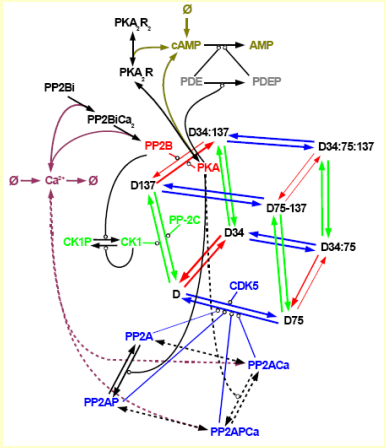
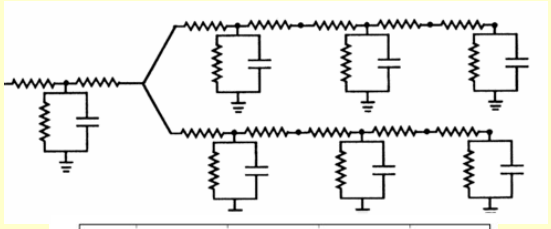
Pink Seminar

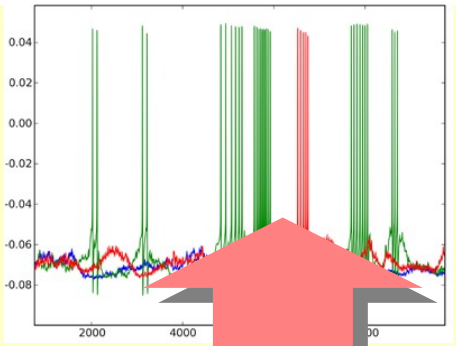
Nicolas Le Novère, EMBL-EBI

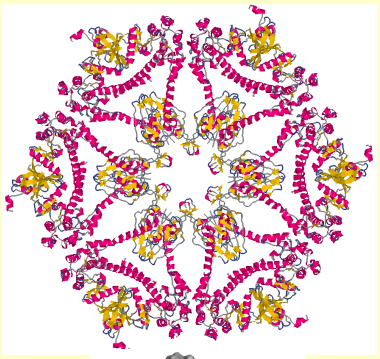
compneur group themes and projects

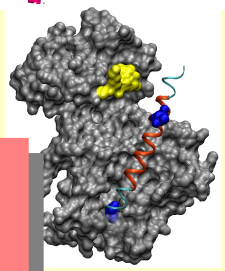
Computational Neurobiology

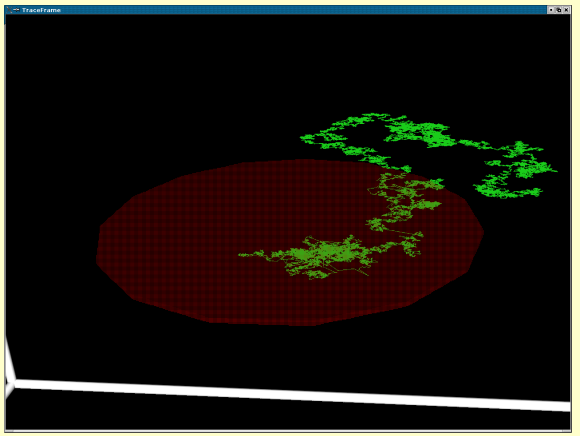






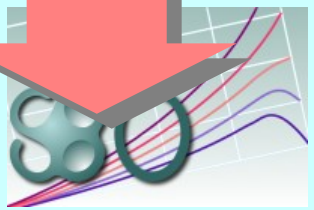


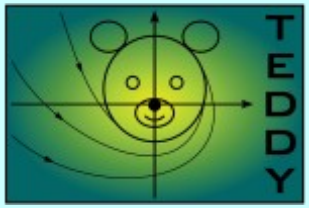




SBML

SBGN





KISAO

e-MeP

Ligand-Gated Ion Channel database

Computational Systems Biology

MIRIAM

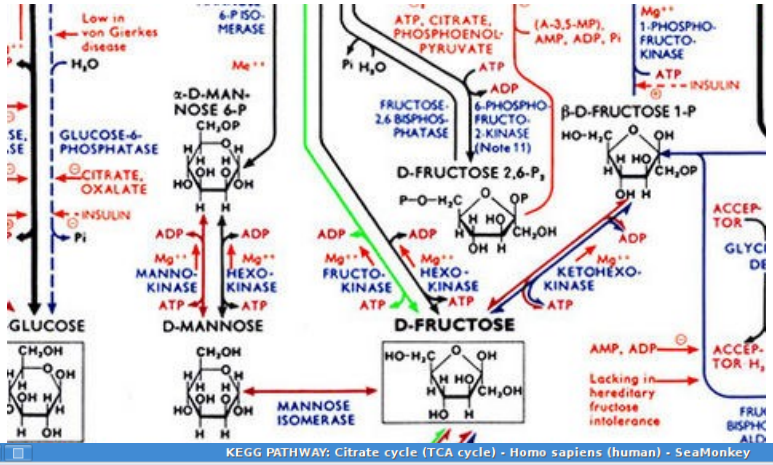
MIASE

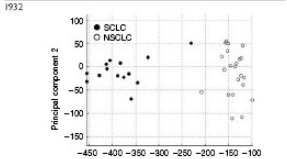
BioModels

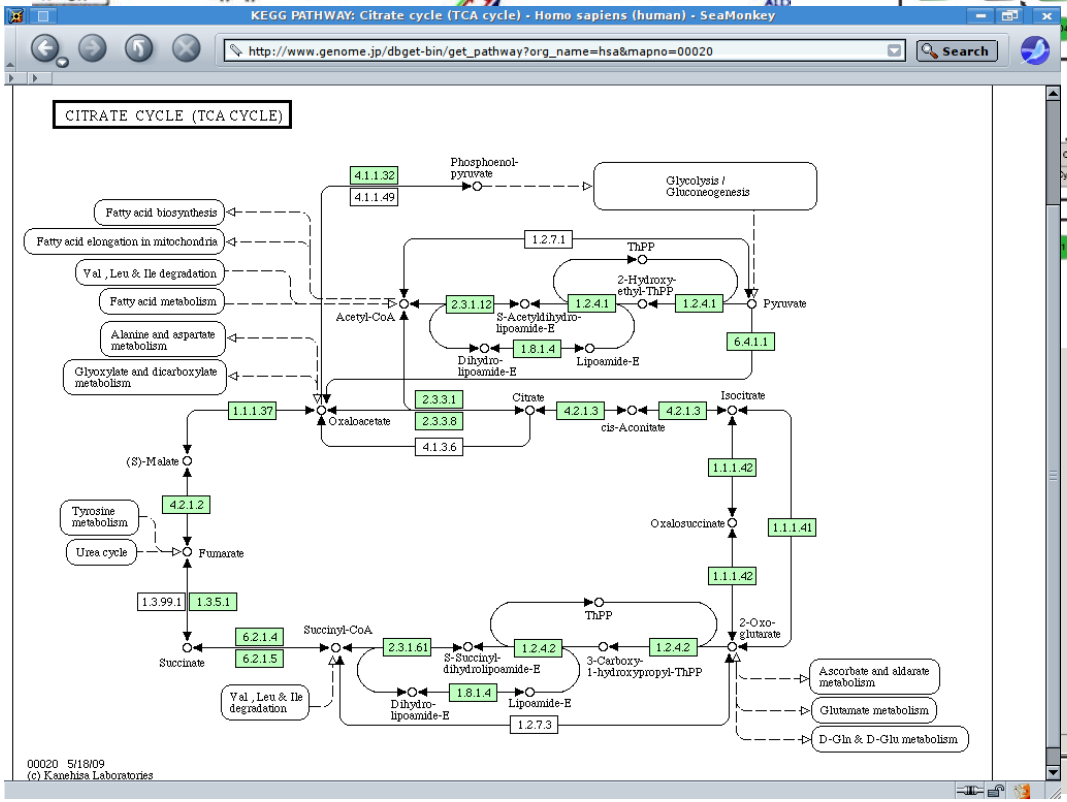
A common layout for the Tower of Babel: The Systems Biology Graphical Notation

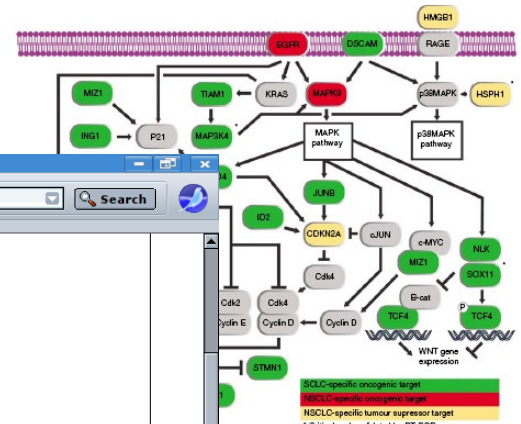
(on the behalf of SBGN editors, authors and contributors)

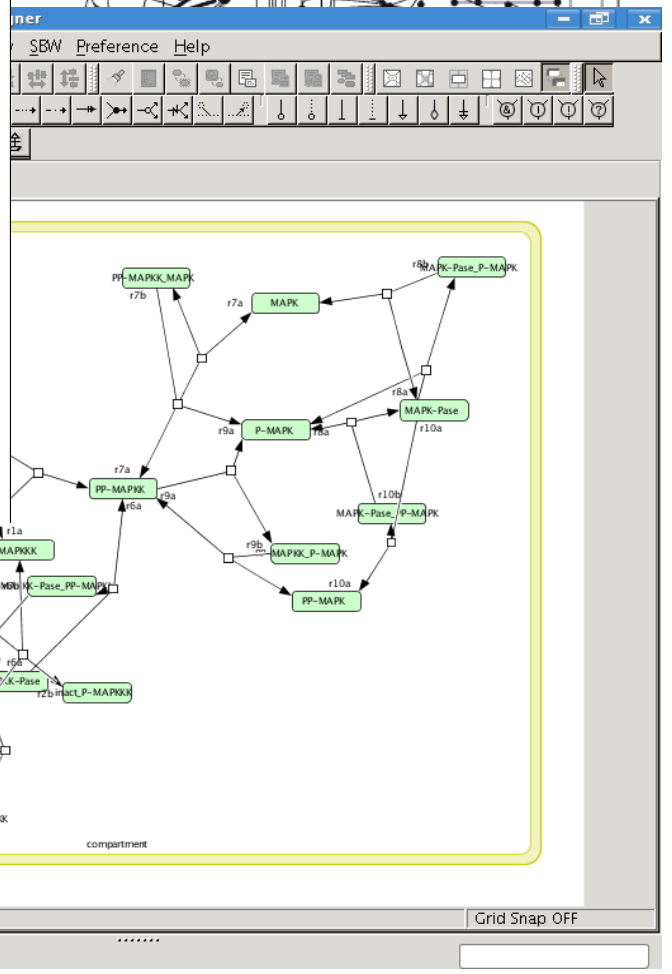
Graphs are everywhere in biology





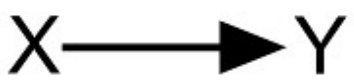






Ambiguity of usual representations

Ambiguity of usual representations



is transformed into

translocates (X "=" Y)

is degraded into

associates into

dissociates into

stimulates the activity of

stimulates the expression of

catalyses the formation of

Ambiguity of usual representations

X inhibits Y

is transformed into

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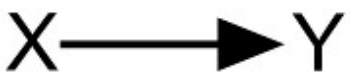
Ambiguity of usual representations



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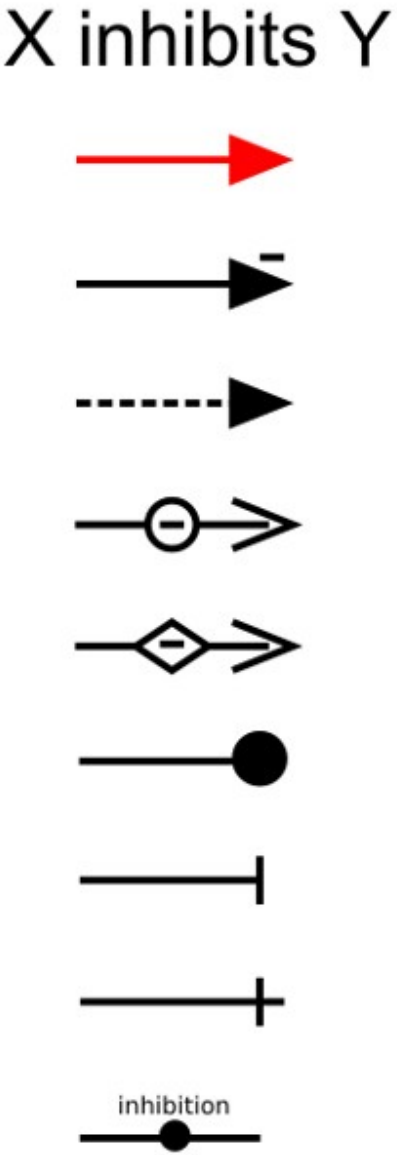
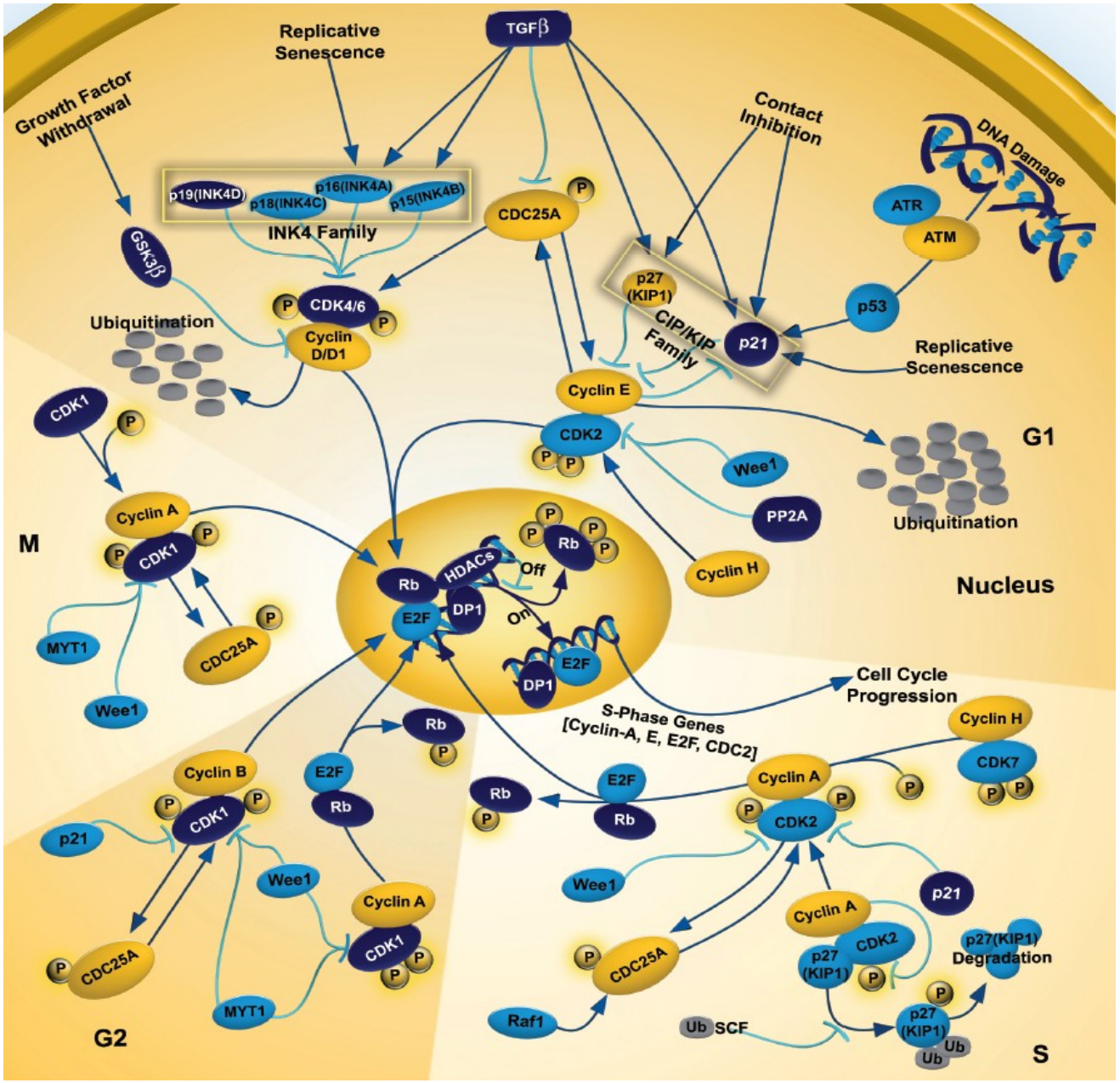


Can-this be understood by biologists?



Can-this be understood by biologists?

Stimulates? but … what exactly?

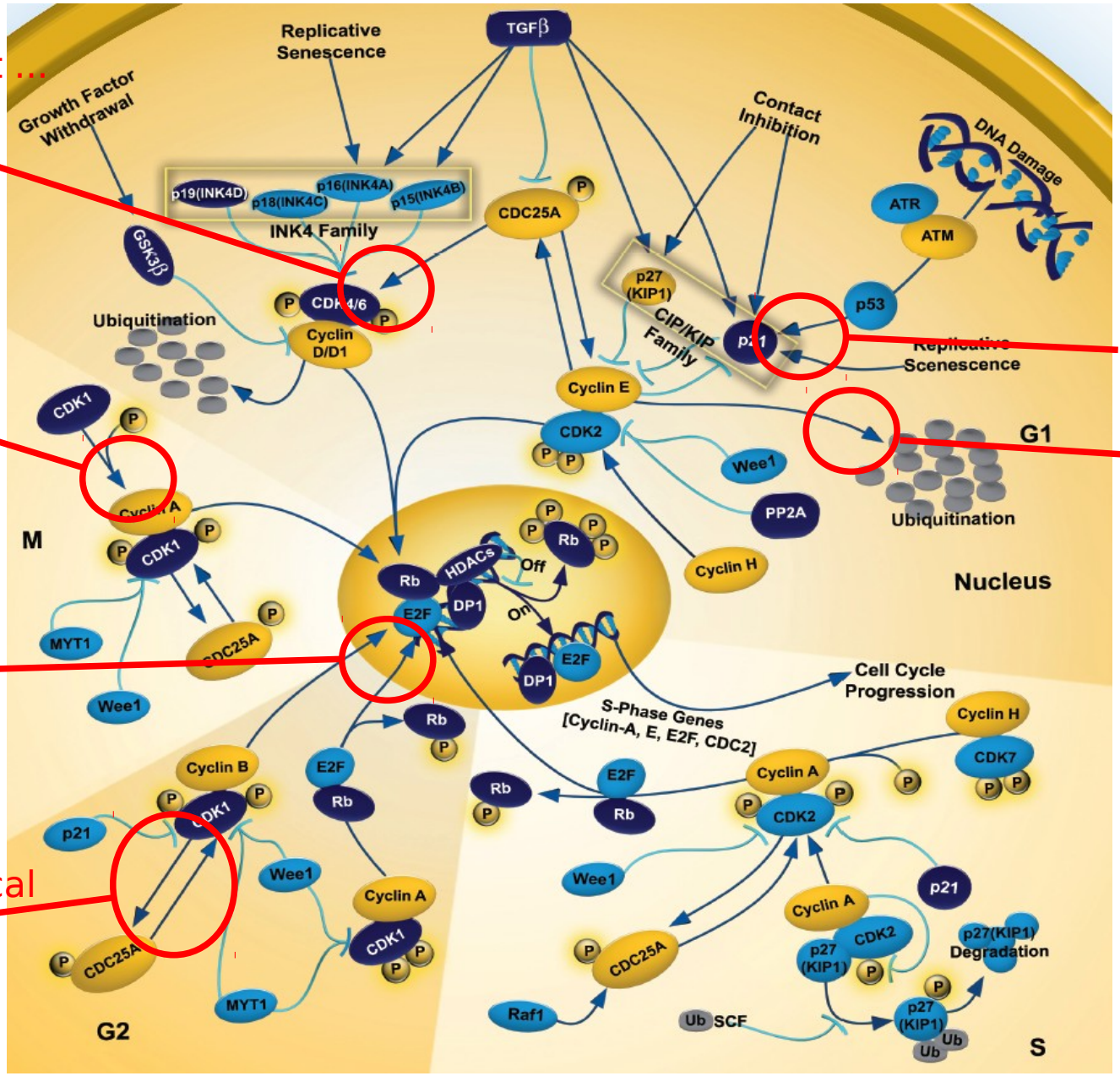
Associates into?

Translocates?

