Digital Biological Cell

Digital Biological Cell (DBC) is a general empathic mathematical model of an eukaryotic cell. The model is inspired by theoretical physics. The notions used in the model are both observed (such as speed in physics) as well as introduced (such as energy). The theoretical model does not primarily open a question, whether the introduced notions can be observed. Contrary to that, the theoretical approach opens a question how the introduced notions can help us to describe, simulate or even predict behavior of the surrounding world, in our case behavior of organism consisting of eukaryotic cells.

The DBC is described as follows:

- Every cell has an internal state. This notion has not been observed; it was introduced.
- The internal state of the cell is determined by ligands (λ) caught by its receptors (ρ).
- The production of ligands (λ) by the cell is determined by the internal state and genetic information identical for all cells within an organism.

Is it enough to conduct a simulation of different biological aspects? It is not, at least we have to presume environment in which the cells are. However, different aspects require different environment. Some aspects should be simulated in a time scale of years (aging), some require days (ontogenesis), some can show different results in minutes (homoeostasis) or even fractions of a second (neural network). Similar differences are with space. Sometimes it's dimension could be insignificant while some other times the space must be three dimensional, the space could be also vacant or occupied and so on. There could be also different requirements for diffusion model; cells in a blood stream have different access to ligands than cells in a skin.

Even if we would have an unified environment, it is not enough. To simulate an aspect we have to add more additional laws into presumptions. As an example, if we simulate splitting of a cell during ontogenesis, we have to add a law describing how does the cell divide geometrically. While the additional law is crucial for this simulation, it can be completely irrelevant for another (ex. for neurons). This was the primal reason for exclusion of the additional laws from general DBC.

However, the specific laws are added to each specific implementation of DBC resulting in DBX, the Digital Biological X. The DBX does not necessarily represent a (observed) type of a cell; the DBX is designed to describe a specific biological aspect. Typically one DBX matches one cellular phenotype. As an example DBN (Digital Biological Neuron) is a model of a neuron. However, the same DBX used for simulation of immune system is used for all types of cells in the organism, which participate on the immune reaction.

Also DBX specification is the place, where the environment requirements must be formulated. The picture below shows how different biological aspects are implemented by different DBX. The cells should be still able to interfere with each other as they are all based on DBC.

Sometimes we would like to have a possibility to simulate a behavior, which consists of two or more aspects. As an example we would like to study how homoeostasis influence immune system and vice versa. Let's assume we already have two Virtual Laboratories, which are programs to conduct the simulations, one for the immune system and another for homoeostasis. Since we have both laboratories based on DBC, there should be a way, how the laboratories can share the results. First of all, the additional laws of each DBX in the shared simulation must not be contradictory. Since each DBX model has been created with regard to maximal compatibility with other models, this condition is easily met. Whereas the DBC model determines ligands and receptors as the only mean of communication between the cells, the only interface between the laboratories is shared ligands and appropriate receptors.

I: ρλ

Of course, the environmental differences must be also considered, but these are solved on case-by-case basis. The most important result of the DBC modeling is, that it does not create obstacles for further extensions by future DBX, but still allows compatibility and shared simulation.

As any other theory, this one should prove it's credibility by showing how much the description, simulation or prediction reflects the surrounding world. As seen, DBC is a theoretical platform and does not offer any mean to be compared to a general eukaryotic cell behavior (*). However, each of the DBX presented in these pages or by our colleagues, deserves to be judged and to be judged separately.

(*) General eukaryotic cell does not exist anyway, any observed or existing eukaryotic cell is highly specialized and not general, therefore should be simulated by DBX instead of DBC.