



Online resources for mathematical modeling in biology

Resources in the Web

First step in modeling: Collecting pathway/ molecular information

Making models: Learning from old models

Parameter estimation: Collecting numerical values for parameters

Collecting pathway/ molecular information

No substitute of reading existing publications

The image displays two web interfaces. The top interface is the PubMed website, featuring the NCBI logo, navigation links for Resources and How To, a search bar with a dropdown menu set to 'PubMed', and a 'Search' button. Below the search bar, there is a banner image of books and a tablet, followed by the text: 'PubMed comprises more than 26 million citations for biomedical literature from MEDLINE, life science journals, and online books. Citations may include links to full text content from PubMed Central and publisher web sites.' The main content area is divided into two columns: 'Using PubMed' with links to 'PubMed Quick Start Guide', 'Full Text Articles', 'PubMed FAQs', and 'PubMed Tutorials'; and 'PubMed Tools' with links to 'PubMed Mobile', 'Single Citation Matcher', 'Batch Citation Matcher', and 'Clinical Queries'. The bottom interface is a Google Scholar search bar, showing the Google Scholar logo and a search input field with a search button.

Collecting pathway/ molecular information

Pathway databases: KEGG, Reactome, Panther, WikiPathways



The image displays two web interfaces for biological pathway databases. On the left is the KEGG PATHWAY Database, featuring a colorful logo and a navigation menu with options like PATHWAY, BRITE, and MOD. It includes a search bar for selecting a prefix (map or Organism) and a list of pathway categories such as Metabolism, Genetic Information Processing, Environmental Information Processing, Cellular Processes, Organismal Systems, Human Diseases, and Drug Development. On the right is the Reactome website, which has a dark blue header with the Reactome logo and the tagline 'A CURATED PATHWAY DATABASE'. The main navigation bar includes links for About, Content, Documentation, Tools, Community, Download, and Contact. Below this are six large buttons: Browse Pathways, Analyze Data, Reactome FIViz app, User Guide, Data Download, and Contact Us. A search bar on the right of the navigation bar contains the text 'e.g. O95631, NTN1, signalin'. A 'Tweets' section on the far right shows a tweet from Gramene Database (@GrameneDatabase) mentioning the current version of Reactome as V59 and providing a link to a publication on Plant Reactome.

KEGG PATHWAY Database
Wiring diagrams of molecular interactions, reactions, and relations

Menu PATHWAY BRITE MOD

Select prefix
map Organism Enter

Pathway Maps

KEGG PATHWAY is a collection of molecular interaction and reaction data.

1. Metabolism
 - Global/overview Carbohydrate
 - Cofactor/vitamin Terpenoid
2. Genetic Information Processing
3. Environmental Information Processing
4. Cellular Processes
5. Organismal Systems
6. Human Diseases

and also on the structure relationship

7. Drug Development

REACTOME
A CURATED PATHWAY DATABASE

About Content Documentation Tools Community Download Contact

e.g. O95631, NTN1, signalin Search

Browse Pathways **Analyze Data** **Reactome FIViz app**

User Guide **Data Download** **Contact Us**

Tweets

Current Version: Reactome V59

reactome Retweeted

Gramene Database
@GrameneDatabase

nar.oxfordjournals.org/cgi/content/fo... Checkout the first publication on Plant Reactome a resource for plant pathways

@reactome @CSHL @OregonState @embl

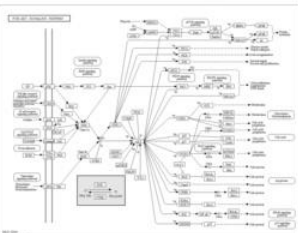
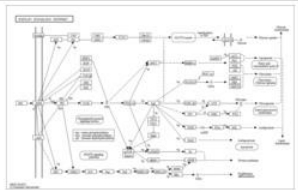
Using KEGG

