A simulator for digital microfluidic biochips

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Abstract

A lab on chip is a concept that in recent years became a very popular alternative to traditional laboratories. A digital microfluidic biochip is one of the devices that are strictly connected to the lab on chip concept.

Digital microfluidic biochips are very small devices capable of replacing conventional laboratories by performing all the necessary biochemical functions using droplets with volumes as low as picolitres.

A digital biochip is composed of a two-dimensional array of identical cells, together with reservoirs for storing the substances. Each cell consists of several control electrodes, used for moving the droplets on the array. This is done by applying voltages to required electrodes.

Any biochemical application can be decomposed into a series of basic microfluidic operations (e.g., creating a droplet with a precise volume, mixing two droplets, diluting a droplet with a buffer solution). Performing such operations requires transporting droplets on the array according to a certain pattern, therefore a sequence of electrodes activation is required.

Given a biochemical application in the form of a set of microfluidic operations, together with the activated electrodes at each moment, a simulator provides a graphical representation of the droplets movement on the array, either as a realistic model showing the exact droplet movement or as a simplified model, with modules representing the operations. The simulator also captures specific situations that may appear during the execution of the application, like an incorrect execution of operations.

The simulator can provide useful information on the efficiency of the current design, before an actual chip goes into production.

This thesis provides brief theoretical information about the microfluidics field and the biochips. Furthermore, a simulator concept is provided, followed by the detailed information on its design and implementation, including two aforementioned models (simplified and realistic) and faults simulation. Finally, a technical documentation on the tool itself is provided, followed by a list of possible future extensions.

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Chapter 1

Digital microfluidic biochips

This chapter presents an introduction to the theory behind the digital microfluidic biochips. It includes basic information about the whole microfluidics field, explains the difference between main types of microfluidic biochips and finally some in-depth information about how does a digital microfluidic biochip exactly work. At the end there is a small section devoted only to the on-chip errors.

1.1 Microfluidics

As the name suggests, microfluidics is an area dealing with the behavior of the low-volume liquids, where low-volume usually indicates less than 1nl. The major difference between macro- and microfluidics is what properties are the most important ones. An example of such a property can be the gravity, which plays a big role in case of macrofluidics, but is not such a significant factor in microfluidics. In contrast, surface tension which is not the most important property to follow while studying macrofluidics plays a very important role when microscopic amounts of fluids are taken into account. Obviously there are much more factors that may favour the micro- over macrofluidics, but they are irrelevant for the purpose of this project. Some key application areas of microfluidics are:

- engineering (micro-scale pneumatics, mechanics, etc.),
- physics,
- chemistry (bio-smoke alarm¹),
- biotechnology (cell separation, protein analysis),
- crime scene investigation,
- technology (inkjet printhead)

1.1.1 Lab on a chip

In some of these areas a concept of **lab on chip** is used. This means that microfluidics can be used to produce a single chip that would be able to integrate one or more duties usually performed in a full size laboratory. Such chips are small in size (usually no more than several square centimeters) and can be used for several purposes, from a simple mixing operation in chemistry to DNA extraction from the blood samples or bacteria, virus, etc. detection.

This technology provides the researchers with some significant advantages. First of all - effectiveness. This includes automatization (no men involved), significant reduction in costs (smaller amounts of reagents needed), efficiency "per sample" (e.g. there is only a small blood sample available - much more tests can be carried out if it is split into micro volumes), integration (chips can be used by different applications) as well as space savings (miniaturization lab-on-chip devices are much smaller than any laboratory equipment).

These devices also provide their users with enhanced safety. Unstable, exothermic or radioactive mixtures are safer to work with, because throughout almost the whole process they are contained within a strictly limited space and any energies that they may store are also strictly limited.

Finally, these devices are usually fast, it takes much less time to perform the same operation on a chip than on a regular laboratory equipment. They can also be - to some extent - precisely controlled, for example it is much easier to uniformly heat a small droplet than a large volume of liquid.

¹http://nanopatentsandinnovations.blogspot.com/2010/06/ carbon-nanotube-wearable-bio-smoke.html

1.1 Microfluidics

Lab on chip is not a perfect solution though, mainly because it is a relatively new technology, which means that it is still in a development stage. Many of the design or manufacturing challenges stem from the very nature of the microfluidics, as some of the effects may become extraordinarily important when they are applied to small volumes. An example of such situation may be surface smoothness. On a micro scale it may be so coarse that friction forces simply make small fluid amounts stop there.

Another problem is that scalability of this technology is not linear - examining tools for biochips are not as accurate as their "normal size" counterparts. Also SNR (signal-to-noise ratio) in such an environment is usually much lower than on a macro scale, which also must be taken into account.[2]

1.1.2 Continuous flow vs. digital microfluidics

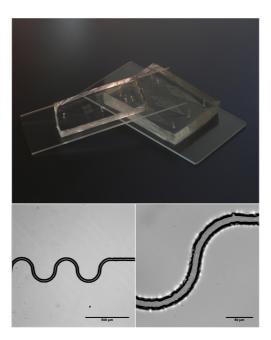


Figure 1.1: An example of a continuous-flow device.

There are two main types of microfluidic chips - continuous flow and digital ones. The former consist of a number of channels through which the fluids circulate (see figure 1.1 taken from Wikipedia - zoomed fragments show a single channel and the imperfections in its structure). Flow of the liquid is enforced via a set of microscopic pumps, various pressure sources, devices utilizing some basic physical properties, etc. Such a design may be useful for some of the simplier applications, but due to its nature it possesses a number of vital disadvantages. The main source of problems is that all the channels are firmly etched into the chip's structure. This means that the chip has its specific purpose and no reconfiguration is possible, which also results in a much lower fault tolerance level. Continuous flow biochips are also hardly scalable which disqualifies them from many applications.

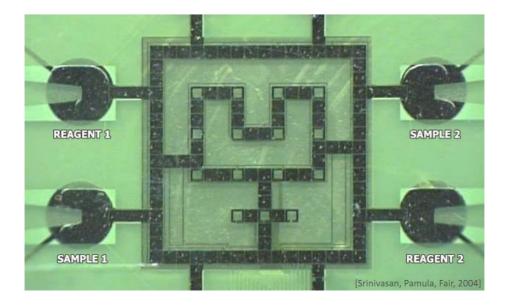


Figure 1.2: An example of a digital microfluidic biochip.

The second main type of the biochips are digital biochips. Contrary to the continuous flow biochips, these structures operate in a discrete universe. The discrete state applies both to liquid volume (droplets of a specific size are used) and droplets position on the biochip (a droplet cannot stop at any arbitrary place on the chip, it can only stay on the centre of a "cell" - see below). The most literal explanation of this discretization (or digitalization) is that the whole process can be considered as a set of operations, and an operation includes moving a single volume of liquid (droplet) over a specified, unit distance.

A digital microfluidic biochip consists of a number of identical (to enable reconfigurability) cells which are used to move the droplets around using electrowetting (for details, please refer to section 1.2.1). In short - such a construction eliminates all the flows of a continuous-flow biochip. If it is well designed, it can be easily reconfigurable, which leads to a much higher fault

tolerance level. It also allows much finer control over the whole system - by controlling the cells independently it is possible to control each of the droplets seperately, while in a continuous-flow biochip the system is controlled as a whole.

Next section will describe in more details the working principles of the digital microfluidic biochips. It will also present the exact biochip features that are covered by this project. Finally, it will describe what errors can be encountered in such a system and how the system behaves under erroneous conditions.

1.2 Digital Microfluidic Biochip

1.2.1 Working Principle

As pictured in figure 1.2 [4], a digital microfluidic biochip consists of a number of identical cells, represented by squares, and a few reservoirs on the edges to store the needed substances. A single cell is shown in details in figure 1.3 [1]. It is formed of 2 glass plates, a top and bottom one, that form a "sandwich" with a droplet between them. Top plate has a ground electrode and the bottom one consists of an array of electrodes used to move the droplet in a specific direction.

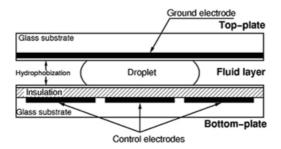


Figure 1.3: Biochip cell.

The droplets move - generally speaking - to an active electrode. This means that if droplet needs to be moved right, the electrode on the right to the droplet needs to be activated (control voltage applied to the electrode changes the hydrophobicity of its coating) and soon after that the one that the droplet stayed on needs to be switched off. All the operations are based on this principle. The biochip uses the electrowetting as a way of moving the droplets. Electrowetting is - by definition - changing the wetting properties of a surface by an application of an electric field. Moving deeper, wetting describes - simply speaking - ability of the liquid to maintain contact with solid surface. In this case turning the control electrode on makes the contact between the droplet and the electrode much firmer. This is why a droplet is attracted to an active electrode and the principle behind the droplets' movement on the chip. In other words - the electrode is hydrophobic (literally "afraid" of liquid) when inactive and hydrophilic (attracting the droplet) when it is switched on.²

There are several alternatives to electrowetting, e.g. ultrasonic wetting or optical wetting, but these are not under consideration here.

1.2.2 Operations

The whole process taking place on the biochip can be split into single operations. There are several distinct types of operations that can be distinguished:

- dispensing droplet is created and moved from a reservoir onto the chip.
- mixing two droplets are merged into one.
- dilution a droplet is diluted in a solvent droplet.
- splitting division of one droplet into two smaller droplets.
- transportation simply moving the droplet around the chip.
- detection during this operation droplet stays on the cell that has a detector installed. It can be an optical device or any other device that measures certain characteristics of the droplet.

1.2.3 Synthesis

Before a biochip can serve its purpose, i.e. it can be manufactured and a biochemical application can be run on it, a number of processes need to be performed (design, testing, etc.). The typical chain of actions include a behavioral model (for example a sequencing graph) which serves as an input for

 $^{^2 \}rm Digital microfluidics by electrowetting, Duke University <code>http://microfluidics.ee.duke.edu/</code>$

the architectural-level synthesis (producing a general macroscopic biochip structure). After the architectural-level synthesis a geometry-level synthesis is performed, which results in a full model of the biochip, ready for manufacturing. The aim of the synthesis is to optimize the biochip cost-wise, i.e. by ensuring the most efficient use of biochip's resources.[1]

Four main steps of the synthesis process can be distinguished:

- Resource binding
- Scheduling
- Module placement
- Droplet routing

To start a synthesis process, a sequencing graph is needed. Such a graph shows the order in which operations are performed and dependencies between them. Once it is known what operations need to be carried out, resources can be bound to them. This process simply allocates necessary biochip area for a specified amount of time, for example a 4x5 (cells) area is allocated for mixing operation that takes 10 seconds to finish. Each operation is allocated both area and time. Both of them are evaluated on experimental results. An example of a sequencing graph is presented in figure 1.4 (taken from [1]).

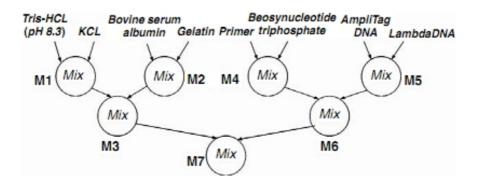
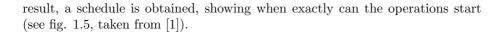


Figure 1.4: An example of a sequencing graph.

Once the execution times are known, the operations can be scheduled, based on the sequencing graph and the times obtained after resource binding. As a



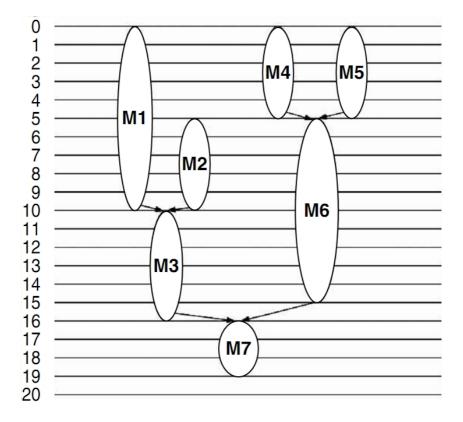


Figure 1.5: Operation schedule.

The next part is module placement, which is probably the most important part in obtaining an efficient biochip application. At this stage resources allocated in the binding process - now considered "modules" - need to be placed on a biochip. A module covers the execution operation from start to end. This means that - if one wants to visualize the process - modules will be appearing and disappearing from the biochip along the timeline.

There are two main problems that make this issue a challenge:

• Modules cannot overlap with each other, as this can potentially lead to droplet collisions.

• Modules' placement must be optimal, to minimize the overall execution time and maximize the usage of biochip's space.

Modules can be reconfigurable or not. The former include for example mixing or splitting modules, which simply consist of a number of cells. The latter are fixed and need to be placed on the biochip beforehand. An example of a non-reconfigurable device can be a detector or a waste disposal reservoir. The main challenge is to place the modules in such a way, that a maximum possible number of operations can be performed parallelly and distances between modules of subsequent operations is as small as possible. Details on algorithms used in module placement optimization are extensively covered in [1].

Finally, once modules are placed, routing needs to be done. This process establishes the sequence of droplet movements from the starting point to the ending point during the operation. When routing, a number of things needs to be taken into account:

- Initial position of the droplet,
- Ending position, which will be the initial position for the subsequent operation,
- Optimal route within the module, taking into account for example the most efficient step sequences for a given operation.

To check whether these four stages were performed optimally, a simulator can be used. Instead of a costly series of experiments on actual devices, a tool may be used to visualize the module placement and/or the actual routes taken by the droplets. One could easily see if the modules optimally utilize available space or if droplets are moving in a desired way. More information on such a tool is presented in chapter 2.

1.2.4 Faults

As in any system, there is no guarantee that all the operations will be performed without any errors. There are certain errors that can happen on the biochip an they can be divided into sudden "spontaneous" errors and intrinsic errors.

The first group - spontaneous errors - can include basically any undesired behaviour that occured. This may be an accidental merge, when two droplets

are brought too close to each other, a situation when a droplet is permanently stuck on an active electrode or a sudden electrode breakdown. Apart from these, there can also be droplet volume errors, e.g. when a split is not a perfect 50:50 split. As far as the spontaneous errors are concerned, only volume errors are considered further. This project does not deal with structural errors of the biochip - it considers only droplet volume errors.

The other group are intrinsic errors. An intrinsic error limit can be specified for any operation type and simply describes the bounding values of the resulting droplet, e.g. if an 0.2 intrinsic error limit for a dispensing operation indicates that the droplet that is dispensed from a reservoir can have its volume anywhere between 80 and 120% of the default volume. For the value distribution a Gaussian distribution can be used, with the *mean* being the default droplet volume and the intrinsic error limit as a *variance*.

The most important feature of the intrinsic errors is that they propagate through the schedule. This means that - if we consider the schedule of operations as a tree - an error value at the output of the first operation in the branch is taken as an input by all its successor operations. The situation is repeated until the last operation in the branch is finished. In practice - if the intrinsic error limit values are high and the schedule is very complicated - the resulting droplets can have volumes significantly different from desired.

Formulae are specified for five operation types [3]:

• Dispensing (E_{Ds}) is an intrinsic error limit value for dispensing operation). The error limit value at the end of dispensing operation is therefore:

$$1 \pm E_{Ds}$$

• Mixing (E_{Mix}) . Mixing operation is a successor of two operations. Thus, if the error limits at their outputs were I_1 and I_2 , the error limit value at the output of the mixing operation is equal to:

$$\sqrt{(0.5I_1)^2 + (0.5I_2)^2 + E_{Mix}^2}$$

• Splitting (E_{Slt}) . For split operation we have only one predecessor, but two successor operations. Thus, for input error value I the output (for each of the droplets) is equal to:

$$\sqrt{I^2 + (2E_{Slt})^2}$$

• Dilution (E_{Dlt}) . Dilution is similar to mixing, with two inputs with their values equal to I_1 and I_2 . The error limit value at the end of a dilution operation is therefore equal to:

$$\sqrt{(0.5I_1)^2 + (0.5I_2)^2 + (2E_{Dlt})^2}$$

• Transportation (E_{Tran}) . This is an operation with a single predecessor (with its error limit value I) and a single successor. The output value for the transportation operation equals:

$$\sqrt{I^2 + E_{Tran}^2}$$

Please note that at the current stage intrinsic errors for transportation and splitting operations are not considered, since the operations themselves are not implemented. However - as it will be explained further in this paper - it is very easy to include those two as well.

