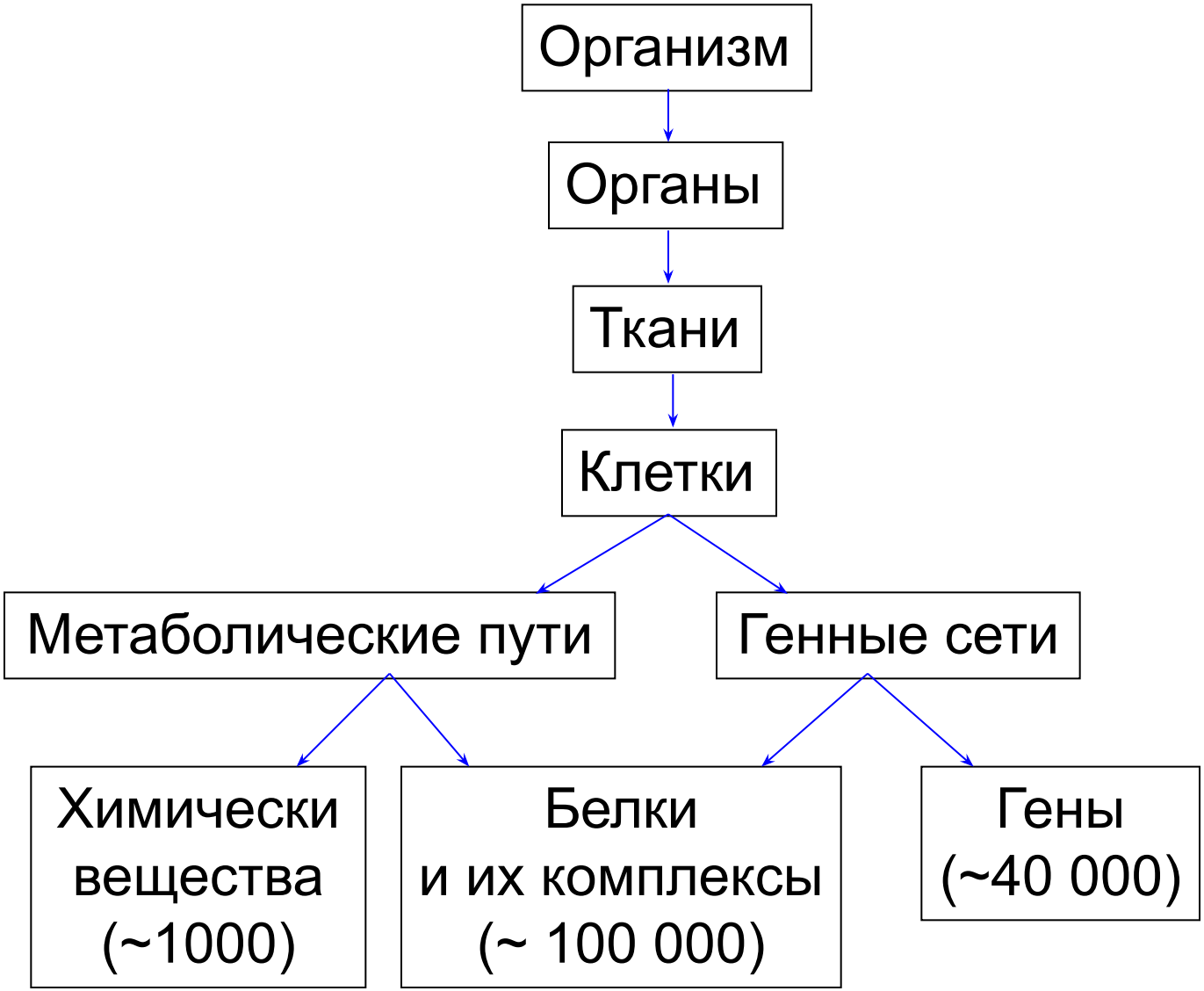
# Комплексный подход для формального описания, графического представления и моделирования широкого круга биологических и других сложных систем

**Biosoft.Ru**

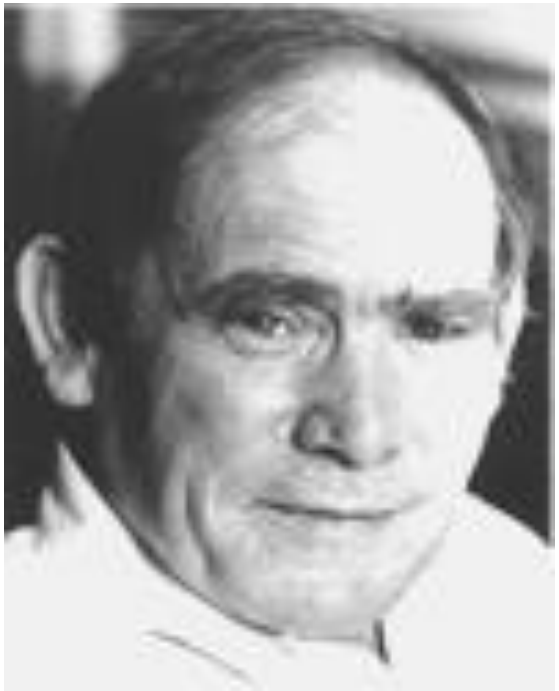
DevelopmentOnTheEdge.com

Лабоработория Биоинформатики КТИ ВТ СО РАН

**http://www.biouml.org**




Базы данных
(более 500 баз данных, общий объем сотни гигабайт)