<http://www.genome.jp/kegg/pathway.html>


Pathway Text Search

Number of entries in a page

Page : of 4 Items : 1 - 20 of 77

Entry	Thumbnail Image	Name	Description	Object	Legend
map04151		PI3K-Akt signaling pathway	The phosphatidylinositol 3' - kinase(PI3K)-Akt signaling pathway is activated by many types of cellu...	...07208 (RHEB) K07207 (TSC2) K07206 (TSC1) K04456 (AKT), 2.7.11.1 K06276 (PDPK1), 2.7.11.1 5290 (PIK3C...	...BPs eIF4B S6K1/2 Raptor mTOR GβL Rheb TSC2 TSC1 AKT PDK1 PI3K p53 signaling pathway mTOR signaling ...
map04910		Insulin signaling pathway	...pendent protein kinase 1 (PDK1), which activates Akt, a serine kinase. Akt in turn deactivates glyco...	...(PPARGC1A) K06086 (SORBS1) K07208 (RHEB) K04456 (AKT) K00922 (PIK3C), K02649 (PIK3R) K07194 (RHOQ) K...	... PEPCK G6PC mTOR PDE3 FBP Exo70 PGC-1α CAP Rheb Akt PI3K TC10 GSK-3β SREBP-1c GRF2 CrkII aPKC APS ...

Using KEGG



Search

Database: GENES - Search

hsa:55355
no KO assigned | (RefSeq)

hsa:11005
no KO assigned | (RefSeq)

hsa:10000
K04456 RAC serine/threonine PKBG, PRKBG, RAC-PK-g

hsa:207
K04456 RAC serine/threonine ALPHA, PRKBA, RAC, RA

hsa:84335
K16184 proline-rich AKT1 s

hsa:64400
no KO assigned | (RefSeq)

hsa:208
K04456 RAC serine/threonine PRKBB, RAC-BETA; AKT s

ptr:740898
K04456 RAC serine/threonine kinase 1

ptr:467979
no KO assigned | (RefSeq)

ptr:456035
K04456 RAC serine/threonine

ptr:736031
no KO assigned | (RefSeq)


