
14th Brainstorming Week on *Membrane Computing*

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Three weeks ago we, a group of students from the University of Barcelona, were given the possibility of going to Seville, in order to attend a Workshop on *Membrane Computing*. The seven of us that went to the Workshop are all physics students and until the day we received the mail making us aware of that event, I had never heard about *Membrane Computing*, so I was kind of surprised the first time I read about it. In the university we have learned how to program with Python and Fortran. It was mostly on how to deal with physics problems, and how to find a solution using numerical methods. But what we saw when we arrived there was completely different, it was like entering another world of computation. While dealing with physics we are always reminded of how important is to keep in mind the physical part of the problem (i.e. how a given system is supposed to react when a field is applied, or if the result makes sense with what we can see in the reality), when programming with that new computational way you try to think how to model things but once you get it, you abstract (somehow) from reality and work with maths, or that is what I understood the first days. It was really difficult, specially at the beginning, as I was completely lost and maybe it could have been a better idea to have been previously informed about what the talks were about, or even to have an idea of what *Membrane Computing* meant.

During the days I spent there I got to know that this picturesque way of computing is based on a system analogous to how alive cells behave or how elements in these ones evolve, using P-Systems (a computational model based on the structure of living cells that permits to perform calculations). Indeed, the inspiration came from how processes take place in cells. This new computing paradigm makes use of the structure of the cells, working with their different membranes and even with the environment. But it is not only something involving one cell, they also work with multiple ones, and so there are different models on which they can work. The most usual one is the cell-like system, which is the one I have already talked about. There are also other kinds of models, such as tissue-like or neural-like systems; the first ones are typically used to represent interaction between cells, or better said to

implement exchanges of elements between cells. The second one is used to analyse the behaviour of neurons, and tries to represent synapsis' process.

To work with all that stuff, a new language is needed, and so P-lingua takes action. P-lingua is a programming language to define P-Systems and it is highly used, as it is a language close to scientific notation, as well as from my point of view really visual of what it is going on. While we were attending the talks, we were invited to participate by doing a small project where we could use what we were learning, so our first idea was how could we use it in our own field, physics. We decided to reproduce two physical situations in order to see the process: the final result as well as their intermediate stages. These two projects were about: i) the Stern-Gerlach experiment, by modifying it a bit and ii) the Uranium-238 Decay Chain. At the beginning of our project, we tried to program a small code to get a bit used to the language, and I was truly surprised when I saw that it was not that weird to write it, and that by following one example one could understand almost perfectly what we were expressing. Nevertheless, I am aware that I only got a small view of how it works and that, for sure, it turns more difficult when you keep on programing more advanced things.

However, even though it was not easy to understand most of the parts of the talks, people was extremely nice with us. One of my biggest fears was to break the dynamic of the event, as we could probably slow down the pace of it with our low level, but it surprised me a lot when everyone was inviting us to make as many questions as we wanted. Of course I did not want to disturb the pace of the event, but sometimes it was almost impossible to follow explanations, although I consider I learned a lot during that week, so to say, we got a slight insight on the general topic, but nothing really deep.

Most of the conferences were interesting as it was another way of thinking, one which we are not so used to. Nevertheless, there was one that made me think of other fields and possible further applications. It was about the concept of Eco-P colonies. It is based on systems of only one membrane and in each of them we can find the objects that we want to study or see the final product of evolution. In Eco-P colonies, these objects do interact with a shared environment and this was the main point of the talk, titled *P Colonies with Dynamic Environment*. In order to evolve, the objects inside the membrane interact with the environment by some rules, specially rewriting and communication ones. The first ones basically transform the object into another one, or even into multiple objects. They are also called evolution rules and are basically applied inside the same membrane/entity (or even called agent), whereas the second kind of rules are based in an exchange between objects inside the membrane and objects outside it (environmental objects, usually symbolized by e). To sum up, Eco-P colonies would be a way to show mechanisms of generation and consumption from the environment. The system halts when no more rules can be applied to the objects, or no more exchange

between the agents and the environment can be done.

In fact, before the talk began, Petr Sosík, who gave the conference, showed us a video where we could see some bacterias multiplying, and we could see how the growth was really fast. This reminded me of a conference we were given some months ago, about cancer cells and which are their mechanisms to propagate cancer. I was wondering, when I heard about Eco-P colonies and their rules, if they could have some applications to Medicine, by adapting some of their rules to how cancer cells behave, or even in other cases. In fact, *Membrane Computing* modelizes non-deterministic processes, so somehow we could be able to implement the probabilities of a possible mutation (that produces the beginning of the disease).

Another thing that surprised me was the characteristic of maximal parallelism when working with P-systems. At what we are used to, we have an order, so the first written commands are the first to be displayed, whereas in maximal parallelism, more than one rule can be executed at the same time. Indeed, it is based in the fact that the maximum number of rules that can be applied in each step, are applied, maximizing the number of processes that can be done at one time.

To sum up, this experience has been really advantageous. First of all because I still do not know which is the field that interests me the most, but I have seen that computation keeps attracting me, and now even more than ever. Secondly, going there has made me realize of how vast this area can be and that it does not only reduce to solve some problems by numerical approximations but they are also a useful tool to visualize some difficult experiments or processes. And to end up with, it was a kind of personal growth, where we got to work together as a team and got the chance to talk with great people that taught us about science in general and more about research.