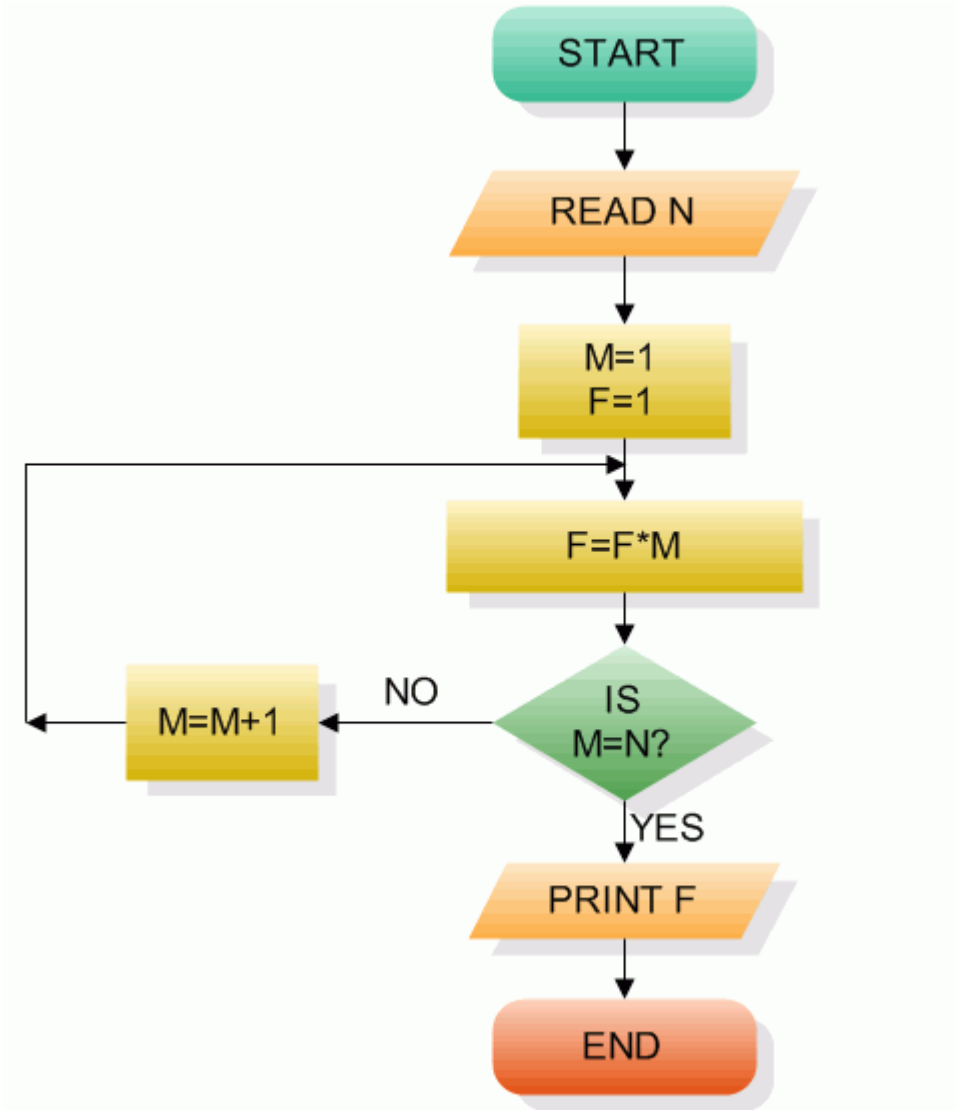
No idea. Reciprocal stimulation?

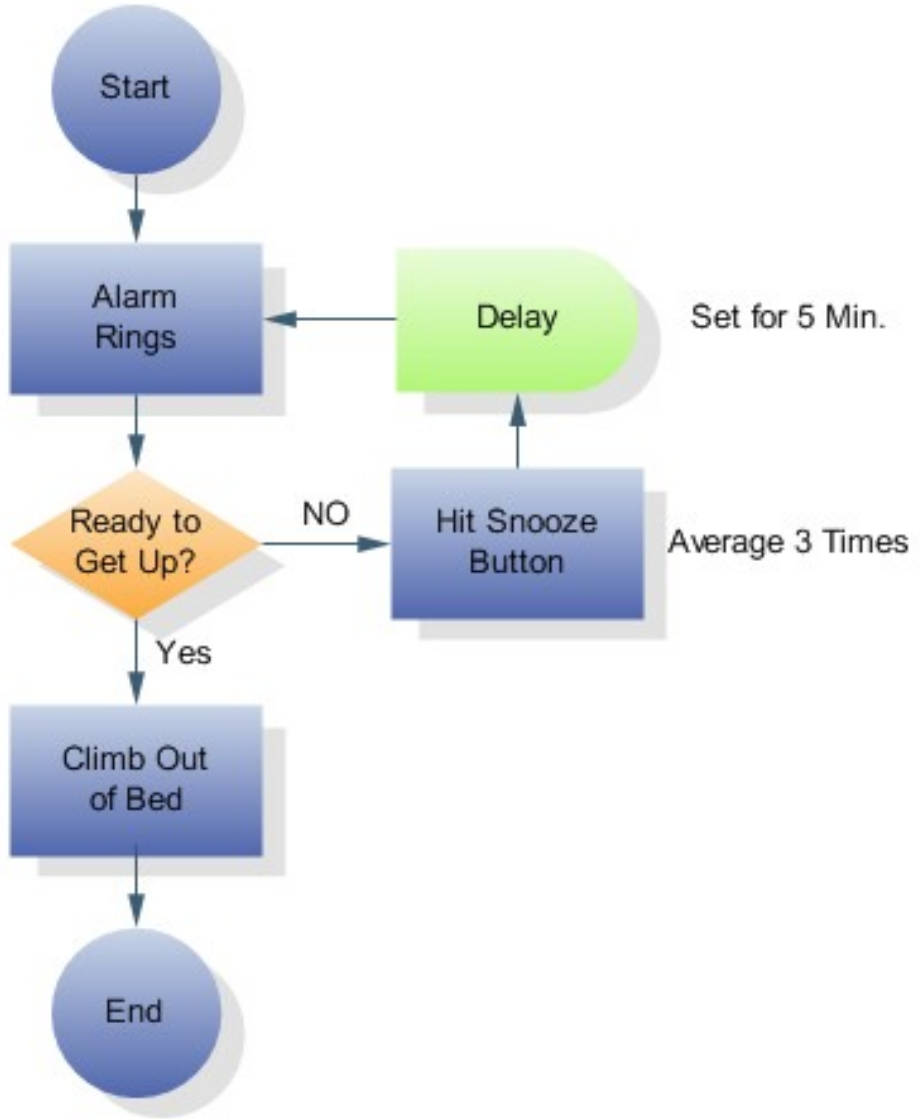
Stimulates gene transcription?

Is degraded?

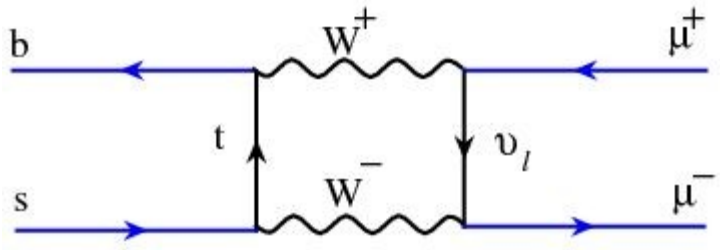


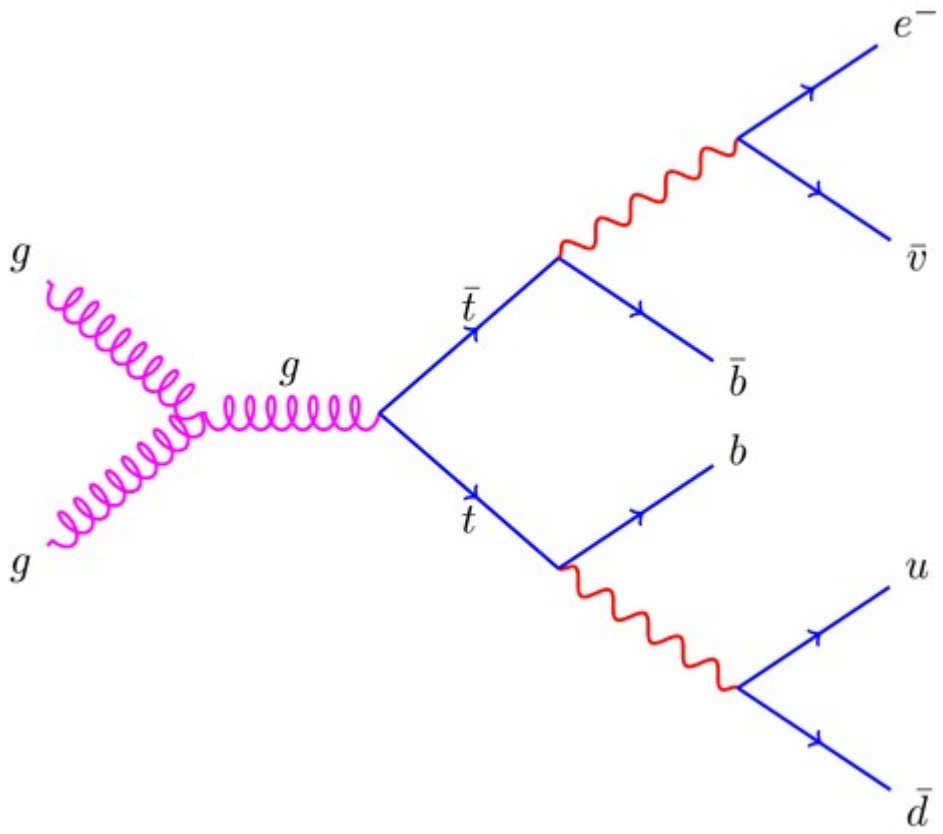
Every computer scientist understands those



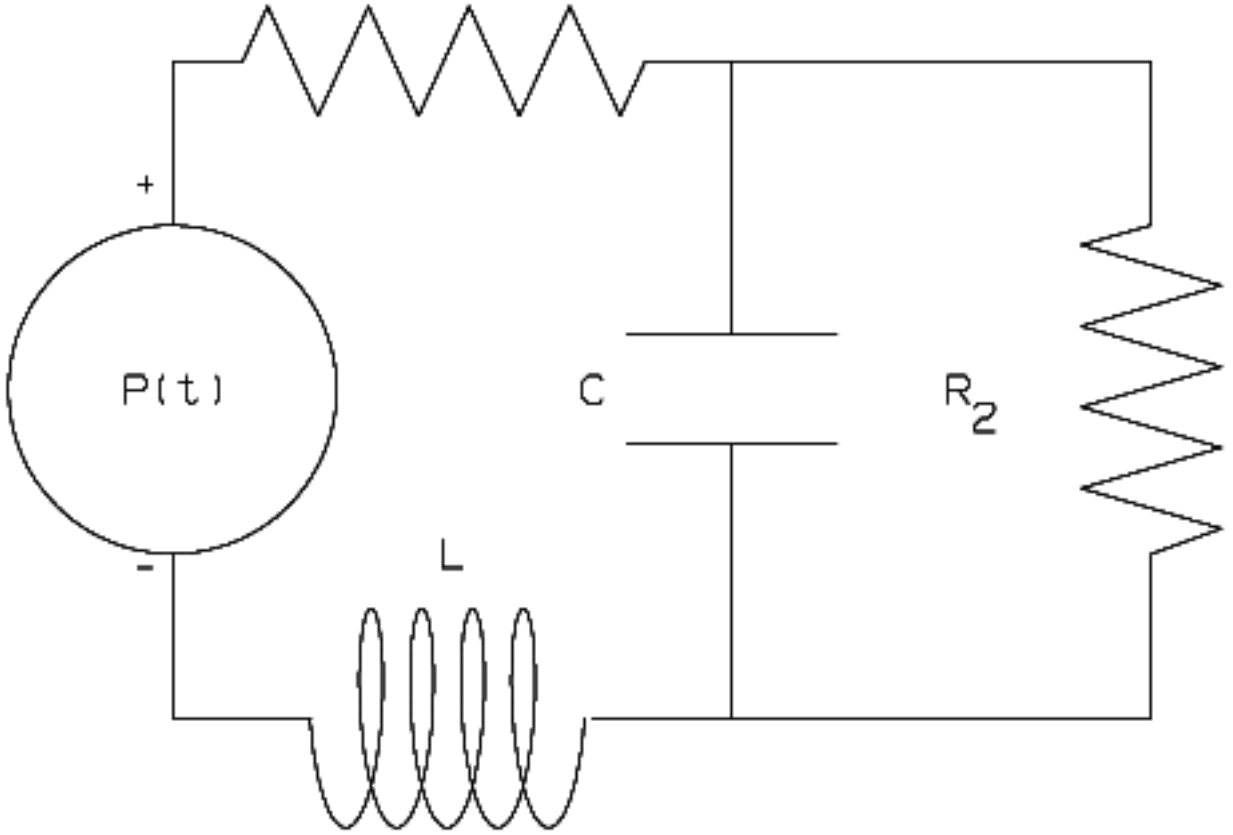


Every physicist understands those

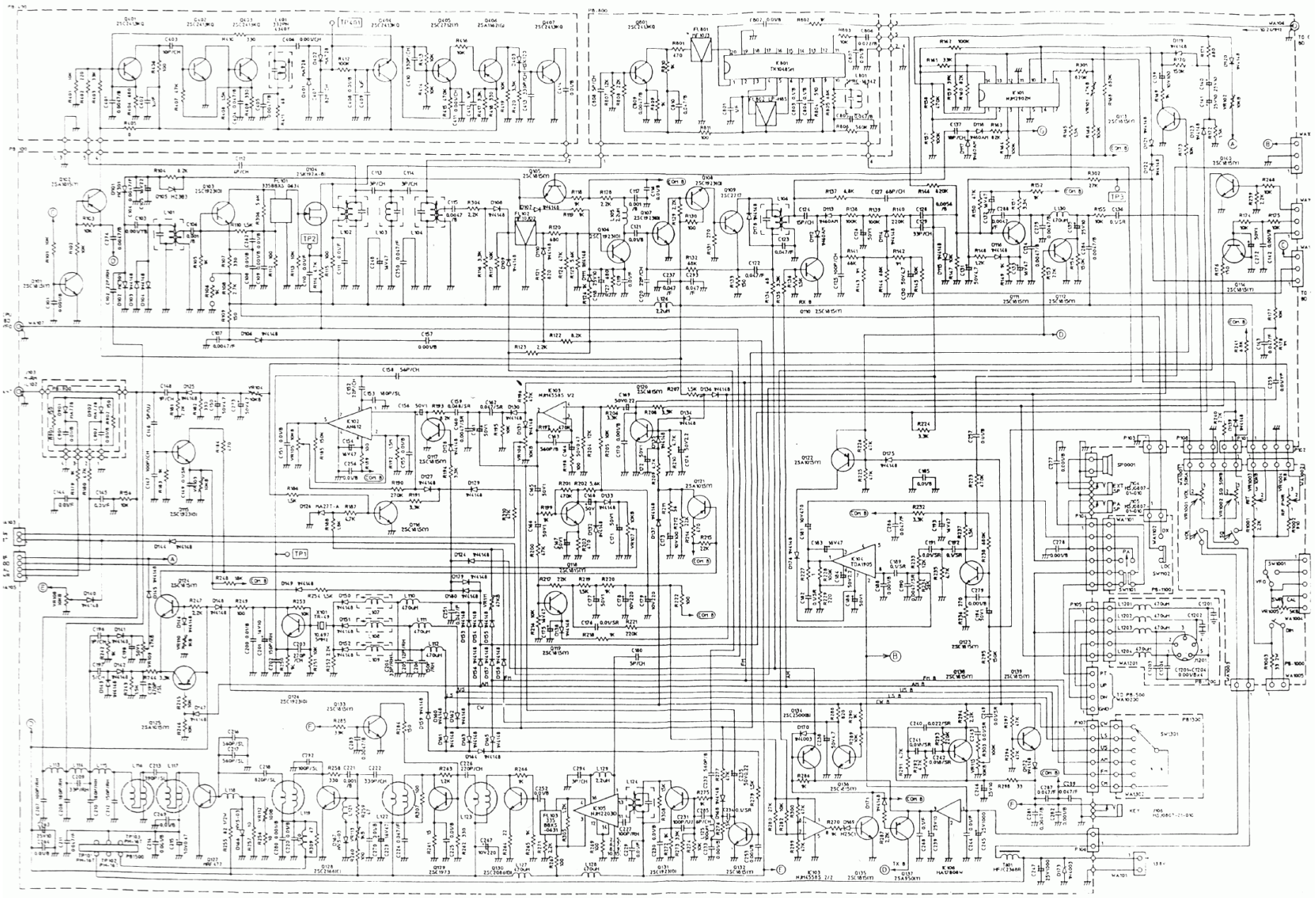




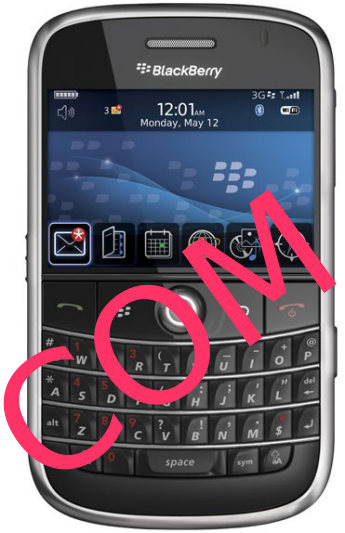
Every engineer understands that



Or that as a matter of fact



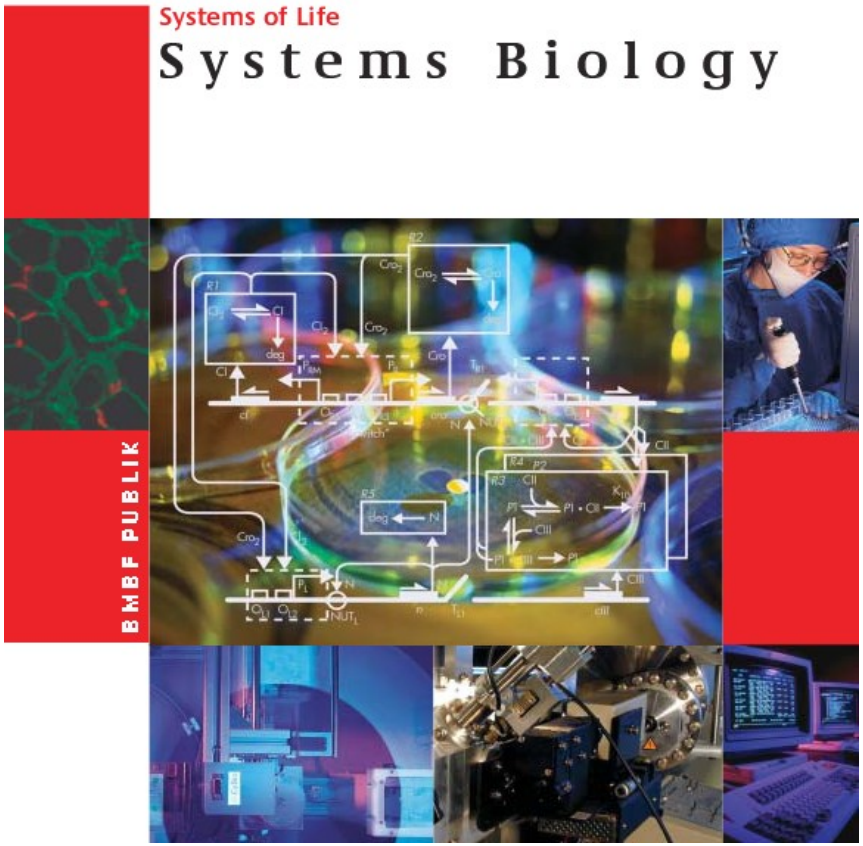
What did-those diagram bring?