ptr:456218

Menu PATH

Search

Search

Enter org



Homo sapiens (human): 207

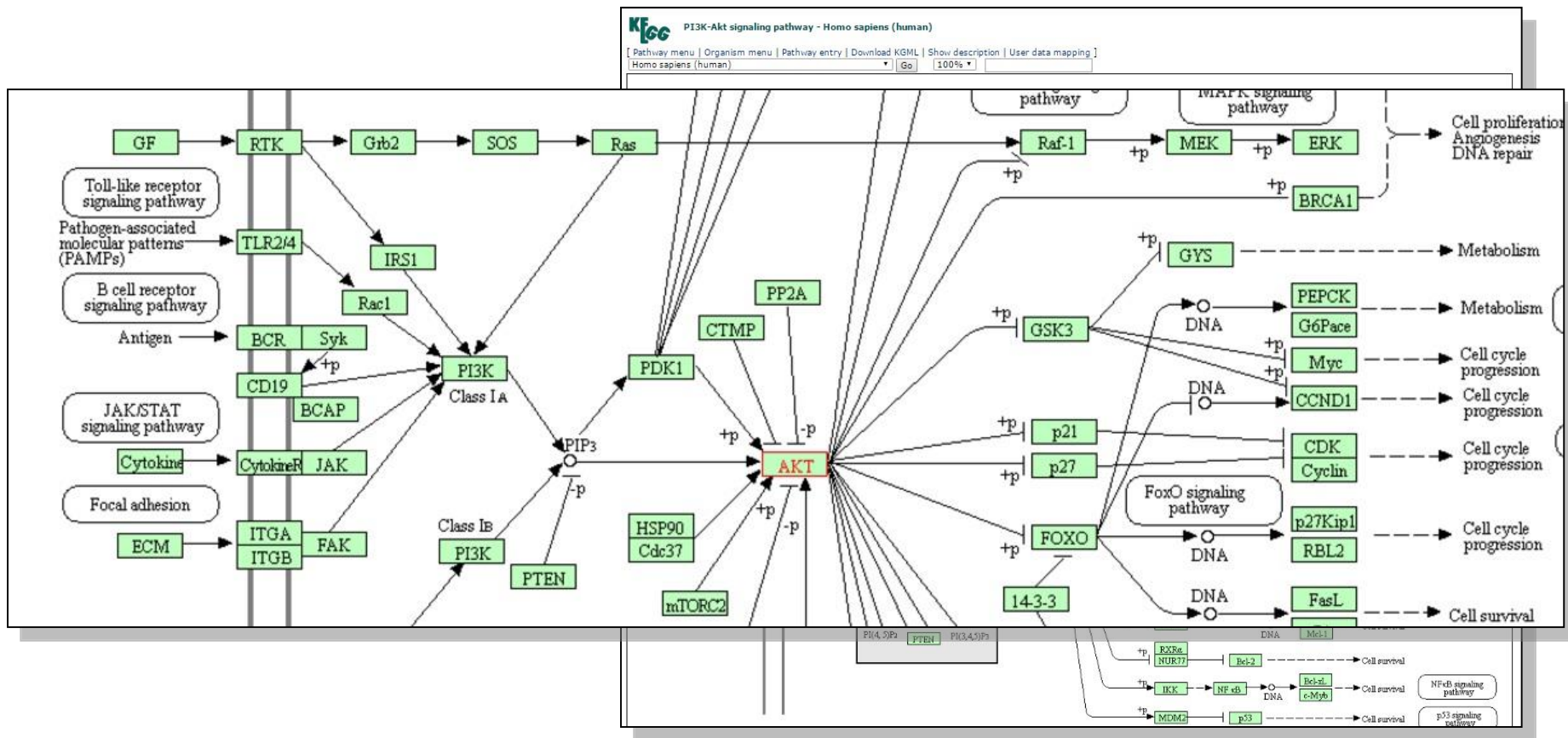
Help

Entry	207	CDS	T01001
Gene name	AKT1, AKT, CWS6, PKB, PKB-ALPHA, PRKBA, RAC, RAC-ALPHA		
Definition	(RefSeq) AKT serine/threonine kinase 1		
KO	K04456 RAC serine/threonine-protein kinase [EC:2.7.11.1]		
Organism	hsa Homo sapiens (human)		
Pathway	<p>hsa01521 EGFR tyrosine kinase inhibitor resistance</p> <p>hsa01522 Endocrine resistance</p> <p>hsa01524 Platinum drug resistance</p> <p>hsa04010 MAPK signaling pathway</p> <p>hsa04012 ErbB signaling pathway</p> <p>hsa04014 Ras signaling pathway</p> <p>hsa04015 Rap1 signaling pathway</p> <p>hsa04022 cGMP-PKG signaling pathway</p> <p>hsa04024 cAMP signaling pathway</p> <p>hsa04062 Chemokine signaling pathway</p> <p>hsa04066 HIF-1 signaling pathway</p> <p>hsa04068 FoxO signaling pathway</p> <p>hsa04071 Sphingolipid signaling pathway</p> <p>hsa04072 Phospholipase D signaling pathway</p> <p>hsa04150 mTOR signaling pathway</p> <p>hsa04151 PI3K-Akt signaling pathway</p> <p>hsa04152 AMPK signaling pathway</p> <p>hsa04210 Apoptosis</p> <p>hsa04211 Longevity regulating pathway</p> <p>hsa04213 Longevity regulating pathway - multiple species</p> <p>hsa04261 Adrenergic signaling in cardiomyocytes</p> <p>hsa04370 VEGF signaling pathway</p>		

All links

- Ontology (4)
 - KEGG BRITE (4)
- Pathway (75)
 - KEGG PATHWAY (74)
 - KEGG MODULE (1)
- Disease (10)
 - KEGG DISEASE (3)
 - OMIM (7)
- Drug (5)
 - KEGG DRUG (4)
 - KEGG DGROUP (1)
- Chemical reaction (1)
 - KEGG ENZYME (1)
- Genome (1)
 - KEGG GENOME (1)
- Gene (23)
 - KEGG ORTHOLOGY (1)
 - RefGene (3)
 - NCBI-PROTEINID (1)
 - NCBI-Gene (1)
 - UniGene (1)
 - HGNC (1)
 - HPRD (1)
 - Ensembl (1)
 - RIKEN BRC-DNA (11)
 - OC (1)
 - VEGA (1)
- Protein sequence (11)
 - UniProt (2)
 - SWISS-PROT (1)

