1 step to get any speed at all
    if(srd_motorx->max_s_lim == 0)
        srd_motorx->max_s_lim = 1;
    }
    // Find out after how many steps we must start deceleration.
    / n1 = (n1+n2)decel / (accel + decel)
    tmp=uint64_mul32(step, decel);
    tmp=uint64_div32(tmp, (accel+decel));
    srd_motorx->accel_lim = (uint32_t)(tmp);
    // \overline{We must accelrāte at least 1- step before we can start deceleration.}
    if(srd motorx->accel_lim == 0)
        srd motorx->accel lim = 1;
    }
    // Use the limit we hit first to calc decel.
    if(srd_motorx->accel_lim <= srd motorx->max_s_lim){
        srd_\overline{motorx->decel_val = srd_motorx->accel_lim - step;}
    }
        srd_motorx->decel_val = -((int32_t)srd_motorx->max_s_lim*accel)/decel;
    }//
    // We must decelrate at least 1 step to stop
    if(srd_motorx->decel_val == 0)
        srd_motorx->decel_val = -1;
    }
    // Find step to start decleration.
    srd_motorx->decel_start = step + srd_motorx->decel_val;
    // If the maximum speed is so low that we dont need to go via accelration state.
    if(srd_motorx->step_delay <= srd_motorx->min_delay){
        srd_motorx->step_delay = srd_motorx->min_delay;
        srd_motorx->run_state = RUN;
    }
        srd_motorx->run_state = ACCEL;
    }
    // Reset counter.
    srd_motorx->accel_count = 0;
    }
    OCR1A=100;
    sm start timer();
318 }
1319
1320 void speed_cntr_Init_Timer1(void)
```

```
srd_sm1.run_state = STOPPED;
// Timer/Counter 1 in mode 4 CTC (Not running).
TCCR1B = (1<<WGM12);
// Timer/Counter 1 Output Compare A Match Interrupt enable.
TIMSK |= (1<<OCIE1A);
28 }
1329
1331 void Motor_Init(void)
1332 {
1333 // Init of IO pins
1334 sm_driver_reset();
1336 sm_motor_init(&srd_sm1, 32, 750, 100);
1337 sr\overline{d}_sm1.\overline{d}river_state}e=0
1338 SM_\overline{CLK_0;}
1340 // Init of Timer/Counter1
    speed_cntr_Init_Timer1();
42 }
1343
1345 void sm1_driver_Step(void)
1346 {int8_t next_xidx,next_yidx;
1347 uint\overline{8}_t step_flag=0;
1348
1349 sm_set_iphase(srd_sm1.i_phasea, srd_sm1.i_phaseb);
1351 if(srd_sm1.microstep_inc>0) srd_sm1.abs_position++; else srd_sm1.abs_position--;
1352 srd_sm1.mstep_counter+=srd_sm1.microstep_inc;
```



```
1354
1355 else if(srd_sm1.mstep_counter<=0) { if(srd_sm1.mstep_counter<0)
357 _ srd_sm1.mstep_counter+=MICROSTEPS_TABSIZE;
1359
1360
1361
1362
1363
1364 i
if(step_flag==1 ) { step_flag=0; //set SPM1CLK to 1
        SM_CL\overline{K_1; //set SPM1CLK to 1}
        srd_sm\overline{1}.driver_state & =0x07;
        SM_CLK_0; ///set SPM1CLK to 0
    next_yidx=(0x66>>srd_sm1.driver_state) & 0x01;
    next_xidx=srd_sm1.mstep_counter+'srd_sm1.microstep_inc;
    if(next_xidx>=MICROSTEPS__TABSIZE) { next_xidx=0;
                next_yidx^=0x01;
    if(next_xidx<0){ next_xidx+=MICROSTEPS_TABSIZE;
        next_yidx^=0x01;
        }
    srd_sm1.i_phaseb=(srd_sm1.max_iphase/100)*(microstep_tab[next_yidx][next_xidx]);
    srd_sm1.i_phasea=(srd_sm1.max_iphase/100)*(microstep_tab[next_yidx^0x01][next_xidx]);
    82 }
1383
1385 //void sm1 update(void)
1386 SIGNAL(SIG_OUTPUT_COMPARE1A)
1387 {
388 OCR1A = srd_sm1.step_delay;
1388 OCR1A = 
1390 switch(srd sm1.run state)
1390 switch(srd_
1391
        case STO\overline{P}
            srd_sm1.step_count = 0;
            srd_sm1.step_coun
            sm_stop_timer(); // Stop Timer/Counter 1.
            sm_stop_timer(); // Stop Timer
            sr\overline{d}_sm1.run_state = STOP\overline{PED;}
            srd_sm1.run_state = STOP\overline{PED;}
            break;
        case ACCEL:
            sm1_driver_Step();
            srd_sm1.step_count++;
            srd_sm1.acce\overline{l_count++;}
            srd_sm1.new_step_delay = srd_sm1.step_delay - (()2 * (int32_t)srd_sm1.step_delay)
            - - + srd_sm1.rest)/(4 * srd_sm1.accel_count + 1));
            srd_sm1.rest = ((2 * (int32_t)srd_sm1.step_delay) +
                srd_sm1.rest)%(4 * srd_sm1.accel_count + 1);
            // Check if we should start decelration.
            if(srd_sm1.step_count >= srd_sm1.decel_start) {
                srd_sm1.accel_count = srd_sm1.decel_val;
                srd_sm1.run_state = DECEL;
            }//
            // Check if we hitted max speed.
            else if(srd_sm1.new_step_delay <= srd_sm1.min_delay)
                    srd_sm1.last_accel_delay = srd_sm\overline{1}.new_ste\overline{p_delay;}
                    srd_sm1.new_step_delay = srd_sm1.min_delay;
                    srd_sm1.rest = 0;
                    srd_sm1.run_state = RUN;
            }
            break;
        case RUN:
            sm1 driver Step().
            sm1_- viver_Step();
```



```
1527 //const char *pstr=str_unknown;
1528
last_speed=speed;
srd motorx=&srd sm1
if(!speed || !volume) return
if(speed>5000) speed=5000
if(volume<0) {sign=-sign
    volume=-volume
    };
    //calculate number of steps for required volume
    steps= uint64 mul32(volume,((uint32 t) 32*FSPR*1000))
    steps= uint64_div32(steps, (uint32_乞)PUMP1_VOL_PER_REVOLUTION);
    stepsdir=(int\overline{3}2_t)steps
    stepsdir*=sign;
    //calculate speed in radians per second *1000
    tmp=uint64 mul32(speed, ((uint32 t) 1000*6283)),
    tmp+=(uint32_t)PUMP1_VOL_PER_REVOLUTION*60/2; //decrease rounding error
    tmp=uint64_div32(tmp,((u\overline{int32}_t)PUMP1_VOL_PER_REVOLUTION*60));
    //adjust acceleration and deceleration
    //accel=(speed/1000)*628;
    tmp2=speed*628
    accel=(uint16_t)(tmp2/1000)
    if (accel<628) accel=628;
srd_motorx->max_iphase = 750
    if(speed>=100) srd_motorx->max_iphase = 1000;
    if(speed>=1000) srd_motorx->max_iphase = 1500;
    speed_cntr_Move(stepsdir, accel, accel, (uint16_t)tmp);
    //print information
    printf_P(PSTR("\n\rStarting BR pump. Pumping %dul @ %dul/min."),volume*sign,speed);
64 }
565
1566 void stop_pump(void)
    (speedRampData *srd motorx;
568
569 srd_motorx=&srd_sm1;
5 7 1 ~ i f ( s r d \& m o t o r x - > r u n ~ s t a t e ~ = = ~ D E C E L ) ~ r e t u r n ; ~ / / r e t u r n ~ i f ~ a l r e a d y ~ d e c e l e r a t i n g ~
2 while(\overline{srd_motorx->run_state == ACCEL); //wait until acceleration is ove}
if(srd_motorx->run_state == RUN){
                    }rd_motorx->step_count = srd_motorx->decel_start;
    printf_P(PSTR("\n\rBR Pump has been stopped."));
    7 }
578
579 //checks if pump is running
580 uint8_t get_pump_status(void)
81 {speedRampData *srd_motorx=&srd_sm1;
1582
if(srd_motorx->run_state == STOPPED) return (OFF);
584 else
85 return(ON);
586 }
5 8 8 ~ / / c h e c k s ~ t h e ~ p u m p i n g ~ p r o g r e s s . ~ r e t u r n s ~ 0 ~ i f ~ t h e ~ p u m p ~ i s ~ s t o p p e d , ~ o t h e r w i s e ~ 1 ~
589 uint8 t get pump progress(brtask statistics *stats)
590 {spee\overline{dRampDäta *'srd_motorx=&srd_sm1;}
591 uint32_t tmp;
592 // uint3}32_t time2end
5 9 3 ~ / / u i n t 8 ~ \overline { t ~ p e r c e n t ~ d o n e ; }
1594 uint8_t rtn_val;
1595 if(srd_motorx->run_state == STOPPED) {rtn_val=0;
                                    stats->percent done=100
                                    stats->time2en\overline{d}=0
                                    // printf_P(PSTR("\n\rBR pump is stopped.\n\r"));
    else{
            tn val=1
            tmp=100UL*srd_motorx->step_count;
            stats>>percent_done=(uint8_t)(tmp/srd_motorx->decel_start);
            if(srd_motorx->decel_start > srd_motorx->step_count)
```



```
            stats->time2end=(tmp*srd_motorx->min_delay)/25\overline{0}000UL;
        // printf_P(PSTR("\n\rBR pump is running.\n\r"));
        // printf_P(PSTR("\n\rBR pump status: \n\rProgress %d %% \n\rTime to end: %d sec"),
    //
    return(rtn_val);
    7 }
1 8
1618
619
61 void get medchange stats(brtask statistics *stats, int16 t volume, uint16 t speed)
6 2 2 ~ \{ b r t a s k ~ s t a t i s t i c s - ~ s t a t 1 ; ~
1623 uint32_t total_time2end;
625 total time2end=(60UL*(abs(volume)+abs(CALIBRATED DEAD VOLUME)))/speed;
626 //printf_P(PSTR("\n\rTotal time to end: %u\n\r"),total_time2end);
```

| 1628 | if (progress [1] < 5) \{stats->percent_done=0; |
| :---: | :---: |
| 1629 | stats->time2end $=$ total_time2end; |
| 1630 | \} - |
| 1631 | else if(progress[1]<6) \{ |
| 1632 | stats->time2end= (60ul*abs (CALIBRATED_DEAD_VOLUME)) /speed; |
| 1633 | get_pump_progress(\&stat1); |
| 1634 | stats->time2end += stat1.time2end; |
| 1635 | stats->percent_done=100- |
| 1636 | (uint8_t) ( 100 UL*stats->time2end+total_time2end/2)/total_time2end); |
| 1637 | \} - - - |
| 1638 | else if(progress[1]<8) \{ |
| 1639 | stats->time2end = (60ul*abs (CALIBRATED_DEAD_VOLUME))/speed; |
| 1640 | stats->percent_done=100- |
| 1641 | (uint8_t) ( 100 L *stats->time2end+total_time2end/2)/total_time2end); |
| 1642 | \} |
| 1643 | else\{ |
| 1644 | get_pump_progress (\&stat1) ; |
| 1645 | stats->time2end = stat1.time2end; |
| 1646 | stats->percent_done=100- |
| 1647 | (uint8_t) ( 100 UL*stats->time2end+total_time2end/2)/total_time2end); |
| 1648 | \} - |
| 1649 | if(stats->percent_done>100) stats->percent_done=0; |
| 1650 |  |
|  |  |
| 1652 | void get_mix_stats (brtask_statistics *stats, int16_t volume, uint16_t speed) |
| 1653 | \{brtask_statistics stat1; |
| 1654 | uint32_t total_time2end; |
| 1655 |  |
| 1656 | total_time2end= (60ul* (abs (volume) ) ) /speed; |
| 1657 | //printf_P(PSTR("\n\rTotal time to end: \%u\n\r"), total_time2end); |
| 1658 |  |
| 1659 | if (progress [3] < 5) \{stats->percent_done=0; |
| 1660 | stats->time2end=total_time2end; |
| 1661 | \} |
| 1662 | else\{ |
| 1663 | get_pump_progress(\&stat1) ; |
| 1664 | stats->time2end = stat1.time2end; |
| 1665 | stats->percent_done=100- |
| 1666 | (uint8_t) ( $100 \mathrm{UL*}$ stats->time2end+total_time2end/2)/total_time2end); |
| 1667 | \} |
| 1668 | if(stats->percent_done>100) stats->percent_done=0; |
| 1669 |  |
| 1670 |  |
| 1671 | void get_prepsamp_stats(brtask_statistics *stats) |
| 1672 | (brtask_statistics stat1; |
| 1673 | uint32_t total_time2end; |
| 1674 - - |  |
| 1675 | total_time2end=60ul*(abs (BR1_MIX_VOL) )/BR1_MIX_SPEED; |
| 1676 | total_-time2end+=60ul* (abs (BR1_SAMP_VOL) )/BĒ1_SĀMP_SPEED; |
| 1677 |  |
| 1678 |  |
| 1679 | if (progress [4] ==0) ( |
| 1680 | get_mix_stats (stats, BR1_MIX_VOL,BR1_MIX_SPEED) ; |
| 1681 |  |
| 1682 - - - - - |  |
| 1683 | stats->time2end+=stat1.time2end; |
| 1684 stats->percent done=100- |  |
| 1685 (uint8_t) ( $\left(\overline{1} 000 L^{*}\right.$ stats->time2end+total_time2end/2)/total_time2end); |  |
| 1686 \} - |  |
| 1687 | else\{ |
| 1688 get mix_stats(stats, BR1_MIX_VOL, BR1_MIX_SPEED) ; |  |
| 1689 stāts->percent_done=100-- - - |  |
| 1690 (uint8_t) ((100UL*stats->time2end+total_time2end/2)/total_time2end); |  |
| 1691 |  |
| 1692 if(stats->percent_done>100) stats->percent_done=0; |  |
| $1693\}$ |  |
| $1694$ |  |
| $1695$ |  |
| 1696 void br_status (void) |  |
| 1697 fuint8_E i; |  |
| 1698 brtask_statistics stat1; |  |
| $1699$ |  |
| 1700 /* |  |
| 1701 | br_status_flags |
| 1702 br1_pump_speed |  |
| 1703 valves - |  |
| 1704 pump: percent done |  |
| 1705 pump: time to end |  |
| 1706 1707 | 1707 task: percent done |
| 1708 task: time to end |  |
| 1709 |  |
| 1710 perfusion speed |  |
| 1711 medium change speed |  |
| 1712 medium change volume |  |
| 1713 */ |  |
| 1714 i2c_txflush(); |  |
| 1715 |  |
| 1716 i=0; |  |
| 1717 if(br1_perfusion) il=0x01; |  |
| 1718 if (br1_make_sample) il $=0 \times 02$; |  |
| 1719 if (br1-changing_medium) il $=0 \times 04$; |  |
| 1720 if (get_pump_status () $==0 \mathrm{~N}$ ) $\mathrm{i} \mid=0 \times 80$; |  |
| 1721 i2c_putchar(i); |  |
| 1722 /* ${ }^{\text {c }}$ |  |
| 1723 if (br1_changing_medium) \{ |  |
|  | i2c_putchar(medium_change_speed/256); |
| 1725 | i2c_putchar (medium_change_speed\%256); |
| 1726 | \} - - - |
| 1727 | else\{ |
| 1728 | i2c_putchar (br1_pump_speed/256); |
| 1729 | i2c_putchar (br1_pump_speed\%256); |