Digital microfluidic biochips

Chapter 2

Simulator

The simulator is designed to visualize a set of scheduled operations performed on the biochip, which greatly helps in understanding what is happening when these operations are executed and detect possible mistakes in the synthesis process. It may help detect possible errors in the scheduling, but most importantly in module placement and droplet routing. Use of such a tool may generate significant cost reductions, as there is no need to manufacture a biochip over and over again just to see that the design is still not optimal.

2.1 Overview

There are several principles behind the design - or idea - behind this tool. First of all, this simulator is not an "intelligent" tool, which means that - generally no randomising algorithms are incorporated into the code. As a result, given set of input files will always produce the same simulation output. The only exception to this is when a presence of random errors is desired, but it is somewhat self-explanatory.

Second goal is to give user a full insight into what happens on the biochip. This means that it must be possible to go over the simulation again and again if needed, pause at a given moment to investigate the current situation, save the current status information for future reference or comparison with other simulations, etc.

Finally, the goal is to provide different abstraction levels. This is to cater to the variety of scenarios that need to be covered. Thus, three (or four, depending on how one wants to count them) different abstraction levels are provided:

- 1. A simplified model,
- 2. A realistic model,
- 3. A model with errors introduced (this apply to both models, so we obtain a simplified model with errors and a realistic model with errors)

For information on exact design of the simulator please refer to the design and implementation section.

2.2 Simplified model (modules)

A simplified model - as the name suggests - does not provide full information about the situation on the biochip. What it does is to represent each of the operations as a module - a shape (in this case a rectangle) covering a number of biochip cells. This module covers an area used by a given operation, i.e. the boundaries within which a droplet moves during that operation. Such a simplification proves useful in several situations:

- No detailed information is needed. Sometimes it is sufficient to see only that a given operation is running, not an exact route taken by the droplet.
- Detection of overlapping modules. When operation are represented as modules it can be clearly seen if any of them overlap during the execution of the operations. On a real biochip such a situation may result in a contact between two droplets and subsequently an accidental merge or a straight collision.
- Efficient use of biochip surface. It can be easily seen when there is a large unused space on the biochip. This is not always a bad thing, however may indicate that the operations could have been scheduled more efficiently (timewise).

As it was mentioned before, this model can also include errors (spontaneous or intrinsic) that may happen during operation execution.

2.3 Realistic model (droplets)

Usually the simplified model is too general for the desired use. Instead, user may want to see what does exactly happen on the biochip. For this purpose a realistic model is provided. Like the name suggests, it provides at least all the information about actions taking place on the biochip (it may also provide some additional information about previous biochip state like previous positions of the droplets). This model may be preferred over the simplified one for the following reasons:

- Provides a detailed insight into the situation on chip. At any given moment all the droplets currently present on the chip can be seen.
- Helps with collision detection. The fact that two modules overlap does not necessarily imply a collision. When a realistic model is applied, one may precisely see if a collision occurs during the experiment.
- Visualizes the routing algorithms. One may precisely see if the routing algorithms that were used ensure that the droplets do not move to close to each other. In other words, it is clearly seen on this model if two droplets may accidentally merge.
- Can also help with an efficiency assessment. Again, large empty spaces between the droplets may indicate that their paths could have been designed more efficiently.

2.4 Errors

The most detailed model is one that incorporates errors (see section 1.2.4). The situation in which each operation is executed perfectly is rather seldom. Therefore it is essential to provide the user with a possibility to check how the whole system behaves in the presence of errors.

Simulation when the errors are introduced provides the following:

• Shows how exactly is the volume of the droplet affected by a given error,

- In case of the intrinsic errors shows how the error propagates from operation to operation,
- May help in designing an improved schedule.

Chapter 3

Design and implementation overview

When designing my solution and implementing it, I established a set of principles that I wanted my program to meet. These can be summed up as:

- Simplicity all the solutions are designed in the most efficient, logical and easy to comprehend way.
- Extensibility any fragments where the code can be updated in order to accomodate new features are as simple as possible. Most of simple improvements would not require any changes to any functions, only variables, such as lists or dictionaries.
- User Friendliness, which includes two things. Firstly, a simple interface with clearly described buttons. Secondly, clear communication with the user, which means that any undesired acting will be stopped and the user will be alerted by a short, but informative message.
- Flexibility by applying common and widely available formats and techniques, it is possible to use the simulator for a wider range of applications only by small alterations to the code.
- Easy customization user is able to alter the way the simulation looks, either by using controls provided in the main application window or by

altering simple, single variables within the source code, and those variables are clearly marked. None of these changes require massive changes to the code.

3.1 Overview

The simulator has been divided into two applications - a simplified simulator, operating on a module level and a realistic one, based on droplets. Such a design is justified by the fact that each of those simulators have a slightly different purpose. Moreover, one or two features are added for the realistic simulator, thus also the window looks different.

The overall mechanism for the simulators, both the simplified and the realistic one, can be put in three separate steps: Loading the data, generating the simulation and simulation itself. An overview of the design is presented below, and it applies to both the simplified and the realistic simulator, thus no details are specified here. This section's purpose is to give an impression of a general behaviour of the simulator.

Loading the data - where all the data is read in, file by file. My idea was to make this step as user-friendly as possible, so originally it was just three 'load' buttons (one for schedule, one for graph, optionally one for error input file) and the program tried to generate the simulation instantly, based only on the input given. However such a solution was acceptable only and only if following precautions have been observed:

- Input files were properly prepared, which included careful construction of the XML file and putting all the necessary information in the file,
- Input file for the graph matched the input file for the schedule,
- (Optional) input file with errors matched the graph and the schedule.

If such a solution is applied, the procedure becomes a much simpler one including only two steps: Loading combined with automatic simulation generation and the simulation itself. However this would be working correctly only and only if the precautions mentioned above are observed - there is no safety mechanism applied. Thus, when the work progressed I changed the principles to following:

- The order in which files are to be loaded is strictly specified: schedule, then graph and if those two are loaded - error file (if needed). This is perfectly justified, as the input schedule includes all the information needed to generate a visual simulation, whereas graph includes only information about the dependencies between the operations, and those are irrelevant to the simulation itself. Errors are naturally useless if there is no schedule to apply them to, so there is no point in allowing the user to load the error file when there is no schedule loaded.
- Once a graph is loaded, it is matched against the schedule to ensure that the two files belong together (details on the matching mechanisms will follow in subsequent chapters). In the same way the error file is matched against the schedule and the graph.
- All the input files are verified against their respective XSD schemas to ensure that they are properly formatted and include all the necessary information.

If any of these requirements is not met, an error is produced and simulation cannot be generated. In other words, at this stage it is determined whether all the files are correct from the technical point of view and whether they match, i.e. the graph is representing the operations in the schedule file and the errors can be applied to the given schedule. If these conditions are met, simulation can be generated. The flow chart for this process is presented on figure 3.1. Please note that it is only a generalization of the whole process. More detailed descriptions of each step will be presented later in this paper.

Generation, at which point the program uses information from the input files to determine the following: From the schedule file:

- Size of the biochip, so it can render the biochip in a size that fits the simulation window,
- Locations of all the operation modules (for simplified model),
- Locations of the reservoirs from which the droplets are dispensed (for realistic model),
- Routes taken by the droplets (for realistic model),
- Times at which droplets (or modules) appear and disappear from the view,
- Identification information like operation number and type, needed to somehow label the modules or droplets,

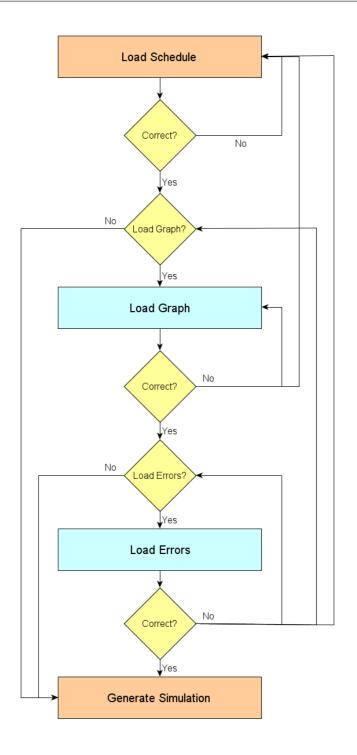


Figure 3.1: General process flow for loading the simulation files.

• Locations of 'special' cells, for example optical sensors,

From the graph file:

• Dependencies between the operations

From the error file:

- Information about errors happening to particular operations,
- Error limit values for intrinsic errors

The overall process of simulation generation is presented on figure 3.2. Please note that this is again a simplified model, the details of generation are presented in further sections.

At this stage the biochip and the graph are rendered, and (optionally) errors are scheduled. Therefore, user is able to execute the simulation and possesses a number of control possibilities over its playback.

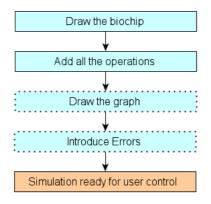


Figure 3.2: Simplification of generation process.

Simulation - a visual representation of the data collected and produced during two previous steps. Simulation is designed to provide user with numerous features:

• Full information display - operations currently being executed, errors happening, etc.,

- Playback control, with possibility of pausing the playback, jumping to an arbitrary timestamp and changing the speed of the simulation,
- Changing the appearance of the simulation view,
- Saving the screenshot of an arbitrary frame to an external file,
- Saving the error log file,

Obviously user is also allowed to restart the simulation, re-generate it, load new files or change error settings without restarting the application.

3.2 Choice of tools

Suitable choice of a programming language was probably the first important choice to make. My initial range of languages was: C++, Java and Python, because I had previous experience with all of them and initially they seemed equally suitable for this task.

After some consideration it turned out that the first thing when choosing a programming language is not how comfortable it is to use it, but rather how good GUI libraries it provides. Since basically whole program operates on a graphical level, it is particularly important to use libraries that are most flexible when it comes to GUI programming.

With almost no hesitation I decided not to use Java, as its most popular Swing library is anything but user friendly. Instead, Qt came to my mind. It is a relatively new framework currently developed by Nokia, providing an extremely useful and flexible platform for GUI based applications. It's main advantages are:

- clear syntax, which is its main advantage over Swing.
- great support, both from developer's side and from the community. I had no trouble finding a solution to any problem that arose during the project.
- it's a cross-platform framework, thus the program is not platform-limited.

Among big names that use Qt one can find Google (Google Earth), KDE, Opera or Skype, so it is by no means a niche technology.

The Qt itself uses standard C++, but there are numerous language bindings that provide full Qt support for many languages. There are bindings for both Java (Qt Jambi) and Python (PyQt). After some consideration I opted for Python, mainly for the following reasons:

- Coding in C++ is really time-consuming and the possibilities of making a mistake are vast.
- Qt wrapper for Java still uses (mostly) C++ code, which leads directly to the previous points.
- PyQt completely integrates Qt with Python, which means that Python's principles can be used while coding.

Apart from these, the Python itself has numerous advantages due to its very nature:

Python is an interpreted, object-oriented, high-level programming language with dynamic semantics. Its high-level built in data structures, combined with dynamic typing and dynamic binding, make it very attractive for Rapid Application Development (...). Python's simple, easy to learn syntax emphasizes readability and therefore reduces the cost of program maintenance. Python supports modules and packages, which encourages program modularity and code reuse. The Python interpreter and the extensive standard library are available in source or binary form without charge for all major platforms, and can be freely distributed.

Often, programmers fall in love with Python because of the increased productivity it provides. Since there is no compilation step, the edit-test-debug cycle is incredibly fast. Debugging Python programs is easy: a bug or bad input will never cause a segmentation fault. Instead, when the interpreter discovers an error, it raises an exception. When the program doesn't catch the exception, the interpreter prints a stack trace. A source level debugger allows inspection of local and global variables, evaluation of arbitrary expressions, setting breakpoints, stepping through the code a line at a time, and so on. The debugger is written in Python itself, testifying to Python's introspective power. On the other hand, often the quickest way to debug a program is to add a few print statements to the source: the fast edit-test-debug cycle makes this simple approach very effective.¹

¹What is Python? Executive Summary - http://www.python.org/doc/essays/blurb/

As for the input files, the most logical solution (and the first that came to my mind) was to use XML. First of all, it's a standard format that is easy to read and understand. Moreover, simple XML files - like those used in this project - are quick to parse, and the number of parsers available is huge (same goes for XML libraries themselves). Finally, it is extremely easy to check if the files are correct, for example by validating them against a correct XSD Schema.

Qt provides great XML libraries that can perform all the needed actions, be it parsing or validation. As most of the Qt libraries, these are extremely pleasant to use and result in a clear, neat and readable code.

3.3 Data structures

In every program an optimal choice of data structures is required, especially in one like this, dealing with real-time calculations which are additionally required to finish within a given timeframe. By real-time calculations I mean for example functions redrawing the simulation view every n miliseconds. If the code used there is written inefficiently (for example by using unoptimal data structures), the simulation will be simply unable to keep up with the timeline. This section provides information on principles behind choosing specific data structures.

3.3.1 Simple types

Python does not require to specify a type when declaring the variable. Thus, in most cases type casting is performed when the variable is to be used, just for the sake of simplicity. The only place where the value types are strictly specified is the XSD schema, but it does not influence the program itself.

3.3.2 Collections

Three different structures are used in the program: list, set, and dict (dictionary). General principle is:

• For simple collections, **set** has been used, as it provides much better performance than any other structure and the program performs a great number of lookups.

In case of sets of custom classes it was required to provide them with

__hash() __ attribute in order to allow them to be stored in a set - elements of the set must be hashable.

- For any collection that needed a key:value assignment, dict has been used, which is Python's version of a hash table. Look up by key provides the optimal performance and ensures that there is no waste of performance at this stage.
- If for any reasons it is impossible to store the desired data in any of the two above, lists are used. There is only one list used in the code a (sorted) list of relevant timestamps, as their chronological order is essential.

3.3.3 Qt classes

Since most of the coding is done using PyQt libraries, it is obvious that its classes are used throughout the project. To minimize the incompatibility-related risks, number of these classes has been minimized. Simple types, like QString, were left out in favour of their native Python counterparts. Any class that is used can be classified in one of the following groups:

- Main Window and additional windows. See section 3.4.
- Window elements. These include buttons (QPushButton and QCommandLinkButton), sliders and scroll bars (QScrollBar, QSlider), Switches, choice boxes, etc. (QCheckBox, QComboBox) and display, layout or informational elements (QLCDNumber, QLabel, QGroupBox, QFrame)
- Simulation view classes. QGraphicsView and QGraphicsScene. Detailed information on simulation view and rendering of the simulation is included in section 3.5.
- XML related classes. Two of them were used QXmlSchema and QXmlSchemaValidator and they greatly simplified the process of XML validation. Also QFile has been used instead of native Python file object in order to simplify the code where the validation is performed.

3.3.4 Custom classes

A number of custom classes had to be generated in order to accomodate some of the simulator features. Such classes combine a number of features that would normally be handled by two or more different objects into one, more complex object. Examples of such classes are Module, Error or Droplet, and they will be explained in details in the subsequent chapters.