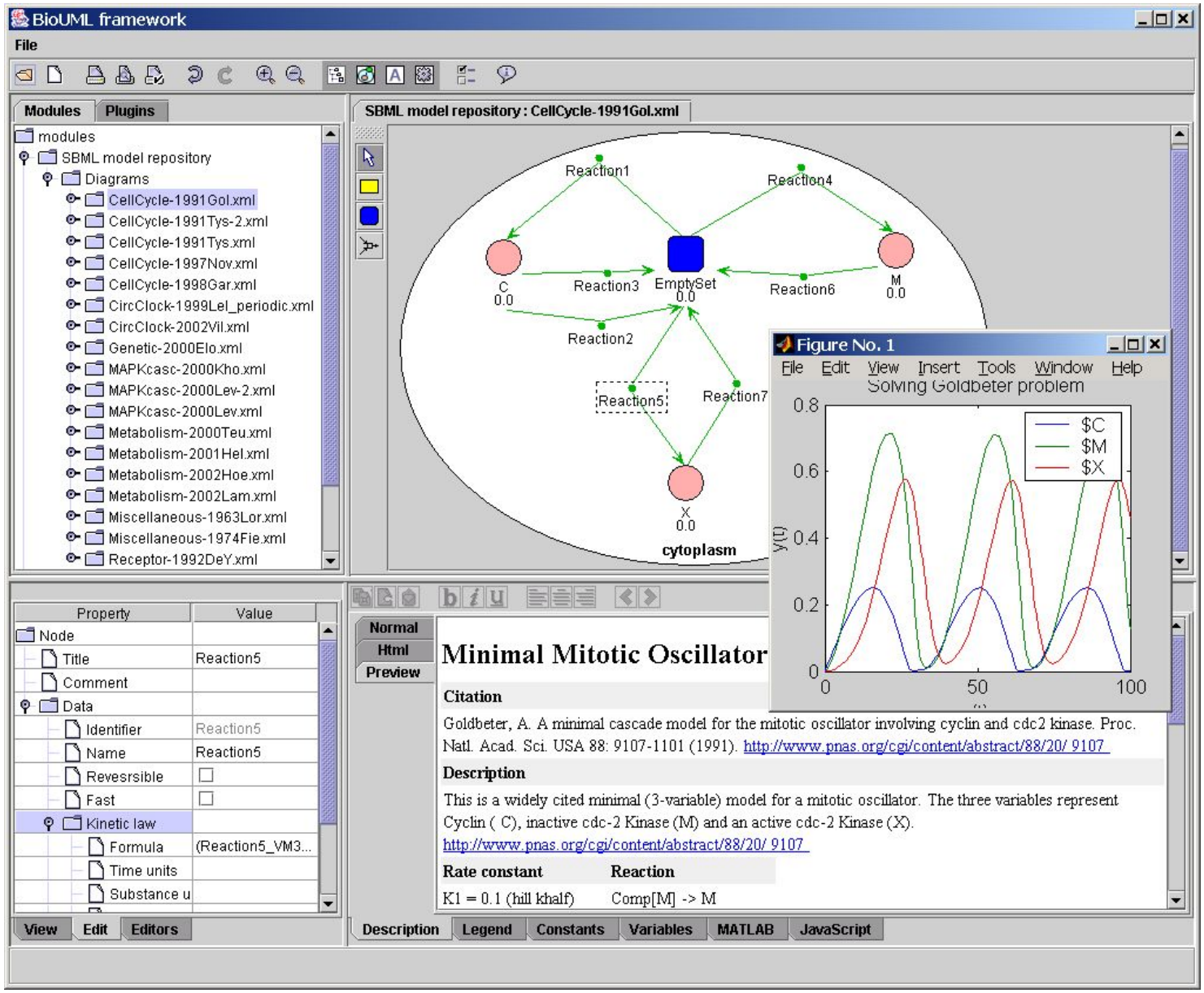
Сидней Бреннер, лауреат Нобелевской премии 2002 года в области медицины

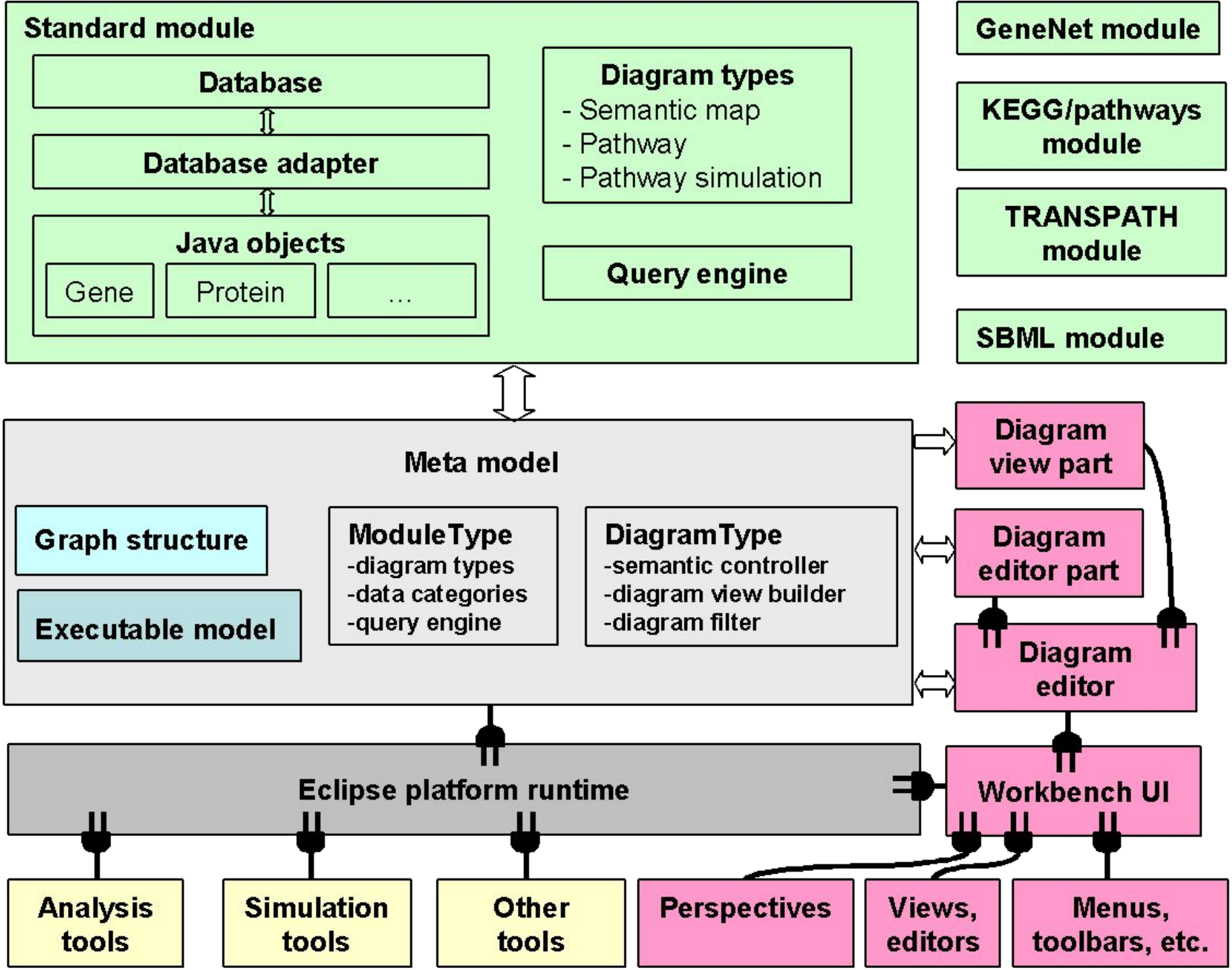
*Сейчас у нас есть беспрецендентная возможность собирать и накапливать данные о природе, тем не менее в современной биологии развивается кризис, который состоит в том что полностью неструктрированные данные не улучшают нашего понимания. Нам нужна система (framework) в которую мы могли бы поместить все эти знания и данные – это то и становится проблемой в биологии.*

*Мы достигли уровня когда мы больше не можем разговаривать друг с другом – мы стали слишком специализированы. Нам нужна система, используя которую люди могли бы сказать: “Да, я понял.”. Создание такой системы является действительно большим вызовом.*

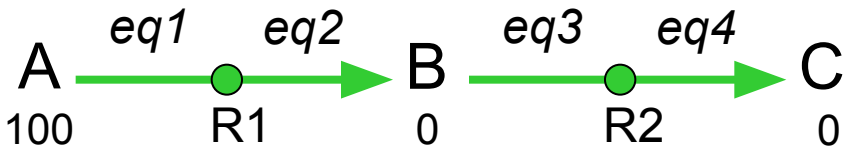
Sydney Brenner, 2003

# BioUML - Biological Unified Modeling Language




Standard module
Database
Database adapter
Java objects
Gene
Protein
...
Diagram types
- Semantic map
- Pathway
- Pathway simulation
Query engine
GeneNet module
KEGG/pathways module
TRANSPATH module
SBML module
Meta model
Graph structure
Executable model
ModuleType
-diagram types
-data categories
-query engine
DiagramType
-semantic controller
-diagram view builder
-diagram filter
Diagram view part
Diagram editor part
Diagram editor
Eclipse platform runtime
Workbench UI
Analysis tools
Simulation tools
Other tools
Perspectives
Views, editors
Menus, toolbars, etc.