```
*/
i2c_putchar(last_speed/256);
i2c_putchar(last_speed%256);
i=PINA&0x3F;
i|=PINC&0xC0;
i2c_putchar(i).
get_pump_progress(&stat1)
i2c putchar(stat1.percent done);
i2c - putchar(stat1.time2en\overline{d}/256);
i2c-putchar(stat1.time2end%256).
if(brl_make_sample) get_prepsamp_stats(&stat1);
else if(br1 changing medium)
    get_medchange_stats(&stat1,medium_change_vol,medium_change_speed);
i2c_putchar(stat1.percent_done);
i2c_putchar(stat1.time2end/256);
i2c_putchar(stat1.time2end%256);
i2c_putchar(br1_pump_speed/256);
i2c_putchar(br1_pump_speed%256);
i2c_putchar('\n');
*
757
60 compare string with message in RX buffer
1760 unsigned char buf_strcmp(PGM_P stringp,const char *strbuf)
1762 char tmp[20];
1764 len=strlen_P(stringp); // get length of string to compare
1765 if(len>19) len=19;
1766 for(i=0;i<len;i++){tmp[i]= *strbuf++;
1768 tmp[i]=0\times00;
1769 i=strcasecmp_P(tmp,stringp);
1770 i=strcasecmp_P(tmp,stringp);
1771 if(i) return(1);
return (0):
1773 }
5 void send_status(void)
776 {
1 7 7 7
1778 printf_P(PSTR("\r\nCURRENT STATE: "));
779 if(srd_sm1.run_state==STOP) printf_P(PSTR("STOP \r\n"));
780 if(srd_sm1.run_state==RUN) printf_ P
1781 if(srd_sm1.run_state==ACCEL) printf_P(PSTR("ACCELERATING \r\n"));
1782 if(srd_sm1.run_state==DECEL) printf_P(PSTR("DECELERATING \r\n"));
1783
1784 }
1786 char* find_number(char *position)
1787 {
1788 while(!isdigit((int)position) && (*position!='+') && (*position!='-')){
1789 position++;
1790 1791 }
1792 return(position);
1793 }
1795 char* find_next_number(char *position)
1795 ch
while(isdigit((int)position)) { position++;
                                    if(position>=rxbuf+RXBUFSIZE) return(NULL);
    #, }
    position=find number(position);
    return(position);
|
803
804
1805
1806
807
808 //********************** BIOREACTOR ROUTINES ***************
1809
811 uint8_t br1_init(void)
1812 {
1813 control_solenoid(BR1_V1, OFF);
814 control_solenoid(BR1_V2, OFF);
1815 control_solenoid(BR1_V3, OFF);
1816 control_solenoid(BR1_V4, OFF);
1817
1818 return(STEP_FINISHED);
819 }
1820
1822 uint8_t br1_change_medium(int16_t volume, uint16_t speed)
1823 {
1824 //first stop the pump
1825 if(progress[1]==0) {
```



```
828 return(STEP_RUNNING);};
1829 //then switch all valves to correct position
1829 //then switch all valves to correct position 
    progress[1]=2;
```

```
1832 
if(progress[1]==2) {if(dela\overline{y_timer_br) return(STEP_RUNNING);}
progress[1]=\overline{3}
    control solenoid(BR1 V2, ON);
    delay_timer_br=20;
    return(STEP RUNNING);},
if(progress[1]==3){if(delay__timer_br) return(STEP_RUNNING);
    progress[1]=}=\overline{4
    control solenoid(BR1 V3, OFF);
    control-solenoid(BR1_V4, OFF);
    delay t\overline{imer br=20;}
    return(STEP-br=20;
//start the pump at medium change speed and volume
if(progress[1]==4){if(delay_timer_br) return(STEP_RUNNING);
            progress[1]=5;
            start_pump (volume, speed)
            return(STEP_RUNNING);};
if(progress[1]==5) {if(get_pump_status()==ON) return(STEP_RUNNING);
    progress[1]=6
    control_solenoid(BR1_V1, OFF);
    control_solenoid(BR1_V2, OFF);
    delay_timer_br=20;
    return(STEP_RUNNING);};
if(progress[1]==6){if(delay_timer_br) return(STEP_RUNNING);
    progress[1]=\overline{7}
    control_solenoid(BR1_V3, ON)
    delay_timer_br=20;
    return(STEP_RUNNING);};
//start the pump at medium change speed to flush the medium from calibrated tubing
if(progress[1]==7) {if(delay_timer_br) return(STEP_RUNNING);
    progress[1]=8;
        start pump(CALIBRATED_DEAD VOLUME,speed)
        return(STEP RUNNING);};
    if(progress[1]==8){if(get pump-status()==ON) return(STEP RUNNING)
        progress[1]=9;
    control_solenoid(BR1_V3, OFF);
    delay timer br=20
    return(STEP_RUNNING);};
//END
if(progress[1]==9){if(delay_timer_br) return(STEP_RUNNING);
        progress[1]=0
        return(STEP_FINISHED);
    };
    //this is never reached
    return(STEP_RUNNING);
2 }
uint8_t br1_sample(int16_t volume, uint16_t speed)
f //
if(pst stop the pump
if(progress[2]==0) {
        progress[2]=1
        stop_pump();
        return(STEP_RUNNING); ;
    //then switch all valves to correct position
if(progress[2]==1){if(get_pump_status()!=OFF) return(STEP_RUNNING);
        progress[2]=2;
        control solenoid(BR1_V1, ON)
        delay tímer br=20;
        return(STEP_RUNNING);};
if(progress[2]==2){if(dela\overline{y_timer_br) return(STEP_RUNNING);}
    progress[2]=\overline{3}
    control solenoid(BR1 V2, ON)
    delay tímer br=20;
    return(STEP RUNNING);}
if(progress[2]==3){if(delay__timer_br) return(STEP_RUNNING);
        progress[2]=}
        control_solenoid(BR1_V4, ON)
    delay timer br=20
    return(STEP RUNNING);}
if(progress[2]==4){if(delay__timer_br) return(STEP_RUNNING);
    progress[2]=5
    control_solenoid(BR1_V3, OFF);
    delay_timer_br=20;
    return(STEP_RUNNING);},
//then run the pump at samp
if(progress[2]==5){if(delay_timer_br) return(STEP_RUNNING);
    progress[2]=
        start_pump (volume, speed)
        return(STEP_RUNNING);};
    //then switch off all valves
if(progress[2]==6){if(get_pump_status()==ON) return(STEP_RUNNING)
        progress[2]=7;
        control_solenoid(BR1_V1, OFF);
        control_solenoid(BR1_V2, OFF);
        control_solenoid(BR1_V4, OFF);
        delay_timer_br=20
        return(STEP_RUNNING);};
    //END
        =7) {if(delay_timer_br) return(STEP_RUNNING);
        progress[2]=\overline{0}
        return(STEP_FINISHED);
        ret
    //this is never reached
    return(STEP_RUNNING);
```

```
    uint8_t br1_mix_sample(int16_t volume, uint16_t speed)
1936 {
1937 //first stop the pu
if(progress[3]==0){
    return(STEP RUNNING); }
//then switch all valves t\overline{o correct position}
if(progress[3]==1){if(get_pump_status()!=OFF) return(STEP_RUNNING);
        progress[3]=2;
        control_solenoid(BR1_V3, ON)
        delay t\overline{imer br=20;}
        return(STEP RUNNING);}
if(progress[3]==2){if(dela\overline{y}_timer_br) return(STEP_RUNNING);
        progress[3]=\overline{3}
        control solenoid(BR1_V4, ON)
        delay timer_br=20
        return(STEP_RUNNING);}
if(progress[3]==3){if(delay_timer_br) return(STEP_RUNNING);
        progress[3]=4
        control_solenoid(BR1_V1, OFF);
        control_solenoid(BR1_V2, OFF);
        delay_timer_br=20;
        return(STEP_RUNNING);};
//take the time point and wait mix tim
if(progress[3]==4) {if(delay__imer_br) return(STEP_RUNNING);
        progress[3]=5;
        if(get_pump_status()==OFF) start_pump(volume, speed)
            return(STEP_RUNNING);)
//then switch off all valves
if(progress[3]==5){if(get_pump_status()==ON) return(STEP_RUNNING)
        progress[3]=6;
        control_solenoid(BR1 V3, OFF);
        control solenoid(BR1-V4, OFF);
        delay timer br=20
        return(STEP RUNNING) ; ;
    //END
if(progress[3]==6) {if(delay timer_br) return(STEP RUNNING);
        progress[3]=0
        return(STEP FINISHED)
        };
//this is never reached
return(STEP_RUNNING);
79 }
981 uint8_t br1_prepare_sample(void)
982 {uint\overline{8}_t result;
984 //first fill the calibrated tubing length with the old medium
985 if(progress[4]==0) {result=br1_change_medium(BR1_SAMP_VOL,BR1_SAMP_SPEED)
if(result==STE\overline{P}_RUNNING) return(\overline{STEP_}\mp@subsup{\overline{R}}{~}{\prime}UNNING);
    progress[4]=1
        return(STEP_RUNNING);}
    //then flush that volume into the dilution container and mix with air
    if(progress[4]==1) {result=br1_mix_sample(BR1_MIX_VOL,BRI_MIX_SPEED);
        if(result==STEP_RUNNING) return(STEP_RUNNING);
        progress[4]=0;
        return(STEP_FINISHED);};
    //this is never reached
    return(STEP_RUNNING);
997
1 9 9 9 \text { void bioreactor_sequencer(void)}
{uint8 t status;
if((!br1 make sample) && (!br1_changing_medium)) {
        if(br1_perfusion)
                                    if(get pump status()==OFF)
                                    start_pump(BR1_PERFUS_VOL, BR1_PERFUS_SPEED);
            else{
                //if(get_pump_status()==ON) stop_pump();
                };
if(brl_make_sample) {if(br1_make_sample==1) {br1_make_sample++;
        eeprom_write_byte((uint8_t \overline{ }) EE_\overline{BR1_MAKESAMPLE,br1_make_sample);}
        printf_P(PST\overline{R}("\n\rprepar̄ing sample"));}
        status=br1_prepare sample();
        if(status==STEP_FINISHED) {
            br1_make_sample=0;
            eeprom_write_byte((uint8_t *)EE_BR1_MAKESAMPLE,br1_make_sample);
            printf_P(PSTR("\n\rsample ready"));
        }
        }
    if(br1_changing_medium && (!br1_make_sample))
    if(br1_changing_medium==1) {br1_changing_medium++;
        printf_P(PSTR("\n\rstart of the medium change"));
        status=brl change medium(medium change vol,medium change speed);
        if(status==STEP_FINISHED)
            brl_changinggmedium=0;
            ~
        }
,
2034
2035
```