Using KEGG



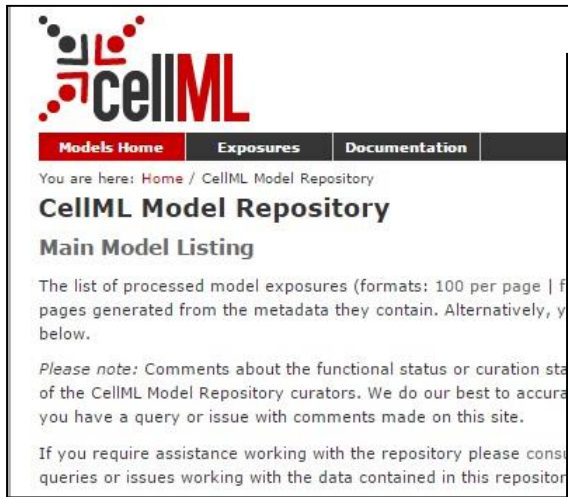
Learning from old models

Databases for biological models:

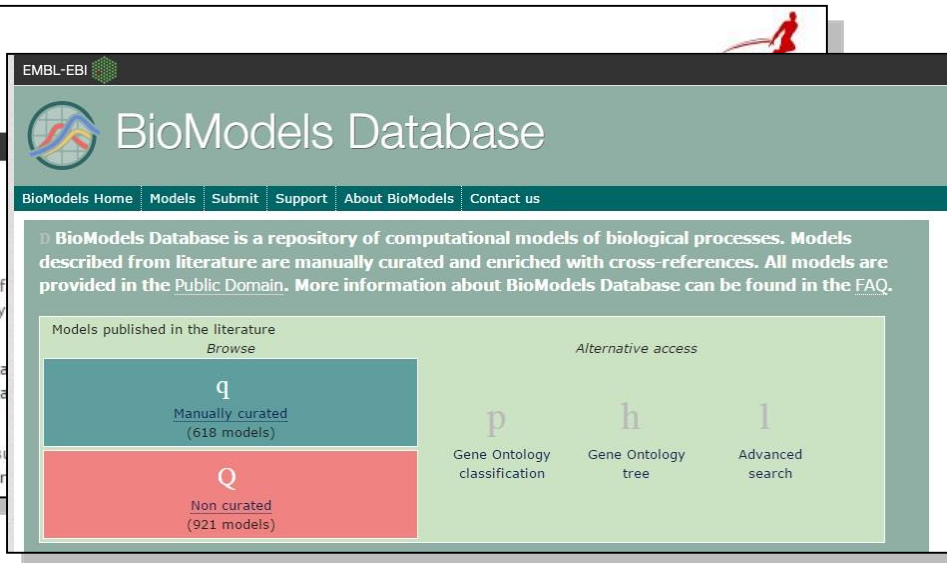
BioModels database: <https://www.ebi.ac.uk/biomodels-main/>