**Пример двух последовательных химических реакций**



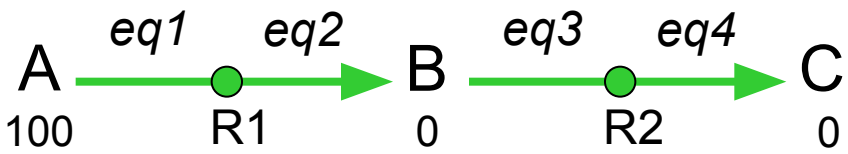

**Соответствующая ему математическая модель**

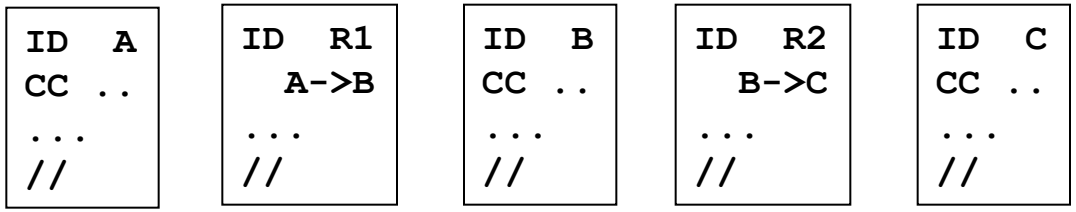
$$\frac{dA}{dt} = eq1$$

$$\frac{dB}{dt} = eq2 + eq3$$

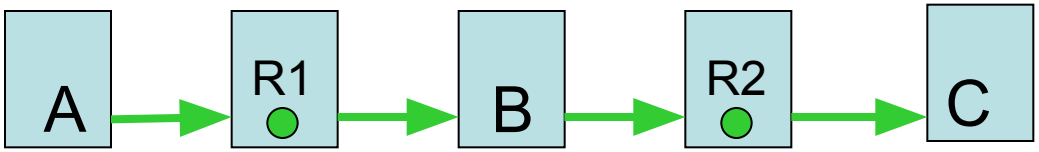
$$\frac{dC}{dt} = eq4$$

# BioUML мета-модель позволяет описать сложную систему на 3 уровнях

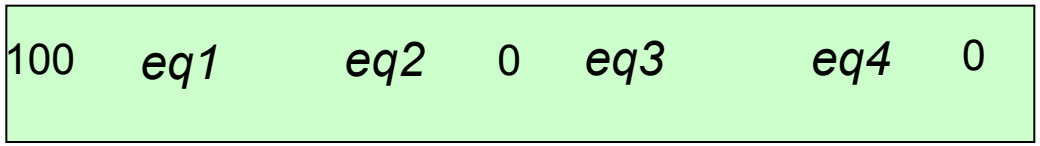



**Описание компонентов системы в базе данных**

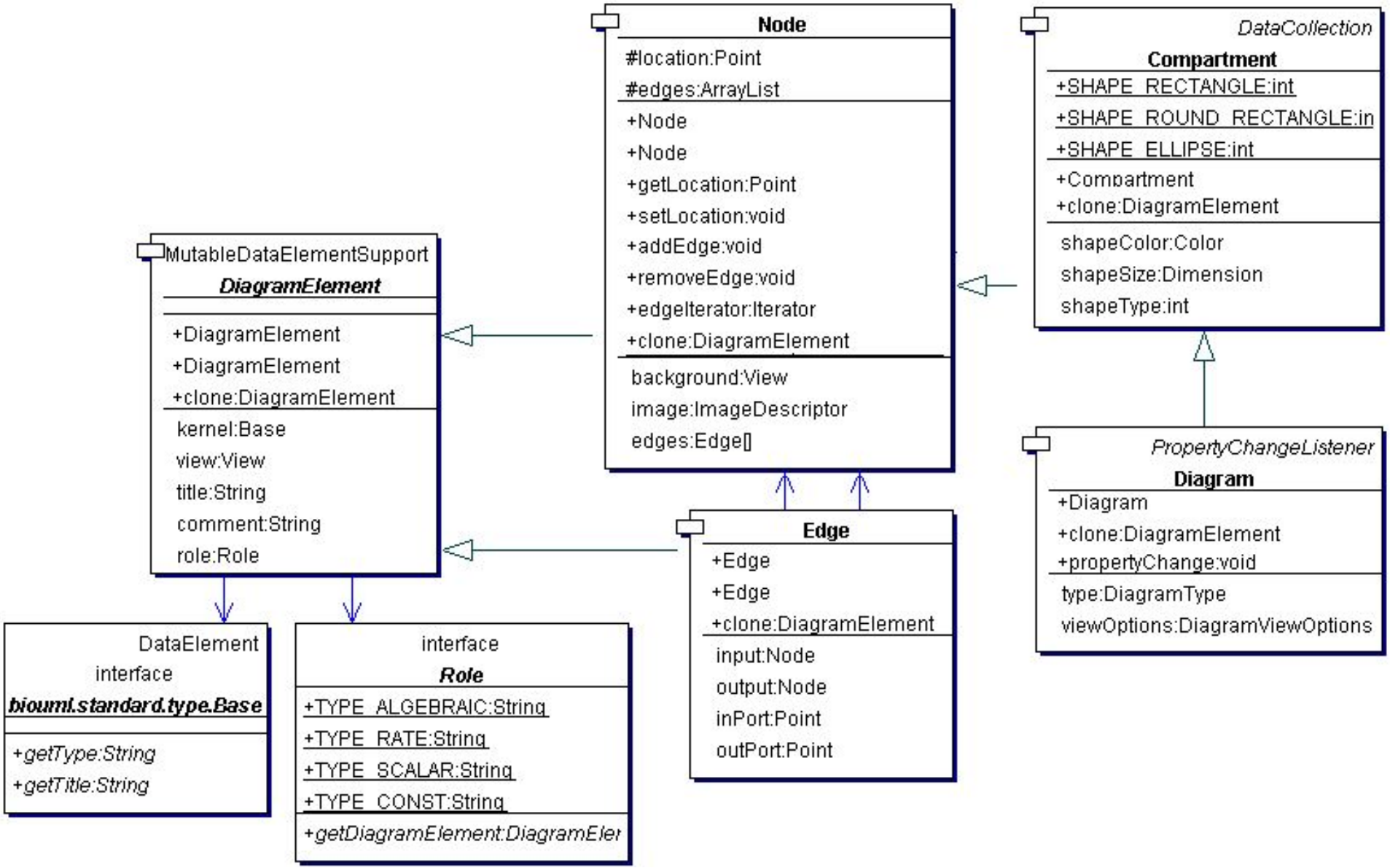



**Описание структуры системы в виде графа**

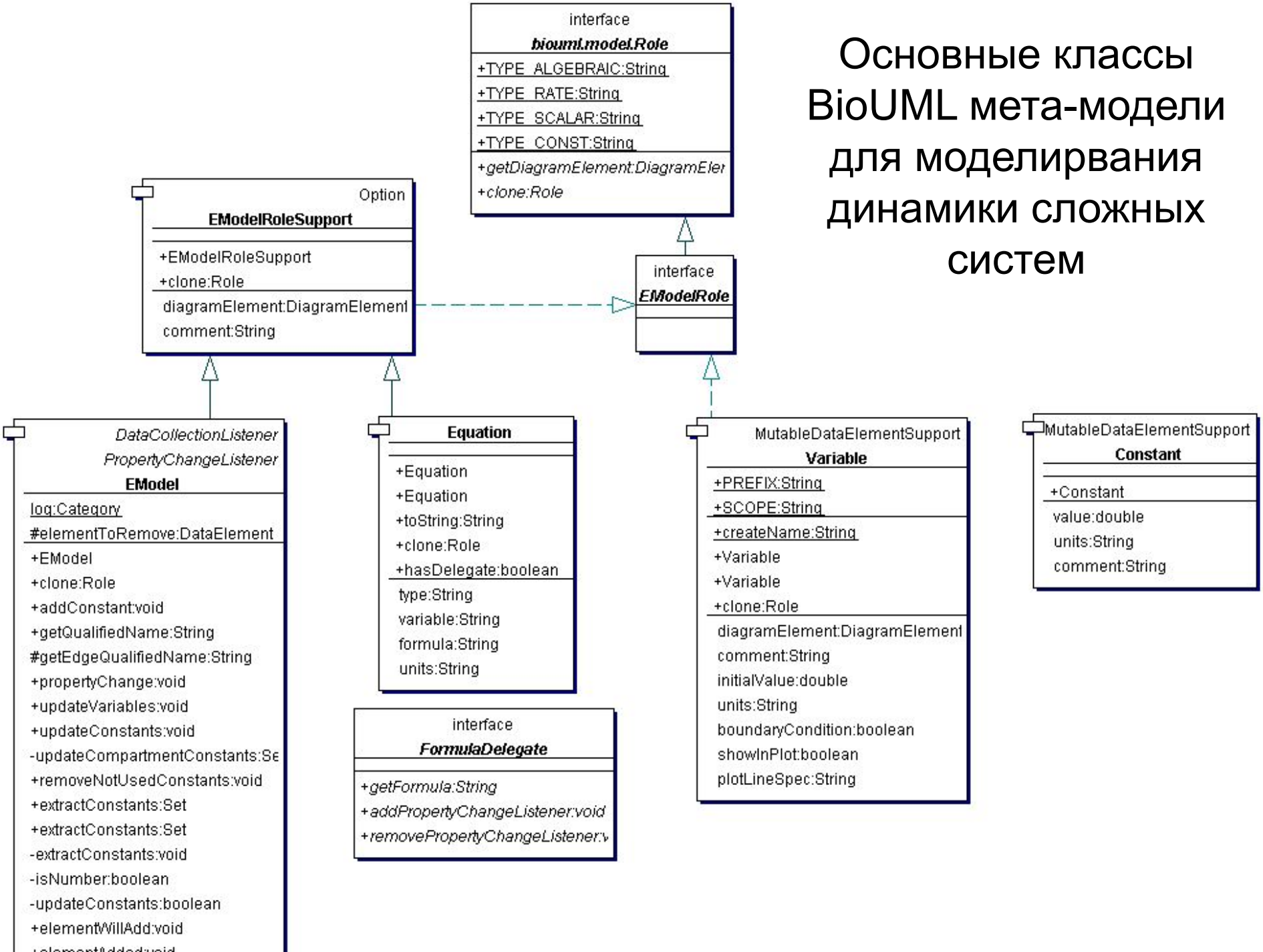


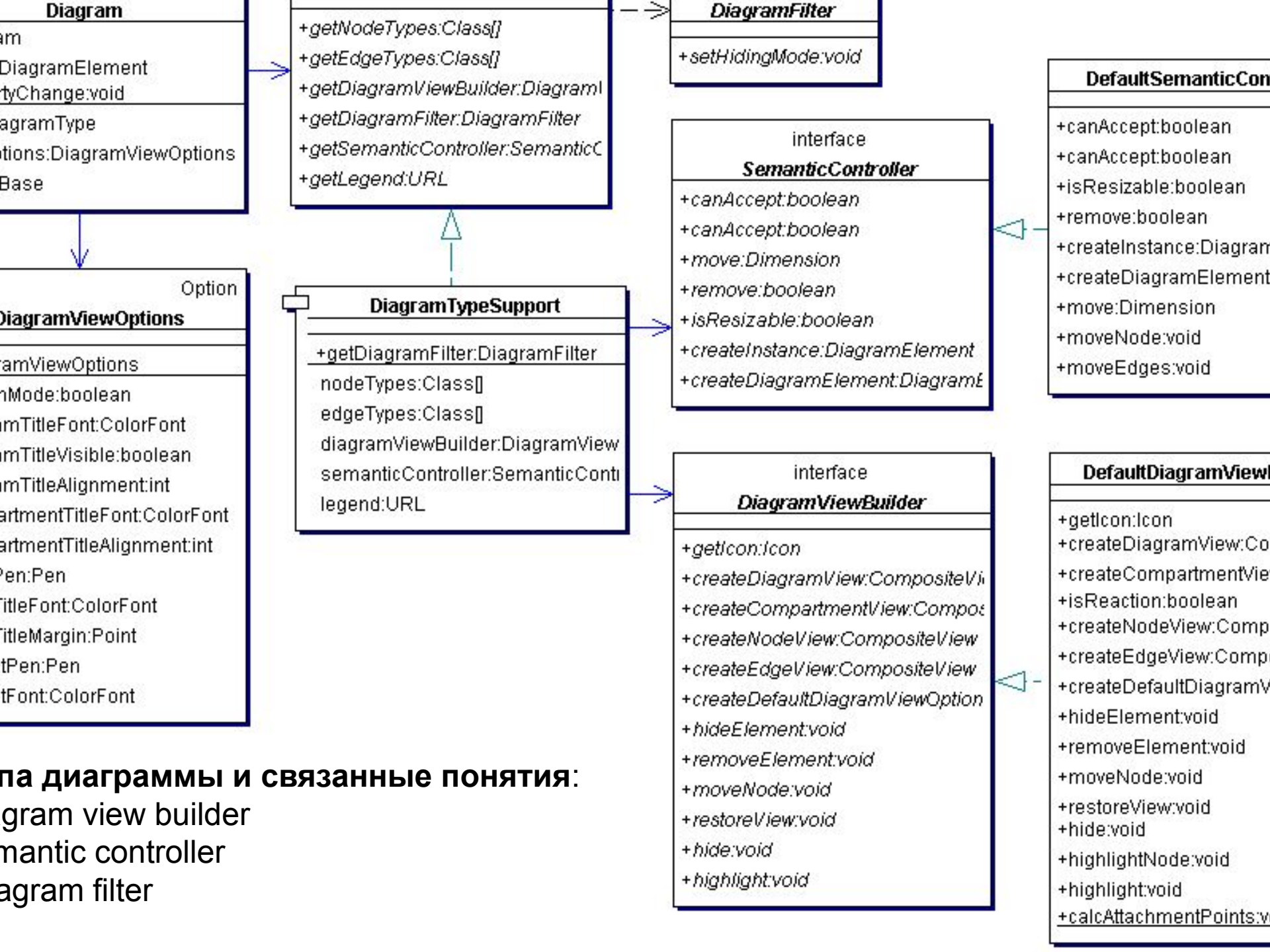