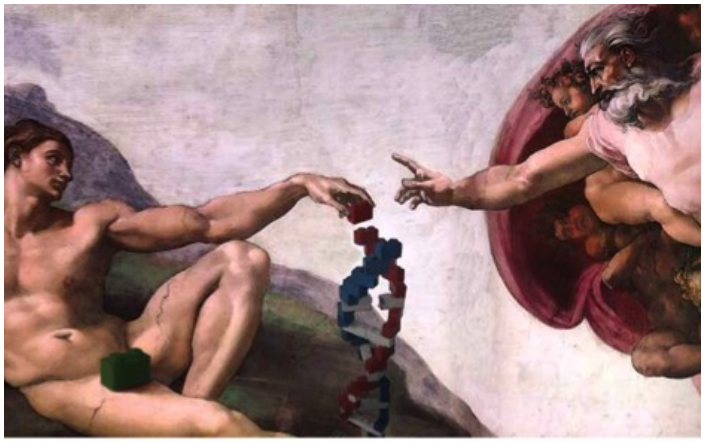
What do-we expect in modern (future) life science

Federal Ministry
of Education
and Research

Basic science



Technology



EXTREME GENETIC ENGINEERING

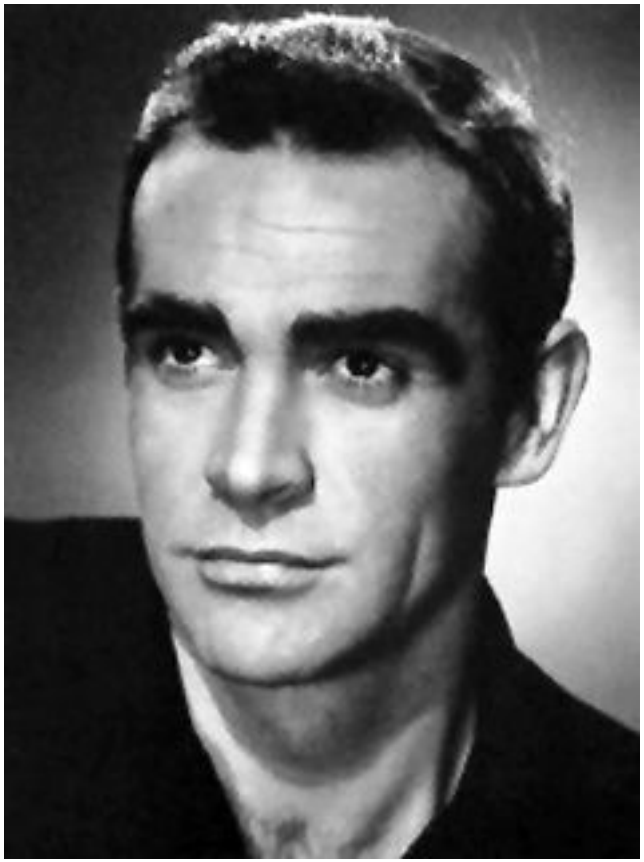
An Introduction to Synthetic Biology

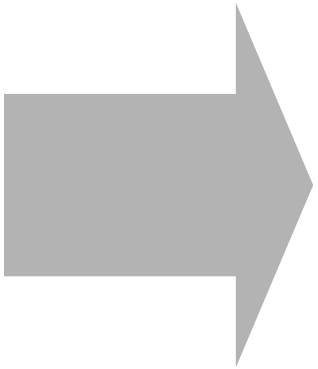
etc group

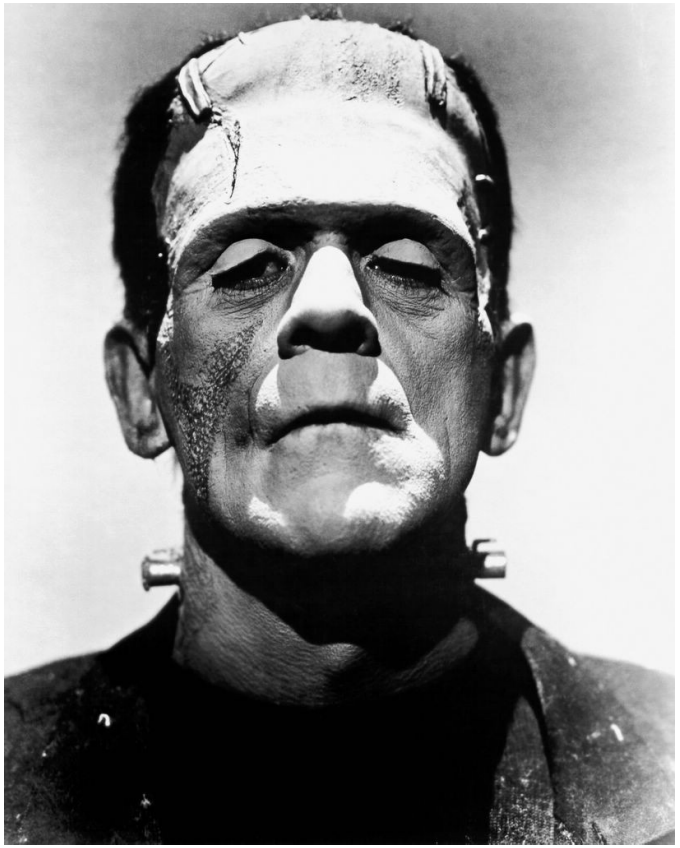
January 2007

What happens if one cannot read the blueprint

What happens if one cannot read the blueprint



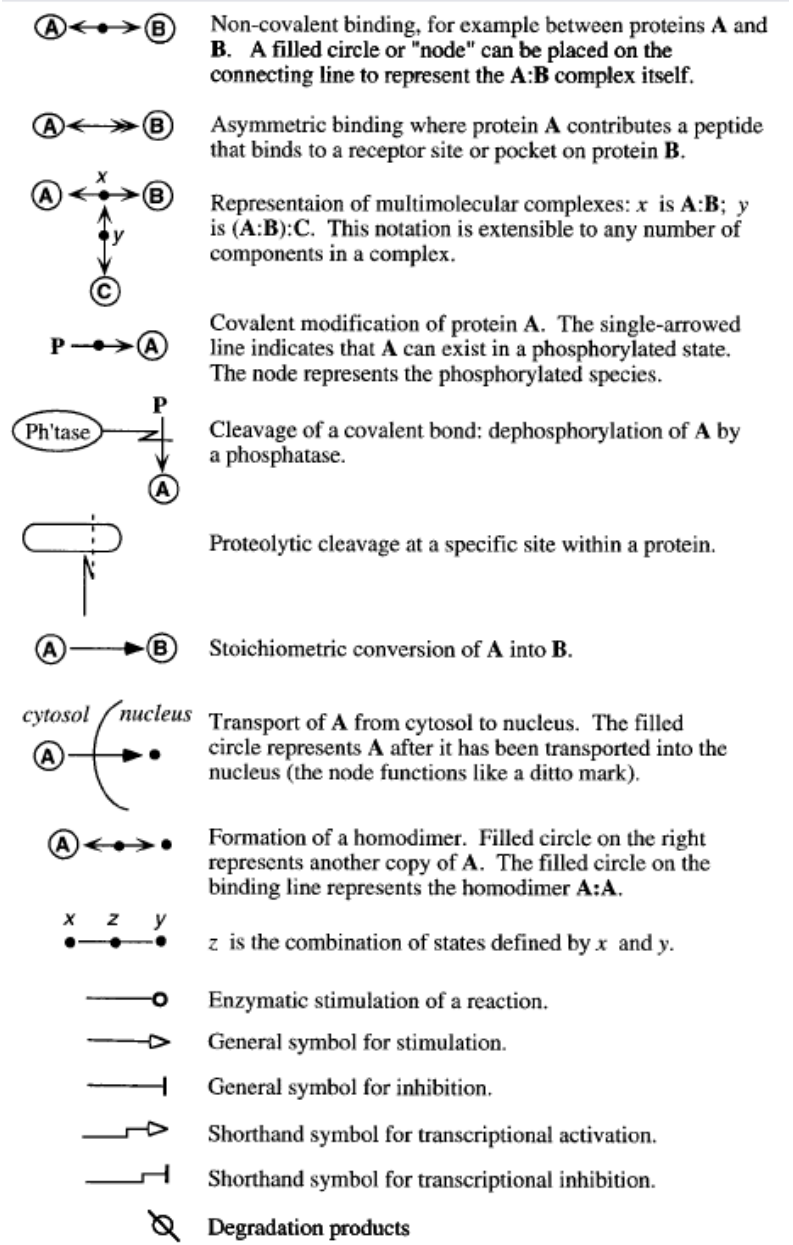


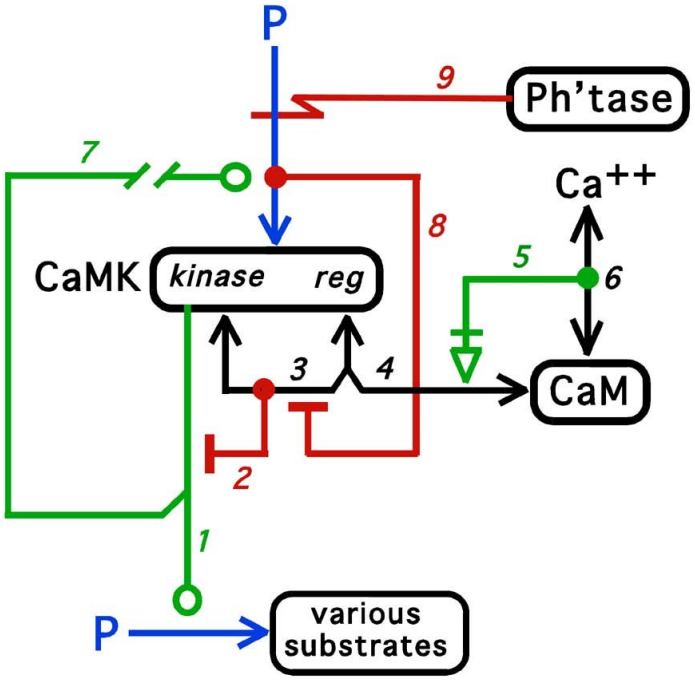


Why can-we understand electric diagrams?

- Standard symbols
  - Simple shapes, easily recognisable
  - Limited number of basic symbols (<70)
  - Similarity of shapes reflects similarity of functions
- Unambiguous interpretation of the circuits
- Endorsed by the community for practical reasons
  - End-users: manufacturers
  - Tool developers
  - Publishing industry
  - Teaching communities

Kohn's Molecular Interaction Maps





- Kurt W Kohn (1998) *Oncogene*, 16: 1065-1075
- Kurt W. Kohn (1999) *Mol Biol Cell*, 10(8):2703-2734

Cell Cycle in MIM

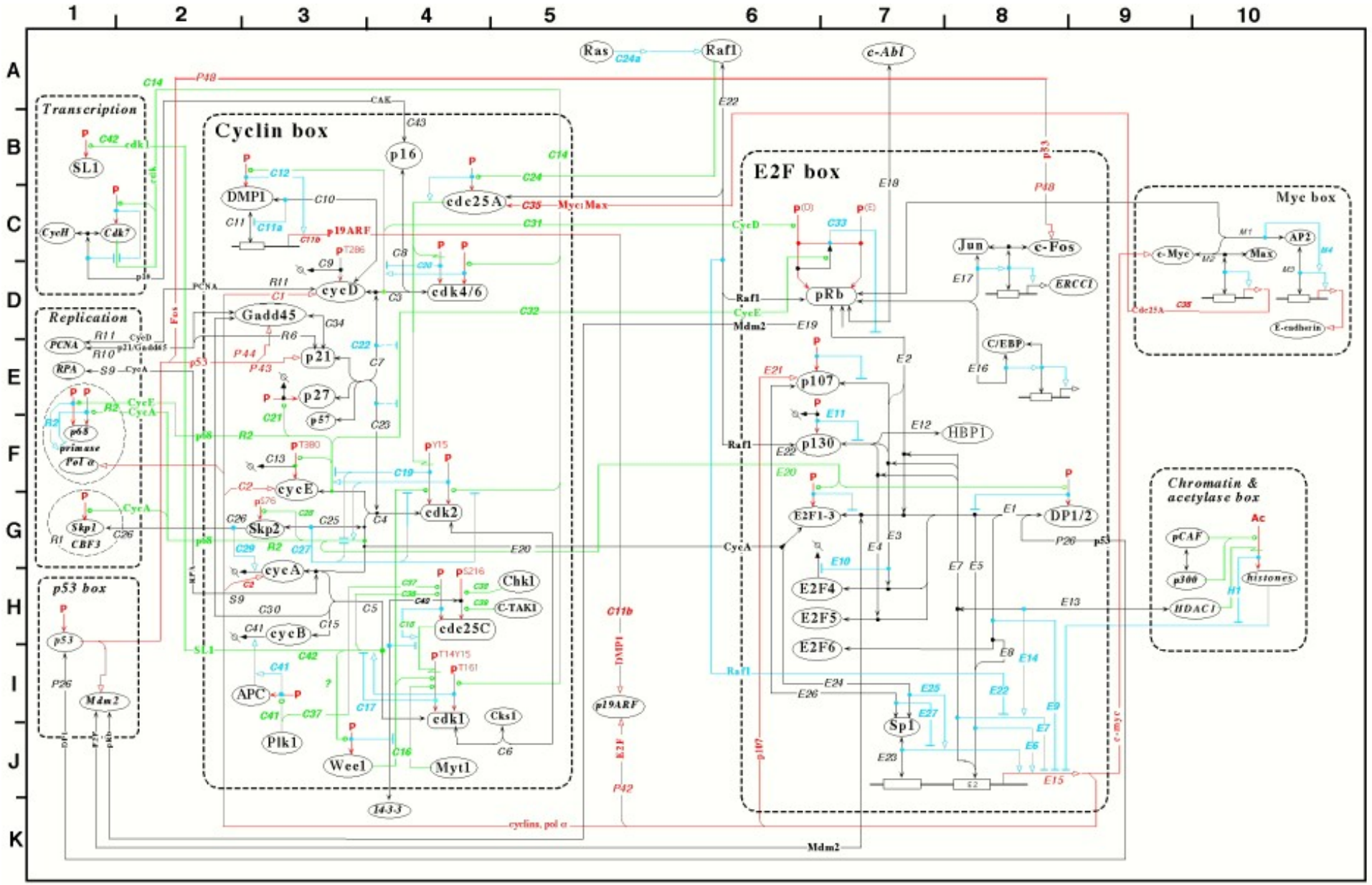
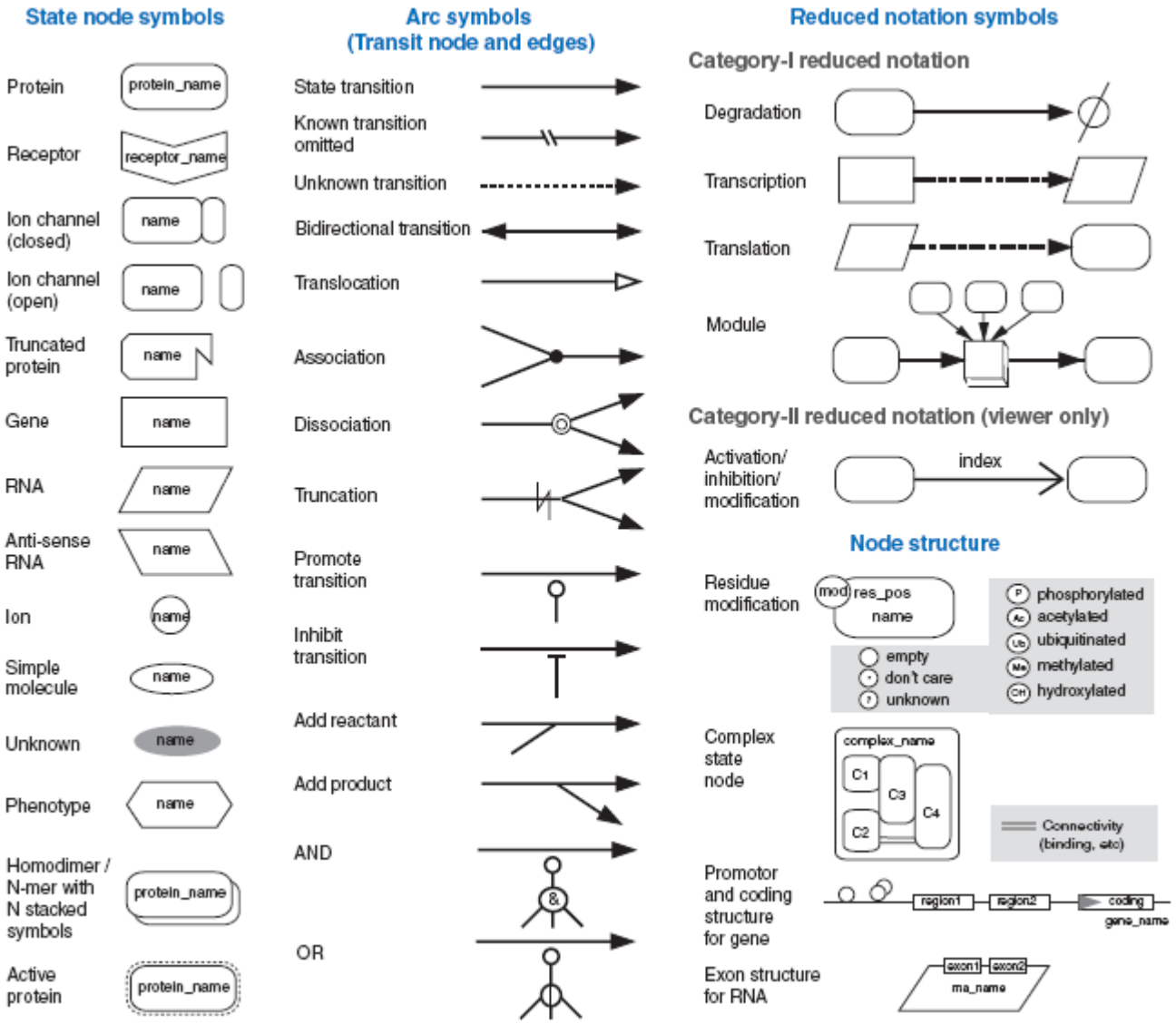


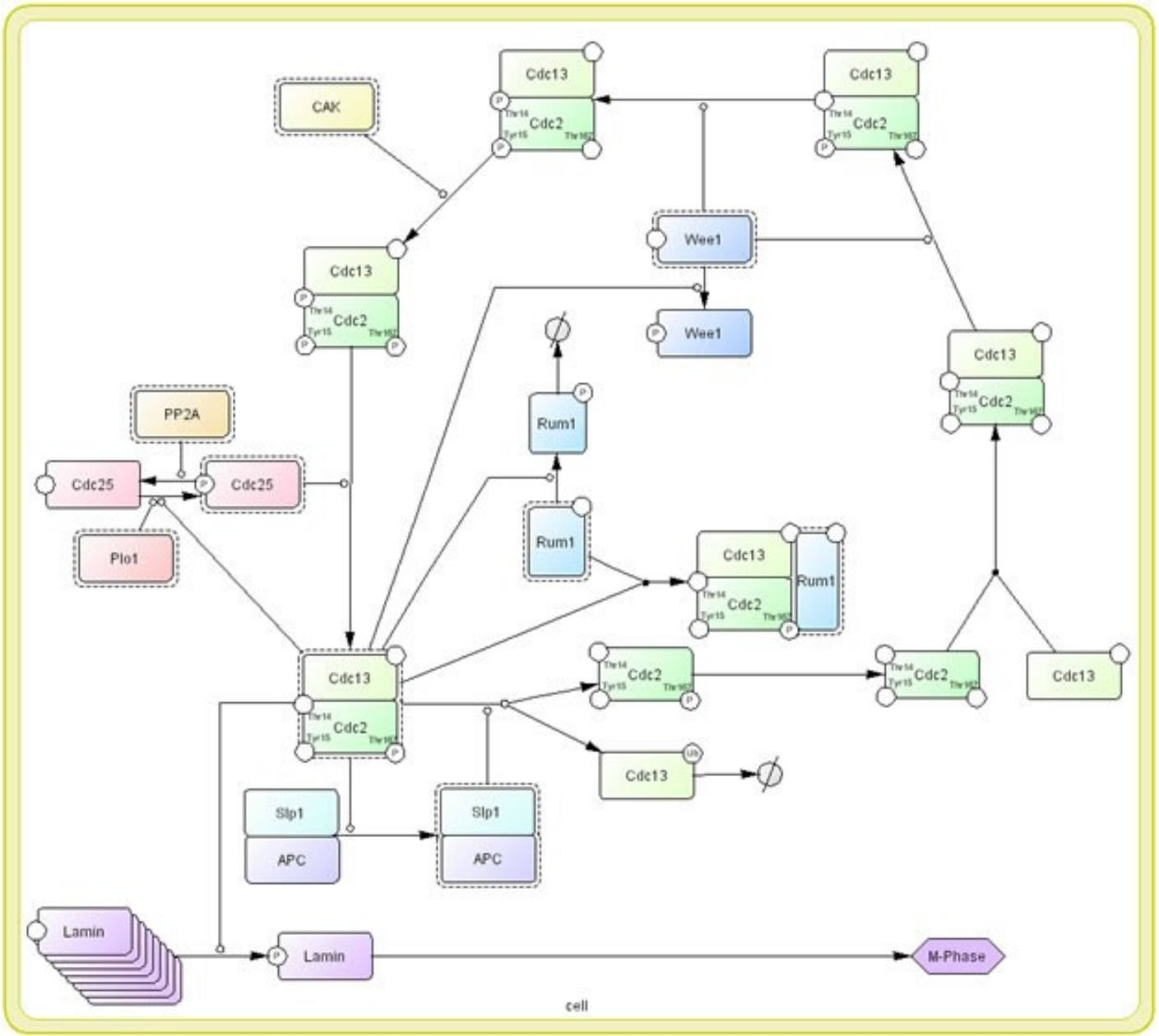
Figure 6A: The Cyclin - E2F cell cycle control system (version 3a - June 8, 1999)

Kitano's Notation



- Kitano (2003) *Biosilico*, 1: 169-170
- Kitano et al (2005) *Nat Biotech*, 23: 961-966

Cell Cycle in Kitano's Process Diagram



Why those pioneer efforts did not make it

- Somehow fuzzy semantics
  - No structured data model or ontology behind the notation
  - Overlapping concepts rather than sub-classing
  - Gaps in the coverage of biochemistry or modelling
  - Ambiguous interpretation of the graph
- Little software support (except CellDesigner for Kitano's Process Diagrams)
- No community involvement
  - No systematic bug tracking and consistency checking
  - No comprehensive coverage (focussed on some use-cases)
  - No endorsement by the tool developers or by the end-users

Enters
The Systems Biology Graphical Notation

http://www.sbgn.org/

What is SBGN?