```
2037
2039 void parse_msg(void)
2040 {uint8_t cmderr=CMD_ERR_CMD;
2041 char *msgptr;
2042 int16_t cmdparameters[8];
2043 brtask__statistics mstats;
2044
2045
2047
2048
//switch on/off the solenoid valve
2050 if(!buf_strcmp(cmd_valve,msgptr)) {cmderr=CMD_OK;
msgptr+=strlen}(cmd_valve)
2052 //read the 1st parameter - the valve number
2053 cmdparameters[0]=(uint16_t) strtol(msgptr, &msgptr, 0)
2054 if(cmdparameters[0]<1 || cmdparameters[0]>8) cmderr=CMD_ERR_PARAM;
2055 if(*msgptr != ' ') cmderr=CMD_ERR_PARAMCNT;
2056 //read the 2nd parameter - on(1) of off(0)
if(cmdparameters[1]!=0 && cmdparameters[1]!=1) cmderr=CMD_ERR_PARAM;
2059 if
2061 
063 //start pump
2064 else if(!buf_strcmp(cmd_startpump,msgptr)) {cmderr=CMD_OK;
2065
2066
2067
2068
2069
2070
2071
2072
2073
2074
2075
2078
2079
2080
2081 }
2082 //stop pump
2083
2084
2085
2086
2086
2088
2089
2090
2091
2093
2094
2095
2096
2097
2100
2101
2102
2104
2106
2107
2108
2111
2112
2114
2115
2117
21190 //
2120
2121
2123
2123
2124
2125
2126
2127
2128
2129
2130
2131
2132
2133 //chan
2134 //change the cultivation medium
2135
    else if(!buf_strcmp(cmdb_changemed,msgptr)) {cmderr=CMD_OK;
    msgptr+=strlen(cmd\overline{b}_changemed);
    msgptr+=strlen(cmdb_changemed); (lread the 1st parametium volume to change
```

```
2138
    if(cmdparameters[0]<-100000 || cmdparameters[0]>10000) cmderr=CMD_ERR_PARAM;
    if(*msgptr != ' ') cmderr=CMD_ERR_PARAMCNT;
        //read the 2nd parameter - the pump speed
        cmdparameters[1]=(uint16_t) strtol(msgptr, &msgptr, 0);
        if(cmdparameters[1]<1 || cmdparameters[1]>500) cmderr=CMD_ERR_PARAM;
        if(cmderr==CMD OK)
            medium change vol=cmdparameters[0]:
            medium change-
            br1 chänging medium=1;
                    }
    }
    //sample the cultivation medium
    else if(!buf_strcmp(cmdb_sample,msgptr)) {cmderr=CMD_OK;
    msgptr+=strlen(cmdb sample);
    //read the 1st parameter - the medium volume to chang
    cmdparameters[0]=(uint16_t) strtol (msgptr, &msgptr, 0)
    if(cmdparameters[0]<0 || cmdparameters[0]>10000) cmderr=CMD_ERR_PARAM;
    if(*msgptr != ' ') cmderr=CMD_ERR_PARAMCNT;
        //read the 2nd parameter - the pump speed
        cmdparameters[1]=(uint16_t) strtol(msgptr, &msgptr, 0);
        if(cmdparameters[1]<1 || cmdparameters[1]>500) cmderr=CMD_ERR_PARAM;
    if(cmderr==CMD_OK)
        while(br1_sample(cmdparameters[0],cmdparameters[1]) != STEP_FINISHED)
    }
    //mix the sample during dilution
    else if(!buf strcmp(cmdb mix,msgptr)){cmderr=CMD_OK;
    msgptr+=strlen(cmdb_mix);
    //read the 1st parameter - the air volume to pump
    cmdparameters[0]=(uint16_t) strtol(msgptr, &msgptr, 0)
    if(cmdparameters[0]<1 || cmdparameters[0]>30000) cmderr=CMD_ERR_PARAM;
    if(*msgptr != ' ') cmderr=CMD_ERR_PARAMCNT;
        //read the 2nd parameter - the pump speed
        cmdparameters[1]=(uint16 t) strtol(msgptr, &msgptr, 0).
        if(cmdparameters[1]<1 || cmdparameters[1]>500) cmderr=CMD_ERR_PARAM
    if(cmderr==CMD OK){
            while(br1_mix_sample(cmdparameters[0],cmdparameters[1]) != STEP_FINISHED)
            }
    }
    //mix the sample during dilution
    else if(!buf_strcmp(cmdb_prepsample,msgptr)){cmderr=CMD_OK;
        if(cmderr==CMD_OK)
            br\overline{1_make_sample=1}
                eeprom_write_byte((uint8_t *)EE_BR1_MAKESAMPLE,br1_make_sample)
            }
    }
    //change washing manifold pump speed
    else if(!buf_strcmp(cmdb_setspeed,msgptr)) {cmderr=CMD_OK,
    msgptr+=strlen(cmdb_setspeed);
    //read the 1st parameter - the bioreactor perfusion speed
    cmdparameters[0]=(uint16_t) strtol(msgptr, &msgptr, 0);
    if(cmdparameters[0]<1 || cmdparameters[0]>500) cmderr=CMD_ERR_PARAM;
    if(cmderr==CMD_OK) {
                br1_pump_speed=cmdparameters[0];
                eeprom_write_word((uint16_t *)EE_BR_SPEED,br1_pump_speed);
                    }
    }
    //mix the sample during dilution
    else if(!buf_strcmp(cmdb_stop,msgptr)){cmderr=CMD_OK;
        if(cmderr==CMD OK) {
            br1_chānging_medium=0;
            br1 make sample=0;
            eeprom write byte((uint8 t *)EE BR1 MAKESAMPLE,br1 make sample);
            progress[0]=0;
            progress[1]=0;
            progress[2]=0;
            progress[3]=0;
            progress[4]=0
            br1_init();
            }
    }
    if(cmderr==CMD_OK) printf_P(resp_ok);
    else if(cmderr==CMD_ERR_CMD) printf_P(resp_err_cmd);
    else if(cmderr==CMD_ERR_PARAM) printf_P(resp_err_param);
    else if(cmderr==CMD_ERR_PARAMCNT) printf_P(resp_err_paramcnt);
    new_msg=0;
    rx_ptr=0;
    }
    2229
    2230
    2231
    2 3 3 \text { void load backup(void)}
    234 {
    235 br1 make sample=eeprom read byte((uint8 t *)EE BR1 MAKESAMPLE);
    2236 br1 perfusion=eeprom read byte((uint8 t }\mp@subsup{}{}{-}\mathrm{ *) EE BR1 PERFUSION).
    2237 br1_pump_speed=eeprom_read_word((uint16_t *) EE _BR_SPEED);
2238
2239 if(br1 make sample==0xFF) {br1 make sample=0;
```

```
2240
```

2240
2241
2241
2243
2243
2244
2244
2245
2245
2246
2246
2247
2247
2248
2248
2249
2249
2250
2250
2251
2251
2252
2252
254 int main( void)
254 int main( void)
2255 ///unsigned char i;
2255 ///unsigned char i;
2256 //int tmp;
2256 //int tmp;
2257
2257
2258
2258
259 steps = 200;
259 steps = 200;
2260 acceleration = 2000;
2260 acceleration = 2000;
2261 deceleration = 2000;
2261 deceleration = 2000;
262 speed=10;
262 speed=10;
2263
2263
2264
2264
2265
2265
266 GICR=0x01; //move interrupt vectors to appl section
266 GICR=0x01; //move interrupt vectors to appl section
2267 GICR=0\times00;
2267 GICR=0\times00;
2268
2268
2269 ioinit()
2269 ioinit()
2 2 7 0 uartinit(baudrate);
2 2 7 0 uartinit(baudrate);
2271 fdevopen(uartsend,0);
2271 fdevopen(uartsend,0);
272 printf_P(PSTR("\n\rBIOREACTOR DRIVER START\n\r"));
272 printf_P(PSTR("\n\rBIOREACTOR DRIVER START\n\r"));
2273 T0_start();
2273 T0_start();
2274 adc start();
2274 adc start();
2274 adc_start();
2274 adc_start();
2276 i2c_init(I2C_100k);
2276 i2c_init(I2C_100k);
2277
2277
2 2 7 8 ~ s e i ( ) ;
2 2 7 8 ~ s e i ( ) ;
2279 tim ena=1;
2279 tim ena=1;
2280 Motōr_Init()
2280 Motōr_Init()
2281
2281
2282 LEDR ON;
2282 LEDR ON;
2283 delaȳ(250);
2283 delaȳ(250);
284 LEDR OFF;
284 LEDR OFF;
2285 LEDG_ON;
2285 LEDG_ON;
2286 delaȳ(250);
2286 delaȳ(250);
2287 LEDG_OFF;
2287 LEDG_OFF;
2288
2288
2289
2289
2290
2290
2291 SOL_SET_5V;
2291 SOL_SET_5V;
2292 br1_init();
2292 br1_init();
2293 loa\overline{d_backup();}
2293 loa\overline{d_backup();}
2294 /*
2294 /*
2295 i2c_putchar('1');
2295 i2c_putchar('1');
2296 i2c_putchar('2')
2296 i2c_putchar('2')
2297 i2c_putchar('3'),
2297 i2c_putchar('3'),
2298 i2c_putchar('\n');
2298 i2c_putchar('\n');
2299 */
2299 */
2300 while(1) {
2300 while(1) {
2302 if(new msg) parse msg();
2302 if(new msg) parse msg();
2303 if(i2c_newmsg) parse_i2c_command();
2303 if(i2c_newmsg) parse_i2c_command();
2304 bioreactor_sequencer();
2304 bioreactor_sequencer();
2306 if(i2c buserror) {TWCR=0;
2306 if(i2c buserror) {TWCR=0;
2308 //i2c_buserror=0;
2308 //i2c_buserror=0;
i2c_iñit(I2C_100k);
i2c_iñit(I2C_100k);
};
};
2309
2309
2310
2310
2310
2310
2311
2311
2312
2312
2313
2313
2314
2314
return 0;

```
return 0;
```


## Appendix 11 - Listing of the source code for control unit for

## smart drivers