**Математическая модель системы**

# Основные классы BioUML мета-модели для описания структуры графа



# Основные классы BioUML мета-модели для моделирвания динамики сложных систем






**па диаграммы и связанные понятия**:

gram view builder

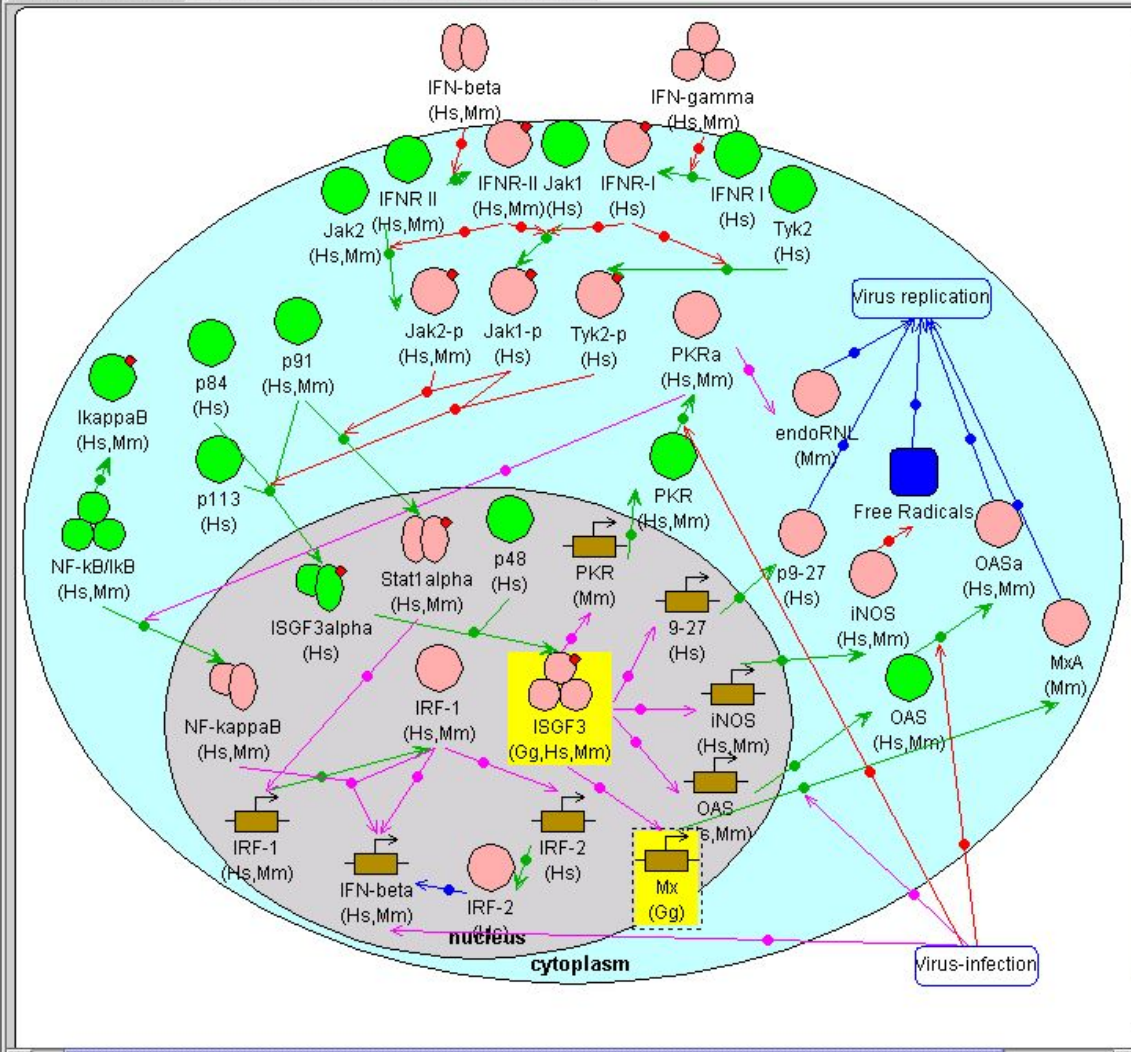
mantic controller

agram filter

BioUML Viewer

modules
- GeneNet module
  - Data
    - cell
    - compartment
    - expert
    - gene
    - literature
    - organism
    - process
    - protein
    - relation
    - rna
    - substance
  - Diagrams
    - Antiviral response
    - Antiviral response (dynar
    - Cholesterol
    - Embryo maturation
    - Environmental stress res
    - Erythroid differentiation
    - ethylene
    - HSP70-autoregulation
    - Leptin (organism level)
    - plant-pathogen
    - plant-pathogen general
    - redox-regulation
    - Seed reserve mobilisatio
    - Seed reserve mobilisatio
    - Seed reserve mobilisatio
    - Seed reserve mobilisatio
    - Seed reserve mobilisatio
    - seed-proof
    - Steroidogenesis (glucoc
    - Steroidogenesis (testost
    - Storage protein biosynthe
    - Storage proteins biosynth
    - tobacco

Antiviral response | Embryo maturation | Erythroid differentiation




| Property | Value |
|---|---|
| Diagram filter | |
| Filter | ☑ |
| Species filter | |
| Gallus gallus | ☑ |
| Homo sapiens | ☐ |
| Mus musculus | ☐ |
| Cell type filter | |
| Inducer filter | |
| Filter mode | highlight |
| Highlighter | yellow |

