Plasma membrane, compartmentation, transport, and imprecisions*

Óscar Moya Mesa

Department of Biology,
University of the Balearic Islands,
07122 Palma de Mallorca (Spain)
E-mail: omoya@uib.es

A cell is delimited by its plasma membrane. It is a compartmentation that allows qualitative and quantitative differences between its inner contents and the environment.

A cell, or even a group of cells, can be considered different compartments where membrane properties determine the communication between them due to their properties:

- they act as highly selective filters and molecular transport mechanisms for;
- they control the entry of nutrients and exit of residual products;
- they generate differences between contents and environment;
- they have systems to detect external signals allowing the cellular compartment to react to environmental (external compartment) changes.

There is a basic common structure in all eucariotic cell membranes. Phospholipids are disposed in a bilayer, as those assimetric molecules create spontaneously this structure in an aqueous environment. A phospholipid has a head group attached via a phosphat group to a 3-carbon glycerol backbone, and two fatty acid tails attached to the remaining two carbons of the glycerol. The head is polar, property that confers this part of the molecule affinity to water, in contrast to the tails that are hydrophobic. The simpler phospholipid membrane structure would be a liposome, where the polar heads are exposed to water because of their hydrophilic properties and the tails are in the middle of the bilayer. But a plasma membrane is much more than a liposome: proteins, glucosacarids and cholesterol are other components. Proteins are specially important as they play a key role in transport, signal detection, and regulation.

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Without proteins, lipid membranes would be relatively impermeable to ions and many other small molecules, but permeable to water. In fact, they are permeable to almost all molecules: apolar and polar molecules without electrochemical charge can freely go from one side to the other; even polar charged ones can, as it is only a matter of time that they cross from one side to the other. Molecular size and polarity will determine the speed of molecular interchange between both sides, but in biological terms of funtionality we can say that proteins are necessary to mediate transport to allow cellular activity.

Living organisms, and in fact cells, need to communicate with their environment, they need the entry and exit of ions, simple, and complex molecules. Most of the small molecules and ions need help to cross the membrane in form of transmembrane channels or active transport. This transport can be passive, depending on concentration and electrical potential gradients, or active (against gradients and with energy use). The first case correspond to the channels, the second to active transport proteins.

These cellular structures, their characteristics of compartmentation and communication have been used in mathematic modelling, in membrane computing. At a first stage very simple models have arisen, where some standard rules can explain how the molecules are placed in the different compartments and how they "move" from one to the other. But biological structures are much more complex. Even more, is not only a matter of complexity what characterizes biological systems, randomness has a lot to say in these processes. Now, the tendence is trying to incorporate these properties in the new models, to get a better approach to reality or simply to try other kinds of computation to test their possibilities. There are models that handle imprecisions, that search how to incorporate the stochasticity associated to biological processes in their calculations.

To do that it is necessary to have a more realistic view about plasma membranes. They are active structures in different ways, one is its fluidity. Both monolayers are not static, their components move along its surface in a more or less aleatory form. This movement is chaotic and depends both on chance and environmental factors. Although the cell has some control, concentrating some specific molecules in concrete zones, depending on needs and functionality, this control is relative and the molecules still move freely and chaotically in theses regions. Chemical reactions have certain degree of randomness as well, molecules do not interact always in the same way, even with a very similar final result.

Biological systems are complex, even our scarce knowledge lets us notice how complicate they can be, how difficult it is to know and control all the factors that are implied. The most simple mechanisms or reactions are regulated and affected by environmental and cellular conditions. There are many sources of imprecision related to:

- transport systems: their specificity, regulatory mechanisms...
- the molecules that will be transported: concentration, difussion rates, gradients,

electrochemical charge, solubility, similarity...

- membrane properties: fluidity, surface, dinamics, membrane electrochemical potential, quantity and distribution of their components...
- inner and outer cell physicochemical conditions: pH, temperature, ionic concentration...

In summary there is imprecision due to the lack of knowledge about which factors interfer, how they do it, and to the stochasticity of biological and chemical dinamics. Randomness and complexity in biological systems are the two main causes of imprecision that should be taken into account for membrane computing in a more realistic scenario.

From a biologist point of view, at a first stage it would be preferable to work with well known systems, as modelling them is much easier and the complexity factor can be better controlled. Randomness is still present and could be incorporated via probabilistic calculations. A good first choice could be to model the sodium-potassium pump, a transport system with a key role in osmotic equilibrium and stabilization of cellular volume. Its biological relevance has been the focus of many research efforts in learning how they work, their regulation systems and how external conditions affect their activity.