```
94 #define EE_TENA1 
96 #define EE_TENA3 0x72
#define EE TENA4 0x73
#define EE TENA5 0x74
#define EE-TENA6 0x75
#define EE-TENNA7 0x75
#define EE_TENA7 0x76
#define EE_TENA8 0x77
#define EE_TFIRST_START1 0x80
#define EE_TFIRST_START2 0x88
#define EE TFIRST START3 0x90
#define EE-TFTRST- START4 0x98
#define EF-TFTRST- START5 0xA0
#define F-MFISST- SARG 0xA8
```



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#define EE_TFIRST_START8 0xB8
#define EE_TNEXT_START1 0xC0
#define EE_TNEXT_START2 0xC8
#define EE_TNEXT_START3 0xD0
#define EE_TNEXT_START4 0xD8
#define EE_TNEXT_START5 0xE0
#define EE_TNEXT_START6 0xE8
#define EE_TNEXT_START7 0xF0
#define EE_TNEXT_START8 0xF8
void timer_init(void);
void update_schedule status(uint8_t channel)
void recalculate_schedule(uint8_t channel);
void print_global_diag(void);
extern uint8_t SmallFont[],
extern uint8_t BigFont[];
extern uint8_t Dingbats1_XL[];
// Remember to change the model parameter to suit your display module
UTFT myGLCD (ITDB50,38,39,40,41)
UTouch myTouch (6,5,4,3,2);
// Finally we set up UTFT Buttons :)
UTFT_Buttons myButtons(&myGLCD, &myTouch);
// Init the DS3231 using the hardware interface
DS3231 rtc(SDA, SCL);
// Init a Time-data structure
Time t;
int inByte = 0; // incoming serial byte
byte x = 0;
unsigned char i2c_txbuf[16];
int but0, but1, but2, but3, but4, but5, but6;
int but7, but8, but9, butDEL, butOK, butBACK;
int but_perstart, but_perstop, but_medstart;
int but_sampstart, but_reset, but_timer, but_sched;
int but_v1, but_v2, but_v3, but_v4, but_pump;
uint8_t i2c_adr_tab[8];
uint1\overline{6}_t medchg_vol_tab[8];
uint16_t medchg_speed_tab[8];
char* dw tab[]={"Mon","Tue","Wed","Thu","Fri","Sat","Sun"};
#define MAX REPEATES 10
#define MAX INTERVAL HOURS 99
#define INTERCHANNEL_DELAY 3
uint8 t timer intervals hour[8];
uint8 - t timer intervals minutes[8];
uint8_t timer_repeates__total[8];
uint8 t timer_repeates left[8];
uint8_t timer_enables[8];
Time timer_next_start[8];
Time timer_first_start[8];
char diag_msg[128];
uint8_t br_connections[8]={0,0,0,0,0,0,0,0};
void save_start_time_eeprom(uint8_t channel, Time* src)
f
EEPROM.write(EE_TFIRST_START1+8*(channel-1)+0, src->sec);
EEPROM.write(EE_TFIRST_START1+8*(channel-1)+1, src->min);
EEPROM.write(EE_TFIRST_START1+8*(channe1-1) +2, src->hour);
EEPROM.write(EE_TFIRST_START1+8*(channel-1)+3, src->date);
EEPROM.write(EE_TFIRST_START1+8*(channel-1)+4, src->mon);
EEPROM.write(EE_TFIRST_START1+8*(channel-1)+5, (src->year)/256);
EEPROM.write(EE_TFIRST_START1+8*(channel-1)+6, (src->year)%256);
EEPROM.write(EE_TFIRST_START1+8*(channel-1)+7, src->dow );
}
void load_start_time_eeprom(uint8_t channel, Time* dest)
{uint8_t error = 0;
    dest->sec= EEPROM.read(EE TFIRST START1+8*(channel-1)+0);
    if(dest->sec > 59) {dest->sec=0; error++;}
dest }>\mathrm{ >min= EEPROM.read(EE TFIRST START1+8*(channel-1)+1);
if(dest->min > 59) {dest->min = 0}\mathrm{ ; error++;}
```