CellML Model Repository: <http://models.cellml.org/cellml>

JSim Model Archives: <http://www.physiome.org/jsim/models/index.html>

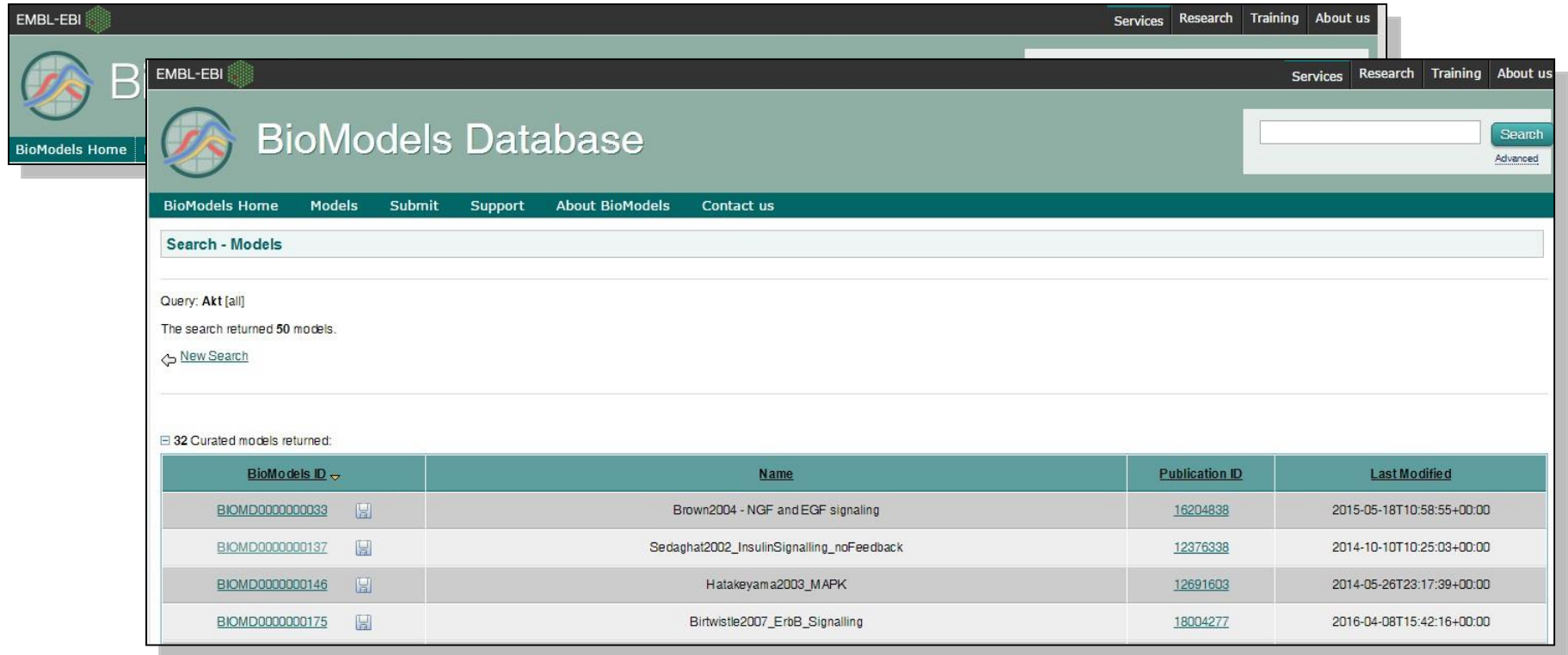


The screenshot shows the CellML Model Repository website. At the top is the CellML logo, which consists of a stylized network of nodes and edges in red and black, followed by the text 'cellML' in a bold, sans-serif font. Below the logo is a navigation bar with three tabs: 'Models Home' (highlighted in red), 'Exposures', and 'Documentation'. Below the navigation bar, the text 'You are here: Home / CellML Model Repository' is displayed. The main heading is 'CellML Model Repository' in a bold, black font, followed by 'Main Model Listing'. The text below states: 'The list of processed model exposures (formats: 100 per page | f pages generated from the metadata they contain. Alternatively, y below.' A 'Please note' section follows, mentioning comments about functional status or curation status. At the bottom, it says: 'If you require assistance working with the repository please cons queries or issues working with the data contained in this repository'.



The screenshot shows the BioModels Database website. At the top is the EMBL-EBI logo, which includes the text 'EMBL-EBI' and a green hexagonal icon. Below the logo is the 'BioModels Database' title in a large, white font. A navigation bar below the title contains links: 'BioModels Home', 'Models', 'Submit', 'Support', 'About BioModels', and 'Contact us'. The main content area has a green background and contains the text: 'BioModels Database is a repository of computational models of biological processes. Models described from literature are manually curated and enriched with cross-references. All models are provided in the Public Domain. More information about BioModels Database can be found in the FAQ.' Below this text is a section titled 'Models published in the literature' with a 'Browse' link. This section is divided into two columns. The left column has two boxes: a teal box labeled 'q' for 'Manually curated (618 models)' and a red box labeled 'Q' for 'Non curated (921 models)'. The right column is titled 'Alternative access' and contains three boxes: 'p' for 'Gene Ontology classification', 'h' for 'Gene Ontology tree', and 'l' for 'Advanced search'.