3.4 Application windows

This section includes information about the window structure of the application, including the main window, the graph window and any other possible windows that may appear during execution.

3.4.1 Main window

The main window of the application is slightly different from a typical application window with menu bar, status bar etc. Therefore there was no need to implement it as such an object (QMainWindow). There are two most reasonable choices to implement an application window that is not a typical main window - QDialog or QWidget. Widget is a base class for all application window, thus it may seem reasonable. However use of a dialog is slightly more suitable. Dialog - after Qt reference guide available at http://doc.qt.nokia.com/4.6/ - is a *top-level window mostly used for short-term tasks and brief communications* with the user.

An initial thought is that it is not that well suited for a main application window, however it is a really powerful class that is extremely easy to manipulate and customize. This means that all the elements needed can be easily added to this window, as well as it is easy to maintain its layout. The main window for the simulator (in this case the realistic one) is presented in figure 3.3. White frame on its right side is the simulation view, and its contents are described in section 3.5.

3.4.2 Graph window

Graph window - as the name suggests - is used to display the graph, and it is its only function. A dialog has been used in this case for the same purposes as in case of main window. The only content of this window is a view frame in which QGraphicsView is placed (see section 3.5). Please note that graph window depicted in fig. 3.4 is an early stage and will be subjected to major changes in the nearest future.

S Digital microfluidic biochip simulator		? ×
Input files	1x	
→ Load schedule None		
➔ Load graph None		
→ Load errors None		
Appearance		
Cell size		
Droplet Size		
Errors		
Error settings for simulation: Simulation with pre-set errors (from file)	-	
Error probability (per op.):		
Misc.	0.01x	
Generate Simulation! Show/Hide graph	rev. Event Play/Pause Save screenshot Ne	ext Event

Figure 3.3: Main application window

3.4.3 Error message windows

Two types of error messages can be specified: settings errors (see fig. 3.5) and simulation errors (fig. 3.6). The former indicate that something has been done wrong with the loading of the files, e.g. schedule file failed verification against the schema. The latter are informational ones, as they provide information that an error - that was either randomly generated or loaded from a file - actually appeared during simulation.

Both types of these error messages utilize QMessageBox class. Windows of this class are usually seen as classic Abort/Retry/Cancel windows. Their main advantage is great configurability. Buttons can be added to them, certain functions (like the button closing the window) can be disabled, etc. Moreover, buttons can have their roles set, for example to Abort, which means that this button will inherit all the actions usually assigned (in case of a generic message box) to the Abort button.

Taking this into account the errors in loading have a simple window including only one possibility - closing it.

On the other hand, windows displaying information about actual simulation errors have some more features enabled. In short (as they will be described

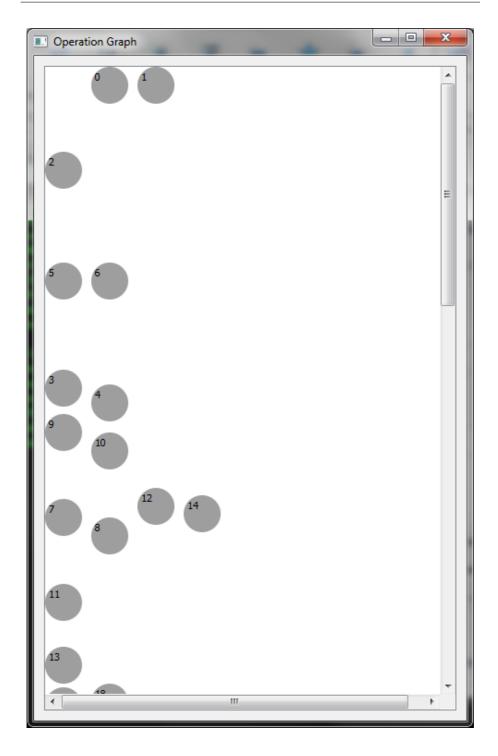


Figure 3.4: Graph window

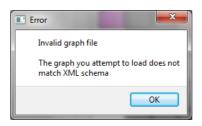


Figure 3.5: Error window example - invalid input file

thoroughly in section 6) - they have some choice buttons and a classic "Show details" button to display the error information. Moreover, for purposes described in section 6 button closing the window has been disabled.

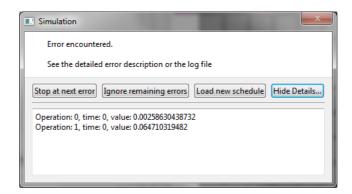


Figure 3.6: Error window example - droplet volume error

3.4.4 Additional windows

There is one more window type utilized by the simulator and it is a file dialog, which is used for loading and saving the files. It is a regular, non-customized file dialog native to the operating system used, well known to the user.

3.5 Simulation view

The main challenge in the design of the visual part was to choose the best way of rendering the data. Qt is quite a powerful environment and has a lot of ways to render graphics, therefore it is quite difficult at first to choose the right one. On the other hand, the variety of options makes it almost certain that one will find a solution that is suitable for a given application.

In case of the biochip simulator I decided to implement it using item-based graphics. The main concept here is a graphics scene, provided by class QGraphicsScene, which provides a surface for managing a large number of 2D graphical items². In other words, it can be considered a canvas on which various items are drawn. If one wants to view the graphics scene it is needed to associate the scene with a graphics view (provided by QGraphicsView class), which allows to view the scene, either as a whole or only a part of it. In the simulator graphics view is placed in the white frame on the right side of the main simulator window and in the graph window (almost whole window).

Graphics scene is populated with items. These can be either base QGraphicsItem class items, or one of the specific types, e.g. QGraphicsLineItem. The main advantage is that once an item is added to the scene, it can be manipulated in a variety of ways - rotated, moved, colored, resized, set invisible and many others. This is a great advantage over other drawing techniques, since it does not require a construction of a fresh scene every time a new frame in the simulation is needed.

The application of this technique in case of the biochip simulator can be summarized in following points:

- Biochip is drawn as a set of rectangles (one for each electrode), which are static and placed on the backmost plane,
- (In realistic simulator) reservoirs are drawn as similar rectangles (just like the biochip electrodes), but are drawn with a different color,
- If a detector is placed over a specific electrode, a graphic effect is applied to its rectangle in order to emphasize the fact that this particular cell

 $^{^2{\}rm PyQt}$ class reference - http://www.riverbankcomputing.co.uk/static/Docs/PyQt4/html/qgraphicsscene.html

is a detector. Applying a graphic effect to an item is another way of manipulating the items placed in the scene,

- (In simplified simulator) modules representing operations are added to the scene and turned visible when the operation is in progress. Turning the items visible or invisible is another example of action applied to a graphics item,
- (In realistic simulator) droplets are used in a similar way as modules, but in addition they are moved around the biochip surface. The ability to move an item was the most important feature that decided on choosing item-based graphics for this program,

Details on the graphics scene use are included in sections 4.6 and 5.6 for simplified and realistic model respectively.

3.6 Timers

There is one last thing to outline before going into details of the simulator, and this are timed events. Simulator must obviously be able to play the simulation automatically, i.e. without the necessity of user changing the frames manually. Again, there are numerous ways to implement this solution, but the best one is to use a timer.

Timer is basically a feature that triggers a specific function every n miliseconds. This function is called timerEvent and can include basically any code. In this case the timer event is responsible basically for updating the current scene to a correct one (by moving the items, setting them visible or invisible, etc.) together with checking all the conditions on which does the current situation depend.

Timer based events are an easy way to implement a simulation playback, however two things need to be taken into account:

- Timer interval needs to be large enough so the code inside the timer event can be executed within the given time frame,
- Timer interval needs to be larger than system's ability to resolve the time. According to [5] currently its safe value for most systems is 20ms. The

values in the simulator have been adjusted accordingly, i.e. the slider responsible for the simulation speed cannot be set for timesteps smaller than 20ms. For details on implementation of timer events please see sections 4.7 (simplified simulator), 5.8 (realistic simulator) and 6.10 (errors).

Chapter 4

Simplified model (modules)

This section presents a description of the simplified simulator. This include an extended description of a general design presented in the previous section as well as purely technical details of how it was implemented in Python code. Also - since a big part of the code is common for the simplified and realistic simulator - this section will use flow diagrams where possible, since detailed information will be included in the realistic simulator section as well and I do not want to repeat it twice. Moreover, the simplified simulator is literarily simpler, therefore it is easier to describe its structure using diagrams - the most detailed description of what happens in parts common to both simulators is included in the description of the realistic simulator.

4.1 Input files

For a full regular, error-free simplified simulation, a set of two input files has to be read in - a schedule of the operations and a graph. The latter - although not required for the simulation generation - provides some useful information, thus it is considered essential. However - once again - it is theoretically not needed to generate a valid simulation. A schedule of the operations include - above all - the information about biochip size, i.e. its x and y dimensions and a list of operation elements. Each operation element includes following attributes:

- operation number
- operation super type
- operation start time
- operation end time
- module location on the biochip (its lower-left corner)
- module x size
- module y size

A schema for a schedule for a simplified, module-level simulator is presented in figure 8.3 and an example of a valid schedule for a simplified simulator is presented in appendix A.

```
<xsd:schema attributeFormDefault="unqualified" elementFormDefault="\leftrightarrow
    qualified "version = "1.0" xmlns: xsd = "http://www.w3.org/2001/
    \tt XMLSchema">
  <rpre><xsd:element name="schedule" type="scheduleType" />
  <rpre><xsd:complexType name="scheduleType">
    <rpre>xsd:sequence>
      <xsd:element maxOccurs="unbounded" name="operation" type="\leftrightarrow
           operationType" />
    </xsd : sequence>
    <xsd:attribute name="xsize" type="xsd:string" />
<xsd:attribute name="ysize" type="xsd:string" />
  </xsd:complexType>
  <rpre><xsd:complexType name="operationType">
    <rpre><xsd:attribute name="deviceLength" type="xsd:string"</pre>
                                                                   />
    <xsd:attribute name="deviceWidth" type="xsd:string"</pre>
                                                                 />
    <xsd:attribute name="endTime" type="xsd:string" />
    <rpre><xsd:attribute name="leftBottomCorner" type="xsd:string" />
    <xsd:attribute name="opNumber" type="xsd:string" />
    <rpre><xsd:attribute name="opSuperType" type="xsd:string" />
    <rpre><xsd:attribute name="startTime" type="xsd:string" />
  </xsd:complexType>
</xsd:schema>
```

Figure 4.1: XSD schema - schedule for simplified simulator

Apart from the schedule, user can also read in a graph, consisting simply of information on the operations and dependencies between them. The XML file consists of a list of nodes, and each node includes the following:

- node (operation) number
- operation super type
- operation type
- "in" nodes, i.e. parent nodes (or empty if none)
- "out" nodes, i.e. child nodes (or empty if none).

Schema for a graph is presented in figure 4.2 and an example of a valid graph input file can be found in appendix C.

```
< \tt xsd: \tt schema \ \tt attributeFormDefault = "unqualified" \ \tt elementFormDefault = " \leftrightarrow " \leftrightarrow " \in [t] \ \tt schema \ \tt attributeFormDefault = " \leftrightarrow " \ \tt schema \ \tt attributeFormDefault = " \ \tt schema \ schema \ \tt schema \ \tt schema \ sch
                     qualified" version = "1.0" xmlns: xsd="http://www.w3.org/2001/\leftrightarrowXMLSchema">
         < \tt xsd:element name="graph" type="graphType" />
         <rpre><xsd:complexType name="graphType">
                    <xsd:sequence>
                              <xsd:element maxOccurs="unbounded" name="node" type="nodeType" \leftrightarrow
                                                    />
                     </xsd : sequence>
          </xsd:complexType>
          <re><xsd:complexType name="nodeType">
                  <rre><rsd:attribute name="in" type="xsd:string" /><rsd:attribute name="nodeNum" type="xsd:string" /></rr>
                   <rpre><rsd:attribute name="opSuperType" type="xsd:string" />
                   <rr></r></r></r></r></r></r>
                    <rpre><rsd:attribute name="out" type="xsd:string" />
          </{\tt xsd}:{\tt complexType}>
  </xsd:schema>
```

Figure 4.2: XSD schema - graph file (same for both simulators)

Schedule is absolutely required before any simulation can take place. Graph - as it has been previously mentioned - is optional. Moreover, it is not possible to load the graph before loading the schedule, and the reasons for such a solution will be described in the design and implementation subsections.

4.2 Variables

One thing needs to be clarified at this point - Python does not require explicit variable declarations. Most of the variables below can be declared when needed, not at the beginning. However to make things more clear - especially for those who are used to more "conventional" languages - I decided to declare all the vital variables at the beginning. This also excludes the possibility of referring to a variable that has not yet been used.

There are many variables that are critical for the simulation. They are responsible for setting certain simulation parameters like sizes, timings, collections, etc. Below

Sizing variables, i.e. ones that directly influence the biochip's appearance in the simulation window:

- SCALE One of the especially crucial variables, it determines the size of the "slot" that can be assigned for a single cell. It is adjusted later in the code after obtaining the numbers of rows and columns in the biochip. This ensures that biochip will occupy maximum possible space in the view.
- **BIOXSIZE** horizontal "spread" of the biochip, i.e. number of cells in each row.
- **BIOYSIZE** same, but for the vertical "spread".
- SCENEXSIZE horizontal size of the scene containing the simulation, hard-coded to match the simulation view area.
- SCENEYSIZE same, but for scene's vertical size.

Variables which affect the appearance of the simulation:

- ELBORDER spacing between the biochip cells.
- MODULEBORDER spacing between modules.
- cellBrush, errBrush and dictionary brushes colors used for different biochip elements (cells, etc.). The aforementioned dictionary is especially important as it is a place where "allowed" operations are specified. Whenever a new, previously not defined operation is used in the schedule it is necessary to add it here as well (with its color), so the simulator can pick up a correct color for it.

Time-related variables and boolean flags:

• INTERVAL - determines the simulation's time step, i.e. the duration of one time unit in the schedule.

- counter indicates the current simulation timestamp. Used to determine the correct scene contents at that timestamp.
- **startingTime** an initial timestamp of the simulation, determined from the schedule (please note that it does not have to be zero).
- finishingTime a timestamp at which the simulation finishes, also determined from the schedule file.
- running a boolean flag indicating whether the simulation is running automatically or is controlled by the user.

Boolean flags indicating certain properties of the simulation:

- schedIsOpen True if a correct schedule file is loaded, False if it is not loaded or is by any means incorrect.
- graphIsOpen same, but for the graph file.
- showGraph determines if the graph window is shown or not.

Boolean flags indicating certain properties of the simulation:

- schedule this set contains all the Module objects. Each of them contains information on the operation and its graphical representation (module). For details on this object please refer to section 4.3.
- nodeList a set of all graph nodes.
- rlvTimes a chronologically sorted list containg all the relevant timestamps (i.e. starting and ending times of operations). A list is used here as its essential to preserve a chronological order of the timestamps.
- nodes a dictionary used to establish references to the graphic items that are representing the graph nodes. An operation number is the key for each entry, and the value assigned is the graphNode graphic item (see sec. ??), which is a graphical representation of a particular node.
- allModules similar, but stores [operation number]:[Module object] pairs. This ensures that a graphics item representing a particular operation can be explicitly referred to by its number.

4.3 Module class

As it has been mentioned earlier, Python classes can be (to some extent) dynamically extended, thus it is not always possible to generate a correct class diagram. Therefore a brief description of the Module class is provided below.