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dest->hour= EEPROM.read(EE_TFIRST_START1+8*(channel-1)+2);
dest->date= EEPROM.read(EE_TFIRST_START1+8*(channel-1)+3);
if(dest->date > 31) {dest->date = 1; error++;}
dest->mon= EEPROM.read(EE_TFIRST_START1+8*(channel-1)+4);
if(dest->mon > 12) {dest->mon = 1; error++;}
dest->year= 256*EEPROM.read(EE_TFIRST_START1+8*(channel-1) +5);
dest->year += EEPROM.read(EE_TFIRST_START1+8*(channel-1)+6);
if(dest->year > 9999) {dest->year = 2000; error++;}
dest->dow = EEPROM.read(EE TFIRST START1+8*(channel-1)+7);
dest->dow = EEPROM.read(EE_TFIRST-START1+8* (
if(error) save_start_time_eeprom(channel, dest);
}
void timer_init(void
{char i;
    for(i=0;i<8;i++){
    timer_intervals_hour[i]=EEPROM.read(EE_TINT_HRS1+i);
        if( t\overline{imer_intervals_hour[i]>MAX_INTERVAL_HOURS) timer_intervals_hour[i]=MAX_INTERVAL_HOURS;}
        timer_inteervals_minütes[i]=EEPROM.read(EE_TINT_MIN1+i);
        if(timer_intervals_minutes[i]>59) timer_intervals_minutes[i]=59;
        imer_repeates_total[i]=EEPROM.read(EE_TREP_TOT1+i);
        f(timer_repeates_total[i]>MAX_REPEATES) timer_repeates_total[i]=MAX_REPEATES;
        timer_repeates_left[i]=EEPROM.read(EE_TREP_LEFT1+i);
        f(timer_repeates_left[i]>MAX_REPEATES) timer_repeates_left[i]=MAX_REPEATES;
        timer_enables[i]=EEPROM.read(EE_TENA1+i);
        f(timer enables[i]>1) timer enables[i]=1;
        load_start_time_eeprom(i+1, &timer_first_start[i]);
        calc_next_start(i+1);
    }
}
void setup()
{char i;
    uint8 t tmp;
    uint1\overline{6}t tmp16;
    Wire.begin(); // join i2c bus (address optional for master)
    Serial.begin(115200)
    // Setup the LCD
    myGLCD.InitLCD()
    myGLCD.setFont(SmallFont);
    // Clear the screen and draw the frame
    myGLCD.clrScr();
    myTouch.InitTouch (LANDSCAPE);
    myTouch.setPrecision(PREC_MEDIUM);
    myTouch.calibrateRead(); //used to properly initialize XPT2046 - and enable the IRQ
    myButtons.setTextFont(BigFont);
    myButtons.setSymbolFont(Dingbats1_XL);
    // Initialize the rtc object
    rtc.begin();
    timer_init();
    for(i=0;i<8;i++){
        tmp=EEPROM.read(EE_I2CADR1+i);
        if(!tmp || tmp>127)}{tmp=127; EEPROM.write(EE_I2CADR1+i,tmp);
        i2c_adr_tab[i]=tmp;
        tmp16=EEPROM.read(EE MEDCHG VOL1+2*i);
        tmp16=tmp16<<8;
        tmp16+=EEPROM.read(EE MEDCHG VOL1+2*i+1);
        if(!tmp16 || tmp16>99}\overline{9}9) (tmp\overline{1}6=9999
                            EEPROM.write(EE_MEDCHG_VOL1+2*i,tmp16/256);
                            EEPROM.write(EE_MEDCHG_VOL1+2*i+1,tmp16&0xFF);
                            };
    medchg_vol_tab[i]=tmp16;
        tmp16=EEPROM.read(EE_MEDCHG_SPEED1+2*i);
        tmp16=tmp16<<8;
        tmp16+=EEPROM.read(EE MEDCHG SPEED1+2*i+1);
        if(!tmp16 || tmp16>500 ){tmp1\overline{6}=50;
                            EEPROM.write(EE_MEDCHG_SPEED1+2*i,tmp16/256);
                            EEPROM.write(EE_MEDCHG_SPEED1+2*i+1,tmp16&0xFF);
                            };
        medchg_speed_tab[i]=tmp16;
        };
    diag_out("System Power ON.");
    for(i=1;i<9;i++) draw_status(i,0);
    print_global_diag();
}
uint8_t is_leap_year(uint16_t year)
return ((year & 3) == 0) && ((year % 400 == 0) || (year % 100 != 0))
}
//returns 1 if thistime os on future
    // returns 0 otherwise
    int8_t is_time_future(uint8_t channel, Time* thistime)
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```
thistime->sec = ((channel-1)*INTERCHANNEL_DELAY)%60;
curtime = rtc.getTime()
if(thistime->year > curtime.year) return(1);
if(thistime->year < curtime.year) return(0);
f(thistime->mon > curtime.mon) return(1);
if(thistime->mon < curtime.mon) return(0);
if(thistime->date > curtime.date) return(1);
if(thistime->date < curtime.date) return(0);
if(thistime->hour > curtime.hour) return(1);
if(thistime->hour < curtime.hour) return(0);
if(thistime->min > curtime.min) return(1);
if(thistime->min < curtime.min) return(0);
if(thistime->sec > curtime.sec) return(1);
if(thistime->sec < curtime.sec) return(0);
return(0)
}
void calc_incr_start(uint8_t channel, Time* begining, Time* result)
}uint16_t tmp_hours,
uint16_t tmp_minutes;
uint8_t day_limit;
Time tmptime;
tmp_hours = timer_intervals_hour[channel-1];
tmp_minutes = timēr_interval`_minutes[channel-1];
tmptime.sec=0;
tmptime.min=begining->min;
tmptime.hour=begining->hour;
tmptime.date=begining->date;
tmptime.mon=begining->mon;
tmptime.year=begining->year;
tmptime.min+=tmp minutes;
    if(tmptime.min>5\overline{9}){tmptime.min-=60; tmptime.hour++;;}
    tmptime.hour+=tmp hours % 24;
    if(tmptime.hour>2\overline{3}) {tmptime.hour-=24; tmptime.date++;};
    tmptime.date+=(tmp_hours / 24);
    day_limit=31
    if(tmptime.mon==1 || tmptime.mon==3 || tmptime.mon==5 | tmptime.mon==7 ||
    tmptime.mon==8 | | tmptime.mon==10 || tmptime.mon==12) day_limit--;
if(tmptime.mon==2){ day_limit=28;
                                    if(is_leap_year(tmptime.year)) day_limit++;
                    };
    if(tmptime.date>day_limit){tmptime.date-=day_limit; tmptime.mon++;},
    if(tmptime.mon>12){tmptime.mon=1; tmptime.year++;};
    result->sec=tmptime.sec;
    result->min=tmptime.min;
    result->hour=tmptime.hour;
    result->date=tmptime.date;
    result->mon=tmptime.mon;
    result->year=tmptime.year;
}
int8 t calc next start(uint8 t channel)
//uint16_t Emp_hours;
    //uint16_t tmp_minutes;
    uint8 t \overline{day limit,i;}
    Time Emptime,
    //tmp hours = (uint16 t)timer repeates left[channel-1] * timer intervals hour[channel-1]
    //tmp_minutes = (uint\overline{1}6_t)timer_repeates_left[channel-1] * timer_intervals_minutes[channel-1];
    tmptime.sec=0;
    tmptime.min=timer first start[channel-1].min;
    tmptime.hour=timer_first_start[channel-1].hour
    tmptime.date=timer_first_start[channe1-1].date
    tmptime.mon=timer first_start[channel-1].mon;
    tmptime.year=time\overline{r}_firs\overline{t}_start[channel-1].year;
    i=timer_repeates_total[channel-1];
    while(i)
        if(is_time_future(channel, &tmptime)) break;
        calc_incr_start(channel, &tmptime, &tmptime);
        i--;
    }
    timer_repeates_left[channel-1]=i
    timer_next_start[channel-1].sec=tmptime.sec;
    timer_next_start[channel-1].min=tmptime.min;
    timer_next_start[channel-1].hour=tmptime.hour
    timer_next_start[channel-1].date=tmptime.date;
    timer_next_start[channel-1].mon=tmptime.mon;
    timer_next_start[channel-1].year=tmptime.year;
    return(1);
}
void br_reset(uint8_t channel)
vo
|
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    diag_out(diag_msg);
    i2c_txbuf[0]=2;
    2c txbuf[1]=0\times32;
    send_i2c_msg(i2c_adr_tab[channel-1],i2c_txbuf);
void control perfusion(uint8 t channel, uint8 t new state)
f if (new state) sprintf(diag}\mathrm{ msg,"Perfusion START 和的 BR unit %d.",channel);
            lse
            sprintf(diag msg,"Perfusion STOP for BR unit %d.",channel);
    diag_out(diag_msg);
    2c txbuf[0]=3
    2c-
    i2c_txbuf[2]=0x00;
    if(new_state) i2c_txbuf[2]++;
    i2c_tx\overline{buf[3]='\n';}
    send_i2c_msg(i2c_adr_tab[channel-1],i2c_txbuf);
}
void control_valve(uint8_t channel,uint8_t valve, uint8_t new_state)
{ if (new_state) sprintf(diag_msg,"Switch Valve%d ON on BR unit %d.",valve,channel);
            else
            sprintf(diag_msg,"Switch Valve%d OFF on BR unit %d.",valve,channel);
    diag_out(diag_msg);
    12c_txbuf[0]=4;
    12c_txbuf[1]=0x38;
    12c txbuf[2]=valve
    i2c_txbuf[3]=0;
    f(new_state) i2c_txbuf[3]++;
    i2c_tx\overline{buf[4]='\n';}
    send_i2c_msg(i2c_adr_tab[channel-1],i2c_txbuf);
}
void set perfusion speed(uint8 t channel,uint16 t pspeed)
{ sprint\overline{f}(diag_msg,"Setting prērfusion speed to %od ul/min for BR unit %d.",pspeed,channel);
    diag out(diag_msg)
    i2c txbuf[0]=4
    2c-txbuf[1]=0\times33.
    i2c-txbuf[2]=(uint8 t)(pspeed/256)
    i2c txbuf[3]=(uint8_t)(pspeed&0xFF)
    i2cttxbuf[4]='\n',
    send_i2c_msg(i2c_adr_tab[channel-1],i2c_txbuf);
}
void start_pump(uint8_t channel, int16_t volume, int16 t pspeed)
{ sprintf(\overline{diag_msg,"SETarting pump of B\overline{R}}\mathrm{ unit %d. Volume : %d, Speed: %d",channel, volume, pspeed);}
    diag_out(diag_msg)
    i2c_txbuf[0]=6;
    i2c_txbuf[1]=0x39;
    12c_txbuf[2]=(uint8_t)(volume/256);
    12c_txbuf[3]=(uint8_t)(volume&0xFF)
    12c_txbuf[4]=(uint8_t) (pspeed/256)
    2c_txbuf[5]=(uint8_t) (pspeed&0xFF)
    2c_txbuf[6]='\n';
    send_i2c_msg(i2c_adr_tab[channel-1],i2c_txbuf);
}
void medium_change(uint8_t channel, int16_t volume, int16_t pspeed)
sprintf(d\overline{iag_msg,"Star}\overline{t}ing medium change
    diag out(diag msg);
    i2c txbuf[0]=6;
    2c txbuf[1]=0\times35.
    2c txbuf[2]=(uint8 t)(volume/256)
    2c- txbuf[3]=(uint8 - t) (volume&0xFF)
    i2c- txbuf[4]=(uint8 ' t)(pspeed/256);
    2c-}\mathrm{ txbuf[5]=(uint8-t)(pspeed&0xFF)
    2c-
    send_i2c_msg(i2c_adr_tab[channel-1],i2c_txbuf);
}
uint8_t get_selected_ch(void)
{uint\overline{8}_t \overline{result;}
int touch_x;
    int touch_y;
    myTouch.read();
    touch_x = myTouch.getX()
    touch_y = myTouch.getY();
    result=touch_y/STAT_SIZEY+1;
    if(touch_x >= STAT_SIZEX) result+=4;
    return(result);
}
#define BUTSIZEX 100
#define BUTSIZEY 50
void draw_keyboard(void)
    but1 = myButtons.addButton(5+0*(BUTSIZEX+10), 479-15-2*BUTSIZEY, BUTSIZEX, BUTSIZEY, "1");
    but2 = myButtons.addButton(5+1*(BUTSIZEX+10), 479-15-2*BUTSIZEY, BUTSIZEX, BUTSIZEY, "2");
    but3 = myButal
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but4 = myButtons.addButton(5+3*(BUTSIZEX+10), 479-15-2*BUTSIZEY, BUTSIZEX, BUTSIZEY, "4"); 
but6 = myButtons.addButton(5+0*(BUTSIZEX+10), 479-5-BUTSIZEY, BUTSIZEX, BUTSIZEY, "6");
but7 = myButtons.addButton(5+1*(BUTSIZEX+10), 479-5-BUTSIZEY, BUTSIZEX, BUTSIZEY, "7");
but8 = myButtons.addButton(5+2*(BUTSIZEX+10), 479-5-BUTSIZEY, BUTSIZEX, BUTSIZEY, "8");
but9 = myButtons.addButton(5+3*(BUTSIZEX+10), 479-5-BUTSIZEY, BUTSIZEX, BUTSIZEY, "9");
but0 = myButtons.addButton(5+4*(BUTSIZEX+10), 479-5-BUTSIZEY, BUTSIZEX, BUTSIZEY, "0");
butDEL = myButtons.addButton(5+5*(BUTSIZEX+10), 479-5-BUTSIZEY, BUTSIZEX, BUTSIZEY, "DEL")
butOK = myButtons,addButton(5+6*(BUTSIZEX+10), 479-5-BUTSIZEY, BUTSIZEX, BUTSIZEY, "OK");
butBACK = myButtons.addButton(5+5*(BUTSIZEX+10), 479-15-2*BUTSIZEY, BUTSIZEX*2+10, BUTSIZEY, "BACK")
myButtons.drawButtons();
}
int16 t read keyboard(int16_t xpos, int16_t ypos, uint8_t len)
lchar num[8];
uint8_t return_home, numptr,i;
int pressed_bütton, result;
if(len>5) len=5;
if(!len) return(0);
myGLCD.setFont (BigFont)
myGLCD.setBackColor(VGA_WHITE);
myGLCD.setColor(VGA_MAROON);
return_home=0;
numptr=0;
while(!return_home)
            if(myTouch.dataAvailable()==true) {
                                    pressed_button = myButtons.checkButtons();
                                    if (pressed_button==but0) (num[numptr++]='0';)
                                    else if(pressed_button==but1) {num[numptr++]='1';}
                                    else if(pressed button==but3) {num[numptr++]='3';
                                    else if(pressed_button==but3) {num[numptr++]='3';
                                    else if(pressed_button==but4) {num[numptr++]='4';}
                                    else if(pressed_button==but5) {num[numptr++]='5';
                                    else if(pressed_button==but6) {num[numptr++]='6';
                                    else if(pressed_button==but7) {num[numptr++]='7';
                                    *)
                                    else if(pressed-button==but9) {num[numptr++]='9'';
                                    else if(pressed button==butDEL) {
                                    if(numptr) numptr--
        else if(pressed_button==butoK) {
                                    return_home=1
                                    if(numptr>len) numptr=len;
                                    for(i=numptr;i<len;i++) num[i]=' ';
                num[len]=0;
                myGLCD.print(num,xpos,ypos);
            }
    sscanf(num,"%d",&result);
    while (myTouch.dataAvailable() == true);
return(result);
}
oid check_num_fields(uint8_t channel)
int result;
    myTouch.read();
    nt touch_x = myTouch.getX();
    if(touch x>190 && touch x<260 && touch y>40 && touch y<80) { //Perfusion speed
                                    myGLCD.setColor(VGA WHITE)
                                    myGLCD.fillRect(200- 50,250,69);
                            result=read keyboard (202, 52,3);
                    if(result<1) result=1;
                    if(result>500) result=500
                    myGLCD.setColor(VGA GRAY)
                            myGLCD.fillRect (200-, 50,250,69);
                            myGLCD.setBackColor(VGA_GRAY);
                    myGLCD.setColor(VGA_RED);
                    sprintf(tmp,"%d",result);
                            myGLCD.print(tmp, 202,52);
                            set_perfusion_speed(channel,result);
                    set
    if(touch_x>0 && touch_x<83 && touch_y>210 && touch_y<260){ //Medium Change Volume
            myGLCD.setColor(VGA_WHITE);
            myGLCD.fillRect(5, 230,5+68,249)
            result=read_keyboard(7, 232,4);
            if(result<1) result=1;
            if(result>9999) result=9999;
            myGLCD.setColor(VGA GRAY);
            myGLCD.fillRect(5, 230,5+68,249);
            myGLCD.setBackColor(VGA GRAY);
            myGLCD.setColor(VGA_RED);
            sprintf(tmp,"%d",result);
            myGLCD.print(tmp,7, 232);
            medchg_vol_tab[channel-1]=result;
            EEPROM.write(EE_MEDCHG_VOL1+2*(channel-1),result/256);
            EEPROM.write(EE_MEDCHG_VOL1+2*(channel-1)+1, result&0xFF);
    f(touch x>190 as touch x<2
                        & & touch y>210 && touch v<260) { //Medium Change Speeed
                        myGLCD.setColor(VGA WHITE);
                        myGLCD.fillRect (200- 230,200+52,249)
                        result=read keyboard(202, 232,3);
```



| 706 |  | myGLCD.fillRect (240+96, 58,240+96+32,77) ; |
| :---: | :---: | :---: |
| 707 |  | myGLCD.setBackColor (VGA_GRAY) ; |
| 708 |  | myGLCD.setColor (VGA_RED) ; |
| 709 |  | sprintf(tmp, "\%02d", result); |
| 710 |  | myGLCD.print (tmp, 240+96, 60); |
| 711 |  | tmp_time=rtc.getTime(); |
| 712 |  | rtc. ${ }^{\text {setTime(tmp_time.hour, tmp_time.min, result) ; }}$ |
| 713 |  | \} |
| 714 | if(touch_x>456 | \&\& touch_x<504 \&\& touch_y>48 \&\& touch_y<87) ( //Day |
| 715 |  | - myGLCD.setColor (VGA_WHITE) ; |
| 716 |  | myGLCD.fillRect (464, 58,464+32,77) ; |
| 717 |  | result=read_keyboard (464, 60,2); |
| 718 |  | if (result<1) result=1; |
| 719 |  | if(result>31) result=31; |
| 720 |  | myGLCD.setColor (VGA_GRAY) ; |
| 721 |  | myGLCD.fillRect (464, 58,464+32,77) ; |
| 722 |  | myGLCD.setBackColor (VGA_GRAY) ; |
| 723 |  | myGLCD. setColor (VGA_RED); |
| 724 |  | sprintf(tmp, "\%02d", result); |
| 725 |  | myGLCD.print(tmp, 464, 60) ; |
| 726 |  | tmp_time=rtc.getTime(); |
| 727 |  | rtc. ${ }^{\text {setDate (result, }}$ tmp_time.mon, tmp_time.year) ; |
| 728 |  | rtc.setDOW(wd (tmp_time.year, tmp_time.mon, result)); |
| 729 |  | \} |
| 730 | if(touch_x>504 | \&\& touch_x<552 \&\& touch_y>48 \&\& touch_y<87) ( //Month |
| 731 |  | myGLCD.setColor (VGA_WHITE) ; |
| 732 |  | myGLCD.fillRect (464+48, 58, 464+48+32,77) ; |
| 733 |  | result=read_keyboard (464+48, 60,2); |
| 734 |  | if (result<1) result=1; |
| 735 |  | if(result>12) result=12; |
| 736 |  | myGLCD.setColor (VGA_GRAY) ; |
| 737 |  | myGLCD.fillRect (464+48, 58,464+48+32,77) ; |
| 738 |  | myGLCD.setBackColor (VGA_GRAY) ; |
| 739 |  | myGLCD. setColor (VGA_RED); |
| 740 |  | sprintf(tmp, "\%02d", result); |
| 741 |  | myGLCD.print (tmp, 464+48, 60) ; |
| 742 |  | tmp_time=rtc.getTime(); |
| 743 |  | rtc.setDate(tmp_time.date, result, tmp_time.year) ; |
| 744 |  | rtc.setDOW(wd (tmp_time.year, result, tmp_time.date)) ; |
| 745 |  | \} |
| 746 | if(touch_x>552 | \&\& touch_x<632 \&\& touch_y>48 \&\& touch_y<87) ( //Year |
| 747 |  | myGLCD. setColor (VGA_WHITE); |
| 748 |  | myGLCD.fillRect (560, 58, 624, 77) ; |
| 749 |  | result=read_keyboard (560, 60, 4) ; |
| 750 |  | if(result<20000) result=2000; |
| 751 |  | if (result>9999) result=9999; |
| 752 |  | myGLCD.setColor (VGA_GRAY); |
| 753 |  | myGLCD.fillRect (560, 58, 624, 77) ; |
| 754 |  | myGLCD.setBackColor (VGA_GRAY) ; |
| 755 |  | myGLCD.setColor (VGA_RED) ; |
| 756 |  | sprintf(tmp, "\%04d", result); |
| 757 |  | myGLCD.print (tmp, 560, 60) ; |
| 758 |  | tmp_time=rtc.getTime() ; |
| 759 |  | rtc. ${ }^{\text {cetDate (tmp_time. }}$ date, tmp_time.mon, result); |
| 760 |  | rtc.setDOW(wd (rēsult, tmp_time.mon, tmp_time.date)); |
| 761 |  | \} |
| 762 | if(touch_x>235 | \&\& touch_x<280 \& \& touch_y>88 \&\& touch_y<127) \{ //Hours of the First Start |
| 763 |  |  |
| 764 |  | myGLCD.fillRect (240, 98,272,117) ; |
| 765 |  | result=read_keyboard (240, 100,2); |
| 766 |  | if (result<0) result=0; |
| 767 |  | if(result>23) result=23; |
| 768 |  | myGLCD.setColor (VGA_GRAY) ; |
| 769 |  | myGLCD.fillRect (240, 98,272,117) ; |
| 770 |  | myGLCD.setBackColor (VGA_GRAY) ; |
| 771 |  | myGLCD. setColor (VGA_RED); |
| 772 |  | sprintf(tmp, "\%02d", result); |
| 773 |  | myGLCD.print (tmp, 240,100) ; |
| 774 |  | timer_first_start[channel-1].hour=result; |
| 775 |  | recalculate_schedule(channel) ; |
| 776 |  | update_schedule_status (channel); |
| 777 |  | save_start_time_eeprom(channel, \&timer_first_start[channel-1]); |
| 778 |  |  |
| 779 | if(touch_x>283 | \&\& touch_ $\mathrm{x}<328$ \&\& touch $\mathrm{y}>888$ \& ${ }^{\text {c }}$ touch_y<127) \{ //Minutes of the First start |
| 780 |  | myGLCD.setColor (VGA_WHITE) ; |
| 781 |  | myGLCD.fillRect ( $240+48,98,240+48+32,117$ ); |
| 782 |  | result=read_keyboard (240+48, 100,2); |
| 783 |  | if(result<0) result=0; |
| 784 |  | if (result ${ }^{\text {c }}$ 59) result $=59$; |
| 785 |  | myGLCD.setColor (VGA_GRAY) ; |
| 786 |  | myGLCD.fillRect (240-48, 98, $240+48+32,117$ ) ; |
| 787 |  | myGLCD.setBackColor (VGA_GRAY) ; |
| 788 |  | myGLCD.setColor (VGA_RED) ; |
| 789 |  | sprintf(tmp, "\%02d", result); |
| 790 |  | myGLCD.print (tmp, 240+48, 100); |
| 791 |  | timer_first_start[channel-1].min=result; |
| 792 |  | recalculate_schedule(channel); |
| 793 |  | update_schedule_status (channel); |
| 794 |  | save_start_time_eeprom(channel, \&timer_first_start[channel-1]); |
| 795 |  | \} - - - - - |
| 796 | if(touch_x>456 | \&\& touch_x<504 \&\& touch_y>88 \&\& touch_y<127) \{ //Day of the First Start |
| 797 |  | myGLCD.setColoror (VGA_WHITE); |
| 798 |  | myGLCD.fillRect (464, $98,464+32,117$ ) ; |
| 799 |  | result=read_keyboard (464, 100,2); |
| 800 |  | if (result<1) result=1; |
| 801 |  | if(result>31) result=31; |
| 802 |  | myGLCD. setColor (VGA_GRAY) ; |
| 803 |  | myGLCD.fillRect (464, 98,464+32,117) ; |
| 804 |  | myGLCD.setBackColor (VGA_GRAY) ; |
| 805 |  | myGLCD. setColor (VGA_RED); |
| 806 807 |  | sprintf(tmp, "\%02d", ${ }^{\text {result) }}$; myGLCD.print (tmp, 464, 100); |



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}
14 void draw brcontrol controls(uint8 t channel)
15 {char msg[24].
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    myGLCD.setColor(VGA_BLACK);
    myGLCD.fillRect(0, 0,799,479);
    myGLCD.setFont(BigFont);
    myGLCD.setFont (BigFont); 
    myGLCD.setBackColor(VGA BLACK);
    sprintf(msg,"BR Unit NR.%d CONTROL",channel);
    myGLCD.print(msg,CENTER,0);
    while (myTouch.dataAvailable() == true);
    myGLCD.setColor(VGA_WHITE);
    myGLCD.drawRect (0, 20,400-2,180-2);
    myGLCD.print("PERFUSION",127,20);
    myGLCD.print("Perf.Speed:",5,50)
    myGLCD.print("ul/min",255,50);
    myGLCD.setColor(VGA_GRAY);
    myGLCD.fillRect(200, 50,250,69);
    but_perstart = myButtons.addButton(25, 150-BUTSIZEY, 150, BUTSIZEY, "START");
    but_perstop = myButtons.addButton(225, 150-BUTSIZEY, 150, BUTSIZEY, "STOP");
    myGLCD.setColor(VGA_WHITE);
    myGLCD.setBackColor(VGA BLACK);
    myGLCD.drawRect(0, 180,400-2,360-2);
    myGLCD.print("MEDIUM CHANGE",95,180);
    myGLCD.print("Volume:",5,210);
    myGGLCD.print("ul",77,230).
    myGLCD.print("Speed:",200,210);
    mYGLCD.print("Speed:",200,210)
    myGLCD.print("ul/min",257,230)
    myGLCD.setColor(VGA_GRAY);
    myGLCD.fillRect(5, 2}30,5+68,249)
    myGLCD.fillRect(200, 230,200+52,249);
    myGLCD.fillRect(200, 230,200+52;
    myGLCD.setBackCo(VI, (VEtColor(VGA RED);
```



```
    sprintf(msg,"%d",me\overline{d}chg_vol_tab[channel-1]);
    nt(msg,7,232);
    sprintf(msg,"%d",medchg_speed_tab[channel-1]);
    myGLCD.print(msg,202,232);