- An unambiguous way of graphically describing and interpreting biochemical and cellular events
- Limited amount of symbols
  Re-use existing symbols

  ☞ Smooth learning curve
- Can represent logical or mechanistic models, biochemical pathways, at different levels of granularity
- Detailed technical specification, precise data-models and growing software support
- Initiated by Hiroaki Kitano. Developed over four years by a diverse community

The Systems Biology Graphical Notation

Nicolas Le Novère[1], Michael Hucka[2], Huaiyu Mi[3], Stuart Moodie[4], Falk Schreiber[5,6], Anatoly Sorokin[7], Emek Demir[8], Katja Wegner[9], Mirit I Aladjem[10], Sarala M Wimalaratne[11], Frank T Bergman[12], Ralph Gauges[13], Peter Ghazal[4,14], Hideya Kawaji[15], Lu Li[1], Yukiko Matsuoka[16], Alice Villéger[17,18], Sarah E Boyd[19], Laurence Calzone[20], Melanie Courtot[21], Ugur Dogrusoz[22], Tom C Freeman[14,23], Akira Funahashi[24], Samik Ghosh[16], Akiya Jouraku[24], Sohyoung Kim[10], Fedor Kolpakov[25,26], Augustin Luna[10], Sven Sahle[13], Esther Schmidt[1], Steven Watterson[4,22], Guanming Wu[27], Igor Goryanin[4], Douglas B Kell[18,28], Chris Sander[8], Herbert Sauro[12], Jacky L Snoep[29], Kurt Kohn[10] & Hiroaki Kitano[16,30,31]

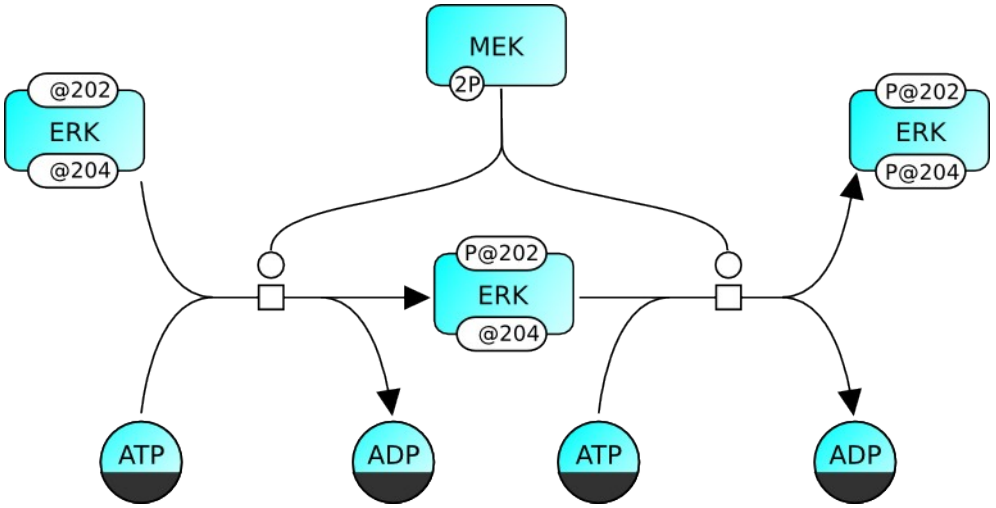
[1]EMBL European Bioinformatics Institute, Hinxton, UK. [2]Engineering and Applied Science, California Institute of Technology, Pasadena, California, USA. [3]SRI International, Menlo Park, California, USA. [4]Centre for Systems Biology at Edinburgh, University of Edinburgh, Edinburgh, UK. [5]Leibniz Institute of Plant Genetics and Crop Plant Research, Gatersleben, Germany. [6]Institute of Computer Science, University of Halle, Halle, Germany. [7]School of Informatics, University of Edinburgh, Edinburgh, UK. [8]Memorial Sloan Kettering Cancer Center - Computational Biology Center, New York, NY, USA. [9]Science and Technology Research Institute, University of Hertfordshire, Hatfield, UK. [10]National Cancer Institute, Bethesda, Maryland, USA. [11]Auckland Bioengineering Institute, University of Auckland, Auckland, New Zealand. [12]Department of Bioengineering, University of Washington, Seattle, Washington, USA. [13]BIOQUANT, University of Heidelberg, Heidelberg, Germany. [14]Division of Pathway Medicine, University of Edinburgh Medical School, Edinburgh, UK. [15]Riken OMICS Science Center, Yokohama City, Kanagawa, Japan. [16]The Systems Biology Institute, Tokyo, Japan. [17]School of Computer Science, University of Manchester, Manchester, UK. [18]Manchester Interdisciplinary Biocentre, Manchester, UK. [19]Clayton School of Information Technology, Faculty of Information Technology, Monash University, Melbourne, Victoria, Australia. [20]U900 INSERM, Paris Mines Tech, Institut Curie, Paris, France. [21]Terry Fox Laboratory, British Columbia Cancer Research Center, Vancouver, British Columbia, Canada. [22]Bilkent Center for Bioinformatics, Bilkent University, Ankara, Turkey. [23]The Roslin Institute, University of Edinburgh, Midlothian, UK. [24]Department of Biosciences and Informatics, Keio University, Hiyoshi, Kouhoku-ku, Yokohama, Japan. [25]Institute of Systems Biology, Novosibirsk, Russia. [26]Design Technological Institute of Digital Techniques SB RAS, Novosibirsk, Russia. [27]Ontario Institute for Cancer Research, Toronto, Ontario, Canada. [28]School of Chemistry, University of Manchester, Manchester, UK. [29]Department of Biochemistry, Stellenbosch University, Matieland, South Africa. [30]Sony Computer Science Laboratories, Tokyo, Japan. [31]Okinawa Institute of Science and Technology, Okinawa, Japan. Correspondence should be addressed to N.L.N. (lenov@ebi.ac.uk).

NATURE BIOTECHNOLOGY VOLUME 27 NUMBER 8 AUGUST 2009

39 authors, 31 affiliations

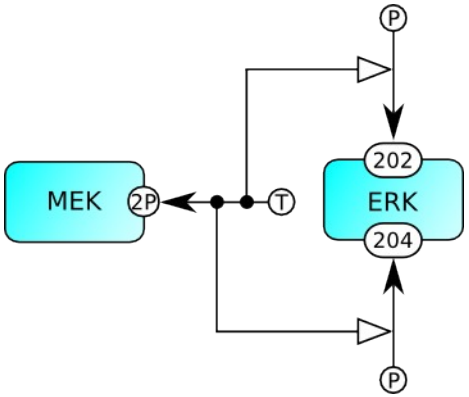
Graph trinity: three languages in one notation

Process Descriptions



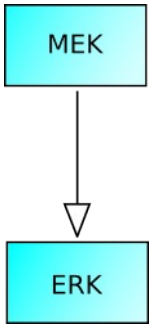
- Unambiguous
- Mechanistic
- Sequential
- Combinatorial explosion

Entity Relationships



- Unambiguous
- Mechanistic
- Non-sequential
- Independence of relationships

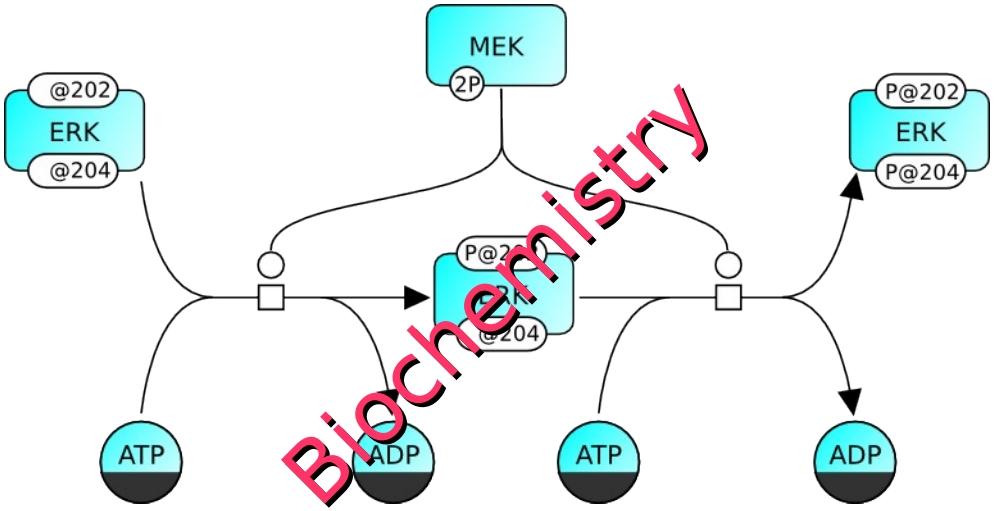
Activity Flows



- Ambiguous
- Conceptual
- Sequential

Graph trinity: three languages in one notation

Process Descriptions



- Unambiguous
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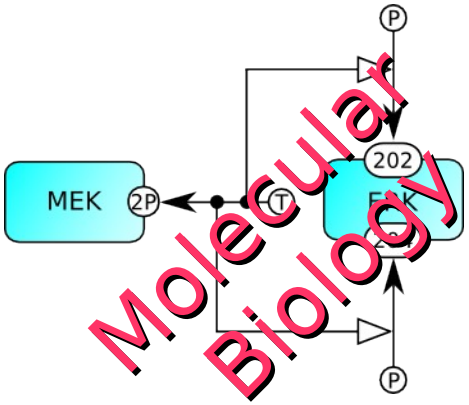
Entity Relationships



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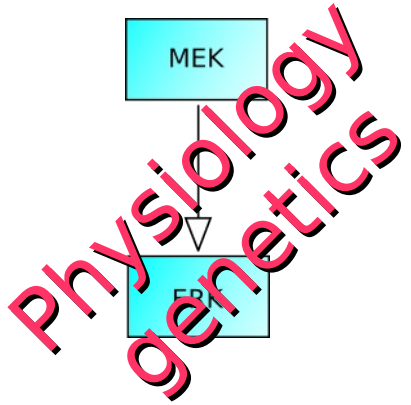
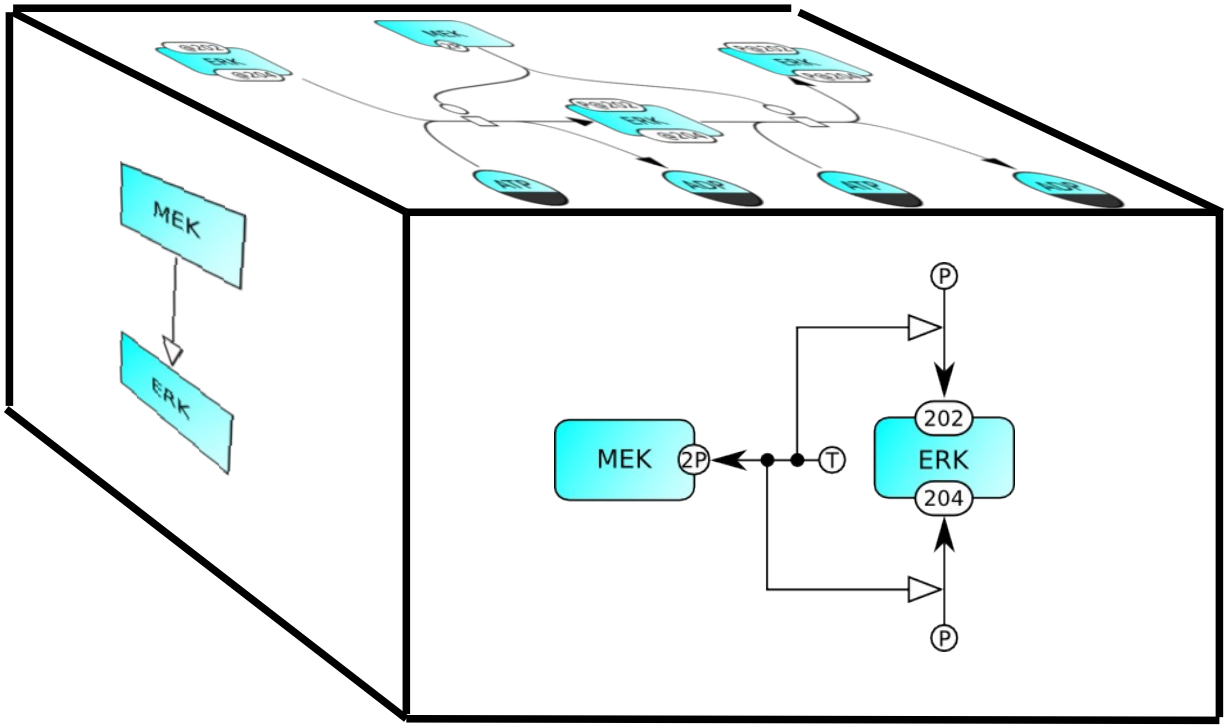
Activity Flows

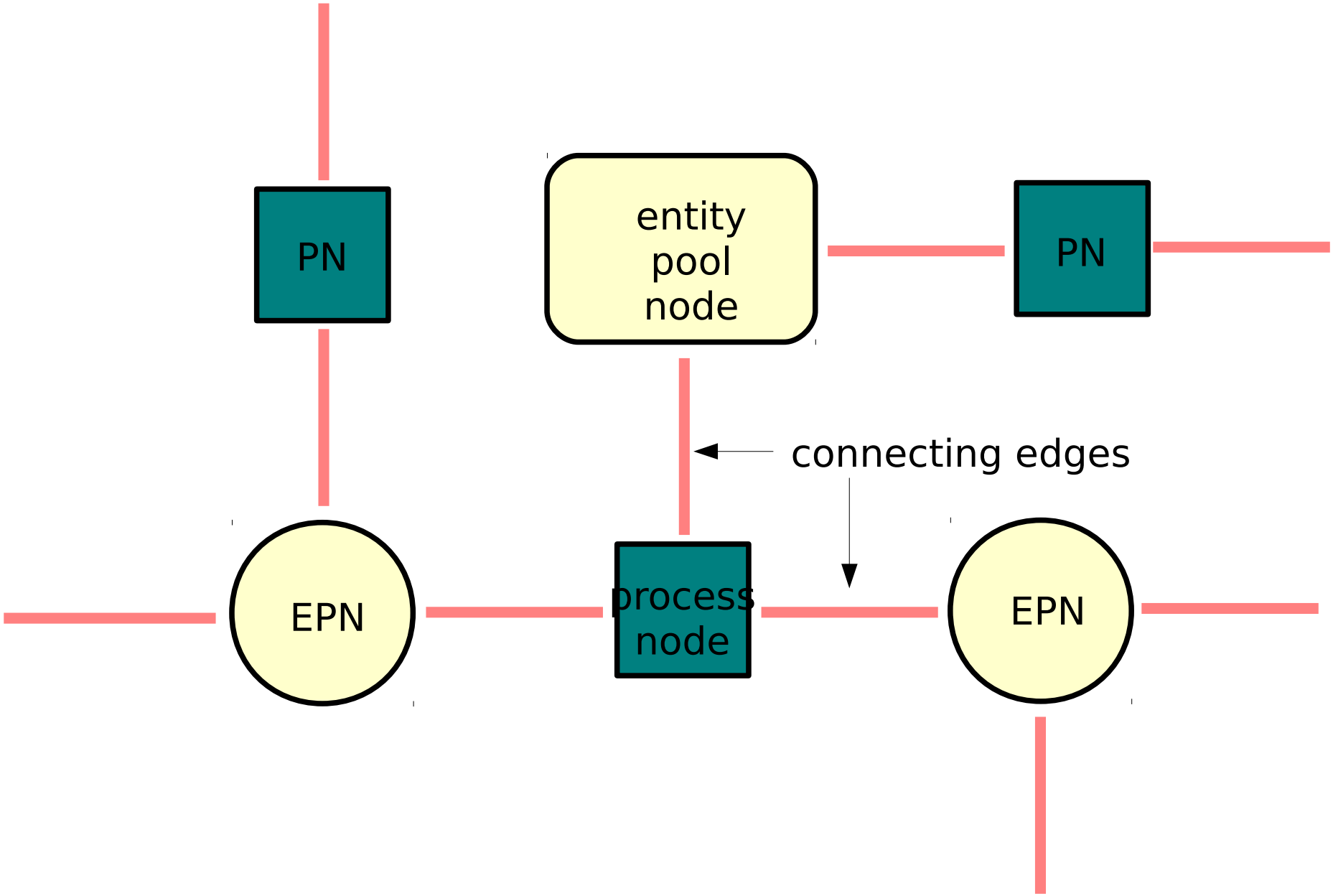


- Ambiguous
- Conceptual
- Sequential

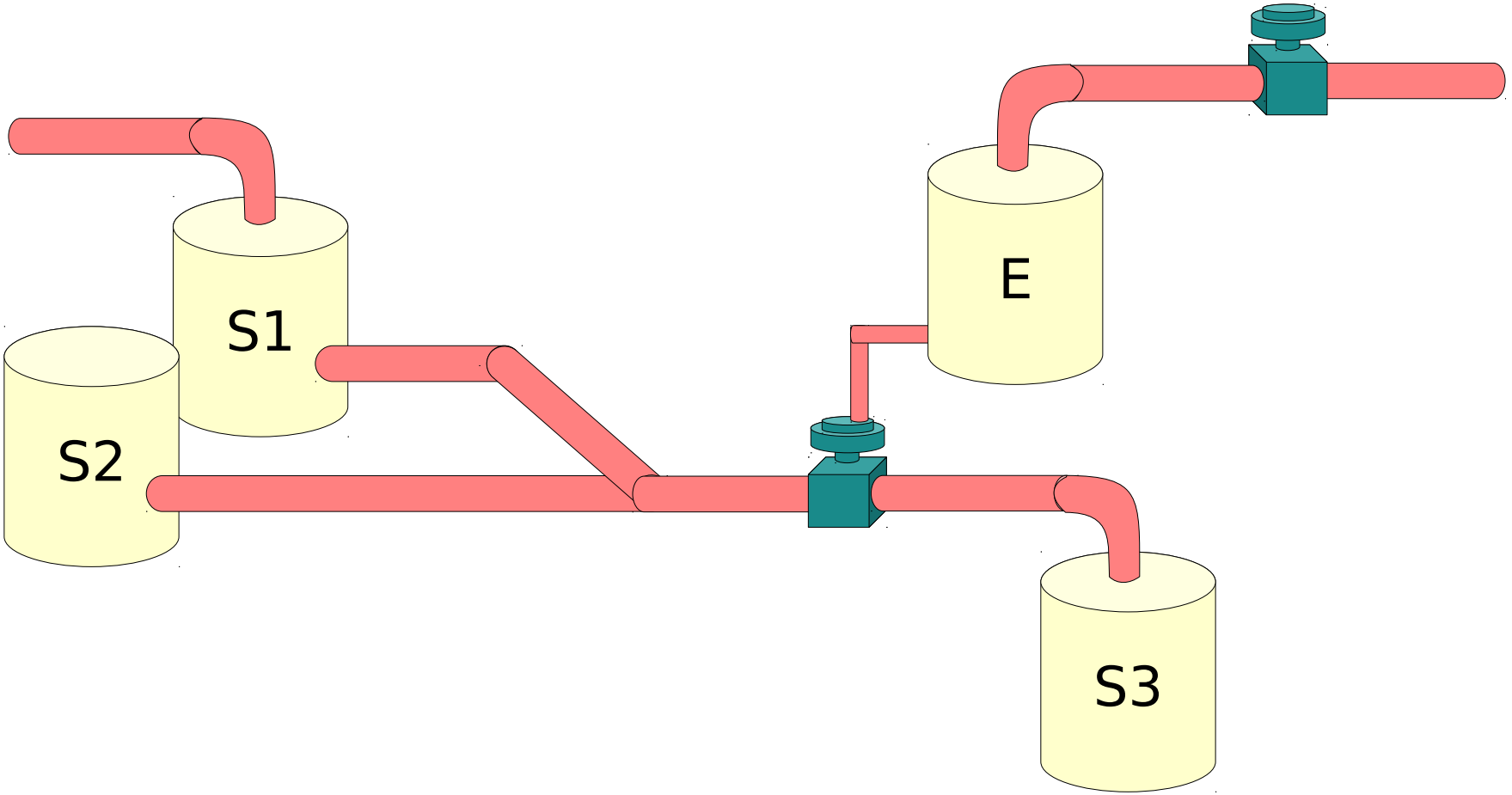
Three orthogonal projections of biology



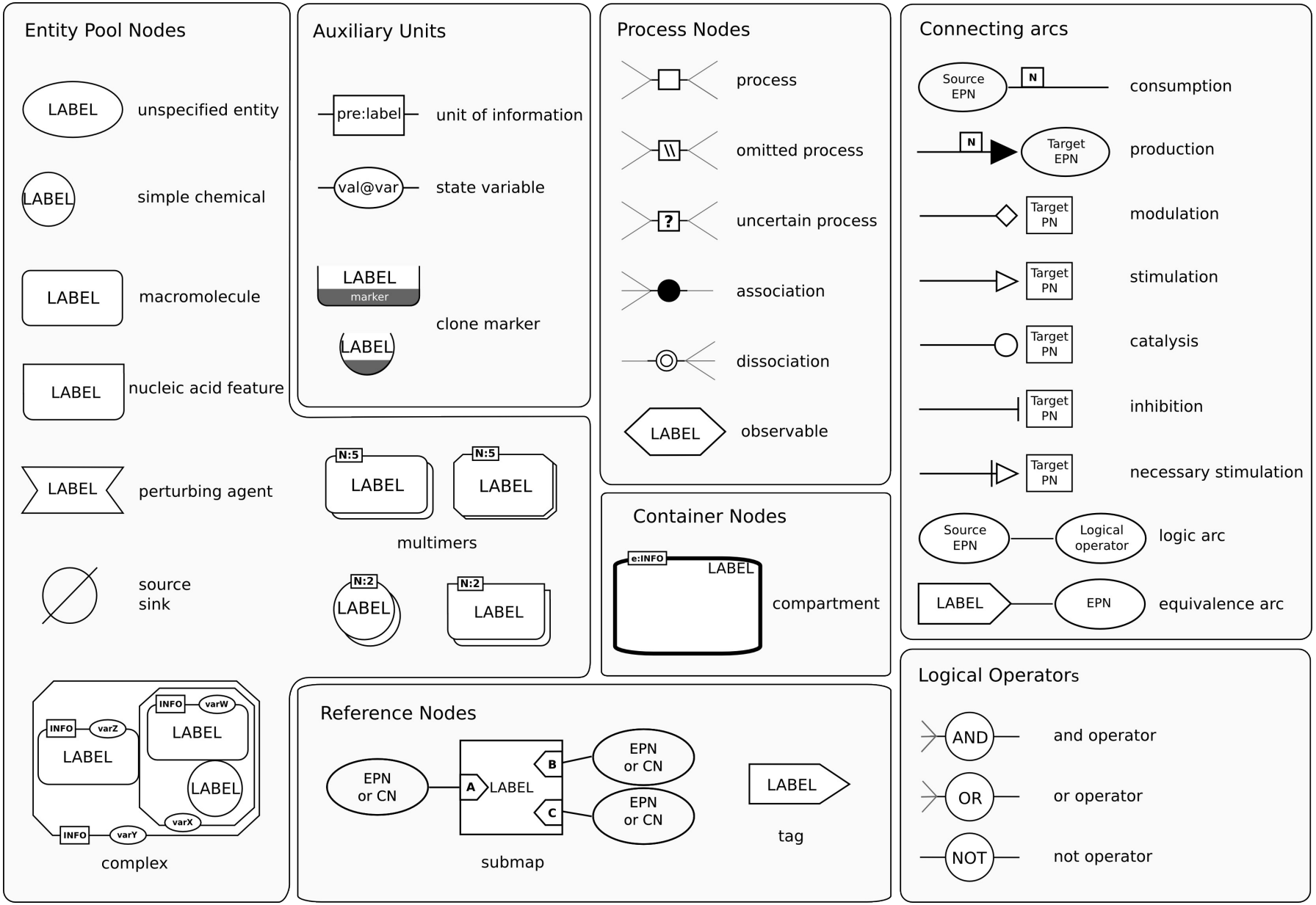
Process Descriptions are bipartite graphs