Module class is extending a QGraphicsItem class. This is because as a graphics item it can be added without any modifications straight to the graphics scene. It combines three basic features:

- Information about an operation.
- Graphic representation of this operation.
- Information on the operation error status (see sec. 6)

When a new Module object is constructed, all the information about the operation (from the schedule file) must be included. This is set in the __init()___, which specifices how many and what arguments are required when constructing a new Module object. Each freshly created object must be passed the following values:

- operation number,
- operation super type,
- operation type,
- operation start time,
- operation end time,
- length of the operation module,
- width of the operation module,
- loceation of the operation module

Another useful method that is common for most classes is __hash()___, which specifies an integer hash value for the operation. In this case hash value is returned as the operation number, since it is simple and provides uniqueness.

As far as the graphic representation is concerned, there are three methods that are by default assigned to a QGraphicsItem class:

- boundingRect specifies the rectangle within which the item is located (in this case it is equal to the module's rectangle)
- shape specifies the shape of the item (in this case a rectangle)
- paint specifies the style pen, fill, effects, etc. in which the item is drawn.

Five variables are needed to determine the graphical representation: dimensions of the module (x and y), size of the module (x and y) and color of the module. Again, these can be dynamically added to the class when needed, but for the clarity they have been added to the class.

One additional method - **status** has been added in order to display main information about the operation as a tooltip activated when mouse cursor is over the module. For operation error features, please refer to chapter 6. A simplified (without generic methods) class diagram for this class is presented below.

	Module	
isCorrupted		
errorLevel		
Х		
У		
xsize		
ysize		
color		
opNumber		
opSuperType		
орТуре		
deviceLength		
deviceWidth		
leftBottomCorner		
startTime		
endTime		
status()		
0		

Figure 4.3: Module - simplified class diagram.

4.4 Loading the schedule

When the user pushes the "Load schedule..." button, function fileOpen connected to clicked signal of this button is executed (signals are simply an interface between actions applied to a given item, e.g. a button, and functions that can be trigerred by this actions). This function is responsible for the following things:

- 1. Reading in the name of the schedule file. This is done by QFileDialog.getOpenFileName, which opens a native file dialog of the operating system, be it Windows, Linux, MacOS, or any other system with such a dialog defined in its graphical user interface. File name is read as a string, which can also be empty (if user closed the file dialog or clicked cancel button).
- 2. File validation against XSD schema. The schema file for a simplified simulation schedule is schedModule.xsd and it is read in as a Qt native QXmlSchema object. There is a safety check if schema.isValid, just in case someone corrupted or deleted the schema. It may be omitted, but for safety's sake some other solution must be implemented, e.g. making the schema read-only or protected.

Once the schema is loaded, a validator needs to be constructed. The disadvantage of Python itself is that its native xml libraries do not include any methods for validating the xml files against XSD schemas. There are several third party libraries that can do it (most common one is libxml), but I really wanted to avoid using any additional packages. Fortunately Qt XML modules are much more capable than Python's and as a result I managed to handle everything using Qt XML modules only. Thus, validator is just another native object, QXmlSchemaValidator. It provides a boolean method validate, so the whole process is as straightforward as possible. Please note that if the file loading has been aborted, the program will show an error here, because no file is passed to the validator.

- 3. Calling the parsing function. If QXmlSchemaValidator.validate returned true, i.e. the input file is correct, two things are done then. Firstly, flag schedIsOpen (which indicates if the correct schedule is loaded) is set to true and text on the informational label next to the "Load schedule..." button is changed to the file path and name. Then, parseFile function is called (see below).
- 4. Providing error messages. If QXmlSchemaValidator.validate returns false, indicating wrong input file, an error message should be displayed to the user. Like in all other cases, it is implemented as a

QMessageBox, with proper information displayed as its content. Moreover, flag indicating that the correct schedule is loaded is set to False and the text on the label showing the loaded file name is changed to "None". Similar error message window should appear if - by any chance - schema itself could not be validated.

A file that has been positively validated against the schema is now parsed. Code of the function responsible for that can be summarized in following steps:

- 1. Reset the necessary variables to 0, empty or False. This step is necessary when a schedule has been reloaded, as it clears all the collections from old operations, etc.
- 2. Parse the input XML file into a simple tree using Python's built in minidom module.
- 3. Determine the biochip size from the file and adjust the scale accordingly (in other words, set the BIOXSIZE, BIOYSIZE and SCALE variables).
- 4. Populate the set of operations schedule. All the operation elements in the input file are converted into objects of custom Module class (see section 4.3). Each module incorporates information from XML, therefore consists of an operation super type, start time, end time, module location, etc.
- 5. Set the flag indicating that the schedule has been loaded (scheduleIsLoaded) to True and display the schedule file path and name on the text label next to the "Load schedule" button.

Loading the schedule file ends here. As it has been mentioned before, the program is designed in such a way that at this point it is possible to generate the simulation (without any graph or error data) or load a graph file (and - optionally - error file).

4.5 Loading the graph

The process of loading the graph is very similar to the one of loading the schedule, but a few additional features have to be added, as the graph depends on the schedule loaded. Again, there is a function graphOpen, which is responsible for initial check of the graph file. Analogically to the schedule load, it is connected via Qt signal clicked to the "Load graph..." button. A step-by-step working principle of this function can be described as follows: Check if schedule is loaded. Since some of the features of the graph rely on information included in the schedule file, it is important that the graph is loaded after the schedule. Such a solution excludes some possibilities of making a mistake and despite causing some difficulties, I consider it an optimal way to deal with this issue.
 If the schedule is loaded, the function proceeds further, otherwise an error

If the schedule is loaded, the function proceeds further, otherwise an error window is shown to the user (QMessageBox, as outlined in section 3.4.3) and the function finishes its execution,

- 2. Load the graph file. This is done in an exact same way as loading the schedule, i.e. by using QFileDialog.getOpenFileName method, which pops up a default "Open file" window.
- 3. Validate the file against the schema. This is done with use of QXmlSchemaValidator, just like in case of schedule validation (the only change is obviously the schema name graph.xsd in this case). Again, if the validation proves unsuccessful, an error message is displayed via QMessageBox and the function stops its execution (this will yield the same result if there was an error during loading the file or the load was cancelled). Otherwise, the program proceeds with loading the graph.
- 4. Once it is checked that the schedule is loaded and that the graph file is correct, it is possible to parse the file (see below), but one more thing must be checked before parsed information can be used. It is essential to determine, whether the graph loaded actually matches the loaded schedule (algorithm for this is described after parsing). If yes, simulation with graph is ready to be generated (as long as no errors are to be included) flag indicating that the graph is loaded (graphIsOpen) is set to True and the informative text label is set to display the graph file path and name. Otherwise, the program displays an error dialog indicating a mismatch and stops the execution of this function.

Similarily to parsing the schedule file, graph parsing function uses Python's default functions from DOM module. It gets the node elements one by one and transforms them into custom Node object (for class description see figure ??). Node object contains information about operation number, type and super type, as well as children and parent node numbers (if any) in a set form. Moreover, it also includes information about starting time of the operation, which is used to set node's position on the graph. This information is taken from the schedule set, as no such data is present in the graph file. This is the main reason for a setup that does not allow loading the graph before schedule. All the Node objects are stored in a temporary set of nodes, which is later on used to check if the graph file matches the node. Moreover, a dictionary is created with operation number as a key and Node object as a value. This

dictionary is later used by the function responsible for calculating the intrinsic error propagation, as it makes the process of traversing the graph reasonably easier.

The check for match between the graph file and the schedule file is really simple. It is designed in a way that it takes the aforementioned temporary set of nodes and the set of operations from the parsed schedule file. Then, node by node, it checks the operation set for the operation with the same number. If found, it compares two values - operation type and operation super type. If for any node-operation pair the super types do not match, flag indicating the correctness of matching is set to False. A simulation cannot be generated if the graph file does not match the loaded schedule.

4.6 Simulation generation

The input files are already loaded and checked, therefore it is possible to generate the simulation now (no input file with errors considered). Function responsible for generating the simulation is **generateSimulation** and its flow diagram is presented in figure 4.4.

One can conclude from the flow diagram that the simulation generation is a two-step procedure (in fact three-step, but at this stage we do not include errors). Firstly, the program checks if a schedule is loaded, and if so - draws the simulation (if not - an error message is displayed). Then, it checks if a graph is loaded. If yes - it is drawn, if not - simulator completes the generation. At this stage errors are produced if the schedule is not loaded, or if the graph does not match the schedule file.

The latter may seem confusing, however is perfectly justified. It came out during testing that if a simulation is generated correctly, and another schedule is loaded, it still uses the old graph. Therefore a solution was urgently needed. One way was to unload a graph when a new schedule is loaded, but this could cause some unnecessary trouble (it can be a common situation that the user wants to load a slightly changed schedule that would still match the previous graph). Another solution was to check the matching once again, and this is the way it works now.

First, and the only mandatory part is to generate an error-free simulation without a graph. This part is enough to see how the droplets behave if the input schedule is applied, however user is neither provided with any graph, nor is he

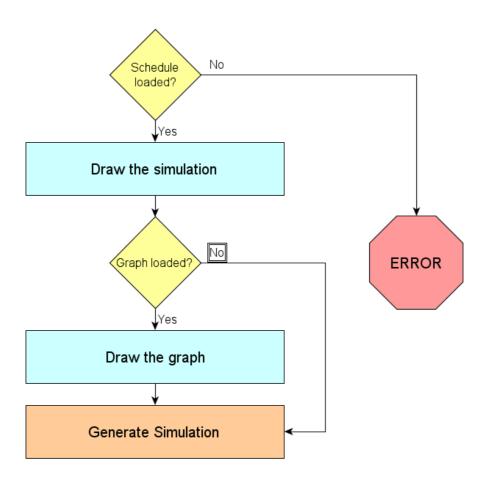


Figure 4.4: Flow diagram for simulation generation function.

able to simulate any erroneous behaviour. The core function responsible for this is drawSim, whose execution can by summarized in the following steps (you can also refer to figure 4.5 for detailed steps of drawing the chip):

- 1. Set default initial values. In the beginning all the necessary values like counters, sliders' positions, etc. should be set to 0, the scene should be erased empty and any sets of objects should be emptied as well. This is necessary when it is a second, third, etc. generated simulation and the remains of an old one must be erased.
- 2. Finding relevant timestamps. All the starting and finishing times of

the operations are collected (these may be considered as "checkpoints" in the simulation). Also a timespread of the simulation is set at this point, i.e. starting time of the first operation and finishing time of the last one.

- 3. Draw the biochip. Draw the rectangles representing the biochip cells.
- 4. Add the modules to the view. Each module created while parsing the file now needs to be added to the scene. Firstly, all the modules are created as a graphical representations of the operations. Then, all of them are added to the scene. Finally, their visibility statuses are set to False, i.e. all of them are placed at once in the scene, but they are invisible until they are needed.

The last action is to set the references to the graphic items representing the modules for good. This process is rather straightforward as the information about module location and size is already included there, thus the only thing to do is to add a rectangular QGraphicsItem of the right size in a specific position.

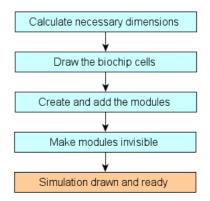


Figure 4.5: Simulation drawing steps - simplified simulator.

The control over modules' visibility is given either to the timer event (section 4.7) or to the user (section 4.8). But in any case it can be simplified to comparing the current timeframe with starting and ending times for each operation. If the frame number is smaller than operation's starting time or larger than its ending time, the module is turned invisible, otherwise it is made visible. An example of two subsequent frames depicting a finishing operation (in this case operation 30 - an optical detection) is presented in figure 4.6.

Drawing the graph. Drawing the graph is - generally - a simplified version of drawing the operation modules. Likewise, it is done node by node (operation by

4 (9	store	e)	6 (9	store	e)	4 (9	store	e)	6 (9	store	e)	
30	(opt)										

Figure 4.6: A finishing operation.

operation). First of all, a graphic object is created. For this purpose I created an object graphNode (simplified class diagram is presented in fig. 4.7), which extends standard QGraphicsItem. This graphNode is then put into a dictionary, so a fixed reference to it can be made, with key being again the node (operation) number. Then the node can be added to the scene of the graph.

It has been a reasonable challenge to find the best way to display the graph. The main problem is that - like the simulation - it needs to be animated, in this case by highlighting the nodes of currently active operations. Therefore it was impossible to use a graph generating program. Finally I decided on a simple solution, which - although leaves space for a lot of improvements - prevails a reasonable level of clarity. Vertical position of each is based on the operation starting time, so the top-down scrolling is preserved. Horizontal position - on the other hand - can be best described as "first come, first served", which means that the node that is currently to be drawn is placed at x = 0 if this position is not occupied. If it would collide with other node, it simply moves by a bit more than node's width to the right.

This means that a lot of crossing arrows may occur on the graph that could have been avoided. This has been left as it is for the following reasons:

- Solving this problem would require some major research in the graph design algorithms which would take a lot of time,
- Python does not provide any native modules addressing this issue, neither am I aware of 3rd party modules serving this purpose,

• Displaying the graph is just a visual help to the simulation itself, the most important thing from the graph file are the dependencies between the operations.

It is also worth noting that solving the problem of a good graph layout may be a good idea for a small project.

	graphNode	
color		
size		
х		
у		
highlight() dim()		

Figure 4.7: graphNode - simplified class diagram.

As the graph is designed to be presented in a separate window, I reckoned it would be a good solution to enable the possibility of turning this window on and off.

4.7 Timer event

The timer event (as described in section 3.6) is executed every n seconds and is responsible for the following things (of course if the simulation is running):

- Updating the currently displayed scene by adjusting the visibility of the modules. This is done by iterating over all the modules, and comparing current time with the module's "lifespan". If the time is lower than the starting time of an operation or higher than its finishing time, the module is set to invisible. It cannot be removed from the scene because the explicit references to this particular module would be lost.
- Stopping the simulation if the counter goes over the finishing time. It is unnecessary to trigger any actions if the simulation has ended, thus once the counter goes over the finishing time, the simulation is paused.
- Adjusting the window elements, i.e. setting the slider's position to the current timestamp and update the display with the current time.

• Displaying an appropriate message box if an error occurs (see section sec:errors),

4.8 User interaction

Updating the scene can also be performed by the user. A number of buttons and controls provided enable user to jump to an arbitrary frame, proceed to the next relevant timestamp (or go back to the previous one). It is also possible to pause/unpause the simulation or export the current frame to a PNG file. For full feature list please refer to chapter 7.

A screenshot of the main window of a simplified simulator is presented below (fig. 4.8).

🕎 Digital microfluidic biochip simulator			? <mark>×</mark>
Input files			
Load schedule None			
Load graph None			
😓 Load errors None			
Appearance			
Cell size			
Module Size			
Errors			
Error settings for simulation: Simulation without errors			
Error probability (per op.):			
Stop at next error			
Save error info log			
Misc.	<		
Generate Simulation! Show/Hide graph	<		4
	Prev. Event	Play/Pause	Save screenshot Next Event
E.			

Figure 4.8: Main application window - simplified simulator.

Chapter 5

Realistic model (droplets)

Realistic simulator coveres a more detailed abstraction level. It basically shows what is exactly happening on the chip, i.e. how the droplets move, where they are created, where the detectors are placed, etc. The only thing that is not covered at this stage are errors. Due to more details, this simulator is also slightly more complicated than the simplified one. This section explains in details its design and the implementation of this design.