    but_medstart = myButtons.addButton(25, 325-BUTSIZEY, 150, BUTSIZEY, "START");
    but_timer = myButtons.addButton(225, 325-BUTSIZEY, 150, BUTSIZEY, "TIMER");
    myGĪCD.setBackColor(VGA_BLACK);
    myGLCD.setColor(VGA_WHITE);
    myGLCD.print("Next:-",10,338);
    if(timer_repeates_left[channel-1] && timer_enables[channel-1]){
        sprintf(msg,"%02d",timer_next_start[channel-1].hour);
            myGLCD.print(msg,106,338);
            sprintf(msg,"%02d",timer_next_start[channel-1].min);
            myGLCD.print(msg,106+48,\overline{338);}
            sprintf(msg,"%02d",timer_next_start[channel-1].date);
            myGLCD.print(msg,106+108,338);
            sprintf(msg,"%02d",timer_next_start[channel-1].mon);
            myGLCD.print(msg,106+108+48,338);
            sprintf(msg,"%04d",timer_next_start[channel-1].year);
            myGLCD.print(msg,106+108+96,3\overline{3}8);
            myGLCD.print(":",106+32,338);
            myGLCD.print(".",106+108+32,338)
            myGLCD.print(".",106+108+80,338);
    }
    else
    myGLCD.print(" --- ",106,338);
    myGLCD.print(" ---
    myGLCD.setColor(VGA WHITE);
    myGLCD.setColor(VGA_WHITE);
    myGLCD.setBackColor(VGA_BLACK);
    myGLCD.drawRect(400, 20,799,180-2).
    mYGGLCD.print("PREPARE SAMPLE",487,20);
    but_sampstart = myButtons.addButton(400+125, 150-BUTSIZEY, 150, BUTSIZEY, "START");
    myGLCD.setColor(VGA_WHITE);
    myGLCD.setBackColor(VGA BLACK)
    myGLCD.drawRect(400, 180,799,360-2)
    myGLCD.print("MANUAL CONTROL",487,180);
    myGLCD.print("I2C ADDR:",405,210);
    myGLCD.setColor(VGA GRAY);
    myGLCD.fillRect(405+144, 210,405+144+52,229);
    myGLCD.setBackColor(VGA_GRAY);
    myGLCD.setColor(VGA_RED);
    sprintf(msg,"%d",i2c_adr_tab[channel-1]);
    myGLCD.print(msg,405+144+2,210);
    but_v1 = myButtons.addButton(400+10, 350-2*BUTSIZEY-10, 75, BUTSIZEY, "");
    but_v2 = myButtons.addButton(400+10+75+10, 350-2*BUTSIZEY-10, 75, BUTSIZEY, "");
    but_v3 = myButtons.addButton(400+10, 350-BUTSIZEY, 75, BUTSIZEY, "");
    but_v4 = myButtons.addButton(400+10+75+10, 350-BUTSIZEY, 75, BUTSIZEY, "");
    but pump = myButtons.addButton(800-150-10, 350-BUTSIZEY, 150, BUTSIZFY, "");
    but_reset = myButtons.addButton(800-150-10, 350-2*BUTSIZEY-10, 150, BUTSIZEY, "!RESET!");
    draw_keyboard();
    myGLCD.setBackColor(VGA BLUE);
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1013 myGLCD.print("V1",4\overline{3}1,249)
1014 myGLCD.print("V2",431+85,249);
1016 myGLCD.print("V4",431+85,249+60);
1017 myGLCD.print("PUMP",720-32,249+60);
1018
1020 void recalculate_schedule(uint8_t channel)
1022 if(timer_repeates_total[channel-1]==0)
                                    timer_repeates_left[channel-1]=0;
                                    return;
1024
calc_next_start(channel);
027 }
9 void update_schedule_status(uint8_t channel)
{char msg[3\overline{0}];
myGLCD.setBackColor (VGA_BLACK);
    myGLCD.setColor(VGA_WHITTE);
    sprintf(msg,"%02d",timer_repeates_left[channel-1]);
    myGLCD.print(msg, 470,300);
    if(timer_repeates_left[channel-1] && timer_enables[channel-1]){
                sprintf(msg,"%02d",timer_next_start[channel-1].hour);
                myGLCD.print(msg,380,330);
                sprintf(msg,"%02d",timer_next_start[channel-1].min);
                myGLCD.print(msg,380+48,330);
                sprintf(msg,"%02d",timer_first_start[channel-1].sec);
                myGLCD.print(msg, 380+96, \overline{3}30);
                    sprintf(msg,"%02d",timer_next_start[channel-1].date);
                    myGLCD.print(msg,604,330);
                    sprintf(msg,"%02d",timer next_start[channel-1].mon);
                    myGLCD.print(msg, 604+48,㣙30);
                    sprintf(msg,"%04d",timer next start[channel-1].year);
                    myGLCD.print(msg,604+96,330);
                            myGLCD.print(get name weekday(wd(timer next start[channel-1].year,
                            timer_next_start[channel-1].mon, timer_next_start[channel-1].date)),540,330);
            myGLCD.print(":",412,330);
            myGLCD.print (":",412+48,330)
            myGLCD.pr1nt(".",588+48,330)
            myGLCD.pr1. (" ",588+9,330)
            myGLCD.print(",",588,330);
            }
            else
            { myGLCD.print("--- ",380,330);
}
void medium_change_schedule(uint8_t channel)
(char msg[30}]
uint8_t i,tmp,return_home;
int pressed_button;
unsigned long nextUpdate=0;
Time curr_time;
while (myTouch.dataAvailable() == true);
        draw_keyboard();
    myGLCD.setColor(VGA_BLACK);
    myGLCD.fillRect(0, 20,799,360);
    myGLCD.setColor(VGA WHITE).
    myGLCD.setBackColor-(VGA BLACK);
    myGLCD.drawRect(0, 20,799,360-2).
    myGLCD.print("Medium Change scheduler settings:",150,20);
    myGLCD.print("Current time: ",20,60);
    myGLCD.setBackColor(VGA BLACK);
    myGLCD.setColor(VGA WHITE);
    myGLCD.setcolor(":" (% 60),
    myGLCD.print(":",272,60);
    myGLCD.print (",",272+48,60);
    myGLCD.print(".",496,60);
    myGLCD.print(".",496+48,60);
    myGLCD.setColor(VGA_GRAY);
    myGLCD.fillRect(240,58,272,77);
    myGLCD.fillRect (288,58,320,77)
    myGLCD.fillRect (336,58,368,77)
    myGLCD.fillRect(464,58,496,77)
    myGLCD.fillRect(512,58,544,77)
    myGLCD.fillRect(560,58,624,77),
    myGLCD.setColor(VGA_WHITE);
    myGLCD.print("First start: ",20,100);
    myGLCD.setBackColor(VGA_BLACK);
    myGLCD.setColor(VGA_WHITE);
    myGLCD.print(":",272,100);
    myGLCD.print(":",272+48,100)
    myGLCD.print(".",496,100);
    myGLCD.print(".",496+48,100);
    myGLCD.print(",",448,100);
    myGLCD.setColor(VGA_GRAY);
    myGLCD.fillRect (240,98,272,117);
    myGLCD.fillRect(288,98,320,117);
    // myGLCD.fillRect(336,98,368,117);
    myGLCD.fillRect(464,98,496,117);
    myGLCD.fillRec( (512, 98, 56,117);
    MYGLCD fillRect (560, 08,624,117);
```

```
myGLCD.setBackColor(VGA_GRAY);
myGLCD.setColor(VGA_RED);
sprintf(msg,"%02d",\overline{timer_first_start[channel-1].hour);}
myGLCD.print(msg,240,100);
sprintf(msg,"%02d",timer_first_start[channel-1].min);
myGLCD.print(msg,240+48,\overline{100);}
sprintf(msg,"%02d",timer_first_start[channel-1].date);
mprliCD.print(msg,240+224,100).
sprintf(msg,"%02d",timer first_start[channel-1].mon);
myGLCD.print(msg,240+224+48,10\overline{0});
sprintf(msg,"%04d",timer_first_start[channel-1].year);
myGLCD.print(msg,240+224+96,10\overline{0});
myGLCD.print(msg,240+224+g., metBackColor(VGA BLACK);
myGLCD.setBackColor( GGA BLAC
myGLCD.setColor(VGA_WHITE);
//sprintf(msg "%s,",rtc.getDOWStr(FORMAT_SHORT));
myGLCD.print(get_name_weekday(wd(timer_first_start[channel-1].year,
    timer_first start[channel-1].mon, timer_first_start[channel-1].date)), 240+160,100);
    sprint\overline{f}(msg,\overline{"%02d",timer_first_start[chañel-1].sec);}
    myGLCD.print(msg,240+96,\overline{100);}
myGLCD.setColor(VGA_WHITE);
myGLCD.print("Change Period: ",20,140);
myGLCD.print("Number of Changes: ",400,140);
myGLCD.setBackColor(VGA_BLACK);
myGLCD.setColor(VGA_WHITE);
myGLCD.print(":",272,140);
myGLCD.setColor(VGA_GRAY);
myGLCD.fillRect(240,138,272,157);
myGLCD.fillRect(288,138,320,157);
myGLCD.fillRect(700,138,700+32,157);
myGLCD.setBackColor(VGA_GRAY);
myGLCD.setColor(VGA RED);
sprintf(msg,"%02d",\overline{timer_intervals_hour[channel-1]);}
myGLCD.print (msg,240,140);
sprintf(msg,"%02d",timer_intervals_minutes[channel-1]);
myGLCD.print(msg,240+48,140);
sprintf(msg,"%02d",timer_repeates_total[channel-1]);
myGLCD.print(msg,700,140);
myGLCD.setBackColor(VGA BLACK);
myGLCD.setColor(VGA_WHITE);
myGLCD.print("Scheduling is switched ",20,220);
but sched = myButtons.addButton(400, 220-BUTSIZEY/2+8, 75, BUTSIZEY, "");
but_sched = myButtons.add
myGLCD.print("Remaining scheduled starts: ",20,300);
myGLCD.print("Next scheduled start: ",20,330);
myGLCD.print(":",380+32,330);
myGLCD.print(":",380+80,330);
myGLCD.print (", ",588,330);
myGLCD.print(".",588+48,330);
myGLCD.print(".",588+96,330);
update_schedule_status(channel);
return home=0;
while(!return_home)
    if (millis() >= nextUpdate){
                                    nextUpdate = millis() + 250; // set up the next timeout period
                                    // Get data from the DS3231
                                    curr_time = rtc.getTime();
                                    myGLCD.setBackColor(VGA GRAY);
                                    myGLCD.setColor(VGA_RED);
                                    sprintf(msg,"%02d",\overline{curr_time.hour);}
                                    myGLCD.print(msg,240,60);
                                    sprintf(msg,"%02d",curr_time.min);
                                    myGLCD.print(msg,240+48,60);
                                    sprintf(msg,"%02d",curr_time.sec);
                    myGLCD.print (msg,240+96,60);
                    sprintf(msg,"%02d",curr time.date);
                    myGLCD.print (msg, 240+22\overline{4},60);
                    sprintf(msg,"%02d",curr time.mon);
                    myGLCD.print(msg, 240+22\overline{4}+48,60);
                    sprintf(msg,"%04d",curr_time.year);
                    myGLCD.print(msg,240+22\overline{4}+96,60);
                    myGLCD.setBackColor(VGA_BLACK);
                myGLCD.setColor(VGA_WHITE);
                sprintf(msg,"%s,",r\overline{tc.getDOWStr(FORMAT_SHORT));}
                myGLCD.print(msg,240+160,60);
                    myGLCD.setBackColor(VGA BLUE);
                    myGLCD.setColor(VGA_WHITE);
                    if(timer_enables[channel-1]==0) myGLCD.print("OFF",415,220);
                else myGLCD.print(" ON ",415-8,220);
            recalculate_schedule(channel);
            update_schedule_status(channel);
                }
    if(myTouch.dataAvailable()==true) {
        check_timer fields(channel);
        pressed_button = myButtons.checkButtons();
        if (pressed_button==butBACK) {
                                    return_home=1;
if (pressed_button==but_sched) {nextUpdate = millis();
            if(timer enables[channel-1]) timer enables[channel-1]=0;
```

```
1217
1218
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12212
1222
1224 while (myTouch.dataAvailable() == true);
1225
1226
1227 myButtons.deleteAllButtons();
228 draw_brcontrol_controls(channel);
1229 }
1231 void draw_brcontrol(uint8_t channel)
232 {char msg[24];
uint8_t i,tmp,return_home;
int pressed_button;
static uint8_t valve_states[8]={0,0,0,0,0,0,0,0};
br_status tmpstatus;
chār err;
unsigned long nextUpdate=0;
err=get_br_status(channel, &tmpstatus);
    if(!err){tmp=1;
        for(i=0;i<8;i++){valve_states[i]=0;
                                    if(tmpstatus.valves&tmp) valve_states[i]++;
                                    tmp=tmp<<1;
                                    }
    }
draw_brcontrol_controls(channel);
return_home=0;
while(\`return_home){
    if (millis() >= nextUpdate){
        nextUpdate = millis() + 250; // set up the next timeout period
        err=get_br_status(channel, &tmpstatus);
        if(!err) (tmp=1;
        for(i=0;i<8;i++){valve_states[i]=0;
            if(tmpstatus.\overline{valves&tmp) valve_states[i]++;}
            tmp=tmp<<1;
            }
        myGLCD.setBackColor(VGA_BLUE);
        myGLCD.setColor(VGA_WHITE);
        if(!valve_states[BR_V1-1]) myGLCD.print("OFF",431-8,249+16);
            el\overline{se myGLCD.\overline{print(" ON ",431-16,249+16);}}\mathbf{}\mathrm{ (})
        if(!valve_states[BR_V2-1]) myGLCD.print("OFF",431+85-8,249+16);
                el\overline{se myGLCD.p}r\mathrm{ rint(" ON ",431+85-16,249+16);}
        if(!valve_states[BR_V3-1]) myGLCD.print("OFF",431-8,249+60+16);
                els\overline{se myGLCD.p}\textrm{print(" ON ",431-16,249+60+16);}
        if(!valve_states[BR_V4-1]) myGLCD.print("OFF",431+85-8,249+60+16);
                else myGLCD.p
            if((tmpstatus.flags&0x80)==0) myGLCD.print("OFF",720-24,249+60+16);
                else myGLCD.print(" ON ",720-32,249+60+16);
            myGLCD.setBackColor(VGA_GRAY);
            myGLCD.setColor(VGA_RED);
            sprintf(msg,"%d",tmpstatus.perfusion_speed);
            myGLCD.print(msg,202,52);
        } }
        }
        if(myTouch.dataAvailable()==true) {
        check_num fields(channel);
        pressed bütton = myButtons.checkButtons();
        if (pressed_button==butBACK) {
                                    return_home=1;
        else if(pressed_button==but_perstart) {
                        control_perfusion(channel,1);
        else if(pressed_button==but_perstop) {
                        control_perfusion(channel,0);
        else if(pressed_button==but_reset) {
                            br_reset(channel);
                    }
        else if(pressed_button==but_v1) {
            if(!valve_states[BR_V1-1]){valve_states[BR_V1-1]=1;
                control_valve(channel,BR_V1,1);
                    }
                            else {valve_states[BR_V1-1]=0,
                        control_valve(channel,BR_V1,0);
                        con
        else if(pressed_button==but_v2) {
            if(!valve_states[BR_V2-1]){valve_states[BR_V2-1]=1;
                                    control_valve(channel,BR_V2,1);
                            }
                            else {valve_states[BR_V2-1]=0;
                                    control_valve(channel,BR_V2,0);
                                    con
            else if(pressed_button==but_v3){
            if(!valv̄v_states[BR_V3-1]){valve_states[BR_V3-1]=1;
                                    control_valve(channel,BR_v3,1);
                                    }
                                    else {valve states[BR V3-1]=0;
                                    contrōl_valve(channel,BR_V3,0);
```

```
else if(pressed_button==but_v4)
        if(!valvē_states[BR_\overline{V}4-1]){valve_states[BR_V4-1]=1;
                                    control_valve (channel,BR_V4,1);
            else {valve states[BR V4-1]=0
                                    contrōl_valve(channel,BR_V4,0)
                                    co
        else if(pressed button==but pump && (!(tmpstatus.flags&0\times7F)))
    l/only in the stanby mode
        if((tmpstatus.flags&0x80)==0) {
            start_pump(channel,medchg_vol_tab[channel-1],medchg_speed_tab[channel-1]);
            } else {
                    start_pump(channel,1,0); //stop the pump
        }
    else if(pressed_button==but_medstart){
        if((tmps\overline{t}atus.flags&\overline{0}\times06)==0) (
        //only if not sampling and not changing the medium
            medium_change(channel,medchg_vol_tab[channel-1],medchg_speed_tab [channel-1])
                }
    if(
    else if(pressed_button==but_timer){
        if(/*(tmpstatus.flags&0x06)==0*/1){
        //only if not sampling and not changing the medium
            myButtons.deleteAllButtons();
                medium_change_schedule(channel)
                }
    }
    while (myTouch.dataAvailable() == true);
    myButtons.deleteAllButtons()
    for(i=1;i<9;i++) draw_status(i,0);
    9
void medium_change_scheduler(void)
{uint8_t i;
    for(i=0; i<8; i++)
            if(timer enables[i])
                    f(timer_repeates_left[i] && (is_time_future(i+1, &timer_next_start[i])==0)){
                    imer_repeatēs_le\overline{ft[i]--;}
                                    medium_change(\overline{i}+1,medchg_vol_tab[i],medchg_speed_tab[i]);
                                    recalculate_schedule(i+1);
                                    print_global_diag();
                                    }
            }
        }
    }
1376 void print_global_diag(void)
    {uint8_t i;
    Serial.print("\r\n")
    sprintf(diag_msg,"BR unit Connections: %d %d %d %d %d %d %d %d",br connections[0],
        br_connections[1],br_connections[2],br_connections[3], br_connections[4], 
        br connections[5],br_connections[6],br_connections[7]);
    diag_out(diag_msg)
    sprintf(diag msg,"M.E. Timer enabled: %d %d %d %d %d %d %d %d",timer enables[0],
                            timer enables[1],timer enables[2],timer enables[3], timer enables[4], 
                            timer enables[5],timer enables[6],timer enables[7])
    diag out(diag \overline{msg);}
    sprintf(diag msg,"M.E. Intervals (hrs): %d %d %d %d %d %d %d %d",timer intervals hour[0], )
                            timer intervals hour[1],timer intervals hour[2],timer intervals hour[3],
                            timer intervals -hour[4],timer intervals - hour[5],timer intervals 'hour[6], \
                timer-intervals hour[7]);
    diag out(diag \overline{msg)}
    diag_out(di
    sprin
            timēr_intervals_minutes[1],timer_intervals_minutes[2],
            timer intervals_minutes[3],timer intervals_minutes[4],timer_intervals_minutes[5], \
            timer_intervals_\overline{minutes[6],timer_intervals_minutes[7]);}
    diag_out(diag_msg);
    sprintf(diag_msg,"M.E. Repats total: %d %d %d %d %d %d %d %d", timer_repeates_total[0], \
            timèr_repeates_total[1],timer_repeates_total[2],timer_repeates_total[\3],\
            timer_repeates_total[4],timer_repeates_total[5],timer_repeates_total[6], )
                    timer_repeates_total[7]);
    iag_out(diag_msg);
    sprintf(diag_msg,"M.E. Repats remaining: %d %d %d %d %d %d %d %d",timer_repeates_left[0], \
            timer_repeates_left[1],timer_repeates_left[2],timer_repeates_left[3], \
            timer_repeates_left[4],timer_repeates_left[5],timer_repeates_left[6], \
            timer_repeates_left[7]);
    diag_out(diag_msg);
    for(i=0;i<8;i++)
        sprintf(diag_msg,"BR%d - 1st M.E. start: %d.%d.%d %02d:%02d, NEXT M.E. start: %d.%d.%d %02d:%02d.",i+1, \
                                    timer_first_start[i].date, timer_first_start[i].mon,timer_first_start[i].year, \
```



```
                            timer_next_start[i].mon,timer_next_start[i].year,timer_next_start[i].hour, )
                    timer-next start[i].min);
    diag_out(diag_msg);
    }
    Serial.print("\r\n").
417 }
1418
1 4 1 9 \text { void diag out(char* dg msg}
```

```
1421 char msg[28];
1422
1423 // Get data from the DS3231
1424 curr_time = rtc.getTime();
1425
1428
1429
1430
1432 void loop()
433 {int pressed_button;
434 static booleān default_colors = true;
1435 static char upd_ch=1;
1436 char i;
4 3 7 \text { static unsigned long nextupdate=0;}
1438 unsigned long timeout=200;
1438 unsigned long timeout=200;
1440 static unsigned int glob_diag_timer=0;
1441
1441 if (millis() >= nextUpdate) {
443 if (millis() >= nextUpdate) nextUpdate = millis() + timeout; // set up the next timeout period
1444
1445
1446
1446
14448
1449
1449
1451
    sprintf(msg,"\r\n%s,%d.%d. %02d:%02d:%02d> ",rtc.getDOWStr(FORMAT_SHORT),curr_time.date, \
    curr time.mon,curr time.hour, curr time.min, curr time.sec).
    Serial.print(msg).
    Serial.print(dg_msg)
}
upd ch++;
if(upd_ch>8) upd_ch=1;
medium_change_scheduler();
glob_diag_timer++;
if(glob_diag_timer>=glob_diag_timeout) {glob_diag_timer=0;
                                    print_globāl_diag();
                                    }
    if (myTouch.dataAvailable() == true)
    {
    i=get_selected_ch();
        Seríal print\overline{((int)i)}
        Serial print("\n)r");
        Serial.print("\n
    dra
1462
1463
1464
```

```
l /********************************************************
*-----------------------------------------------------------
    * Description : supporting library for BR driver controller
    *
    * Author : Martin Baca
    Author : Martin Baca
    * Developed : 07.06.2016 Last Update : 29.12.2017
* Version : 1.2
* * Compiler : arduino
1 * Compiler : arduino
3 *-------------------------------------------------
    ITDB50 - 5" TFT Display 800x480,
    ITDB50 - 5" TFT Dis
    * Target CPU : ATmega2560 @16 MHz, UART: 115200,N,8,1
    * Emulator HW
    #ifndef _BR_Lib_h
    #define -_BR_Lib_h
23
4 //#include <Arduino.h>
# #define STAT_SIZEX 400
# #define STAT_SIZEY 120
28
#define BR_V1
    #define BR_V2
    #define BR_V3
    #define BR_V4
#4 #define BR V1 MASK
    #define BR - V2 -
#6 #define BR V3-MASK
#7 #define BR_V4_MASK
38
39 typedef struct {
    uint8 t flags;
    int16_t pump_speed
    int8_t valves;
    uint8_t pump_percent;
    umin t pump_time2end; //
    ulnt8 total_percent; //
    uint16 t total_time2end;//
    uint16_t perfusion_speed;//
    } br_status;
extern uint8_t br_connections[];
2 void draw_status(uint8_t channel, uint8 t update_mode)
53 uint8_t gēt_br_status(\overline{u}int8_t channel, \overline{br_status *brstatus);}
4 void draw_valve_state(uint1\overline{6}}\textrm{t}\mathrm{ posx, uint16 t posy, uint16 t sizex, uint16_t sizey,
void uint8_t valvenr, uint8_t state, uint\overline{8_t update_mode);}
57
#endif
```