# Node

**Title** Mx

**Data** biouml.genenet.type.Gene@76e5d

**ID** Gg:Mx

**OS** Gallus gallus (chicken).

**SN** Mx

**NM** Mx protein

**SO** Gg:fibroblast

**RE** IFN-alpha
IFN-beta
poly(I).poly(C)
virus infection (NDV)

**DR** TRRD; G001088; Gg:MX
TFGENE; G001088;

```
<!-- BioUML diagrams markup language (DML) v. 0.9.2 -->

<!ELEMENT dml (diagramInfo?, diagram, executableModel?)>
<!ATTLIST dml
   version CDATA "0.9.2"
   appVersion CDATA "0.7.0" >

<!ELEMENT diagramInfo>
<!ATTLIST diagramInfo value CDATA >

<!ELEMENT diagram (compartmentInfo, nodes, edges)>
<!- "diagramType" attribute contains name of Java class ->
<!ATTLIST diagram
    diagramType CDATA #REQUIRED
>

<!ELEMENT nodes (compartment|equivalentNodeGroup|node)*>

<!ELEMENT edges (edge)*>
```

```
<!ELEMENT compartment (compartmentInfo, nodes, edges)>
<!ATTLIST compartment>

<!ELEMENT compartmentInfo (image?)>
<!-
   "kernel" attribute contains complete path for data
      element used as kernel; currently path is relative
      module/Data
  "shape" attribute possible values are:
      0-rectangle; 1-round_rectangle; 2-oval
-->
<!ATTLIST compartmentInfo
   kernel   CDATA  #REQUIRED
   x        CDATA  #REQUIRED
   y        CDATA  #REQUIRED
   width    CDATA  #REQUIRED
   height   CDATA  #REQUIRED
   title    CDATA
   comment  CDATA
   shape    CDATA  "0"
   color    CDATA  "255, 255, 255"
>
```

```
<!ELEMENT node (image?)>
<!ATTLIST node
  kernel   CDATA #REQUIRED
  title    CDATA
  comment  CDATA
  x        CDATA
  y        CDATA
>

<!ELEMENT edge>
<!ATTLIST edge
  kernel   CDATA #REQUIRED
  in       CDATA #REQUIRED
  out      CDATA #REQUIRED
  title    CDATA
  comment  CDATA
  inPort   CDATA
  outPort  CDATA
>
```

```
<!--=================================================== -->
<!-- Executable model                                   -->
<!--=================================================== -->
<!ELEMENT executableModel (constant*, variable*, equation*)>
<!ATTLIST executableModel
   class          CDATA #REQUIRED
   initialTime    CDATA #REQUIRED
   completionTime CDATA #REQUIRED
   comment        CDATA
>

<!ELEMENT constant>
<!ATTLIST constant
   name    CDATA #REQUIRED
   value   CDATA #REQUIRED
   units   CDATA
   comment CDATA
>
```

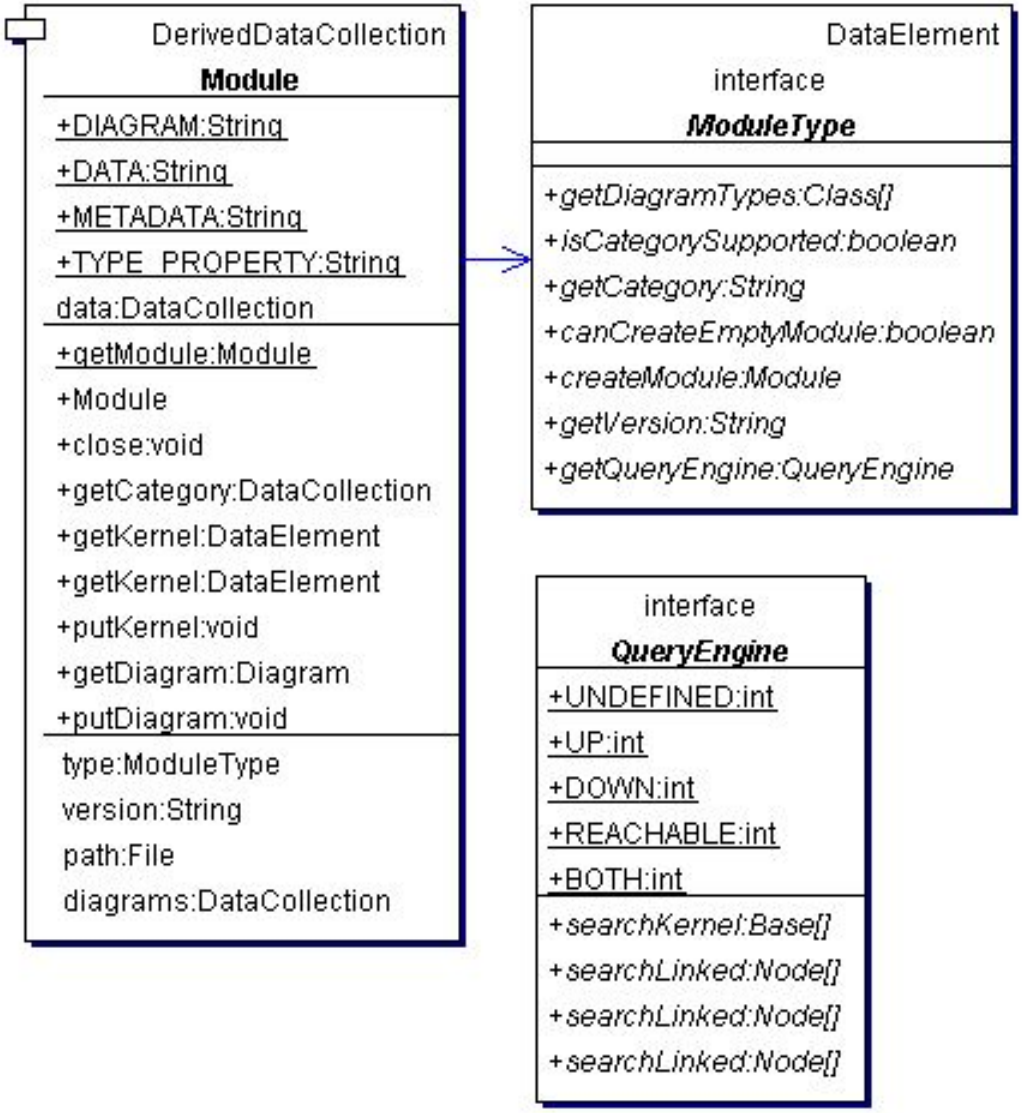
```
<!ELEMENT variable>
<!-- "diagramElement" attribute - diagram element name -->
<!ATTLIST variable
   diagramElement       CDATA  #REQUIRED
   initialValue         CDATA  "0.0"
   boundaryCondition    CDATA  "false"
   showInPlot           CDATA  "true"
   plotLineSpec         CDATA  "-"
   units                CDATA
   comment              CDATA
>

<!ELEMENT equation>
<!-
 "diagramElement" attribute - diagram element name
 "type" attribute - equation type.
  Possible values are:   algebraic, rate or scalar. -->
<!ATTLIST equation
   diagramElement     CDATA  #REQUIRED
   variable           CDATA  #REQUIRED
   formula            CDATA  #REQUIRED
   type               CDATA  "rate"
   units              CDATA
   comment            CDATA
>
```