5.1 Input files

Schedule file to be loaded is basically similar to the one for the simplified simulator, however it includes some new attributes. The main element includes the information about biochip size, i.e. its x and y dimensions (exactly like in the simplified simulator). Subsequently, a list of operation elements is included, with attributes describing:

- operation number
- operation super type
- operation type (each super type can include several types)

- operation start time
- operation end time

The value of the **operation** element itself is a route of the droplet "owned" by this operation. The schema that specifies the input schedule is presented on figure 5.1 and an example of a correct schedule file can be found in appendix B.

```
<xsd:schema attributeFormDefault="unqualified" elementFormDefault="\leftrightarrow
      qualified" version = "1.0" xmlns: xsd="http://www.w3.org/2001/↔
      XMLSchema">
  <rpre><rsd:element name="schedule" type="scheduleType" />
   <rpre><xsd:complexType name="scheduleType">
     <xsd:sequence>
        <xsd:element maxOccurs="unbounded" name="operation" type="\leftrightarrow
               operationType" />
     </xsd : sequence>
     <xsd:attribute name="xsize" type="xsd:string" />
<xsd:attribute name="ysize" type="xsd:string" />
   </xsd:complexType>
  <\!\!\texttt{xsd:complexType} \hspace{0.1cm}\texttt{name}="\hspace{0.1cm}\texttt{operationType}" \hspace{0.1cm}\texttt{mixed}="\hspace{0.1cm}\texttt{true}"\!>
     <red:attribute name="endTime" type="xsd:string" /><red:attribute name="opNumber" type="xsd:string" />
                                                                              />
     <rpre><xsd:attribute name="opSuperType" type="xsd:string"</pre>
     <red:attribute name="opType" type="xsd:string" />
<xsd:attribute name="startTime" type="xsd:string" />
   </xsd:complexType>
</xsd:schema>
```

Figure 5.1: XSD schema - schedule for realistic simulator

Graph loaded is exactly the same as for the simplified simulator, and the principles are exactly the same, i.e. it is not possible to load it before schedule.

5.2 Variables

The list of variables controlling the realistic simulation is slightly bigger than in the case of a simplified one. Most of variables used by the simple simulator are also used by the realistic one, however - for convenience - they are also repeated in the list below:

Sizing variables, i.e. ones that directly influence the biochip's appearance in the simulation window:

• SCALE - size of the "slot" that can be assigned for a single cell.

- BIOXSIZE number of cells in each biochip's row.
- **BIOYSIZE** number of cells in each column.
- SCENEXSIZE horizontal size of the scene containing the simulation.
- SCENEYSIZE scene's vertical size.

Variables which affect the appearance of the simulation:

- ELBORDER spacing between the biochip cells.
- dropletSizeFactor default size of the droplet (expressed as a fraction of a cell size).
- cellBrush, errBrush, resBrush colors used for different biochip parts cells, reservoirs, etc..
- Dictionaries brushes and detBrushes like in the simplified simulator, brushes are also used for defining new operations. Additionally, dictionary detBrushes has been used to define different detector types. As it will be shown on a screenshot later, detectors are painted in a different way than "normal" cells.

Time-related variables and boolean flags:

- INTERVAL interval for subsequent timerEvent executions.
- counter current simulation timestamp.
- startingTime simulation starting time.
- finishingTime time at which the simulation finishes.
- running simulation running status.

Boolean flags indicating certain properties of the simulation:

- schedIsOpen True if a correct schedule file is loaded, False if it is not loaded or is by any means incorrect.
- graphIsOpen same, but for the graph file.
- showGraph determines if the graph window is shown or not.

Boolean flags indicating certain properties of the simulation:

- schedule this set contains all the Droplet objects. Details of Droplet class are described in section 5.3.
- nodeList a set of all graph nodes.
- rlvTimes a sorted list of all relevant timestamps.
- nodes a dictionary used to establish references to the graphic items that are representing the graph nodes, just like in the simplified simulator.
- allDroplets similar, but stores [operation number]:[Module object] pairs. This ensures that a graphics item representing a particular operation can be explicitly referred to by its number.
- reservoirs a set containing all the reservoirs' locations and types.
- detectors similar, but for detectors.

5.3 Droplet class

Droplet serves - on principle - the same purpose as the Module class in case of a simplified simulator, i.e. it provides information about an operation, its graphic representation and the error status of the operation. Exactly like its counterpart, it extends a QGraphicsItem class.

Its __init()__ function is analogical to one in the Module class. This means that when a new Droplet object is created, it needs to be passed some crucial data.

- operation number,
- operation super type,
- operation type,
- operation start time,
- operation end time,
- route taken by the droplet during the operation

Unlike all others (which are attributes in the XML input file), route is the value of the element and provides information about droplet location for every single time unit between operation start and end.

Like in the previous case, each Droplet object has operation number as its hash value.

Graphic representation is also similar to the Module case, with only difference being the shape of this representation, which in this case is an ellipse representing a droplet. Thus, methods connected with drawing have slightly different contents.

- **boundingRect** specifies the rectangle within which the item is located (in this case it is equal to the rectangle bounding the droplet's ellipse (circle))
- shape specifies the shape of the item (in this case an ellipse (circle))
- paint specifies the style pen, fill, effects, etc. in which the item is drawn.

Similarly - four variables are needed to set the droplet's appearance: size of the droplet (no need to split into x and y sizes as it is a circle), droplet's location (x and y) and color of the droplet. Again, these can be dynamically added to the class when needed, but for the clarity they have been added to the class.

status method has been added for the same purpose as earlier - in order to display main information about the operation as a tooltip activated when the mouse cursor is placed over the droplet.

For operation error features, please refer to chapter 6.

Again, a simplified (without generic methods) class diagram for this class is presented below.

5.4 Loading the operation schedule

Loading the schedule is done in a way very similar to the one used in simplified simulator. The only differences emerge from the different information in the input files.

Droplet
color size x y opNumber opSuperType opType startTime endTime route
status()

Figure 5.2: Droplet - simplified class diagram.

- 1. **Reading in the name of the schedule file.** Again, a file open window is shown to the user so the schedule file can be loaded.
- 2. File validation against XSD schema. The schema file for realistic simulation schedule is schedDroplet.xsd and it is processed in the same way as in the simplified simulator.

The validator is constructed in the same way and the validation process is also the same.

- 3. Calling the parsing function. If the input file is correct, the schedule file can be parsed (see below).
- 4. **Providing error messages**. If a schema is wrong, an error is displayed. Another error (or - to be more precise - a warning) is displayed when a new schedule is loaded but there is a graph file already loaded. If they do not match, user is informed about it.

If the file has been positively validated against the schema, it can be now parsed. Parsing is done using function parseFile, which does the following things:

1. Sets all the necessary values to their defaults (usually zeros or empty lists, sets or dictionaries) by executing function setInitialParse, which simply resets all of those values. Like in the simplified simulator, this is to make sure that no information from the previous simulations remains.

- 2. Parses the input XML file into a simple tree using Python's built in minidom module. Again, BIOXSIZE, BIOYSIZE and SCALE values are set at this point.
- 3. Prepares the operation list schedule. All the operation elements in the input file are converted into Droplet objects. The most important of this object's attributes is route. Although it can be saved as a list, it is highly inefficient, as it will be necessary to find droplet's position at a specific time point. Thus, route is saved as a dictionary, with entries of the form key = time, value = location.

At this point the simulation can be generated, though user may want to load also a graph file and errors.

5.5 Loading the graph

Graph is loaded in exactly the same way as in simplified simulator, point by point, thus it is unnecessary to repeat details about it here. Please refer to section 4.5.

5.6 Simulation generation

Once the input files are loaded it is possible to generate the simulation. For this purpose, a function generateSimulation has been created. To make the code clearer and more object-oriented, it provides only two things:

- Checks if everything is set up properly. If schedule file is read in, it executes the function setting up the simulation (drawSim). Then, if graph is loaded it checks if it matches the schedule and, if so, executes the function responsible for painting the graph (paintGraph).
- Displays error messages if anything goes wrong:
 - Schedule is not loaded.
 - Graph does not match the schedule file.

First, and the only mandatory part is to generate an error-free simulation without a graph. This part is enough to see how the droplets behave if the input schedule is applied, however user is neither provided with any graph, nor is he able to simulate any erroneous behaviour. The core function responsible for this is drawSim, whose execution can by summarized in the following steps:

- 1. Reset the window to its defaults. By calling setInitialView all the counters, sliders, etc. are set to their initial positions.
- 2. Reset the scene. The scene that will contain the simulation is recreated from the beginnings, its (0,0) point will be the upper left corner of the biochip and there will be a one cell width margin at each side for possible reservoirs. Finally, this scene will be added to its view.
- 3. Finding relevant timestamps. For all the operations, starting and ending times are collected into a list rlvTimes, as they will be needed later. Moreover, the lowest of relevant times becomes the 'global' starting time and the highest of them - 'global' ending time. This means that the whole timeline for the simulation will be spread from startingTime (usually zero, but simulations starting from, for example, 133 are correct) to endingTime.
- 4. Collect reservoirs' locations. For each of the operations in the operation set schedule, a route taken by the droplet is checked for locations lying outside the biochip. If either of x or y coordinates are -1, a reservoir is located there. It is also true if x equals BIOCHIPXSIZE or y equals BIOCHIPYSIZE. All these locations are collected into one set, so later on they can be added to the scene. Additionally, reservoir types are collected in the same set for future use (each element consists of the information on the reservoir type and its location).
- 5. Collect detectors' locations. It is desired that the cells that are somehow special, for example detectors, are painted in a different way than 'normal' cells. Therefore, locations of the detectors are collected. Operation type is checked for each operation in the schedule. If the type is detection, location is collected from the droplet route (arbitrary element from the route, because droplets do not move during detection operation). At the time being only optical detectors are considered, but changing this situation is easy, as the only update it requires is a new entry in detectors dictionary dictDetectors.
- 6. Draw the biochip. The drawing operation starts with drawing the biochip cells. These are simply rectangles (squares, to be precise), which (if defaults are not changed) are medium grey and have a spacing of two pixels between them. This is done by simply adding such a rectangular

item to the scene, using method QGraphicsScene.addRect, which is a simplication of default addItem method.

- 7. **Draw the reservoirs.** Reservoirs are drawn in the exact same way as the normal cells, they just use another brush for their colour. Additionally, a text label is added on top of the reservoir as an indication of the reservoir type.
- 8. **Highlight the detectors.** There are three ways to make the detectors different from the other biochip cells. One way is to skip them during adding the ordinary cells and draw them later, but such a solution makes the drawing of biochip unnecessarily complicated. Another way is to paint a detector square on top of the cell, but such a solution adds unnecessary items to the scene.

The most optimal solution is to alter the existing cell, and there are two ways to do it. One way is to set a new color for the cell item, but for that purpose at least two more objects need to be created (new brush and a new QPainter object). The other way to do this is to apply an effect to an item. Qt provides a number of such effects, and one of them is QGraphicsColorizeEffect, which simpy colours the item with a given colour, and the strength of this effect can be determined as well.

Therefore, for all detector locations the function invokes method QGraphicsScene.itemAt, which returns a pointer to the biochip cell at this position. Once this pointer is obtained, the aforementioned effect is applied to the cell item.

- 9. Set initial information about droplets. For each operation in the schedule an initial droplet objDroplet is created, and it includes information about operation number, starting and ending times, i.e. times at which the droplet should appear and disappear from the view, and the route the droplet takes during the operation.
- 10. Add the droplets to the view. Each objDroplet created during the previous step now needs to be added to the scene. It is a three step process.

Firstly, all the droplets are created by executing the function createDroplet (see below). Then, all of the droplets are added to the scene - addDroplet, see below. Finally, all of them are turned invisible.

The first thought would be obviously to add the droplets to the scene at their start times and remove them when the operation has finished. Unfortunately this would work only if there was a 'forward-only' timeline, i.e. it would be impossible to move the time slider backwards. All the items are needed on the scene at any time (it does not matter if they are visible or not), so the program can keep track of pointers to all the items. If an item is removed from the scene, and then an exact item is added to the scene, these are not considered the same items and most of the logic behind the program fails. Thus, for the sake of elasticity, all the droplets are present on the scene at all times, and they are turned invisible if their operations are currently not executed.

The steps for drawing the simulation are also presented in figure 5.3.

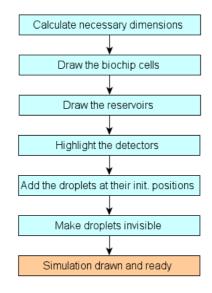


Figure 5.3: Simulation drawing steps - realistic simulator.

Creating the droplets. This process is performed by function **createDroplet** which takes an **objDroplet** object as an argument and is a simple, three line piece of code. It performs two things:

- creates a new object Droplet. It is an extension of standard QGraphicsItem class which acommodates some vital information about the droplet, e.g. its current size or if it has been affected by an error.
- creates a pointer to this particular droplet. This is organized in a form of a dictionary, with key being the operation number, which is unique for a given schedule, and the value is the created **Droplet** object.

Originally all of the droplets are created at point (0,0) - explanation is given below.

Adding the droplets to the scene. This process is handled by function addDroplet, which - again - takes an Droplet object as an argument. This function includes a number of calculations, as it determines the initial position of the droplet. Also it is the one place I used a solution which I know is more complicated, but I could not solve it in a more efficient way.

The problem is that I wanted the droplets to be added to the scene at their starting positions. However, since Qt uses **3** different coordinate systems (one for graphics view, one for graphics scene and one for graphics item), I did not manage to master the transformations between them in a way that would allow me to create the droplets straight at their starting points, as they did not want to pick up correct positions, thus a workaround has been developed.

Firstly, a droplet is added to the scene. Then, a text label is added on top of the droplet, and it is bound to the droplet (QGraphicsItem.setParentItem method creates dependencies between items). Finally, the vector between (0,0) and coordinates for the point at which droplet should appear is calculated and the droplet is moved to that place.

5.7 Moving the droplets

Moving the droplets is probably the most important feature of the simulator, as it simply 'shows' what is happening on the chip. I managed to actually make the logic almost match the reality, i.e. the droplet object actually moves around the chip and nothing is repainted, rerendered, etc.

There are two functions responsible for droplets' movement: setCurrScene, which takes an arbitrary time from the timescale as an input and updates the scene accordingly and setDropletPosition, which needs a objDroplet object passed in, as well as a timeframe from the timescale and moves the droplet to its correct position at a given point in time.

Setting the current scene can be described in the following steps, which are repeated for each objDroplet:

- 1. If the timestamp falls between the start and end time of the operation, its droplet is set to visible and its new position is set by calling the function setDropletPosition. Moreover, if the graph is enabled, this operation's node is highlighted (methods Node.highlight and Node.dim have been described in section 3.4.2).
- 2. If timestamp does not match with the droplet "lifecycle", the droplet is set to invisible and again, if graph is enabled its respective node is

dimmed. Moreover, the LCD displaying the current timeframe is set to the correct position and the same applies to the time slider.

Setting the droplet position happens in a similar way to adding the droplet. The only change is, that instead of calculating the vector between (0,0) and the desired position, a vector between current position and the desired position is calculated. Droplet is then moved by this vector. An image containing two subsequent frames showing the droplets' movement is presented in figure 5.4. It shows three moving droplets and one placed on a detector.

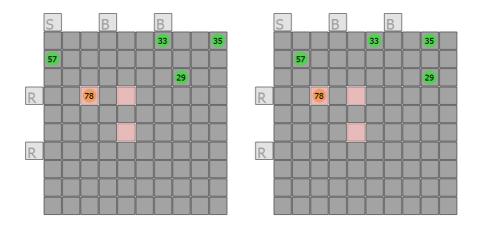


Figure 5.4: Moving droplets.

Setting the scene so it matches the current timestamp can be done in two ways. It can be either a timer event executed automatically every N miliseconds, or a user decision, which can be one of a few options. Both scenarios are described in the subsections below.