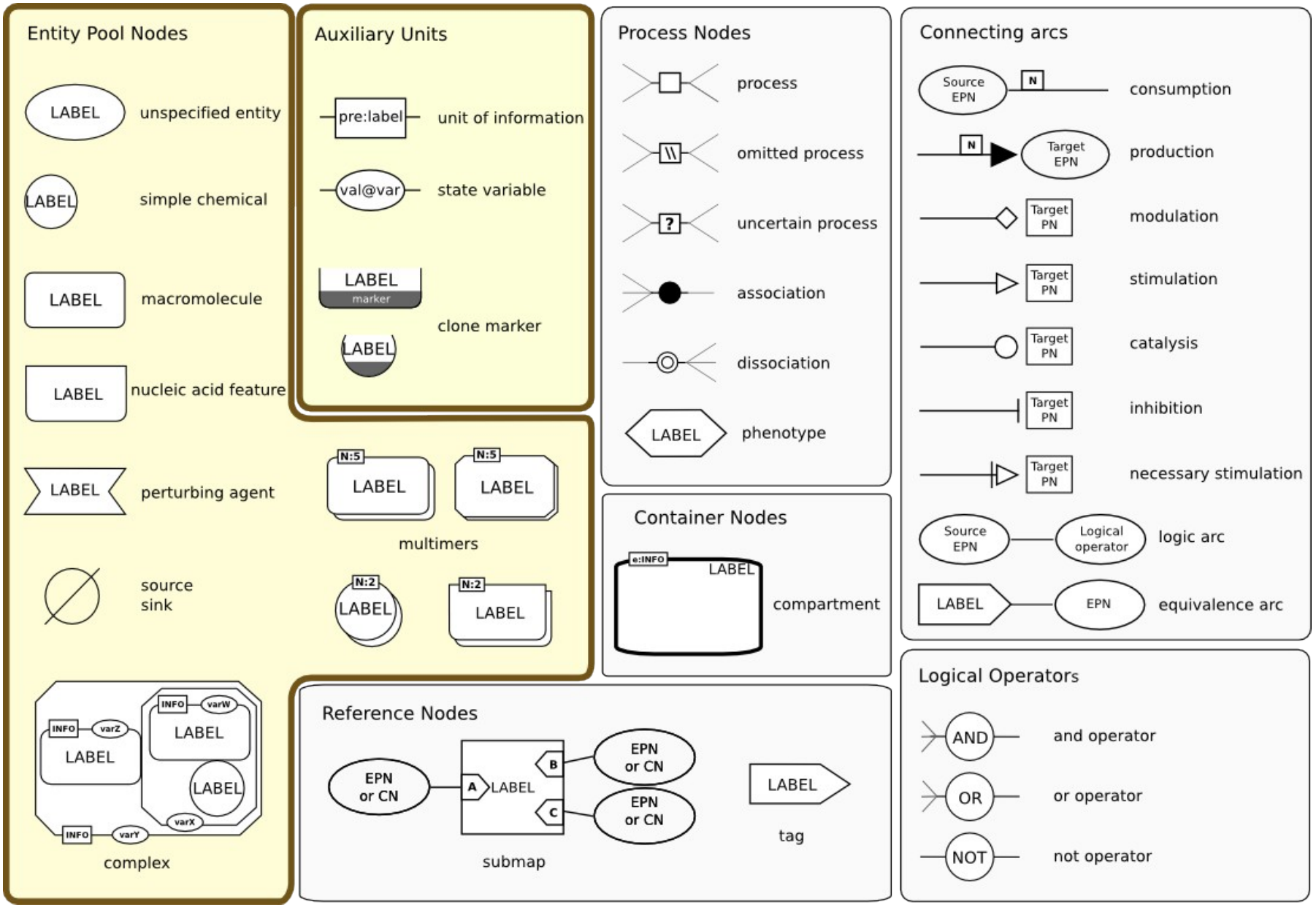
Process Descriptions can be viewed as pipelines



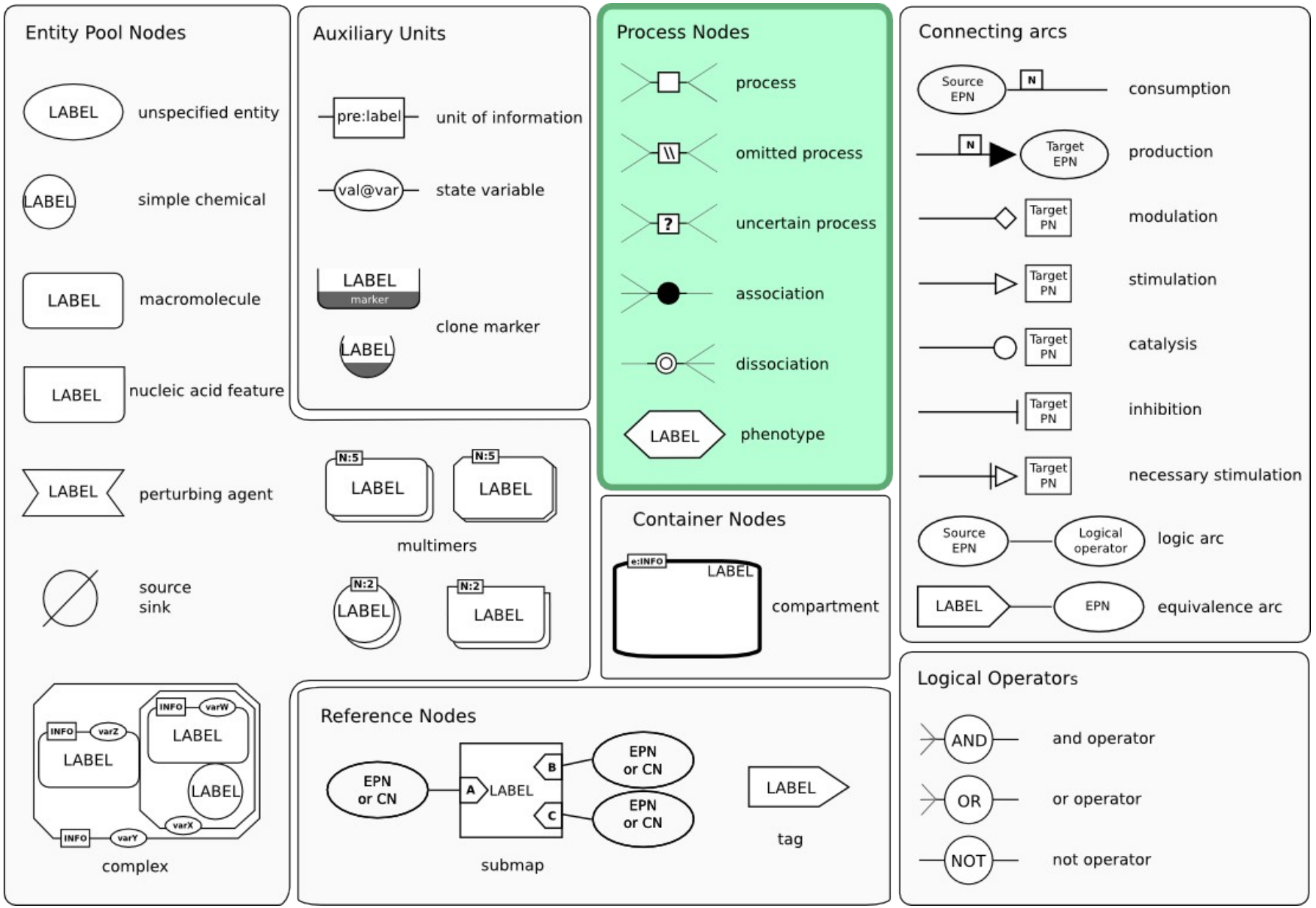
SBGN Process Description L1 V1.1 reference card



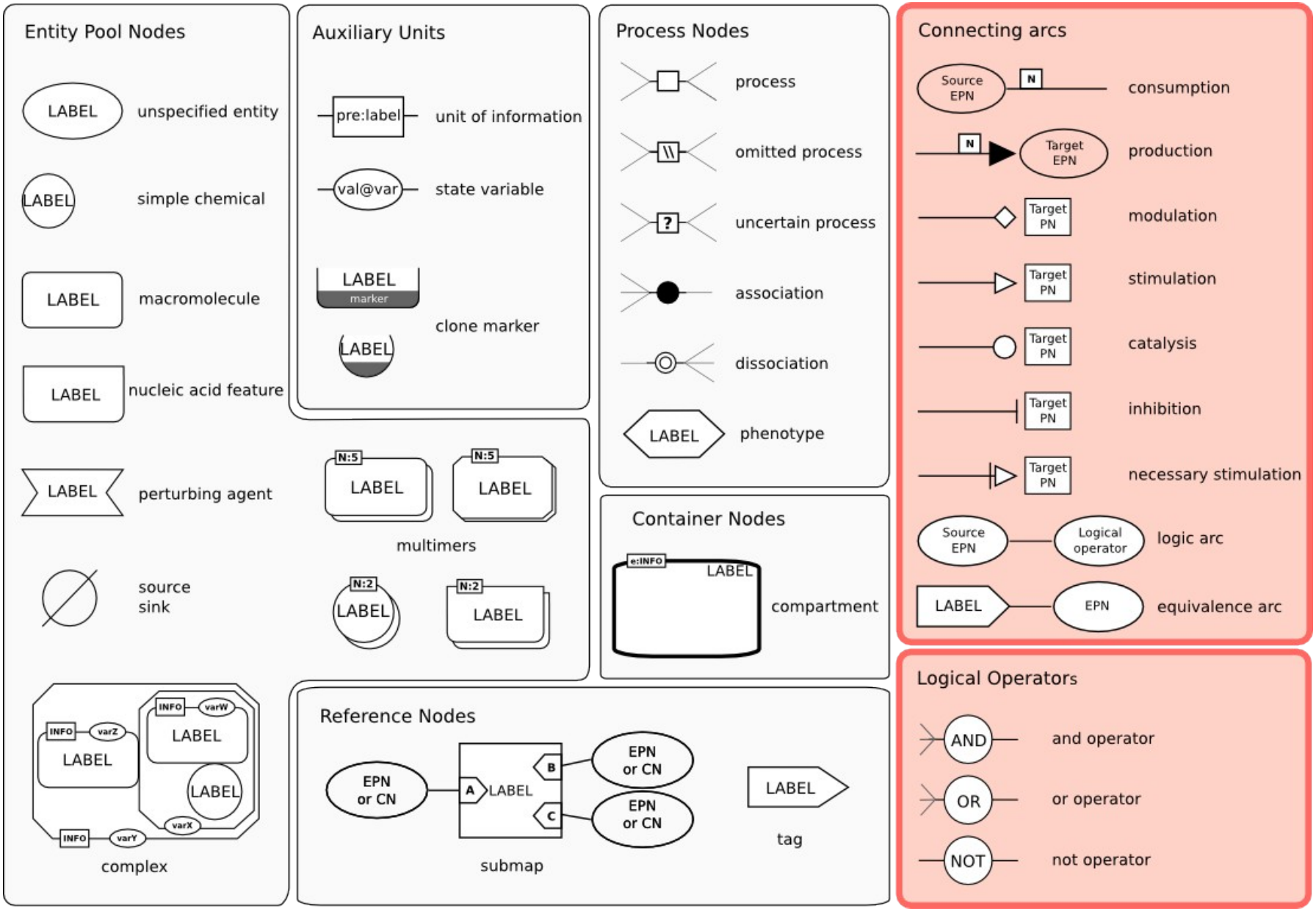
Entity Pool Nodes



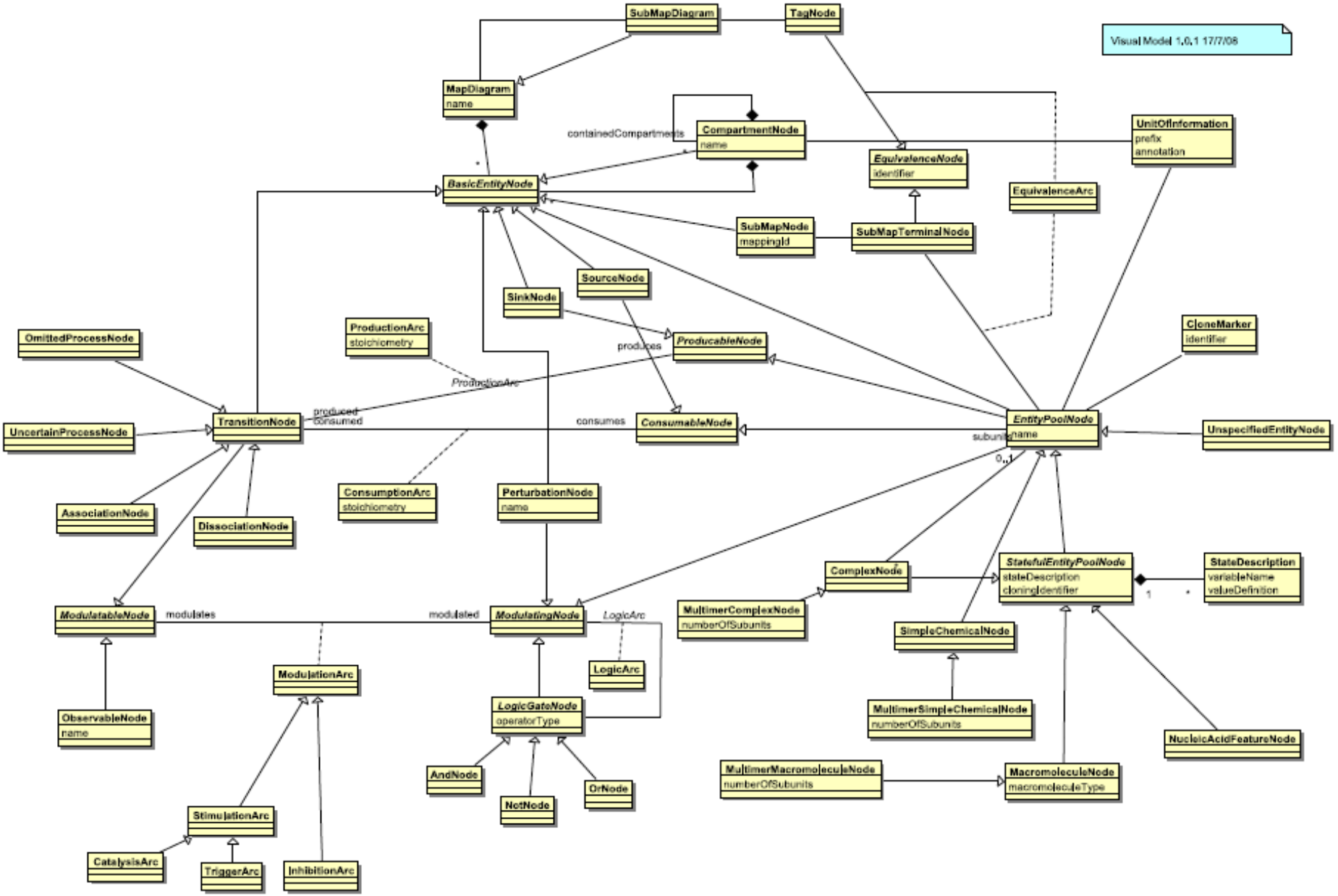
Process Nodes



Edges


Entity Pool Nodes
LABEL
unspecified entity
LABEL
simple chemical
LABEL
macromolecule
LABEL
nucleic acid feature
LABEL
perturbing agent
source
sink
INFO
varZ
LABEL
INFO
varW
LABEL
LABEL
INFO
varY
varX
complex
Auxiliary Units
pre:label
unit of information
val@var
state variable
LABEL
marker
LABEL
clone marker
N:5
LABEL
N:5
LABEL
multimers
N:2
LABEL
N:2
LABEL
Process Nodes
process
omitted process
?
uncertain process
association
dissociation
LABEL
phenotype
Container Nodes
e:INFO
LABEL
compartment
Reference Nodes
EPN
or CN
A
LABEL
B
C
EPN
or CN
EPN
or CN
submap
LABEL
tag
Connecting arcs
Source
EPN
N
consumption
N
Target
EPN
production
Target
PN
modulation
Target
PN
stimulation
Target
PN
catalysis
Target
PN
inhibition
Target
PN
necessary stimulation
Source
EPN
Logical
operator
logic arc
LABEL
EPN
equivalence arc
Logical Operators
AND
and operator
OR
or operator
NOT
not operator