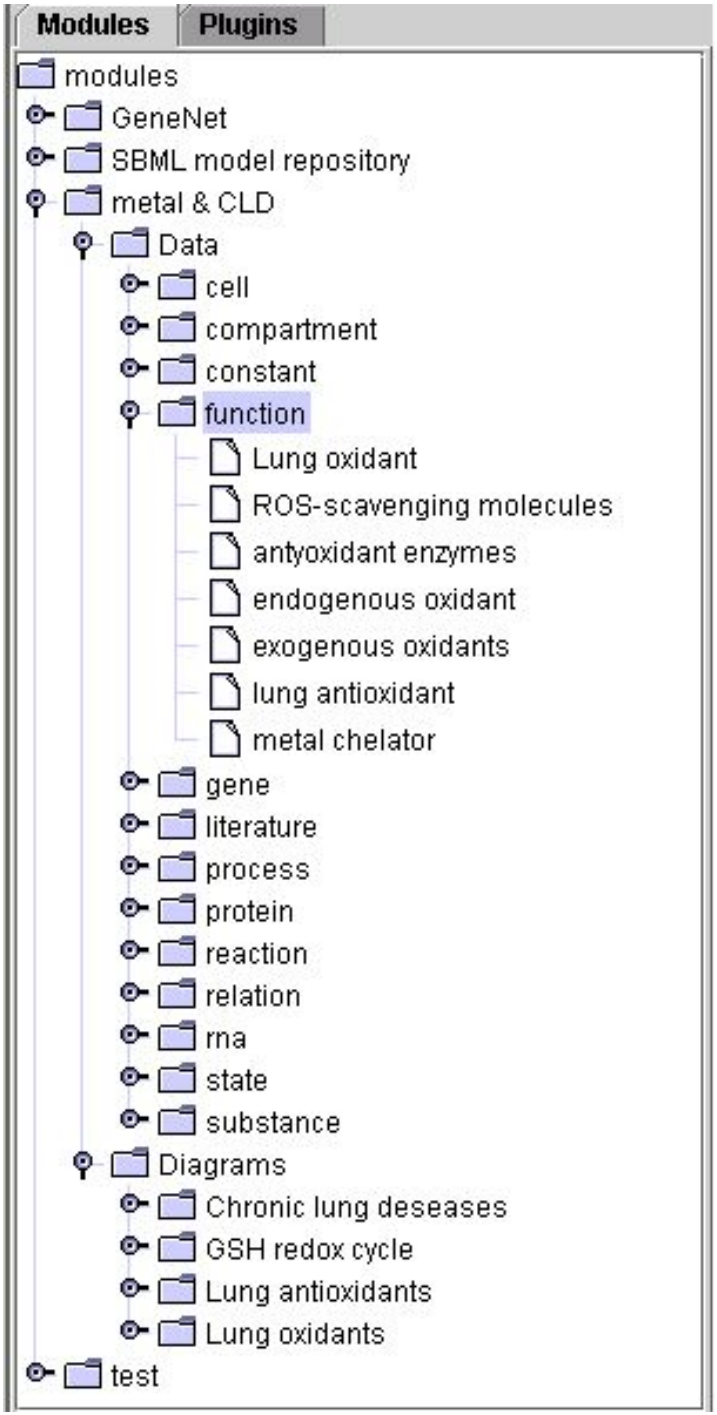
# Концепция модуля

- Чтобы обеспечить интеграцию различных баз данных в среду BioUML, мы вводим концепцию модуля.

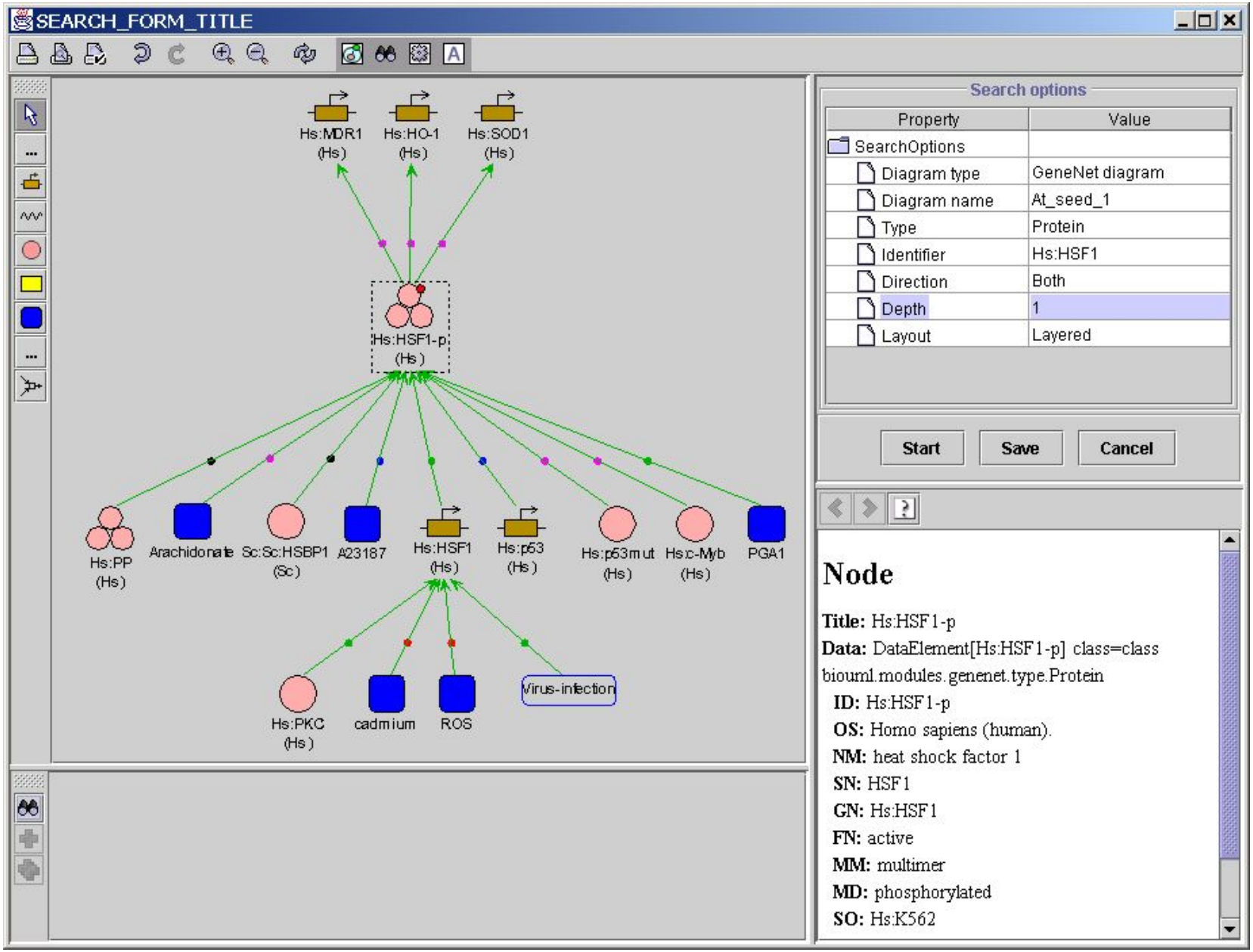
- Как правило, модуль создается для отдельной базы данных и определяет способ представления информации из этой базы данных в виде объектов языка Java. Модуль также может содержать специфичные для этой базы данных типы диаграмм и способы их графического отображения.

