Hello everyone,

1. This will be our presentation of Zelula, a modeling environment for synthetic biologists. This program was developed by Felix Akkermans, Niels Doekemeijer, Albert ten Napel, Thomas van Helden and Jan Pieter Waagmeester.

2. In this presentation we will talk about what this project meant according to us, and how it is relevant to the synthetic biology industry.

Secondly we will talk about what we had planned to do, what we initially designed and how we thought it would work.

Afterwards we will show you the result of our project. You will see that we were pretty conservative, in case of sticking to our design.

Our fourth point is to explain our future plans meaning: If someone is to further develop this product, what would be the next features to implement.

Finally Felix will give a demonstration. We go through some of the features of our program and you will have the possibility to try it out yourself.

3. So we will give a bit of explanation on what this project was all about and how it is relevant to the synthetic biology industry.

Synthetic biology is the science of combining engineering and biology. One of the fields is about the manipulation of cells. By manipulating these cells we can use them similar to how we use small computers. You can make small logical circuits, where the concentrations of proteins represent the amplitudes of signals. This was the basis for our project.

We wanted to create a modeling environment in which we can build and validate circuits. Afterwards we should also be able to simulate the outcome.

This product would be useful for the synthetic biology industry because this would make modeling complex cell systems relatively easy.

4. So here you see our first design of the program. Our aim was to create an online application with an intuitive GUI. Our user should have a good sense what the application does.

This program should of course be able to build, save, open and validate circuits. You should also be able to define the inputs, meaning the proteins within the cells and their concentrations, and simulate the outcome.

You can see in this GUI, you can build circuits and define the proteins as input signals for the gates. On the top side you see a menu. Clicking on simulate would give all the validation, defining inputs and simulation options. The “Brick” menu would contain options like saving and opening. On the left side are your “building blocks” for you biological circuit. Underneath, we left some space for user defined bricks, a concept which we later started calling compound gates.

5. So this is what we eventually built. As you can see, we pretty much stuck to our design. The workspace looks pretty much the same. Another thing we kept in the design was panel on the right side, containing our gates. The top menu has changed. We added a small section where you can set the description and name for your circuit. The brick menu changed to file because this is sort of a standard.

6. So we built this system within a couple of months. We had a lot of ideas but not all of them are implemented. So if anyone would further develop this product, we have some ideas for future features.

One of them is to display the compound gates as single gates instead of loading in the complete circuit. You will see in the demonstration on how it works now.

Another thing is that we would like to have improved zooming functionality. Right now we can zoom in on the site. Instead, we would like to zoom in and out of the workspace. Zooming in on compound gates would show their inner circuit.

We have a lot more ideas like detaching the simulation panel and groupings of gates but we also want to show our demo.

7. So I hereby give the floor to Felix for a demonstration of our program.