Process Descriptions data model

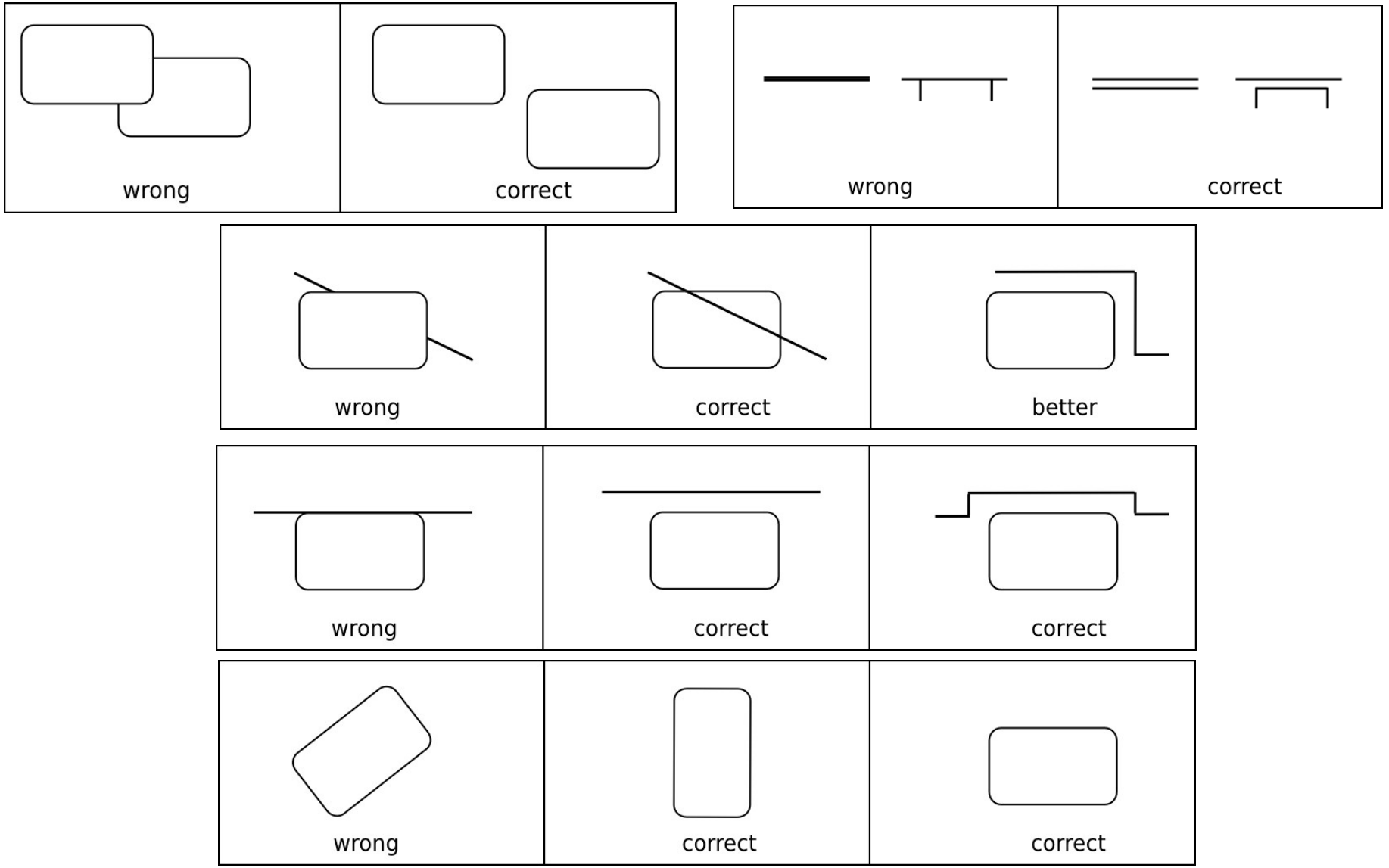


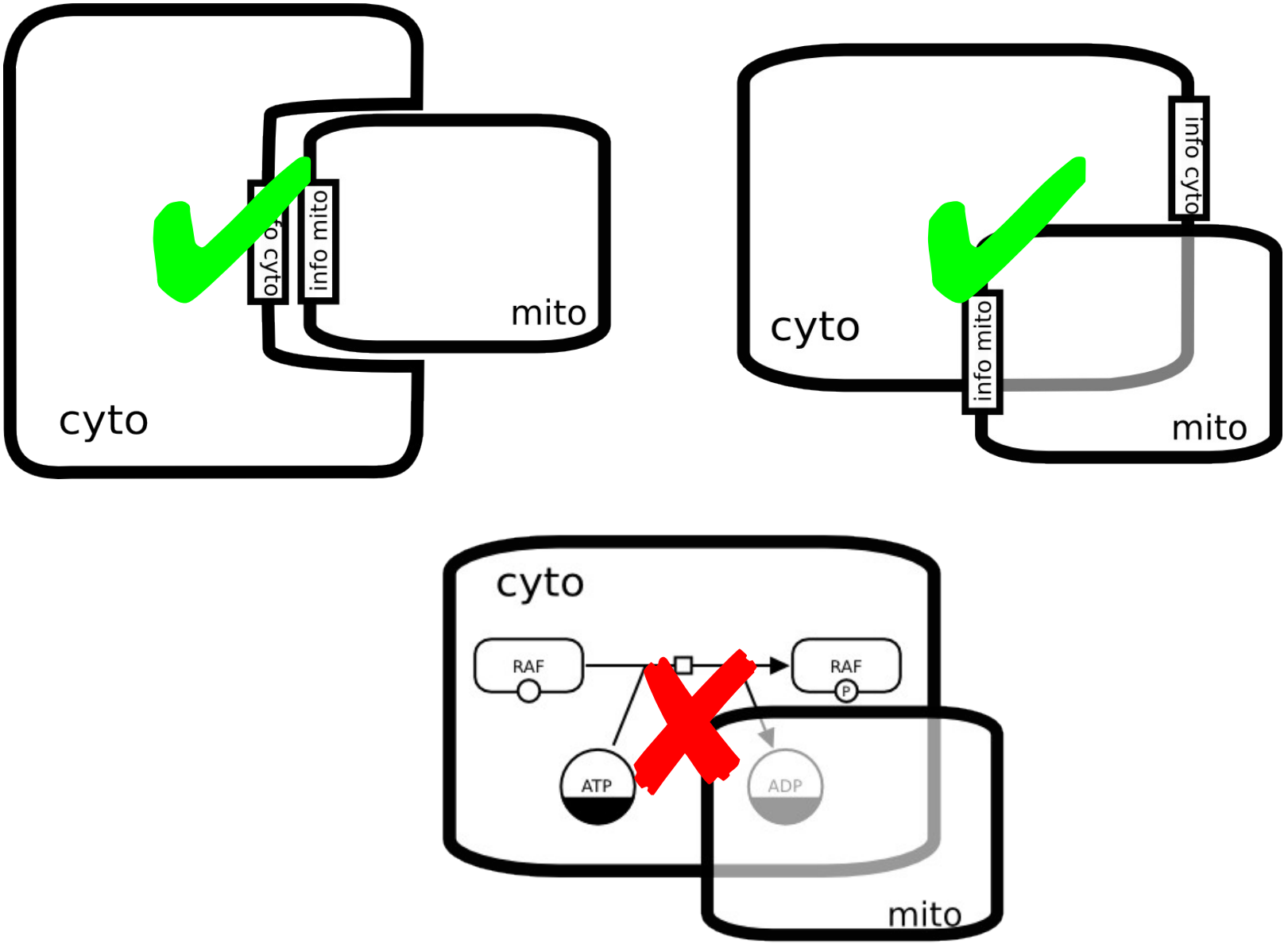
Process Descriptions syntax definition

Arc\EPN	*macromolecule*	*simple chemical*	*unspecified entity*	*multimer*	*complex*	*nucleic acid feature*	*tag*	*source/sink*	*perturbation*	*observable*	*submap*
consumption	I	I	I	I	I	I		I			
production	O	O	O	O	O	O		O			
modulation	I	I	I	I	I	I			I	O	
stimulation	I	I	I	I	I	I			I	O	
catalysis	I	I	I	I	I				I	O	
inhibition	I	I	I	I	I	I			I	O	
trigger	I	I	I	I	I	I			I	O	
logic arc	I	I	I	I	I	I					
equivalence arc	I	I	I	I	I	I	O				O

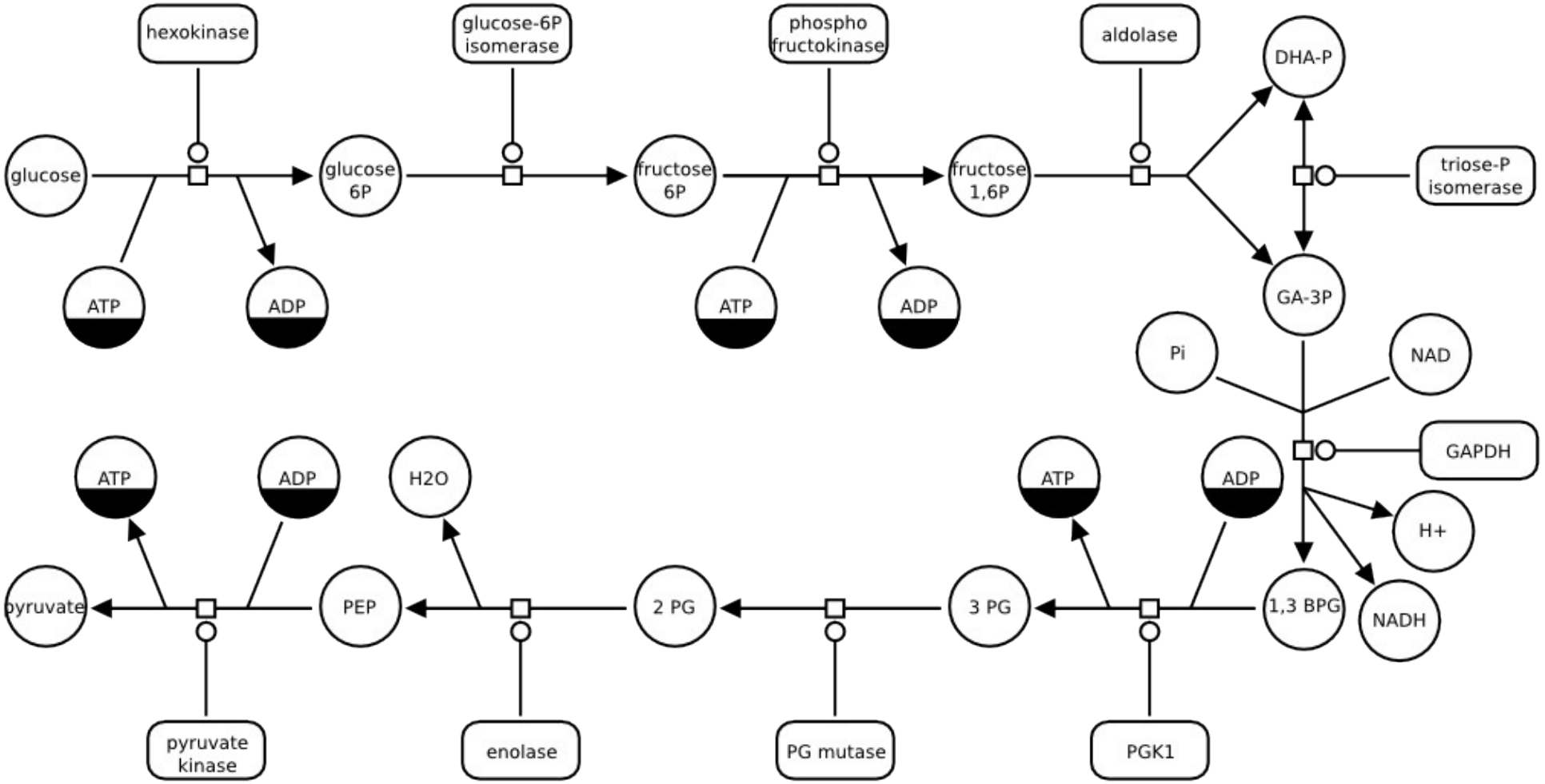
Arc\PN	*transition*	*omitted process*	*uncertain process*	*association*	*dissociation*	*and*	*or*	*not*
consumption	O	O	O	O	O(1)			
production	I	I	I	I(1)	I			
modulation	O	O	O			I(1)	I(1)	I(1)
stimulation	O	O	O			I(1)	I(1)	I(1)
catalysis	O	O	O			I(1)	I(1)	I(1)
inhibition	O	O	O			I(1)	I(1)	I(1)
trigger	O	O	O			I(1)	I(1)	I(1)
logic arc						O	O	O(1)
equivalence arc								

Layout constraints

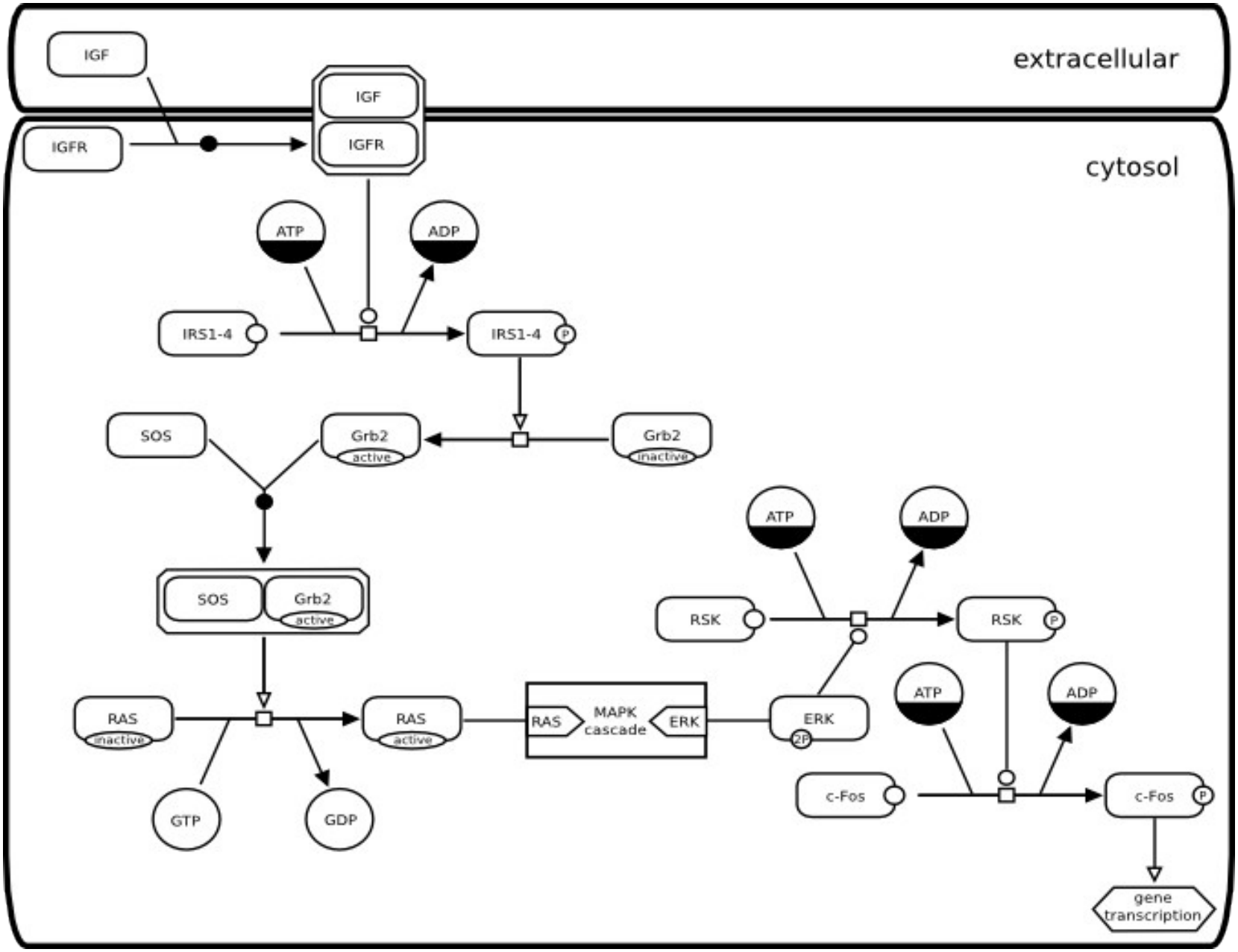



info cyto
info mito
cyto
mito
info cyto
cyto
info mito
mito
cyto
RAF
RAF
P
ATP
ADP
mito

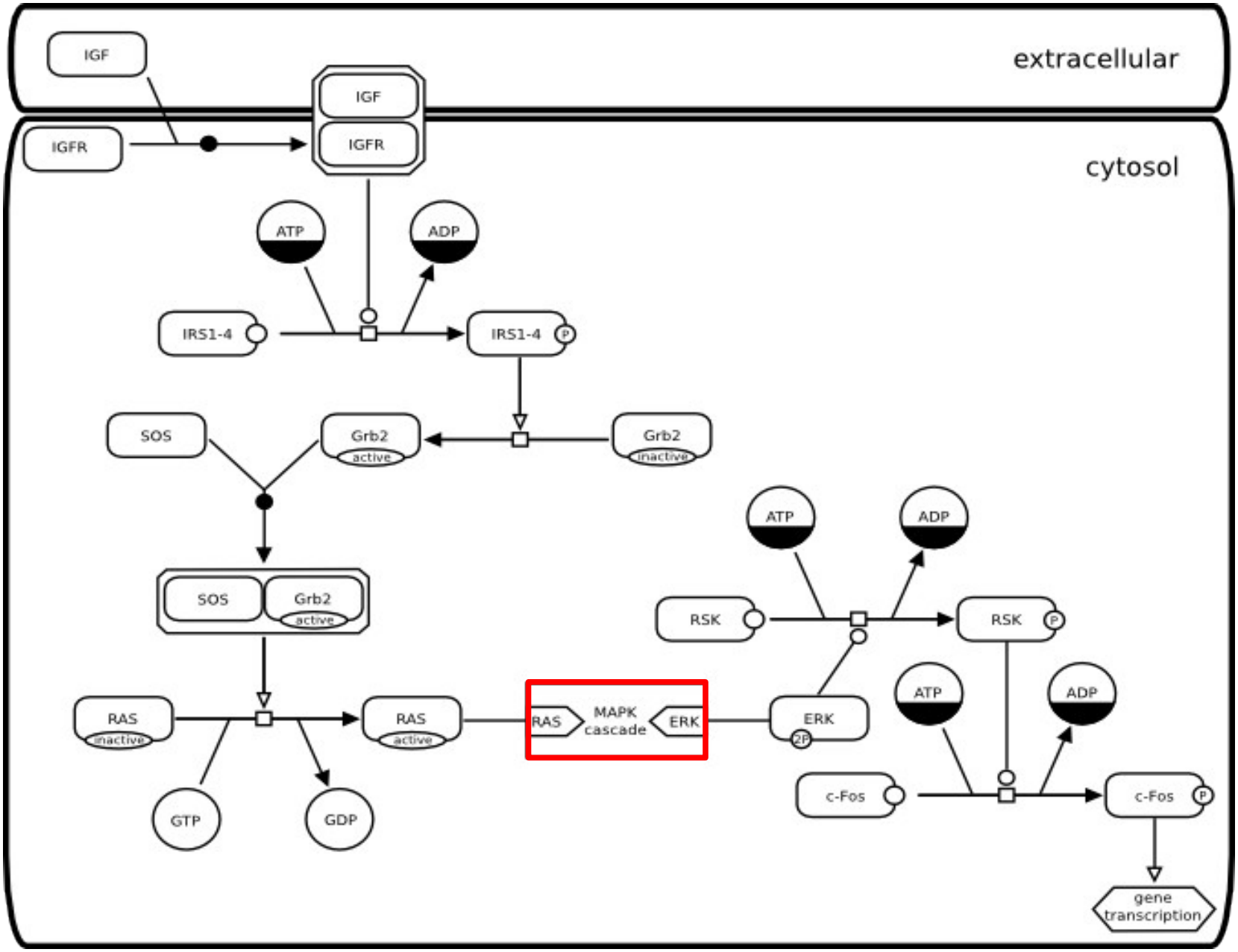
Metabolic network



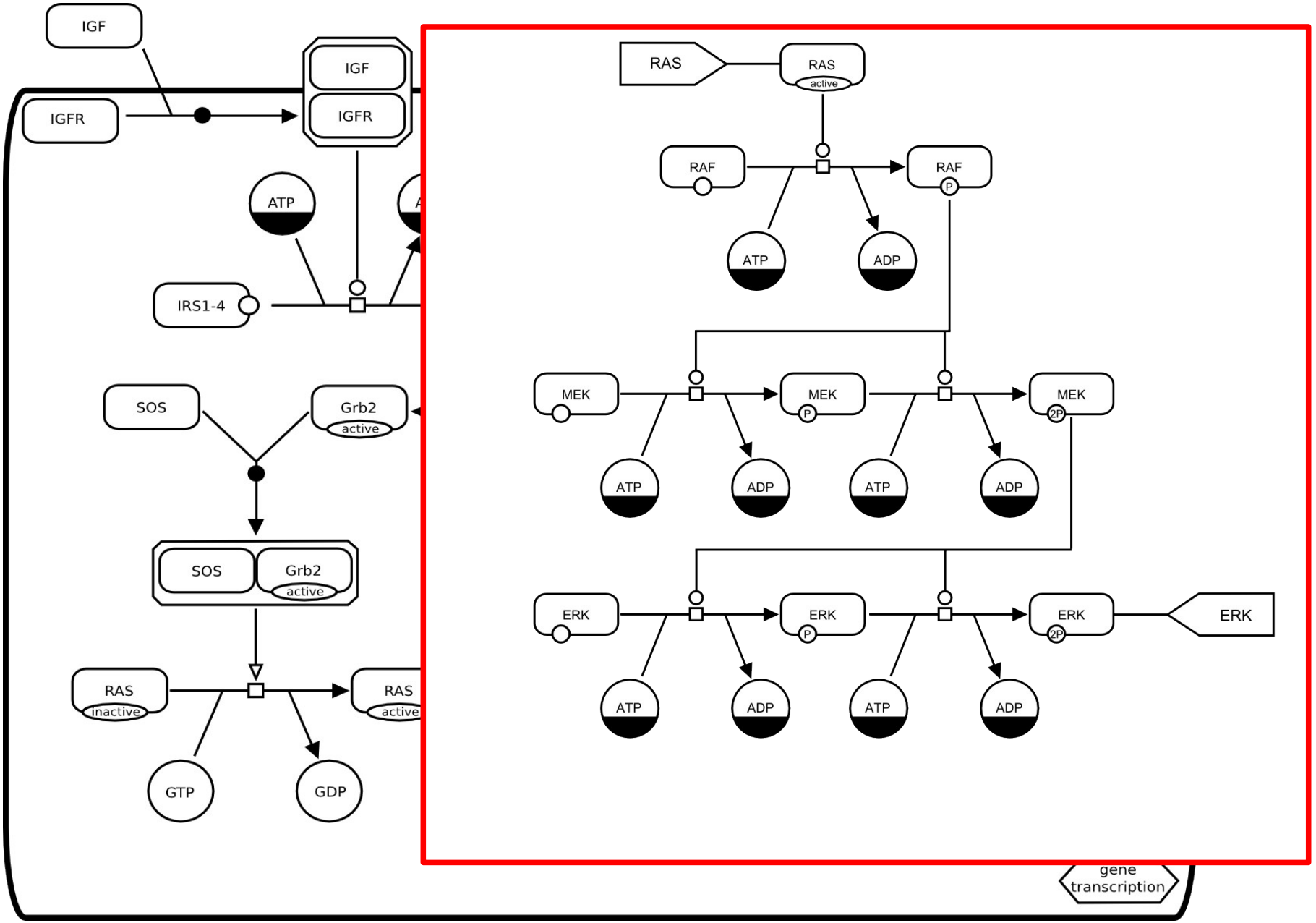
Signalling pathways



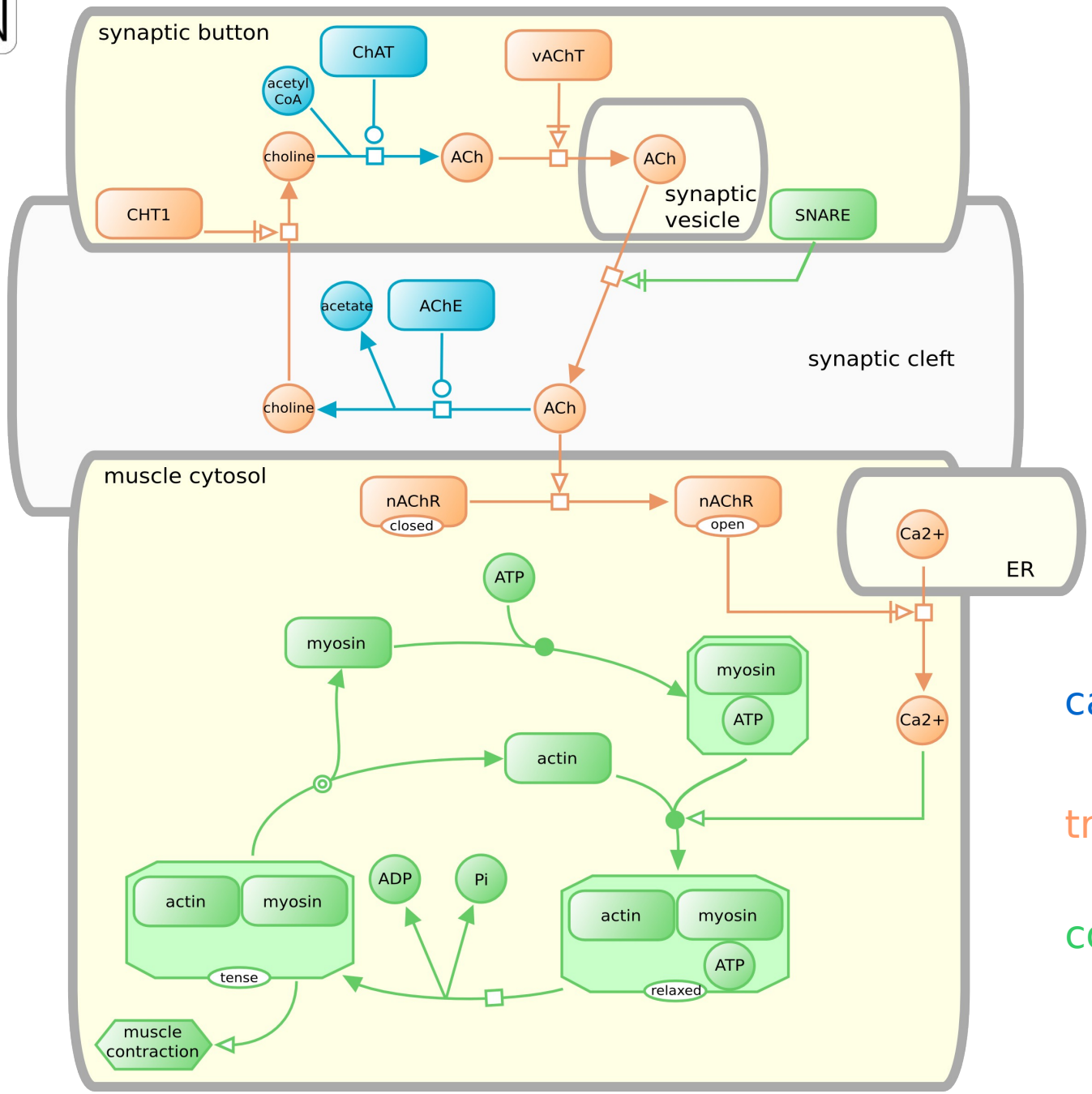
Submaps


extracellular
cytosol
IGF
IGFR
IGF
IGFR
ATP
ADP
IRS1-4
IRS1-4
P
SOS
Grb2
active
Grb2
inactive
SOS
Grb2
active
RAS
inactive
RAS
active
GTP
GDP
RAS
MAPK
cascade
ERK
ERK
2P
ATP
ADP
RSK
RSK
P
ATP
ADP
c-Fos
c-Fos
P
gene
transcription

