

MGSmodelsDB – THE DATABASE FOR STORING MATHEMATICAL MODELS OF MOLECULAR GENETIC SYSTEMS

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Motivation and Aim:

Investigation of molecular-genetic systems mechanisms, patterns of relationship and structure is the system biology fundamental problem demanding the integration of modern experimental and theoretical approaches, in particularly mathematical modeling methods.

The natural hierarchy of gene networks structure allow us to reveal an elementary subsystems (promoters, enzymes etc.) and describe them separately. Thus we can use them for making models of random gene networks structure.

To implement the approach we developed the mathematical models database of elementary cell subsystems that we call MGSmodelsDB.

Methods and Algorithms:

The MGSmodelsDB is developed under the ORACLE database system and uses XML support functionality for storing and retrieving data.

Results:

The database structure was developed for storing mathematical models of two types of elementary cell subsystems: the enzymatic reactions and gene expression regulatory sites. The system has WEB user interface and allows to request mathematical models by setting name of interested reactant which takes part in the elementary cell subsystem. The MGSmodelsDB supports set of reactant synonyms. You can export the selected mathematical model in SBML standard for further analysis by other programs that support the standard.

Conclusion

The database, at the moment, contains 100 elementary mathematical models describing 35 promoters, 60 enzyme reactions in which about 50 metabolites concerning processes of synthesis/utilization of nucleotides and processes of respiration in *E.coli* cell participate.

Each reactant in the database has link at external sources like KEGG and EcoCyc and the synonyms list that compatible with the external sources too.

The database available at: <http://samurai.bionet.nsc.ru/MGSmodelsDB>

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