UDC: 57:[165.2+004.81]

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CONCEPT OF THE METALANGUAGE FOR BIOLOGY FROM VIEWPOINT OF NATURALIST: 1. STEREOTYPES, WHICH ARE SPECIFIC FOR DOMAIN OF BIOLOGY

Modern nature science deals with the plenty of the urgent issues and problems. To solve them the multidisciplinary research are of great importance. The permanently growing rate of the acquisition of knowledge in natural science became another peculiarity of our time. The ability of the intelligence of all humankind is hardly sufficient to apply completely the domain knowledge, which has been accumulated by now. Here we denote the intelligence to be the mean with two determinant attributes: the memory and the ability to do the operations with the information, fed into the memory. Aforementioned circumstance prompts the employment of the joint efforts of artificial and collective human intelligence in order to work out the issues and problems.

The high-level declarative programming languages (also they are defined as the standards for knowledge presentation – SKP) are well-known to serve the indispensable mean for the establishing the advanced intellectual systems. The process of the formal expression of the knowledge in the fields of fundamental and applied biology with the minimum mental transformations would get more convenient, if the multidisciplinary (universal) SKP existed. But such standard has not been developed yet. However, the dissimilar paradigms of the different biological sciences (especially this concerns the mismatch of the names together with the structure of the links between the objects) complicate the achieving of the universality of such a standard.

We are convinced that it is unacceptable to enforce the domain experts to think in the manner of the in ratio structures, accepted by the mathematicians and programmers. It is more reasonably to adapt the SKP to the models which have been practised by the domain experts, since very few natural scientists could easily command the existing standards for the domain knowledge presentation (MathML, SBML etc.). Our work purports the new SKP, which would be: 1) friendly for the wide range of the experts in natural science; 2) multipurpose (to say as invariant as possible) for the numerous areas of biology and related sciences. As the working name for this new standard we propose to use the name «Metalanguage for Biology» (MB). We suggest the MB should be elaborated by the joined team of the experts: programmers and biologists. The current results of MB's elaboration meet the point of view of biologist on which the proposed standard should be. We develop this idea towards the below-mentioned directions: 1) determination and formal definition of the stereotypes, special for biology; 2) development of the syntactic principles; 3) justification of the collection of operators for the construction of expressions by means of the MB. This communication highlights the investigation on the first of the above-listed directions.

In our work «stereotype» is used in the sense of «model, existing in ratio». Note, firstly, we don't deals with the stereotypes, which are common for biology and other subject areas; secondly, the collection of the stereotypes, given here, is not to be the close system – this collection will able to be extended in the course of the further studies in the field of knowledge engineering. Thus, we highlight the sense of the following stereotypes: 1) subject – state – process; 2) the link of origin; 3) the space-based model (SBM).

We cluster the models of subject, state and process into one group, because each of these models fills the syntactic function of the object. The declaration of properties is one of the modes to depict the object by means of the MB (see paper « Concept ...: 2. Specific features of syntax and punctuation»). This mode is accompanied with getting the data structure, which is the same with the two-dimensional table. One of the dimensions serves for the listing of the attributes, which are assigned for object. The values of attributes can be a) non-empty and ungoverned; b) non-empty and governed by argument; c) empty. The number of the non-empty and ungoverned attributes in the model of subject is ≥ 0 , of state $- \geq 1$, of process $- \geq 0$. The numbers of the attributes, which are non-empty and governed by argument, - 0, ≥ 0 and ≥ 1 respectively. The empty attributes pertain with the model of state only. In the model of process besides the records for the description of attributes also the records for the description of arguments are required. Subject can be declared not only in the way of the description of its attributes, but in the way of the depiction of its links with other objects as well. In such case the table of the declaration of properties is not created – this way of modeling allows the subject having no attributes.

The model of the link of origin includes in obligatory mode ≥1 parental,≥1 daughter objects, and one parameter, which specifies the coordinate in which the position of the existence of one object is compared with the position of the other. To explain the link of origin it can be used the following definition: the existence of daughter object is possible exclusively in the presence of the paternal one in the coordinates with the less value. In contrast, the paternal object does not require the obligatory existence of the daughter one. Interestingly, the link of origin possesses the property to be inverted into «the model of eradication» by adding «the logical minus».

It is reasonably to divide the wide diversity of SBMs on two groups: a) SBMs, serving for the reflection of the real space, and b) quasi-spatial SBMs. In turn the last ones include two subgroups: phase spaces and circuit diagrams. To reveal the sense of each group and subgroup of SBM, we employ the ideas of the coordinate addresses, the principle for their setting, as well as the characterization of each group and subgroup on the basis of relation to the real equivalent of the component of SBMs.