Exploring BioModels



The screenshot shows the BioModels Database search results for the query "Akt". The page features a navigation bar with links to Services, Research, Training, and About us. Below the navigation bar, the BioModels Database logo and name are displayed. A search bar with a "Search" button and a link to "Advanced" search is present. The main content area shows the search results for "Akt", indicating that 50 models were returned. A table displays the first four results, including the BioModels ID, Name, Publication ID, and Last Modified date.

EMBL-EBI

Services Research Training About us

BioModels Home

EMBL-EBI

Services Research Training About us

BioModels Database

Search

Advanced

BioModels Home Models Submit Support About BioModels Contact us

Search - Models

Query: Akt [all]

The search returned 50 models.

[New Search](#)

32 Curated models returned:

BioModels ID	Name	Publication ID	Last Modified
BIOMD0000000033	Brown2004 - NGF and EGF signaling	16204838	2015-05-18T10:58:55+00:00
BIOMD0000000137	Sedaghat2002_InsulinSignalling_noFeedback	12376338	2014-10-10T10:25:03+00:00
BIOMD0000000146	Hatakeyama2003_MAPK	12691603	2014-05-26T23:17:39+00:00
BIOMD0000000175	Birtwistle2007_ErbB_Signalling	18004277	2016-04-08T15:42:16+00:00

Exploring BioModels

The screenshot displays the BioModels website interface. The main header includes the EMBL-EBI logo and the BioModels logo. The navigation bar contains links for 'BioModels Home', 'Models', and 'Submit'. The main content area shows the model details for 'BIOMD0000000033 - Brown2004 - NGF and EGF signaling'. The 'Parameters' tab is selected, showing a table of global parameters (48) with columns for the parameter name, value, and type. The table lists parameters such as k_{rb}EGF, k_{ru}EGF, k_{rb}NGF, k_{ru}NGF, k_{EGF}, and K_mEGF, all with constant values. The footer of the page mentions the LASSP, Department of Physics, Cornell University, Ithaca, NY 14853, USA, and provides a link to the model.

EMBL-EBI

BioModels

BioModels Home Models Submit

BIOMD0000000033 - Brown2004 - NGF and EGF signaling

Download SBML | Other formats (auto-generated) | Actions | Send feedback

Model Overview Math Physical entities **Parameters** Curation

Global Parameters (48)

k _{rb} EGF	Value: 2.18503E-5 Constant
k _{ru} EGF	Value: 0.0121008 Constant
k _{rb} NGF	Value: 1.38209E-7 Constant
k _{ru} NGF	Value: 0.00723811 Constant
k _{EGF}	Value: 694.731 Constant
K _m EGF	Value: 6086070.0 Constant

LASSP, Department of Physics, Cornell University, Clark Hall, Ithaca, NY 14853, USA. [\[more\]](#)

Model

How to get the parameter values?

1. Collect from published literature.
2. Collect from old models
3. Perform experiments and estimate parameter by fitting your model
4. Databases for parameter values