59

```
* Description : supporting library for BR driver controller
*
*----------------------------------------------------------------------------------*
* Author : Martin Baca Last Update : 29.12.2017 * *
* Version : 1.2 *--------------------------------------------------------------------------------
* Compiler : arduino
    * Compiler : arduino
    * Source file : BR_lib.h
* Target system : Arduino Mega 2560 board, Rev. }
            ITDB50 - 5" TFT Display 800x480,
            ITDB50 - 5" TFT Di
* DS3231 R1C modul
* Target CPU
    A ATmega2560 @16 MHz, UART: 115200,N,8,1
* Emulator HW
#include <Wire.h>
#include <UTFT.h>
#include "BR_Lib.h"
extern uint8_t SmallFont[];
extern uint8_t BigFont[];
extern uint8_t Dingbats1_XL[];
extern uint8_t i2c_adr_tab[];
// Remember to change the model parameter to suit your display module!
extern UTFT myGLCD;
void send_i2c_msg(uint8_t channel,unsigned char *data)
{unsigned char len;
len=*data++;
Wire.beginTransmission(channel); // transmit to device
while(len--) { Wire.write(*data++); // sends one byte
Wire.endTransmission(); // stop transmitting
}
void draw_progress_bar(uint16_t posx, uint16_t posy, uint16_t sizex, uint16_t sizey,
{char pstring[5];
uint16_t text_xpos;
    if(percent>100) percent=100;
    if(!update_mode) {
    myGLCD.se\overline{tColor(VGA_BLACK);}
    myGLCD.fillRect(posx, posy, posx+sizex, posy+sizey);
    myGLCD.setColor(VGA_BLUE);
    myGLCD.drawRect(posx+1, posy+1, posx+sizex-1, posy+sizey-1);
    } myGLCD.setColor(VGA_BLUE);
    myGLCD.fillRect(posx+1, posy+1, posx+(((long)sizex*percent)/100)-1, posy+sizey-1);
    myGLCD.setFont(SmallFont);
    if(percent<51)myGLCD.setBackColor(VGA_BLACK); else myGLCD.setBackColor(VGA_BLUE);
    myGLCD.setColor(VGA_YELLOW);
    text_xpos=posx+sizex/2-16;
    if(percent<10) text xpos+=8;
    else if(percent<100) text_xpos+=4;
    sprintf(pstring,"%d%%",percent);
    myGLCD.print(pstring, text_xpos, posy+sizey/2-6);
}
void draw_valve_state(uint16 t posx, uint16 t posy, uint16_t sizex, uint16_t sizey, uint8_t valvenr,
                    uint8_\overline{t}}\mathrm{ state, uint8_\ update_mode)
{char tmp[8]
int16_t tmpcolor,tmpx;
if(valvenr<1 || valvenr>8) return;
if(!update_mode) {
    myGLCD.setFont (BigFont);
    myGLCD.setColor(VGA_GRAY);
    myGLCD.fillRoundRec\overline{t}(posx, posy, posx+sizex, posy+sizey);
    myGLCD.setColor(VGA_BLUE);
    myGLCD.drawRoundRect(posx, posy, posx+sizex, posy+sizey);
    }
    myGLCD.setFont(BigFont);
    myGLCD.setBackColor(VGA_GRAY);
    if(!update_mode)\
        sprintf(tmp,"V%d",valvenr);
        myGLCD.setColor(VGA_BLACK);
        myGLCD.print(tmp, posx+sizex/2-16, posy+4);
    }
    tmpcolor=VGA_RED;
    if(state) tmp
    myGLCD.setColor(tmpcolorr);
    sprintf(tmp,"OFF");
    sprintf(tmp,"OFF");
    if(state) {sprintf(tmp," ON ");
```

```
myGLCD.print(tmp, tmpx, posy+4+16+8);
06 }
107
0 9 \text { uint8_t get_br_status(uint8_t channel, br_status *brstatus)}
10 {uint\overline{8}t tmp}[1\overline{6}],i
uint3\overline{2}_t timer=200;
if(channel<1 || channel>8){Serial.print("incorrect channel\n\r"); return(-1);}
tmp[0]=2;
tmp[1]=0\times41;
tmp[2]='\n';
send_i2c_msg(i2c_adr_tab[channel-1],tmp);
delaȳ(80);
// Serial.print("Requesting....");
Wire.requestFrom(i2c_adr_tab[channel-1], (uint8_t) 13); // request 13 bytes from slave device
i=0;
i=0;
while (Wire.available()) { // slave may send less than requested
                                    tmp[i++] = Wire.read(); // receive a byte as character
                                    if(i>13) break;
    if(i<11) {//Serial print(n)
*(1<11) {/Serial.print("not enough data\n\r");
        return(-1);
if(tmp[12]!='\n') {//Serial.print("incorrect data\n\r");
        return(-1);
/*
Serial.print(channel);
serial.print("> ")
                    if (tmp[i] < 16) {Serial.print("0");
                        Serial.print(tmp[i],HEX);
                            Serial.print(' ');
for(i=0;i<13;i++){
    Serial.print("\n\r")
*/
brstatus->flags=tmp[0],
brstatus->pump speed=(tmp[1]<<8)+tmp[2];
brstatus->valves=tmp[3];
brstatus->pump percent=tmp [4]
brstatus->pump_time2end=(tmp[5]<<8)+tmp[6];
brstatus->total_percent=tmp[7];
brstatus->total_time2end=(tmp[8]<<8) +tmp [9];
brstatus->perfusion_speed=(tmp[10]<<88)+tmp[11];
return(0);
53 }
54
56 void draw_status(uint8_t channel, uint8_t update_mode)
{char msg[26];
uint16_t posx,posy;
uint16_t sizex=STAT_SIZEX;
uint16_t sizey=STAT_SIZEY;
br_status tmpstatus;
char err,tmp;
    if(channel<1 || channel>8) return;
    posx=0;
    if(channel>4) posx+=sizex;
posy=((channel-1)%4)*sizey;
    err=get br status(channel, &tmpstatus);
f(!err) -tmp=1; else tmp=0;
if(br_connections[channel-1]!=tmp) {br_connections[channel-1]=tmp; update_mode=0;}
if(!update_mode)
    myGLCD.setColor(VGA_BLACK);
    myGLCD.fillRect(pos\overline{x}, posy,posx+sizex-1,posy+sizey-1);
    myGLCD.setColor(VGA_WHITE);
    myGLCD.drawRect(pos\overline{x}+1, posy+1,posx+sizex-2,posy+sizey-2);
    myGLCD.setFont(BigFont);
    myGLCD.setBackColor(VGA_BLACK);
    myGLCD.setColor (VGA_YELEDOW);
    sprintf(msg,"BR Uni\overline{t NR.%d - ",channel);}
    if(!err) sprintf(msg+15,"Connected");
            else sprintf(msg+15,"Offline");
    myGLCD.print(msg,posx+4,posy+3);
    }
    if(err) return;
    myGLCD.setFont(BigFont)
    myGLCD.setBackColor(VGA BLACK);
    myGLCD.setColor(VGA_WHITE);
    if(!tmpstatus.flags) sprintf(msg,"Standby
    else if(tmpstatus,flags&0\times04) sprintf(msg,"Changing Medium
    else if(tmpstatus.flags&0x02) sprintf(msg,"Preparing Sample ")
    else if(tmpstatus.flags&0x01) sprintf(msg,"Perfusion / Incubation")
    # if(tmpstatus flags&0x80) sprintf(msq "Manual Pump Control ")
    else lf(tmpstatus.1lags&0x80) sprintf(msg,"Manual Pump Control ")
    myGLCD.print(msg, posx+4,posy+sizey-1-16-4-18 );
    if(tmpstatus.flags&0x06 || tmpstatus.flags==0x80) {
    draw progress bar(posx+4,posy+sizey-1-16-4,sizex-104-16,16,tmpstatus.total percent, update mode);
```