# Концепция модуля



# Система поиска взаимодействующих друг с другом компонентов биологических систем



QUERY_FORM_TITLE

| | Identifier | Species | Name | Synoni... | Gene ID | Functio... | Structure | Modifica |
|---|---|---|---|---|---|---|---|---|
| 0 | Hs:IRF-1 | Homo sapi... | interferon regulatory factor -1 | IRF-1 | Hs:IRF-1 | active | monomer | no data |
| 1 | Hs:IRF-2 | Homo sapi... | interferon regulatory factor-2 | IRF-2 | Hs:IRF-2 | active | monomer | no data |
| 2 | Hs:Jak2 | Homo sapi... | Jak2 protein tyrosine kinase | Jak2 | | inactive | monomer | no data |
| 3 | Hs:Jak2-p | Homo sapi... | Jak2 protein tyrosine kinase | Jak2 | | active | monomer | phosph |
| 4 | Hs:OAS | Homo sapi... | 2'-5' oligoadenylate synthetase | OAS | Hs:OAS | inactive | monomer | no data |
| 5 | Hs:OASa | Homo sapi... | 2'-5' oligoadenylate synthetase | OAS | Hs:OAS | active | monomer | no data |
| 6 | Hs:PKR | Homo sapi... | dsRNA-dependent cAMP-independent protein serine/threoni... | PKR | | inactive | monomer | no data |
| 7 | Hs:PKRa | Homo sapi... | dsRNA-dependent cAMP-independent protein serine/threoni... | PKR | | active | monomer | no data |
| 8 | Hs:Tyk2 | Homo sapi... | Tyk2 protein tyrosine kinase | Tyk2 | | inactive | monomer | no data |
| 9 | Hs:p113 | Homo sapi... | Stat2 | p113 | | inactive | monomer | no data |
| 10 | Hs:p48 | Homo sapi... | ISGF3gamma | p48 | | inactive | monomer | no data |
| 11 | Hs:p84 | Homo sapi... | Stat1beta | p84 | | inactive | monomer | no data |
| 12 | Hs:p91 | Homo sapi... | Stat1alpha | p91 | | inactive | monomer | no data |
| 13 | Mm:IRF-1 | Mus musc... | interferon regulatory factor -1 | IRF-1 | Mm:IRF-1 | active | monomer | no data |
| 14 | Mm:Jak2 | Mus musc... | Jak2 protein tyrosine kinase | Jak2 | | inactive | monomer | no data |
| 15 | Mm:Jak2-p | Mus musc... | Jak2 protein tyrosine kinase | Jak2 | | active | monomer | phosph |
| 16 | Mm:OAS | Mus musc... | 2'-5' oligoadenylate synthetase | OAS | Mm:OAS | inactive | monomer | no data |
| 17 | Mm:OASa | Mus musc... | 2'-5' oligoadenylate synthetase | OAS | Mm:OAS | active | monomer | no data |
| 18 | Mm:PKR | Mus musc... | dsRNA-dependent cAMP-independent protein serine/threoni... | PKR | Mm:PKR | inactive | monomer | no data |
| 19 | Mm:PKRa | Mus musc... | dsRNA-dependent cAMP-independent protein serine/threoni... | PKR | Mm:PKR | active | monomer | no data |
| 20 | Mm:Stat1a... | Mus musc... | signal transducer and activator of transcription 1 alpha protein | Stat1alpha | | inactive | monomer | no data |
| 21 | Mm:iNOS | Mus musc... | nitric oxide synthase | iNOS | Mm:iNOS | active | monomer | no data |

Filter | Table columns

| Property | Value | |
|---|---|---|
| FilteringSettings | | |
| Module | GeneNet | |
| Type | biouml.modules.gene... | |
| filter | | |
| Enabled | ☑ | |
| Filters | | |
| Source | ☐ | |
| Identifier | ☐ | |
| Synonims | ☐ | |
| Regulation | ☑ | /.*IFN.*/ |
| Date | ☐ | |
| Structure | ☑ | mon... |
| Name | ☐ | |
| Gene ID | ☐ | |
| Comment | ☐ | |
| Modification | ☐ | |

monomer
homodimer
heterodime
multimer
unknown

Start Cancel

View | Edit

**Protein**

ID Mm:OASa
OS Mus musculus (mouse).
NM 2'-5' oligoadenylate synthetase
SN OAS
GN Mm:OAS
FN active
MMmonomer
MD no data
SO Mm:macrophage Mm:fibroblast Mm:spleen Mm:liver Mm:lung Mm:thymus
RE IFN-alpha

# Универсальная система поиска информации по базам данных

# Модули

***BioUML standard*** – стандартный модуль для описания и моделирования биологических систем (преимущественно на молекулярно-клеточном уровне)

***SBML*** – Systems Biology Markup Language, level 1
http:// www.sbml.org

***GeneNet*** - база данных по генным сетям
ИЦиГ, Новосибирск, http://wwwmgs.bionet.nsc.ru

***KEGG/Ligand*** - Kyoto Encyclopedia of Genes and Genomes, база данных метаболических путей
Kyoto University, Japan, http://www.kegg.com

***TRANSPATH*** - база данных по путям передачи сигнала в клетке
Biobase GmbH, Germany.

***SBML*** – Systems Biology Markup Language, level 2
http:// www.sbml.org

CellML – Cell Markup Language
http://www.cellml.org

***GO*** – Gene Ontology
http://wwwmgs.bionet.nsc.ru

***UMLS*** – Unified Medical Language System
http://www.nlm.nih.gov/research/umls/

***BioPax*** – Biological Pathways Exchange
http://www.biopax.org

Edit View Favorites Tools Help

Search Favorites Media

http://www.biouml.net/index.shtml

Go

developmentontheedge.com
your source of innovative solutions

# http://www.biouml.org

Biosoft.Ru
logo

*BioUML - framework for systems biology*

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- Forum
- Conferences

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- ocumentation
- User guide
- Publications
- Presentations
- Architecture overview
- BioUML meta model
- Diagram markup language
- Module concept
- Extension points
- SBML support

**Welcome to BioUML world**

## What is BioUML?

BioUML is Java framework for systems biology. It spans the comprehensive range of capabilities including access to databases with experimental data, tools for formalized description of biological systems structure and functioning, as well as tools for their visualization and simulations.

Currently BioUML framework consists from following parts:

- Meta model - provides an abstract layer to present structure of any biological system as a clustered graph.
- Viewer - a universal viewer to visualize graphs of biological systems structure as diagrams.
- Editor - universal diagram editor.
- Search engine - provides searching of components with the specified properties in biological pathway databases. The search result can be presented as graph and further edited by a user using BioUML editor.
- Modeler - allows a user to model/simulate dynamics of biological systems using block diagrams.
- Standard diagram and data types - an attempt to standardize data types and graphic notations for biological pathways.
- Database modules - provides incorporation of different databases biological pathways

**Version 0.7**

BioUML workbench version 0.7.1 was released.
More...

**BioUML forum**

The forum aims to co-ordinate a community effort towards of development of BioUML and its application for modelling of biological systems. Here you can ask your questions as well as post your comments and suggestions. More...

enter email address

subscribe

**Have questions?**

If you have any questions please contact us at info@Biosoft.Ru

Internet