5.8 Timer event

If the simulation is running, or in other words, if running flag is set to True, timerEvent is trigerred every n miliseconds (as specified by INTERVAL variable). The actions performed by the timerEvent are:

- Check the current timeframe and update the scene accordingly (see setCurrScene above),
- If error happens at a given timeframe, display an appropriate message box (see section on errors),
- Stop the simulation if the counter goes past the finishing Time.

5.9 User interaction

User is also enabled to pause the simulation and go to an arbitrary timeframe, and thus several features are provided, all of which are simply calling setCurrScene function. The possibilities are:

- Move along the timeline, both forwards and backwards,
- Go to the next (or previous) relevant timeframe (start or end of an operation),

Both possibilities utilize the same principles and functions as the timer event. A screenshot of the main window of a realistic simulator is presented below, so the options are clearly visible (fig. 5.5).

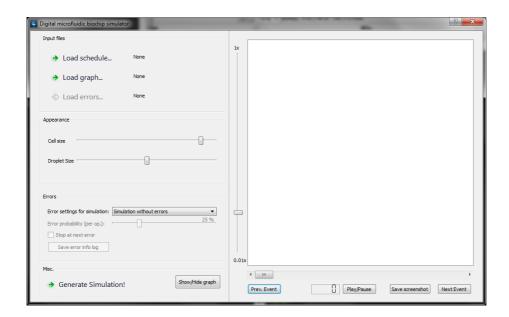


Figure 5.5: Main application window - realistic simulator.

Chapter 6

Faults simulation

Apart from the regular, error free simulation, there is also a possibility to introduce volume errors to the simulation. This feature has been designed to offer three possibilities to the user. Firstly, it is possible to generate random errors to arbitrary operations. Secondly, user can choose to load an error file including such errors, i.e. ones that apply to specific operations and to them only. Finally it is possible to set error limit values for intrinsic operation errors, which would then propagate through the operations.

6.1 Erroneous state of the operation

Both in the simplified simulator and in the realistic simulator it is important to somehow define the erroneous state of the operation. This is one of the reasons why custom Module and Droplet classes have been created. In both of them two variables have been added - boolean isCorrupted and errorLevel (numerical). The first one simply indicates if the operation is erroroneous, whereas the second one determines the actual value of this error (in relation to 1 in the simplified simulator and to the default droplet size in the realistic one). This means that actual generation of an error can be performed by simply changing the mentioned flag to True and setting some error value.

6.2 Input files

There is only one error file type for the simulation, and it covers both intrinsic and "per operation" errors. The main element is **errors** and its attribute **type** determines what kind of errors will be taken into account by the simulator (if the user wants to run the simulation with preset errors) - "i" for intrinsic errors and "o" for "per operation" errors. Details on how to prepare a correct file with errors can be found in section 8.4.5.

Intrinsic errors are determined in a single element **intrinsic_errors**, with the following attributes setting the error limit/threshold values:

- edis error threshold value for dispensing operation,
- edlt error threshold value for dilution operation,
- emix error threshold value for mixing operation,
- etrans error threshold value for transporting operation,
- esplit error threshold value for split operation operation

Last two are currently not used by the simulator, but since they are a part of the whole theory behind the intrinsic errors (see section 1.2.4) I decided to include them. Future improvements may include incorporation of transport and split operations, so those two limit values may prove useful. Please also note that if any of those limits is set to 0 it is treated as if there was no error.

"Per operation" errors are determined in operation elements, one for each error, and each of this elements have two attributes:

- <code>opNumber</code> - <code>number</code> of operation affected by the error - <code>opError</code> - threshold value for the specified error

XML schema for the error input file is presented in figure 6.1, and an example of a correct input file with errors is given in appendix D.

Please note that it is impossible to load a file with intrinsic errors (error type "i") without loading a graph (reasons for this will be given in sections below). An attempt to do so will result in a warning from the program. It should be possible - from the theoretical point of view - to load a list of "per operation" errors (error type "o") as they do not require a graph to work correctly. However such an option has been disabled to minimize the number of checks, and subsequently - a number of mistake opportunities.

```
<xsd:schema attributeFormDefault="unqualified" elementFormDefault="\leftrightarrow
     qualified"
                   version = "1.0" xmlns: xsd = "http://www.w3.org/2001/ \leftrightarrow
     \tt XMLSchema">
  <rpre><xsd:element name="errors" type="errorsType" />
  <rpre><xsd:complexType name="errorsType">
     <rpre>xsd:sequence>
       <xsd:element minOccurs="0" maxOccurs="1" name="intrinsic_errors"\leftrightarrow
              type="intrinsic_errorsType" />
       <rrsd:element minOccurs="0" maxOccurs="unbounded" name="operation↔
" type="operationType" />
     </xsd:sequence>
     <re><rsd:attribute name="type" type="xsd:string" /></re>
  </xsd:complexType>
  <rpre><xsd:complexType name="operationType">
    <\!\!\texttt{xsd:attribute name="opNumber" type="xsd:string"}
                                                                      1>
     <rr></r></r></r></r>
  </xsd:complexType>
  <re><xsd:complexType name="intrinsic_errorsType">
    <xsd:attribute name="edit" type="xsd:string" />
<xsd:attribute name="edit" type="xsd:string" />
    <xsd:attribute name="emix" type="xsd:string" />
<xsd:attribute name="etrans" type="xsd:string"</pre>
    <rpre><xsd:attribute name="etrans" type="xsd:string" />
<xsd:attribute name="esplit" type="xsd:string" />

  </xsd:complexType>
</xsd : schema>
```

Figure 6.1: XSD schema - error input file

6.3 Simulators' extensions

Several new variables needed to be added to both simulators in order to accomodate errors feature:

- Edis, Edlt, Emix, Etrans, Edis and Esplit for storing intrinsic error limit values for five operation types mentioned in section 1.2.4.
- errBrush for setting a color for an erroneous operation (module or droplet).
- Flags errorIsOpen (for indication that a correct error input file has been loaded) and errorOut (indicating that errors happen during the simulation and can be saved in a log file).
- inErrorMode for indicating which kind of errors are loaded (intrinsic or single operation)
- ERRORMODE variable indicating whether simulation is running without errors (0), with randomly generated errors (1) or with errors loaded from a file(2).

- errors set containing all the errors that happen throughout the simulated schedule.
- Dictionary errTimes for a faster access to a specific error.

6.4 Error class

Each of the errors is represented as a single **Error** object. For this purpose a new, really simple class has been created.

A new Error object must be created with the following parameters:

- Operation number,
- Operation super type, to make the error message more informative,
- Time of the error, which is the starting time of an erroneous operation,
- Error value,

A method **errorInfo** has been provided with this class. It returns the error information as a nicely formatted string (please see detailed error information in figure 6.2).

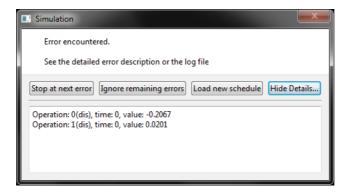


Figure 6.2: Error information.

Like in the case of Node, Module and Droplet classes, this is also hashable, with the hash function returning the operation number.

	Error	
dropletID errorTime errorValue opSuperType		
errorInfo()		

Figure 6.3: Error - simplified class diagram.

6.5 Opening the file

Loading the error file is quite similar to loading the schedule or graph, and the step-by-step working principle is as follows:

- Check if the schedule is loaded and if the graph is loaded. If yes, proceed, otherwise display an error message that they are not loaded and stop execution.
- Choose the file to open. Similarly to the schedule and graph cases, this is done by opening a standard "Open file..." dialog.
- Validate the file using schema error.xsd. If the validation is successful proceed, otherwise display an error message and stop the execution.
- If the validation proved successful parse the error file. This is only the initial parsing, whose main purpose is to check if the errors can actually be applied to the simulation. This means that the operations in the error input file are searched for in the schedule file. If all the operations specified in the error file exist in the schedule, True value is returned and the flag indicating the load status of the errors (errorIsOpen) can be set to true, which means that the errors can be generated.

This is also the place where the last possible errors in the file can be caught, i.e. errors for operations not present in the schedule. If this is the case - error message is produced saying that the errors in the file do not match the schedule and the function is stopped at this place.

6.6 Generating the errors

If everything is loaded correctly, the simulation with errors can be generated. Depending on the initial settings, i.e. if the errors have been loaded from the file or are to be generated randomly, three scenarios can happen. Please note that all the errors - be it random or loaded - are by design generated at this point, together with simulation. This means that if the user wants to change settings for random errors, the simulation needs to be regenerated each time.

6.7 Random errors

Introducing random errors works on an operation-by-operation basis. There are two control parameters for these errors - error probability and error limit value. The first one obviously indicates the chance of an error occuring to a given operation, the second one sets the limit of this error. As for the distribution of the error values - gaussian distribution has been chosen in order to match the theory behind the intrinsic errors.

The simulator is designed in such a way that the user can easily change the error probability through the program interface, whereas the error limit has been hardcoded as a reasonable value of 0.2 (which is set only once in the source code so any adjustments are trivial).

The functions setting the errors (corruptModule and corruptModule in simplified and realistic simulator respectively) do the following things:

- Determine if the error should occur or not. This is done by generic Python random generator. In this case **randint** has been used to generate a random integer between 1 and 100 (**randint** has been chosen to ensure uniform distribution of the results). Subsequently this number is compared to the error probability set by the user. If it is smaller, the operation can be "corrupted", otherwise nothing happens.
- Timestamp for the error is created in order to stop the simulation there (if needed). This is set as exactly one frame after the operation starts, so the error is displayed when the visual representation of the operation (be it a module or a droplet) is already drawn.
- Error variables are updated, which include the flag indicating that the operation started with an error and the value of this error. The value as mentioned before is calculated using gaussian distribution.

- In case of the realistic simulator droplet size is adjusted accordingly and its color is altered to indicate an error.
- Errors are stored in a set for future use. A custom Error object has been created and it includes information about error value, the operation that is erroneous and the time of the error.

6.8 User specified single operation errors

If user chooses to introduce specific errors to the schedule, the process looks only slightly different. First of all, error input file is parsed in order to check the error mode. If one wishes to visualize specific errors, the **type** attribute has to be set to "o". Only then the simulator can introduce the errors specified in the file.

Then, each operation element is read in, or - to be precise - its opNumber attribute. Then a droplet (or module) is looked up in the droplets (modules) set. Finally, program executes the same function that is used in case of random errors, but with probability equal to 100% and the error limit taken from attribute opError. The exact error value is again calculated using gaussian distribution. All the remaining actions are exactly the same as in the previous case.

6.9 User specified intrinsic errors

In case of intrinsic errors the situation is more complicated. First of all - these errors require information from the graph, as they propagate from operation to operation and need information about dependencies between the operations. Therefore an iterative approach is needed.

Every step below is repeated as long as there are nodes that still have error values to be calculated. This is indicated by a boolean flag in each graph node object which is set to True if an error value for this operation node has been calculated.

- If the node has no parents, its value can be determined instantly. It is however applicable only to dispensing operation, as it is the only one that does not have a parent operation.
- If the node has parents, check if all of them have the error values already calculated. If yes, error value can be calculated (using formulae presented in section 1.2.4). Otherwise, proceed to the next iteration.

Having tested numerous input files I deducted that it usually takes at most two iterations to cover all the operations, however I realise that schedules with more complex dependencies may require more of them.

When the errors are populated, they can be applied to operation modules or droplets, just like in the previous two cases. Also all the errors are stored in the error set for future use. Flag indicating that the errors happened (errorOut) is also set to True.

6.10 Visual error information

It is obvious that all the errors would be useless from the user point of view if there was no indication of them at all. Thus the simulator has been designed so as to give the user some control over the error information.

First of all, the full error information can be displayed only if the simulation is running automatically, not when the user is skipping through the frames in pause mode. This is simply a matter of convenience resulting from a number of tests using different settings. Errors popping up when the user simply wants to skip through frames proved highly annoying.

Taking this into account, timerEvent in both simulators has been upgraded to check for errors. It is worth mentioning at this point that it has two levels of "error tolerance", as indicated by the variable RUNNINGSTATUS. If it is set to 0, the simulation runs smoothly and no information about errors is provided. If it is set to 1, the simulation pauses when the next error occurs.

Therefore, if the simulation is set to stop at the next error, after the error occured, information about it is presented to the user. At this point program checks the error set for all errors that occur at this point. As an **Error** class provides a nicely formatted error information message, the program simply collects all this information and provides it to the user.

When an error occurs, user can see the detailed error information, as the error window is constructed as a generic informational window with "See details..." option. At this point he is required to choose one of three options:

- Break the execution of the simulation and choose a load a new schedule (e.g. one that should exclude the possibility of an error),
- Proceed with the simulation and stop at the next error,
- Proceed with the simulation and ignore the remaining errors (this corresponds to setting the RUNNINGSTATUS variable to 0).

However if the user chooses to ignore the remaining errors, he is - at any time - still able to set up a breakpoint at the next error (i.e. change the RUNNINGSTATUS back to 1) by checking the box "stop at next error".

The window shown when an error is encountered has been shown in figure 6.2. Below a simulation screenshot with erroneous droplets is presented (fig. 6.4). Please note the different (erroneous) droplet volumes. Also their color has been changed (in this case to white) to highlight the error's occurrence.

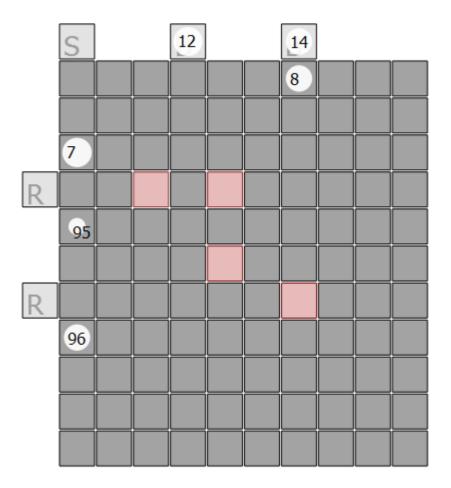


Figure 6.4: Errors in the realistic simulator.

Similar principles apply to modules, though only their colors are changed (not sizes), see fig. 6.5. In this case only one operation has been affected by an error (operation 6 - mixing).

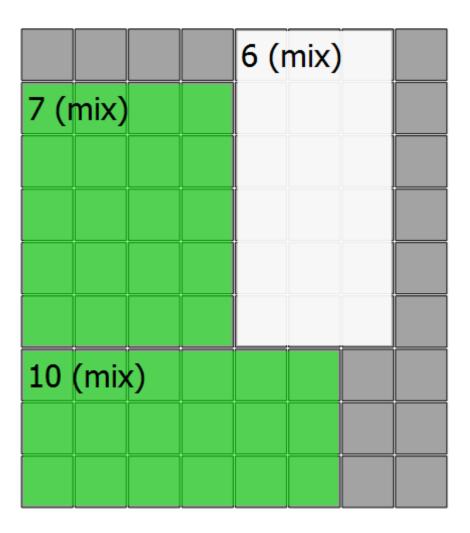


Figure 6.5: Errors in the simplified simulator.

6.11 Error log

The last part of handling the errors is the possibility of saving an error log file. This is the main reason for collecting all the errors in a set, because at this point the program simply collects error information from all the **Error** objects stored there and writes a nicely formatted log text file including all the errors happen. As it was mentioned before, all the errors are generated when "Generate simulation..." button is pressed, therefore the log will include all the errors that happen during the simulation, no matter at which point it is saved. An example of such an error log is presented below.