| 205 | myGLCD. setFont (SmallFont); |
| :---: | :---: |
| 206 | myGLCD. setBackColor (VGA_BLACK) ; |
| 207 | myGLCD.setColor (VGA_YELİOW) ; |
| 208 | sprintf(msg, "End in:\%dmin",tmpstatus.total_time2end/60); |
| 209 | myGLCD.print (msg, posx+sizex-1-4-104, posy+sizey-1-4-12); |
| 210 | \} |
| 211 | else\{ |
| 212 | myGLCD.setColor (VGA_BLACK) ; |
| 213 | myGLCD.fillRoundRect (posx+4, posy+sizey-1-16-4,posx+sizex-4,posy+sizey-1-16-4+16); |
| 214 | \} |
| 215 |  |
| 216 | if(!update_mode) \{ |
| 217 | myGLCD.setFont (BigFont); |
| 218 | myGLCD.setColor (VGA_GRAY); |
| 219 | myGLCD.fillRoundRect (posx+8, posy+24, posx+4+80, posy+24+50); |
| 220 | myGLCD. setColor (VGA_BLUE); |
| 221 | myGLCD.drawRoundRect (posx+8, posy+24, posx+4+80, posy+24+50); |
| 222 | myGLCD.setBackColor (VGA_GRAY); |
| 223 | myGLCD.setColor (VGA_BLACK) ; |
| 224 | myGLCD.print("PUMP", posx+8+8,posy+24+4); |
| 225 | \} |
| 226 | myGLCD.setBackColor (VGA_GRAY) ; |
| 227 | myGLCD.setColor (VGA_BLAC̄K) ; |
| 228 | if(tmpstatus.flags $¢ \overline{0} \times 80$ ) sprintf(msg, "\%dul/min",tmpstatus.pump_speed); |
| 229 | else sprintf(msg," STOPPED"); |
| 230 | myGLCD. setFont (SmallFont); |
| 231 | myGLCD.print(msg, posx+8+4, posy+24+4+12+12); |
| 232 |  |
| 233 |  |
| 234 | draw_valve_state (posx+8+80+10, posy+24, 70, 50, 1, tmpstatus.valves \& BR_V1_MASK, update_mode); |
| 235 | draw_valve_state (posx+8+80+10+75, posy+24, 70, 50, 2, tmpstatus.valves \& BR_V2_MASK, updāte_mode) ; |
| 236 | draw_valve_state (posx $+8+80+10+2 * 75$, posy $+24,70,50,3$, tmpstatus.valves \& BR_V 3 _MASK, update_mode); |
| 237 238 | draw_valve_state (posx+8+80+10+3*75, posy+24, 70, 50, 4, tmpstatus.valves \& BR_V4_MASK, update_mode); |

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