Parameter estimation from experimental data

Perform experiments →

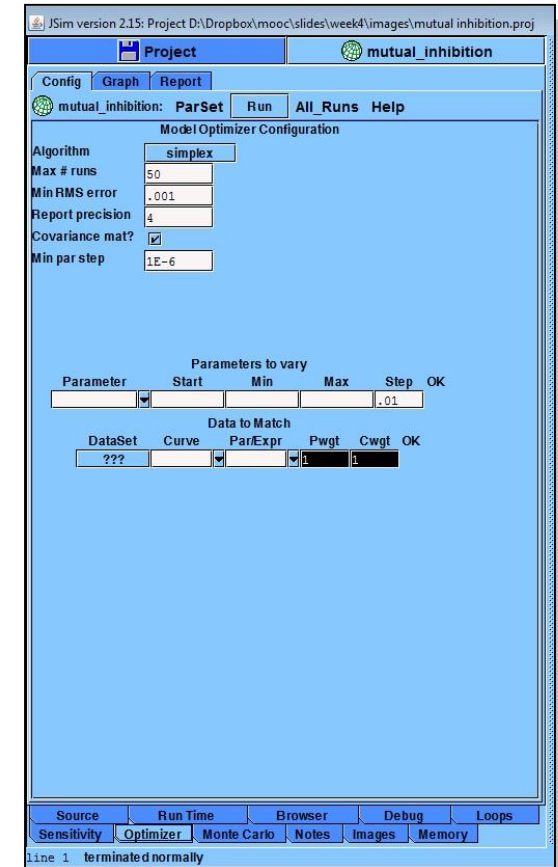
Create mathematical model →

Systematically try different parameter values and fit simulated data

with experimental results →

Identify parameter values that give best fitting

Tools for parameter estimation: JSim, COPASI, Data2Dynamics (D2D)

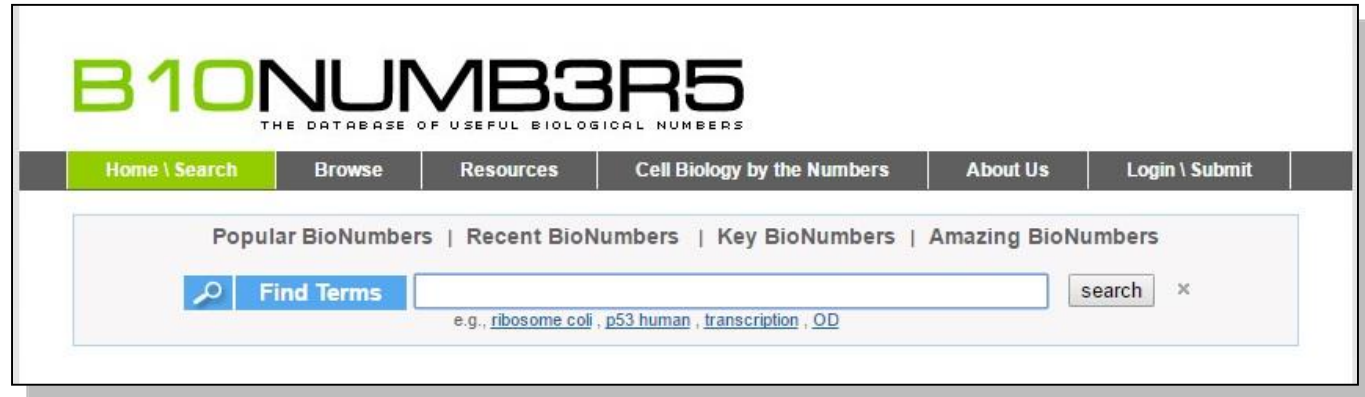


Databases for numerical values

BRENDA: Enzyme information database (<http://www.brenda-enzymes.org/>)

SABIO-RK: biochemical reaction kinetics database (<http://sabio.villa-bosch.de/>)

BioNumbers: Database of biological numbers (<http://bionumbers.hms.harvard.edu/>)



The screenshot shows the BioNumbers website. At the top is the logo "B10NUMB3R5" in green and black, with the tagline "THE DATABASE OF USEFUL BIOLOGICAL NUMBERS" below it. A navigation bar contains links: "Home \ Search" (highlighted in green), "Browse", "Resources", "Cell Biology by the Numbers", "About Us", and "Login \ Submit". Below the navigation bar is a section with links: "Popular BioNumbers", "Recent BioNumbers", "Key BioNumbers", and "Amazing BioNumbers". A search bar is located below these links, featuring a magnifying glass icon, the text "Find Terms", a search input field, a "search" button, and a close "x" button. Below the search bar, there is a hint: "e.g., [ribosome coli](#), [p53 human](#), [transcription](#), [OD](#)".

Key points:

1. The main source of information for building models is published literature. Databases like KEGG help by providing curated information.
2. Published/old models are good starting point for creating a new model: provides information about the system, helps in making mathematical models and provides parameter values.
3. Model databases like BioModels are useful for storing, sharing and recycle of models.
4. Parameter values are usually collected from literature, old models or through parameter estimation from experimental data.