	0, time: $0,$ value: -0.0519335266718
	1, t time:0, t value:-0.0246056254272
Operation:	2, time: 24, value: 0.00492378408244
	4,time: $0,$ value: 0.0360331199652
Operation:	5, time: 40 , value: 0.00328209011747
Operation:	$6, {\tt time:} 75, {\tt value:} -0.00288384829239$
Operation:	7, time: 103 , value: -0.000282241908359
Operation:	11, time: 81 , value: -0.0144442574028
Operation:	12, time: 117, value: -0.0973032945061
Operation:	13, time: 117, value: -0.085529728241
Operation:	$14, {\tt time:} 131, {\tt value:} 0.00838975598521$
Operation:	19, time: 178, value: -0.00285280263556
Operation:	20, time: 204, value: 0.000733058088836
Operation:	60, time: $573,$ value: -0.0337992019842
Operation:	$61, time: 682, time: -1.36601323355 textbf{e} - 05$
Operation:	62, time: 682 , value: $-6.32224878443e-05$
Operation:	63, time: 658 , value: -0.00540860333446
Operation:	67, time: 799, value: 0.00109372606404
Operation:	68, time: 758 , value: 0.0724340326479
Operation:	69, time: 756, value: -0.00501630162506
Operation:	85, time: 69 , value: 0.0245918891858
Operation:	86, time: $21,$ value: -0.0258961905818
Operation:	$90, {\tt time:} 244, {\tt value:} -0.000685358467117$
Operation:	$91, {\tt time:} 207, {\tt value:} -0.0323326526876$
	$95, { t time:} 265, { t value:} -0.0339657903008$
Operation:	96, time: 562, value: -0.00105070150828
Operation:	97, time: $492,$ value: -0.0769251038657

Figure 6.6: Error log

Chapter 7

Program features

This chapter summarizes all the features of both simulators (together with errors). For a bigger readability level the features are grouped by type. Note that only simple explanations are given here as the whole design has been explained in previous sections.

Since most of the features are the same for both the simplified and the realistic simulator, one list covers them both, as it is unnecessary to repeat them twice.



Figure 7.1: File loading buttons.

File loading - three buttons are responsible for loading schedule file, graph file and error file (the last one is disabled unless "Simulation with pre-set errors (from file)" option is chosen in the combo box in error settings.

Appearance		
Cell size		
Droplet Size	0	

Figure 7.2: Appearance settings.

Appearance settings. User can set the size of the biochip cell and either module size (in simplified simulator) or the default droplet size (in realistic simulator).

rrors			
Error settings for simulation:	Simulation with pre-set errors (from file)		Ŧ
Error probability (per op.):		25	%
Stop at next error			
Save error info log			

Figure 7.3: Error (faults) settings.

Error settings. Following features are connected to this part:

- Choosing the error mode. Combo box provides options for error-free simulation, simulation with randomly generated errors or with user-specified errors. It is up to the user whether this errors are intrinsic or only for single operations.
- For a simulation with random errors setting the probability of an error.
- If simulation is running setting (or unsetting) a break point at the next error, if the check box is checked, the simulation will stop when the next error happens.
- Saving error log if there are any errors happening during simulation, it is possible to save them all into a log file.

Misc. settings. Currently these include only the simulation generation and setting the visibility of the graph window.

Playback features.

Misc.		
🔶 Gene	rate Simulation!	Show/Hide graph

Figure 7.4: Misc. settings.

1x			
[
Τ			
0.01x			
	•		Þ
	Prev. Event	Play/Pause	Save screenshot Next Event

Figure 7.5: Playback settings.

- Playing/Pausing the simulation.
- Moving along the simulation timeline. Clicking the slider's arrows will move the simulation 1 step backwards/forwards. Clicking on the slider's background next to the slider will move it 10 steps back/forth.
- Jumping to the previous/next event. Clicking any of those buttons will move the user to the nearest time when an operation finishes or starts.

- LCD-like display shows the current timeframe.
- "Save screenshot" button exports current simulation frame to a PNG file. This is done simply by using a painter that redraws current scene to an external file.
- Changing simulation speed. A vertical slider left to the simulation view adjusts the simulation speed between 1 step per second and 1 step per 20 ms (lowest "safe" time resolution). This option is available only in the realistic simulator.

Features that can be adjusted in source code only.

- Default colors for operations.
- The names for acceptable operations (and colors for these operations)
- Defined types of detectors.

Chapter 8

Instructions of Use

8.1 Requirements

Before it is possible to run the simulator, installation of two things is mandatory:

- 1. Python environment. Version 3.0 or higher is required as the simulator has been developed in Python 3 which is not compatible backward. For the optimal performence version 3.1.x is suggested. It can be downloaded at http://www.python.org, where a number of options are available, including installer for Microsoft Windows and Apple MacOS X (versions 10.3+).
- 2. **PyQt4**. PyQt4 is required as well as it has been the environment in which the graphic interface has been developed. If you are running Microsoft Windows operating system, the installation can be greatly simplified by simply using the binary package available at http://www.riverbankcomputing.co.uk/software/pyqt/download. For PyQt4 installation instructions for other operating systems please refer to the subsection below.

8.1.1 Required Linux packages

The best way is to check which packages cover all the features installed by the binary installer for Windows, i.e.:

- PyQt
- Qt (with database support for MySQL, PostgreSQL, SQLite3 and ODBC)
- Qt Designer
- Qt Linguist
- Qt Assistant
- pyuic4
- pylupdate4
- lrelease
- pyrcc4
- QScintilla

Plus obviously Python itself, as well as SIP (tool generating C++ interface code for Python). Usually it should be enough if Python, PyQt and Qt packages are installed.

If you are running Arch, any Ubuntu mutation or Gentoo, the required packages are:

- Arch python3, pyqt, qt and qscintilla ttogether with all the dependencies,
- Ubuntu python-qt4, qt4-dev-tools, python-qt4-dev and pyqt4-dev-tools together with all dependencies + obviously the Python package,
- Gentoo Python, PyQt and QScintilla packages.

Please make sure that Python is in version at least 3.0 (3.1 preferred, PyQt and Qt are at least 4.0 (4.4 preferred). The version of QScintilla used is 2.2.

8.1.2 Manual PyQt4 installation

If you are running an operating system different from Microsoft Windows - or you are for any reason unable to use the binary installers - you have to perform the following actions:

- Install Python3, most Linux distributions have Python available on their default package lists. If not - source code can be downloaded from http: //python.org/download/.
- 2. Install SIP. This is a tool that generates C++ interface code for Python and is absolutely necessary, as Qt is designed for C++. Most of the Linux distributions usually have SIP available in their package managers (version number is not a very important issue, though at least 4.0 is required and there is no guarantee that the program will work with lower versions). If by any chance SIP package is not available in the package manager or you are running MacOS X or another system different from Windows/Linux you have to download and install SIP manually. SIP can be downloaded at http://www.riverbankcomputing.com/software/sip/download and the detailed installation tutorial is available at http://www.riverbankcomputing.com/software/sip/download.mtml
- 3. Install PyQt4. Again, it should be available in most package managers if you are using any major Linux distribution. If not, or if you are using another operating system, please download PyQt4 source code from http://www.riverbankcomputing.co.uk/software/ pyqt/download and follow the detailed installation instructions available at: http://www.riverbankcomputing.co.uk/static/Docs/PyQt4/ pyqt4ref.html#installing-pyqt.

8.2 Incompatibility issues

Since it is a GUI-based appliation, an operating system with a graphical user interface is obviously required. To minimize the incompatibility chances it utilizes as few interface objects as possible, all of which are considered standard. However it is required that GUI of the operating system includes the following objects:

• Window elements - buttons, radio buttons, sliders, checkboxes, combo lists etc.,

- Message box windows,
- File open and save dialogs,
- Colour pick windows,

All of these features are currently available on the most popular platforms, i.e. Windows, MacOS X and most of the Linux variations. Users of less popular Linux configurations may expect difficulties, depending on the interface used. There was also a known problem of Qt message boxes not displaying the window title on MacOS X, however it is unknown if this problem has been solved or not. It is only a cosmetic issue though.

8.3 Files

The files included are:

- classes.py custom classes written especially for this simulator,
- uiDroplet.py user interface for the realistic simulator, compiled from XML file produced by Qt Designer,
- uiModule.py user interface for the simplified simulator, compiled from XML file produced by Qt Designer,
- simDroplet.py realistic simulator application file,
- simModule.py simplified simulator application file,
- graph.xsd schema for the graph input file,
- schedModule.xsd schema for the schedule input file for the simplified
 simulator,
- schedDroplet.xsd schema for the schedule input file for the realistic
 simulator,
- trnSchedModule.py converter for the schedule files for simplified simulator,
- trnSchedDroplet.py converter for the schedule files for realistic simulator,
- trnGraph.py converter for the graph files

8.4 Instructions of use

8.4.1 Simulator window

Both simulators' windows are very similar. For detailed description of window contents and their actions, please refer to section 7.

8.4.2 Preparing the simulation

After choosing which simulator to run - simplified (simModule.py) or realistic (simDroplet.py) user should follow these steps (it is assumed that all the needed input files are already prepared):

- 1. Choose error mode for the simulation, or leave defaults if a simulation without any errors is desired,
- 2. Load the schedule file.
- 3. Load the graph file (optional).
- 4. Load the errors file (optional). This option is enabled only if simulation with user-set errors has been chosen in step one.
- 5. Adjust the simulation appearance and parameters (optional).
- 6. Generate the simulation.

Once the simulation is generated, user has the control over the running of the simulation.

8.4.3 Running the simulation - basics.

If there were no errors during the simulation, initial frame (at time 0) appears on the right side of the window. Playback controls are present directly below the simulation window. In case of the realistic simulation there is also another slider on the left side of the simulation view.

Now the user has following options available:

- 1. Play/pause the simulation. Clicking this button will change the running status of the simulation instantly.
- 2. Go to an arbitrary point in simulation. Arrows can be used for fine precision of 1 timestamp (centisecond). Clicking on the background of the slider next to the slider skips 10 frames (both ways). Option available both during pause and play.
- 3. Go to the next event (either the nearest start or the nearest end of an operation). Option available both during pause and play.
- 4. Go to the previous event (either the nearest start or the nearest end of an operation). Option available both during pause and play.
- 5. Change the speed of the simulation. Speed can be changed anywhere between 0.5x and 0.01x.
- 6. Export current frame to a PNG file. This will open up a "Save file..." dialog where the destination file can be specified.

8.4.4 Adding the graph

Adding the graph to the simulation is easy. First of all, once the schedule is loaded, please press the "Load graph..." button and choose a valid file (if the file is by any chance wrong a message will be displayed). Please note that graph must be loaded **after** the schedule and **before** pressing the "Generate simulation..." button. Once it is loaded and the simulation is generated the graph can be toggled on and off by pressing the "show/hide graph" button.

8.4.5 Introducing the errors

Before any errors can be loaded, two conditions must be met:

- Error mode must be set to user-input (last option in the combo box)
- File with errors must be properly prepared.

An example of a well prepared file can be found in appendix ??. Three things are essential in this file - error types and well structured input for any of those types.

First of all - it is absolutely necessary to indicate the type of errors that are

loaded. This is done by setting the value of type attribute to either "i"(for intrinsic errors) or "o" (for errors applied to single operations). In the first case, values of all five intrinsic error limits must be set (if there's no error limit value, just enter 0. Note that these are accepted as strings, thus quotations mark are required. Entering non-numerical values will result in program malfunction. For single operation errors an element operation must be specified with attribute values describing the operation number and the error limit value. In case of any problems please use the template file provided with the program or look at an example in the appendices.

8.4.6 Defining and modifying the operations

The simulator can be easily extended with new operations, though this has to be performed by editing source code. In both cases the changes required are the same. To add new operations, please find a line stating:

self.brushes = {}

Underneath there are definitions of all the operations, for example:

self.brushes["opt"] = QColor(255,128,0,127)

To add a new operation, simple copy such a line and change the string in the square brackets to the name of the new operation (it is necessary that it is the same as the operation type within the schedule). Right hand side of this assignment simply specifies the color associated with this operation, in the form of R,G,B,Alpha.

In the case of realistic simulator, there is a possibility of specifying custom detector types. This is done in the exact same way as adding new operations, but the dictionary used for this purpose is named detBrushes and is placed directly below the previous one.

8.5 Additional tools

For the purpose of this project three additional, small tools have been developed. These tools are used to convert plain-text input files I have been provided with into XML files compatible with simulator. The reason for not using the provided files as an input was to make the simulator more independent.

The three tools are XML converters for:

- schedule file for the simplified simulator,
- schedule file for the realistic simulator,
- graph file,

Their working principles are really simple. They read in the text input file, go through it line by line, parse the line word by word, and write the result out to an XML writer. At the end, the whole XML document is written out to a destination file on the disk.

As far as the user interface goes - there is basically none. Upon execution, user is presented with a standard file open dialog and then the input file is chosen. Then the whole conversion process is performed (without any visible indication apart from the default output to the system console) and - when finished another window pops up, this time to choose the destination file for saving.

Examples of plain-text input files are presented in the three figures below.

8	opt 3 3 $(0,6)$ 780 3780
9	opt 3 3 (4,6) 660 3660
6	mix 4 6 (0,6) 490 780
5	mix 3 6 (4,6) 200 660
2	mix 4 6 (0,6) 200 490
7	disR 0 0 $(-1,-1)$ 290 490
0	disS 0 0 $(-1,-1)$ 0 200
1	disR 0 0 $(-1,-1)$ 0 200
3	disR 0 0 $(-1,-1)$ 0 200
4	disB 0 0 $(-1,-1)$ 0 200

Figure 8.1: Schedule for simplified simulator

	2	opt opt 177 207 $[(2,3), (2,3), (2,3), (2,3), (2,3), (2,3), (2,3), (2,3), (2,4)]$
		(3), (2, 3), (2, 3), (2, 3), (2, 3), (2, 3), (2, 3), (2, 3), (2, 3), (2, 3), (2, 4)
		(3), (2, 3),
		(3), (2, 3),
		,3)]
	9	mix mix 131 177 $[(4,2), (5,2), (5,1), (6,1), (6,0), (5,0), (5 \leftrightarrow]$
		$(1), (4, 1), (4, 2), (4, 3), (4, 4), (4, 5), (4, 6), (4, 6), (4 \leftarrow 1)$
		$(5), (4, 4), (4, 3), (4, 2), (4, 1), (4, 0), (3, 0), (3, 1), (4 \leftrightarrow 1)$
		$(1), (4, 0), (4, 0), (5, 0), (5, 1), (5, 2), (5, 3), (4, 3), (3 \leftrightarrow 3)$
		$(3), (3, 2), (3, 1), (3, 0), (4, 0), (4, 1), (5, 1), (5, 0), (4 \leftrightarrow 1)$
		$(0), (4, 0), (3, 0), (3, 0), (2, 0), (2, 1), (2, 2), (2, 2), (2 \leftrightarrow 2)$
		,3)]
	8	mix mix 127 169 $[(2,2), (1,2), (1,3), (1,4), (1,5), (0,5), (0 \leftrightarrow]$
		$(5), (0, 4), (0, 4), (0, 3), (0, 2), (1, 2), (1, 1), (1, 0), (1 \leftrightarrow 1)$
		$(0), (0, 0), (0, 1), (0, 2), (0, 3), (0, 4), (0, 5), (1, 5), (2 \leftrightarrow 1)$
		$(5), (3, 5), (4, 5), (4, 4), (4, 3), (3, 3), (2, 3), (1, 3), (0 \leftrightarrow 1)$
		$(3), (0, 4), (0, 4), (1, 4), (1, 3), (0, 3), (0, 4), (0, 4), (0 \leftrightarrow 1)$
		(5), (0, 6), (0, 6), (0, 5), (0, 4)]
1	7	dis dis 101 131 $[(5, -1), (5, -1), (5, -1), (5, -1), (5, -1), (5 \leftrightarrow -1), (5 \leftarrow -1$
		$,-1), (5,-1), (5,-1), (5,-1), (5,-1), (5,-1), (5,-1), (5,-1), (5 \leftrightarrow$
		$,-1), (5,-1), (5,-1), (5,-1), (5,-1), (5,-1), (5,-1), (5,-1), (5 \leftrightarrow$
		$(-1), (5, 0), (5, 0), (5, 0), (5, 0), (4, 0), (4, 0), (4, 1), (4 \leftrightarrow)$
		(2), (4, 2), (4, 2), (4, 2)]