Submaps


IGF
IGF
IGFR
IGFR
ATP
IRS1-4
SOS
Grb2
active
SOS
Grb2
active
RAS
inactive
RAS
active
GTP
GDP
RAS
RAS
active
RAF
RAF
P
ATP
ADP
MEK
MEK
P
MEK
2P
ATP
ADP
ATP
ADP
ERK
ERK
P
ERK
2P
ERK
ATP
ADP
ATP
ADP
gene
transcription

multi-cellular processes

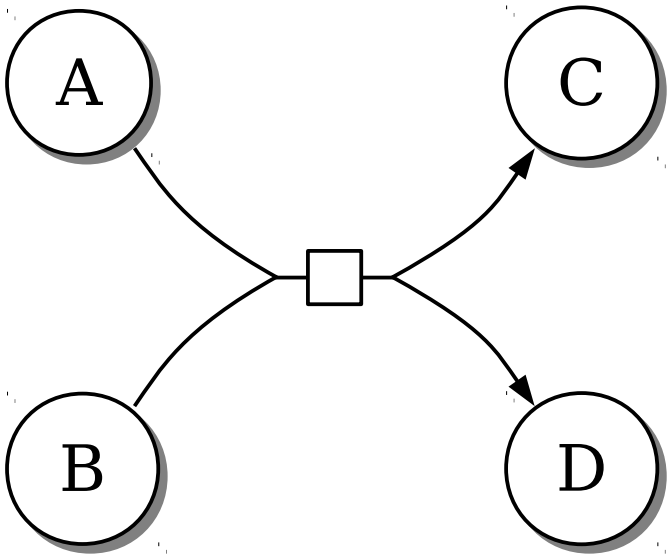


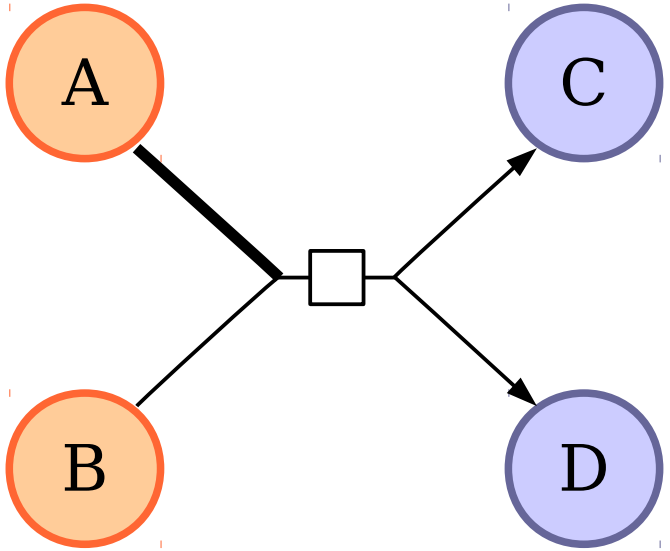
catalytic processes

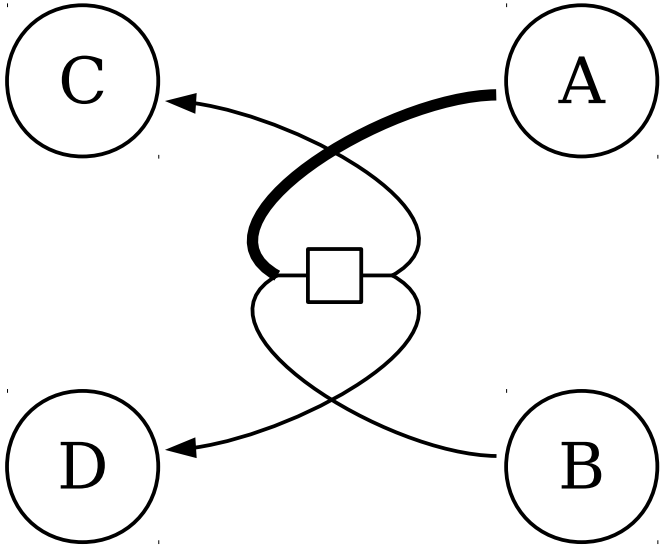
transport processes

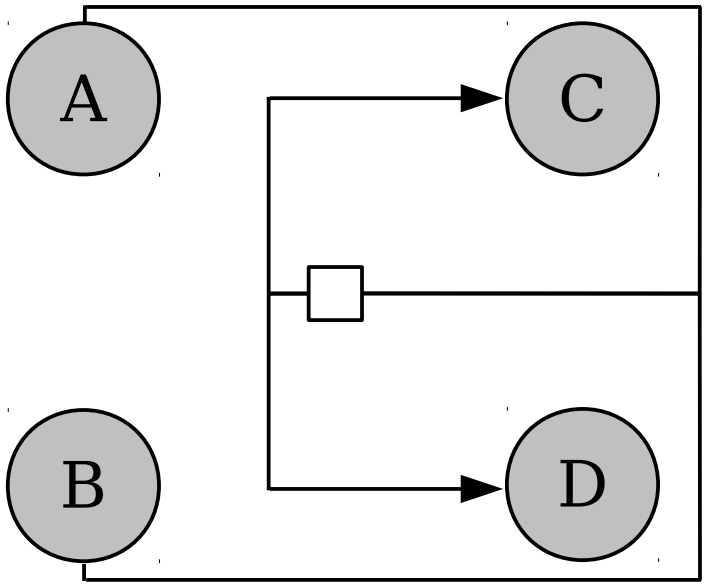
contractile proteins

All those diagrams are identical





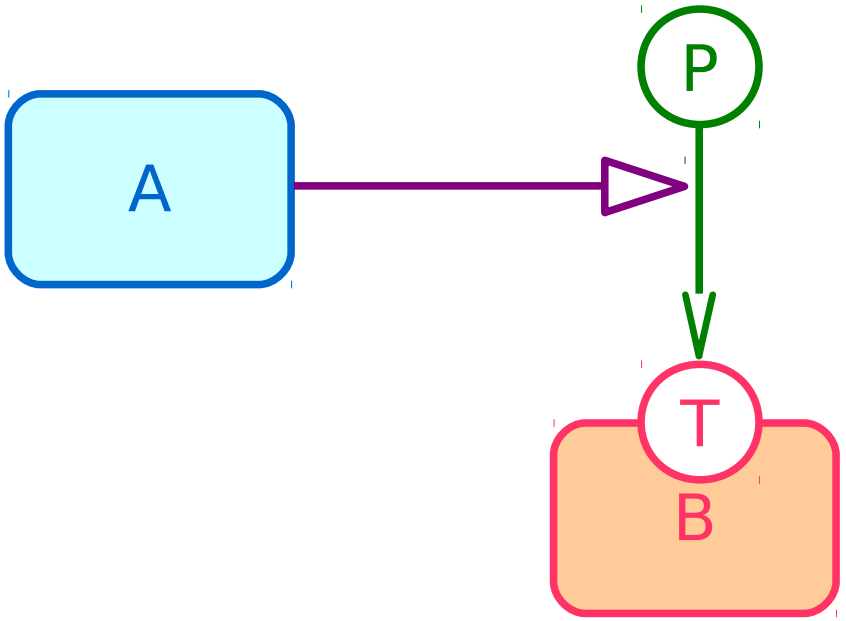




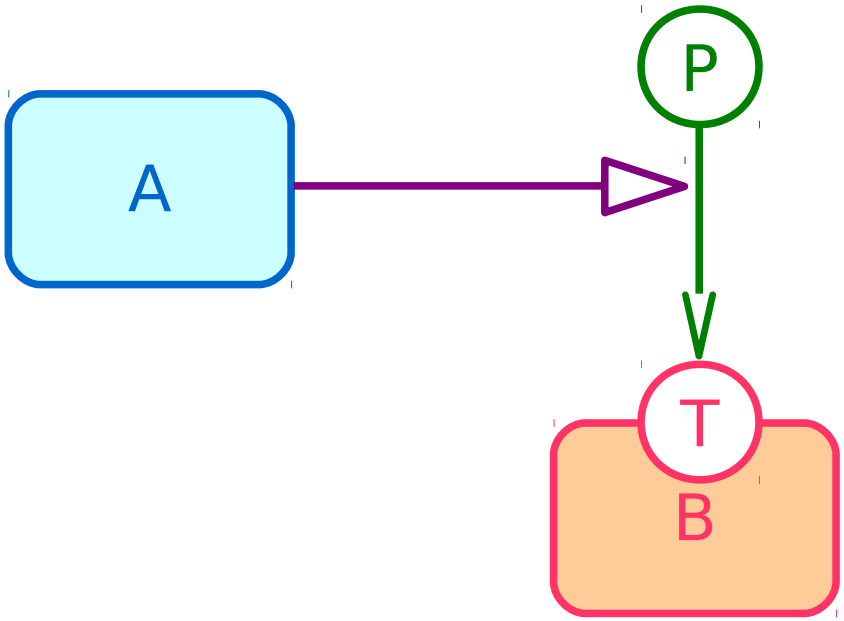
Pending issues

- Generics, i.e, entity pools representing several possible biochemical types. (e.g. MAPK instead of ERK1 and ERK2).
- Trans-compartment (e.g. transmembrane) structures
- Logical combination of state-variable values (and close-world/open-world position)
- Moving and transforming compartments
- Non-chemical entity pool nodes (“voltage”, “pH” ...)

Entity Relationships can be viewed as rules

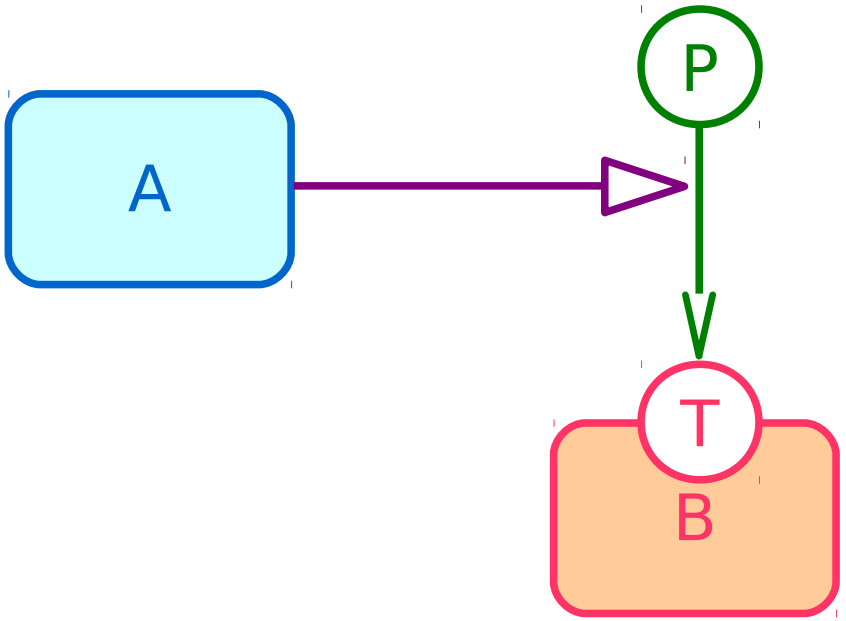


Entity Relationships can be viewed as rules



If A exists, the assignment of the value P to the state variable T of B is increased

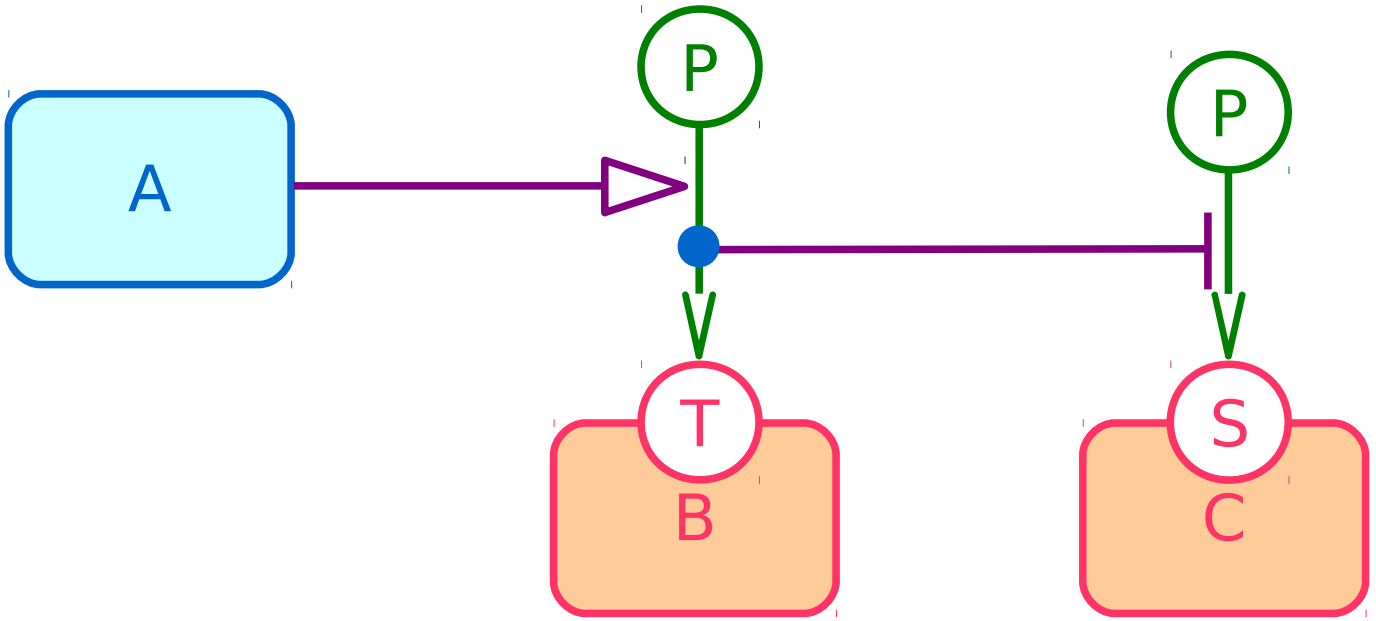
Entity Relationships can be viewed as rules



If A exists, the assignment of the value P to the state variable T of B is increased

(A stimulates the phosphorylation of B on the threonine)

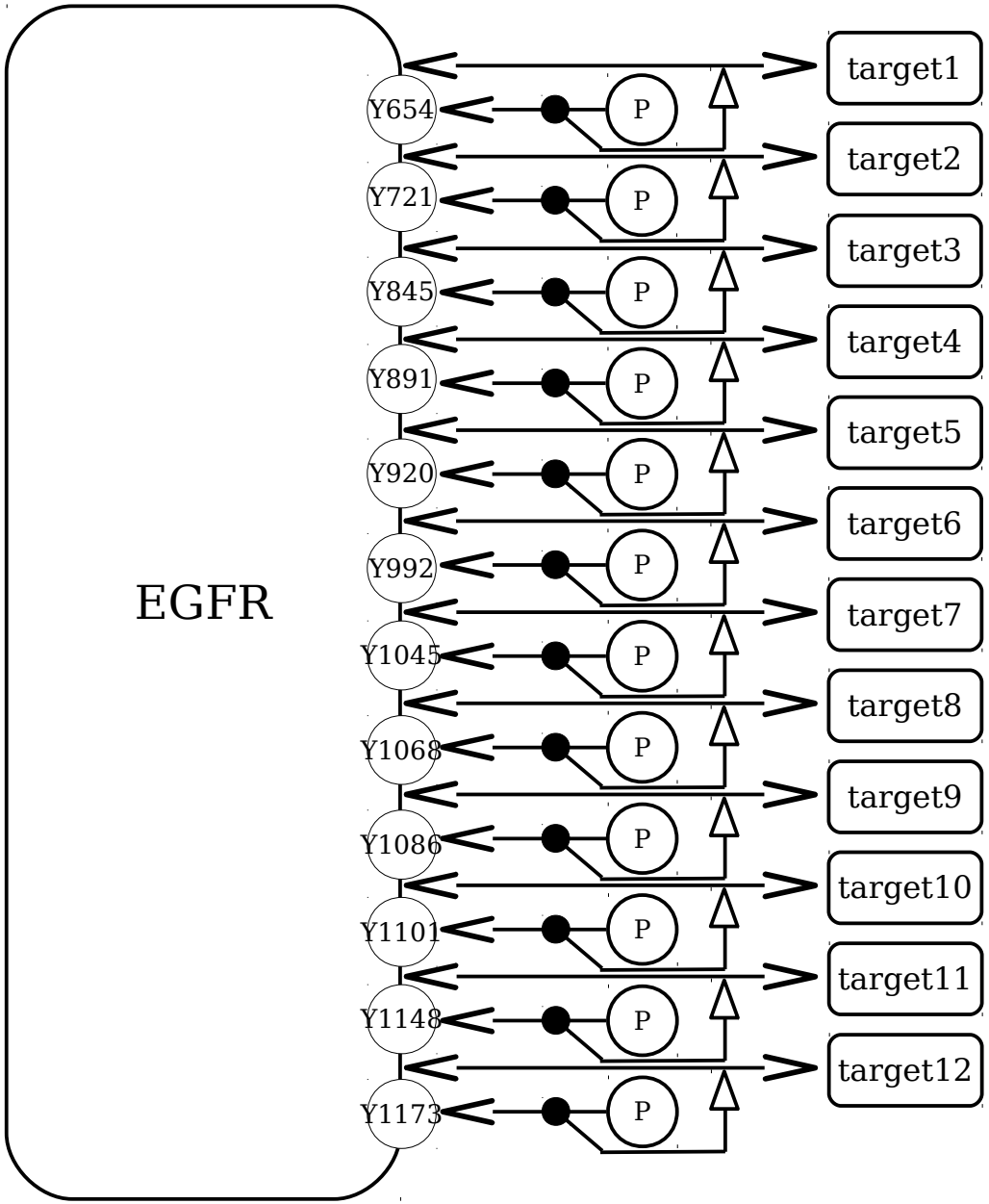
Entity Relationships can be viewed as rules



If A exists, the assignment of the value P to the state variable T of B is increased

If P is assigned to the state variable T of B, the assignment of the value P to the state variable S of C is decreased

