

Standardized Language Dedicated To Biological Function

New Concept For An Ergonomic And Computer Friendly Description Scheme

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ABSTRACT

Since the beginning of biochemical databases, a tremendous amount of data has been accumulated about numerous molecules and biological events. Whereas some data such as kinetics or sequence can be easily processed by computer programs as variables, data relative to functional mechanisms are much more complicated to be undertaken by a program. As part of the *SiliCell* (in Silico Cell simulation) initiative, we developed a knowledge base (*SiliBase*) which is biological functions oriented[1]. Its main purpose is to give biologists the opportunity to take advantage of a knowledge of both biological functions and mechanisms knowledge that can be automatically used into simulation softwares.

The existing databases suffer from a poorly standardized biological functions description: these are based upon textual informations although computer programs are not able to deal with this kind of non formatted data. Moreover, we still need a wide-spread standard to describe complex biological functions in order to facilitate knowledge exchange between databases. Currently, some works attempt to extract the words of interest from these textual informations using specific ontologies, and perform grammatical analysis to give meaning to a computer. By now, these methods are not really operational. To solve these issues, we need to develop new concepts in order to improve the accuracy of biological functions annotations as well as the interactions between current and future simulation softwares.

We propose herein a more precise and standardized function annotation scheme through a new dedicated biochemical language. We recast the concept of biological function through a systemic consideration which leads us to a multiple granular view: *Basic Active Elements*, *Biological Activities*, *Complex Functions* and *Biological Roles*[2]. These four non exhaustive levels describe an increasing complexity in the biological action performed by a molecule: *Basic Active Elements* describe molecular events at a chemical level, whereas *Biological Activities* aim to describe the action of a given functional domain from a molecule. The complexity of a full molecule is described by the *Complex Functions* level through the combination of all *Biological Activities* associated to this molecule. *Biological Roles* intend to allocate these *Complex functions* to identified pathways and to describe their effects. From these new concepts, we will setup

a standardized language for the biological functions description. This language will provide a good ergonomics to allow an easy handling by the biologist community. It also enables an easy integration into simulation softwares in order to improve actual programs with the enormous available quantity of biological knowledge.

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