Figure 8.2: Schedule for realistic simulator

_						
0	dis disS	5				
1	dis disR	2				
	opt opt	•				
	dis disE	,				
-		b				
	mix mix					
	dlt dlt					
6	dis disS	5				
7	dis disR	1				
8	mix mix					
9	mix mix					
ľ						
	ARC a1		t1_0 T	0 +1 4	TYPE	1
	ARC a1		t1_1 T		TYPE	
		-	_	_		
		-	t1_4 T	_	TYPE	
		-	t1_3 T	-	ΤΥΡΕ	
	ARC a1	L_5 FROM	t1_5 T	0 t1_8	TYPE	1
	ARC a1	L_5 FROM	t1_6 T	0 t1_8	TYPE	1
	ARC a1	L_5 FROM	t1_5 T	0 t1_9	TYPE	1
	ARC a1	L_5 FROM	t1_7 T	0 t1 9	TYPE	1
		-	t1_9 T	_	TYPE	
	nno ai		01_0 1	0 01_2	1.1.1	-

Figure 8.3: Graph file

Chapter 9

Conclusions

9.1 Summary

The thesis gives an insight into the possibility of using a simulation tool to verify the synthesis stage of a digital microfluidic biochip. Firstly, the technology behind the biochip has been covered (Chapter 1). Then, the purpose of the simulator has been explained (Chapter 2), as well as the extent to which it covers the issues mentioned in the first chapter. Next four chapters are devoted to the design of the simulator, covering general design principles and overall solutions (Chapter 3), the detailed design and implementation of a simplified, module level simulator (Chapter 4) and a realistic, droplet level simulator (Chapter 5), as well as errors that apply to the biochip (Chapter 6). Rest of the chapters provided a summary of the simulator's features as well as detailed instructions of use.

Summing up, the project gave me an insight into the interesting area of microfluidic biochips. It has shown that a simulation tool can greatly contribute to optimalisation of the synthesis process. And even though not all the planned features made their way to the final version of the project, I am satisfied with the end result. Apart from all those I also gained a lot of experience in three software development areas:

- Programming simulation software,
- Working with GUI based applications,
- Using high-level programming environments for practical applications.

9.2 Future Work

Although the project is finished, it is still missing some features that I would like it to have. Absence of some of them is strictly related to a limited time for the project, but some of them are simply too complex to introduce at this stage. Below, I summarize some ideas that could be implemented in the simulator in the future.

- Showing droplets' movement history. It may be useful to have some kind of indication of the route already taken by the droplet. The idea was to display a "tail" of a user-defined length (but with some sensible limit) that would simply show the last few locations of the droplet. This feature has not been included because it is a reasonable challenge to find a way of an efficient drawing of such a tail so it is refreshed for each new frame. On the other hand, a simplified version showing only one, last location can be included in the nearest future.
- Increase in the information amount given to the user. Currently user is given a reasonable amount of information about what is happening on the chip, but this may be extended further on. For example, a text output (to the console) indicating which operations are starting or ending. This is a feature that can be easily introduced and it should be available within a few weeks.
- Propagation of droplet size information. Currently only droplets representing operations affected by errors inherit size from their predecessors. It would be a nice idea to implement some kind of an algorithm that would propagate the droplet volume information through the whole droplet's life cycle.
- SVG output instead of PNG. SVG graphics are much more suitable for including them in papers. Thus a feature that saves the current frame as an SVG file is desired. Though there is a problem it is easy to output

a specified scene to a PNG painter, but PyQt does not offer an easy solution for converting item-based graphics to SVG, and developing such a tool would simply include a lot of time.

- Nicer graph window. In the cCurrent version of the simulator, graph window is extremely simple, with only one issue in mind that the nodes must not collide. In more complex cases this results in a graph that is far from easily readable. Thus, a nice idea would be to invent a way to draw a graph based on information from the file (nodes and arcs) on a graphics scene. This again is a complex task that would consume quite a large amount of time.
- "Lifelike" animation. Having all the required data, it is possible to generate the animation that would resemble the actual biochip in more details. One may for example model it using OpenGL and 3D graphics. Since (Py)Qt has a built-in OpenGL support, it is not an impossible task, just a time consuming one. Of course other techniques may be used as well.

Application of these features may make the simulator much more useful and even more related to the real-life application.



Example of a schedule input file - simplified simulator

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             startTime="9005"/>
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leftBottomCorner="(3,6)" opNumber="39" opSuperType="opt" ↔</pre>
             startTime="8319"/>
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leftBottomCorner="(3,3)" opNumber="26" opSuperType="mix" ↔</pre>
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leftBottomCorner="(3,3)" opNumber="21" opSuperType="mix" \leftrightarrow
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             startTime = "9721" />
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```

```
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                          startTime = "5564" / >
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                         \texttt{startTime} = "2205" / >
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Appendix B

Example of a schedule input file - realistic simulator

```
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                                             [(2,3), (2,3), (2,3), (2,3), (2,3), (2,3), (2,3), (2,3), (2,3), (2,3), (2,3), (2,3), (2,3), (2,3)] \leftrightarrow
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                                                                                          \begin{array}{c} (1,6) \ ((1,5) \ (0,5) \ ((0,5) \ ((1,5) \ ((2,5) \ ((2,4) \ ((2,4) \ ((2,5) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) \ ((2,6) 
                                                                                                 , (0,6), (0,6), (1,6), (2,6), (2,5), (3,5), (3,6), (2,6), (2,5), (3,5) \leftarrow 
                                                                                                 (3,6), (3,7), (2,7), (2,8), (1,8), (1,9), (0,9), (0,8), (1,8), (1,7) \leftrightarrow
                                                                                                 (1,6), (1,5), (1,4), (1,4), (2,4), (2,3)]
                                             </operation>
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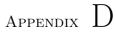
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               mix" startTime="756">
 [(4,1),(3,1),(2,1),(2,0),(3,0),(2,0),(1,0),(0,0),(0,0),(1,0),(0,0) \leftrightarrow
                (0,0),(1,0),(1,0),(0,0),(0,1),(0,1),(0,1),(1,1),(2,1),(3,1) \leftrightarrow
                , (3\,,0)\,, (4\,,0)\,, (4\,,1)\,, (4\,,2)\,, (4\,,3)\,, (3\,,3)\,, (3\,,3)\,, (2\,,3)\,, (2\,,2)\,, (2\,,1) \leftarrow
                ,(2\,,0)\,,(3\,,0)\,,(4\,,0)\,,(4\,,1)\,,(3\,,1)\,,(2\,,1)\,,(2\,,2)\,,(2\,,3)\,,(2\,,4)\,,(2\,,4)\leftarrow
                (1,4),(1,5),(0,5),(0,4),(1,4),(1,5),(0,5),(0,5),(0,4),(0,3) \leftrightarrow
                (0,3), (0,2), (0,2), (1,2), (1,3), (0,3), (0,3), (0,2), (0,2), (0,3) \leftarrow 0
                 (0,4), (0,5), (0,5), (0,4), (0,3), (0,2), (0,2), (0,3), (0,4), (0,5) \leftrightarrow
                ,(1\ ,5)\ ,(0\ ,5)\ ,(0\ ,4)\ ,(0\ ,4)\ ,(0\ ,3)\ ,(0\ ,2)\ ,(0\ ,3)\ ,(0\ ,3)\ ,(0\ ,4)\ ,(0\ ,3)\leftarrow
                (0,3), (0,3), (0,3), (0,3), (0,3), (0,3), (0,4), (0,3), (0,2), (0,3), (0,3) \leftarrow 
                (0,3), (0,4), (0,3), (0,3), (0,3), (1,3), (2,3), (2,2), (3,2), (4,2) \leftrightarrow
                , (4,3)]
</operation>
<operation endTime="856" opNumber="65" opSuperType="mix" opType="\leftrightarrow
               mix" startTime = "785" >
 [(3,5),(4,5),(5,5),(6,5),(7,5),(7,6),(7,7),(8,7),(9,7),(9,8),(9,8)\leftrightarrow
               \begin{array}{c} (9,7), (9,6), (8,6), (8,7), (9,7), (9,6), (9,5), (9,5), (9,6), (9,7) \leftarrow \\ (8,7), (7,7), (6,7), (6,6), (5,6), (5,5), (5,4), (4,4), (4,3), (5,3) \leftarrow \\ (5,2), (6,2), (6,1), (6,0), (5,0), (5,0), (4,0), (3,0), (3,1), (3,1) \leftarrow \\ \end{array}
                ,(2\,,1)\,\,,(1\,,1)\,\,,(1\,,1)\,\,,(2\,,1)\,\,,(3\,,1)\,\,,(4\,,1)\,\,,(4\,,0)\,\,,(3\,,0)\,\,,(2\,,0)\,\,,(2\,,1) \hookleftarrow
                (1,1),(0,1),(0,1),(1,1),(2,1),(3,1),(2,1),(2,1),(2,0),(3,0) \leftrightarrow
                (3,0), (4,0), (4,1), (4,2), (4,3), (4,3), (4,3), (4,4), (5,4), (5,5) \leftrightarrow
                , (4, 5)]
</operation>
<operation endTime="850" opNumber="76" opSuperType="opt" opType="\leftrightarrow
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</operation>
<operation endTime="820" opNumber="71" opSuperType="mix" opType="\leftrightarrow
               mix" startTime="771">
 [(1,3),(0,3),(0,4),(0,5),(0,6),(0,7),(0,7),(0,8),(1,8),(1,7),(0,7)\leftrightarrow
                (0,8) (0,9) (0,9) (0,9) (0,9) (0,9) (0,8) (0,7) (1,7) (2,7) (3,7) (4,7)
                ,(5,7),(5,6),(5,5),(6,5),(7,5),(7,4),(7,3),(7,2),(6,2),(6,1)\leftrightarrow
                , (6\,,0)\,\,, (5\,,0)\,\,, (4\,,0)\,\,, (4\,,0)\,\,, (3\,,0)\,\,, (2\,,0)\,\,, (1\,,0)\,\,, (0\,,0)\,\,, (0\,,0)\,\,, (1\,,0) \leftarrow
                 (1,1), (2,1), (2,2), (2,2), (2,2), (2,2), (3,2), (2,2), (2,3)
</operation>
<operation endTime="799" opNumber="68" opSuperType="dis" opType="\leftrightarrow
              disS" startTime = "758" >
 [(0, -1), (0, -1), (0, -1), (0, -1), (0, -1), (0, -1), (0, -1), (0, -1), (0, -1), (0, -1), (0, -1)] \leftrightarrow
               , (0, -1), (0, -1), (0, -1), (0, -1), (0, -1), (0, -1), (0, -1), (0, -1), (0, -1) \leftarrow 
                \begin{array}{c} (0,-1), (0,-1), (0,-1), (0,0), (0,1), (0,2), (1,2), (1,3), (0,3) \leftrightarrow \\ (0,4), (0,3), (0,2), (0,2), (0,2), (1,2), (1,3), (0,3), (0,2), (0,3) \leftrightarrow \end{array}
                (0,3), (0,2), (1,2), (1,2), (1,2), (1,2)
</operation>
<operation endTime="799" opNumber="115" opSuperType="mergeDlt" \leftrightarrow
               opType="mergeDlt" startTime="778">
 [(8,7),(8,7),(7,7),(7,6),(8,6),(8,5),(8,4),(7,4),(7,3),(6,3),(5,3)\leftrightarrow
                (4,3), (4,3), (5,3), (5,3), (4,3), (5,3), (4,3), (4,3), (4,2), (3,2), (2,2) \leftrightarrow (1,2)]
</operation>
<operation endTime="785" opNumber="66" opSuperType="dis" opType="\leftrightarrow
               disR" startTime = "758" >
 [(-1,3),(-1,3),(-1,3),(-1,3),(-1,3),(-1,3),(-1,3),(-1,3),(-1,3),(-1,3)] \leftrightarrow
                \begin{array}{c} (-1,3), (-1,3), (-1,3), (-1,3), (-1,3), (-1,3), (-1,3), (-1,3), (-1,3), (-1,3), (-1,3), (-1,3), (-1,3), (0,3), (0,4), (1,4), (1,5), (2,5), (2,5), (2,5) \end{array} 
                (2,5),(3,5)
</operation>
</schedule>
```

Appendix C

Example of a graph input file

```
<?xml version = "1.0" encoding = "UTF - 8"?>
      < \texttt{graph} >
      <code in="" nodeNum="0" opSuperType="dis" opType="disS" out="2"/><code in="" nodeNum="1" opSuperType="dis" opType="disB" out="2"/><code in="0 1" nodeNum="2" opSuperType="dlt" opType="dlt" out="6 <</pre>
              7"/>
      <node in="" nodeNum="3" opSuperType="dis" opType="disR" out="5"/>
<node in="" nodeNum="4" opSuperType="dis" opType="disB" out="5"/>
<node in="3 4" nodeNum="5" opSuperType="dlt" opType="dlt" out="8 <</pre>
              9"/>
      <node in="2 10" nodeNum="6" opSuperType="mix" opType="mix" out \leftrightarrow ="14"/>
      <node in="2 11" nodeNum="7" opSuperType="mix" opType="mix" out\leftrightarrow
      ="16"/> = "16"/> <node in="5 12" nodeNum="8" opSuperType="mix" opType="mix" out↔
             ="18"/>
      <node in="5 13" nodeNum="9" opSuperType="mix" opType="mix" out</pre>
      ="20"/>
<node in="" nodeNum="10" opSuperType="dis" opType="dis" out="6"/>
      <node in="" nodeNum="10" opSuperType="dis" opType="dis" out="0"/>
<node in="" nodeNum="11" opSuperType="dis" opType="dis" out="7"/>
<node in="" nodeNum="12" opSuperType="dis" opType="dis" out="8"/>
<node in="" nodeNum="13" opSuperType="dis" opType="dis" out="9"/>
<node in="6 15" nodeNum="14" opSuperType="dit" opType="dis" out="9"/>
             ="22 23"/>
      <node in="" nodeNum="15" opSuperType="dis" opType="disB" out↔
              ="14"/>
      <node in="7 17" nodeNum="16" opSuperType="mix" opType="mix" out↔
="26"/>
<node in="" nodeNum="17" opSuperType="dis" opType="disS" out↔</pre>
             ="16"/>
      <node in="8 19" nodeNum="18" opSuperType="dlt" opType="dlt" out\leftrightarrow
             ="28 29"/>
```

<pre><pre><i "="" <-<br="" nodenum="10" opsupertype="dis" optimize="" optype="disB" out="">="32"/></i></pre> </pre>	
<pre><node in="9 21" nodenum="20" opsupertype="mix" optype="mix" out→<="" td=""><td></td></node></pre>	
<pre><ord><td><pre><node in="9 21" nodenum="20" opsupertype="mix" optype="mix" out↔<="" pre=""></node></pre></td></ord></pre>	<pre><node in="9 21" nodenum="20" opsupertype="mix" optype="mix" out↔<="" pre=""></node></pre>
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Example of an error input file

Example of an error input file

Bibliography

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