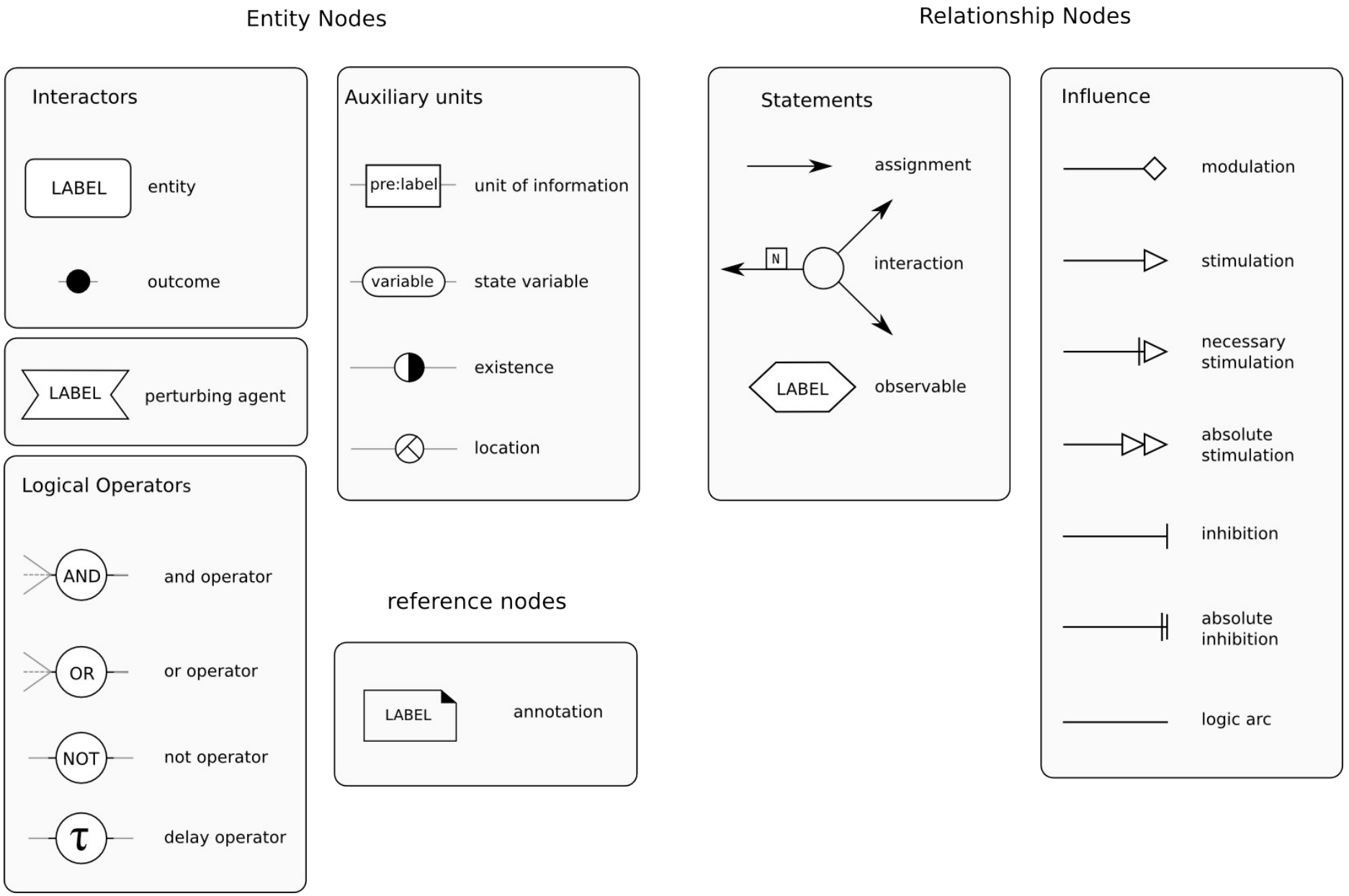
Multistate and combinatorial explosion



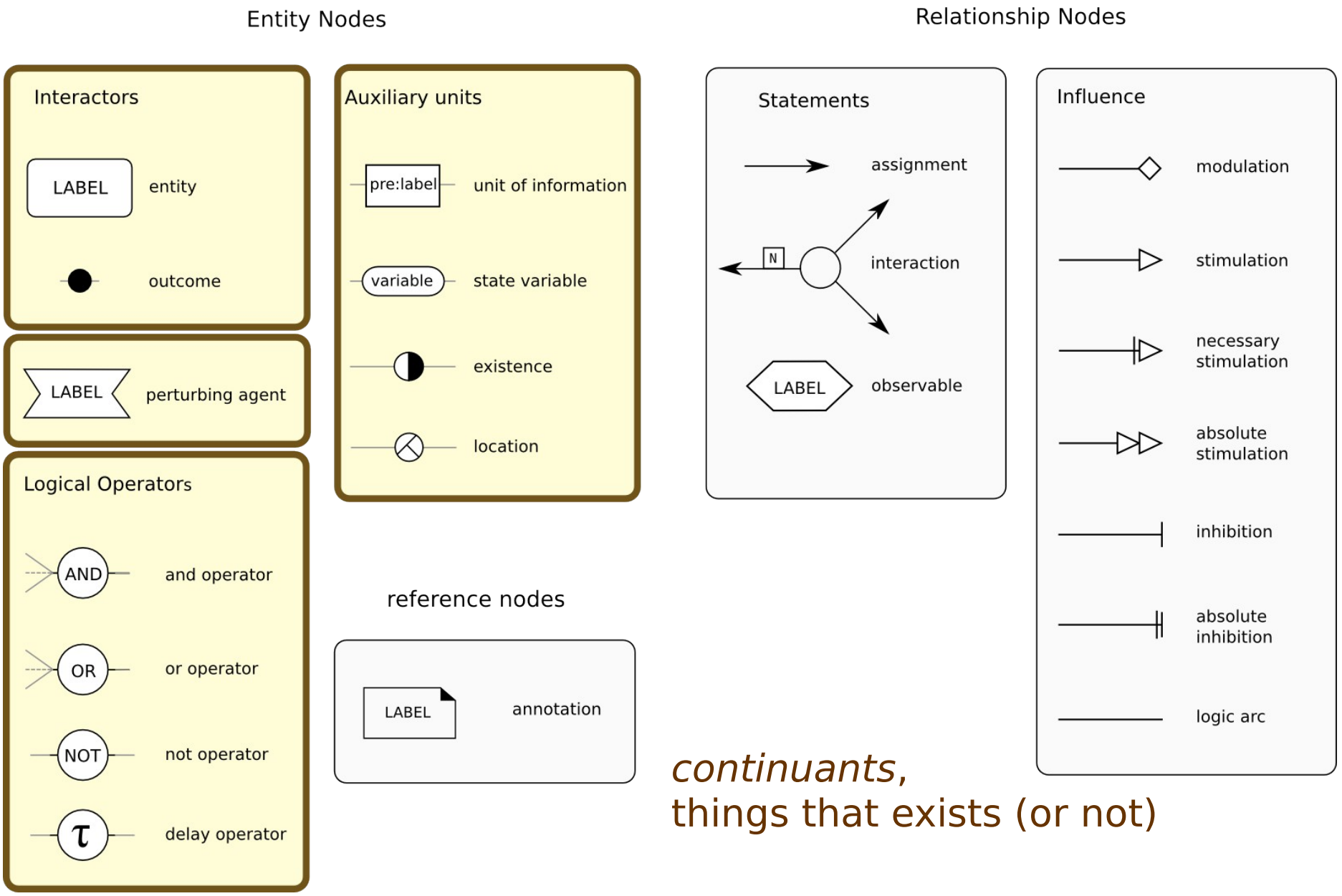
Process Diagram:
“once a state variable value,
always a state variable value”

2^{12} = 4096 states
(i.e. EPN glyphs) for EGFR
and 4096 complexes between
EGFR and targets

SBGN Entity Relationships L1 reference card

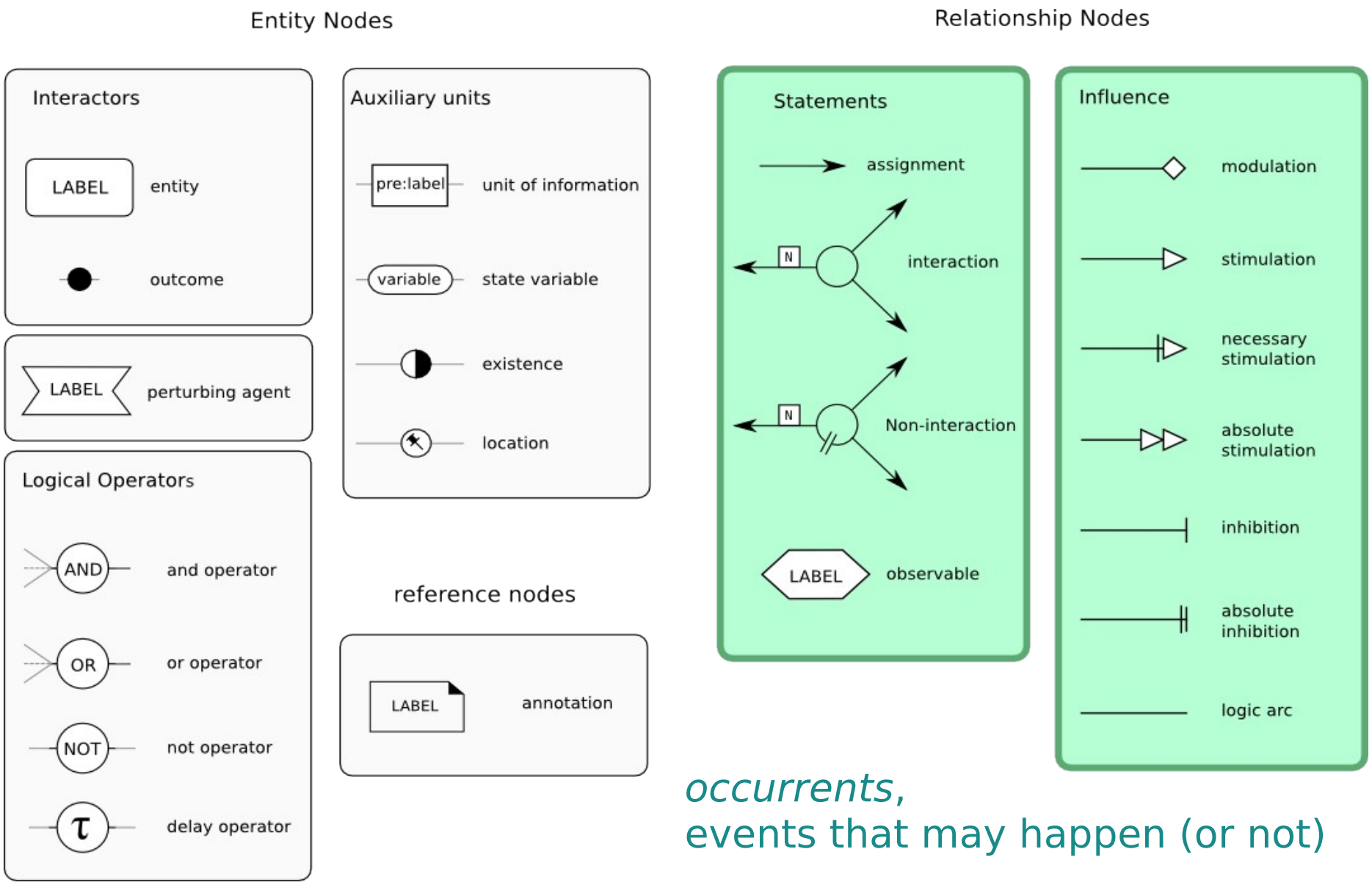


SBGN Entity Relationships L1 reference card



continuants,
things that exists (or not)

SBGN Entity Relationships L1 reference card



occurrents,
events that may happen (or not)

Entity Relationships syntax

symbols \ Arc	*assignment*	*interaction*	*modulation*	*stimulation*	*inhibition*	*necessary stimulation*	*absolute stimulation*	*absolute inhibition*	*logic arc*
entity		IO	I	I	I	I	I	I	I
outcome		I(1)O(1)	I(1)	I(1)	I(1)	I(1)	I(1)	I(1)	I(1)
and			I(1)	I(1)	I(1)	I(1)	I(1)	I(1)	I(1)O
or			I(1)	I(1)	I(1)	I(1)	I(1)	I(1)	I(1)O
not			I(1)	I(1)	I(1)	I(1)	I(1)	I(1)	I(1)O(1)
delay			I(1)	I(1)	I(1)	I(1)	I(1)	I(1)	I(1)O(1)
perturbing agent			I	I	I	I	I	I	I
unit of information		IO							
state variable	I(1)O(1)								
modulation				O	O	O	O	O	
stimulation				O	O	O	O	O	
inhibition				O	O	O	O	O	
necessary stimulation				O	O	O	O	O	
absolute stimulation				O	O	O	O	O	
absolute inhibition				O	O	O	O	O	
assignment				O	O	O	O	O	
interaction				O	O	O	O	O	
phenotype				O	O	O	O	O	

Example of Entity Relationships semantics

3.4.2 Influences

A *modulation* (Section 2.4.3.1) linking an *entity node* E and a relationship R means: "If E exists then R is either reinforced or weakened".

A *stimulation* (Section 2.4.3.2) linking an *entity node* E and a relationship R means: "If E exists then R is reinforced" or "If E exists then the probability of R is increased".

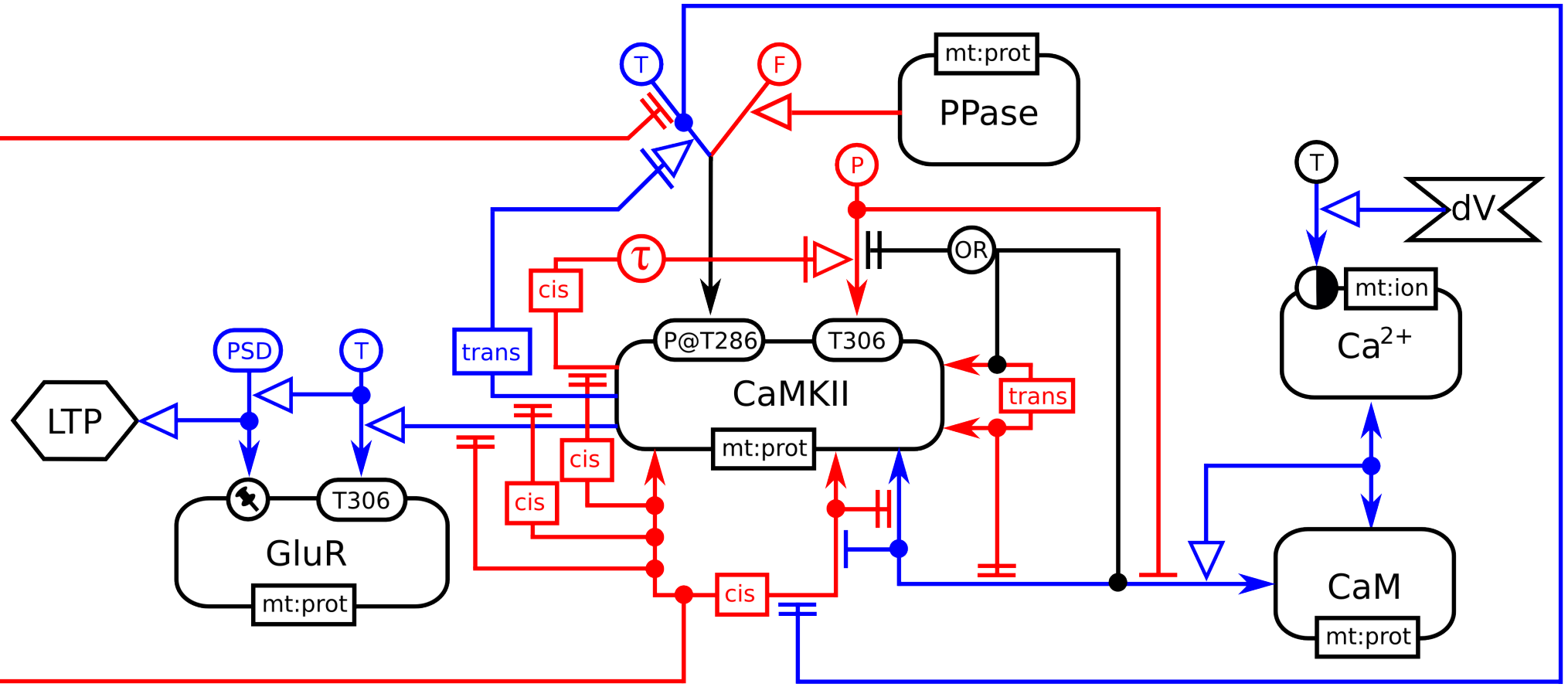
An *absolute stimulation* (Section 2.4.3.6) linking an *entity node* E and a relationship R means: "If E exists then R always takes place".

A *necessary stimulation* (Section 2.4.3.4) linking an *entity node* E and a relationship R means: "R only takes place if E exists.

An *inhibition* (Section 2.4.3.3) linking an *entity node* E and a relationship R means: "If E exists then R is weakened" or "If E exists then the probability of R is lowered".

An *absolute inhibition* (Section 2.4.3.5) linking an *entity node* E and a relationship R means: "If E exists then R never takes place".

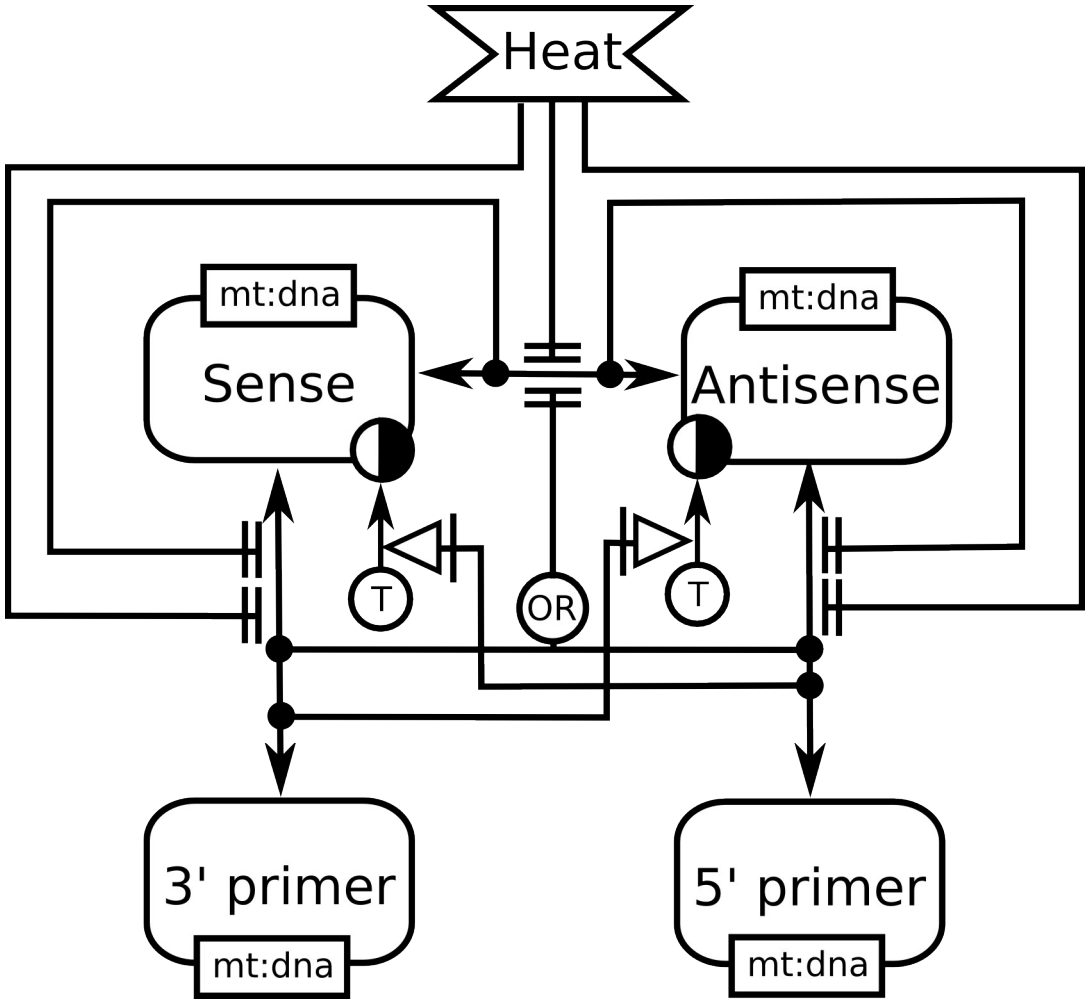
ER map of calcium-regulated synaptic plasticity



increases synaptic weight

decreases synaptic weight

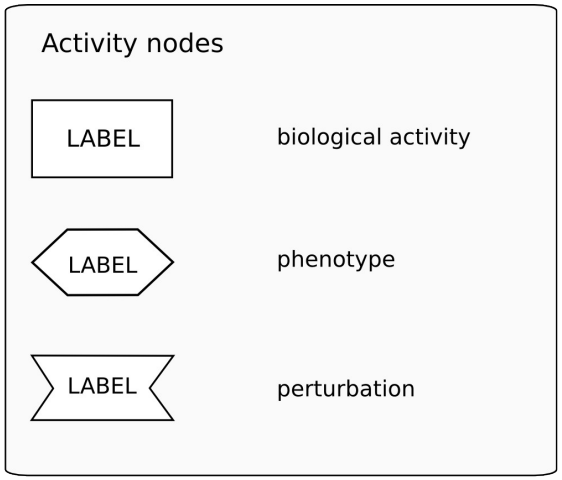
ER map representing PCR

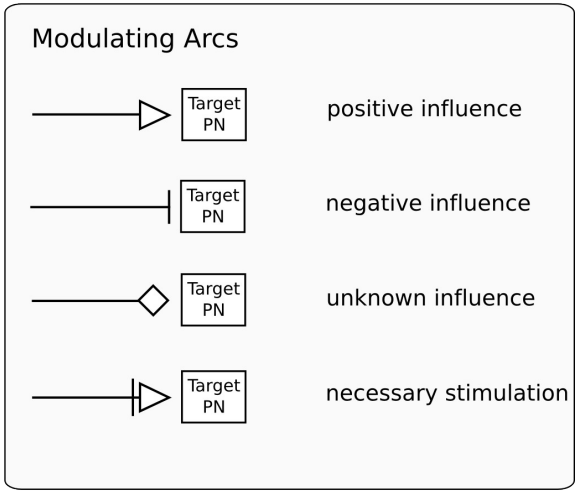


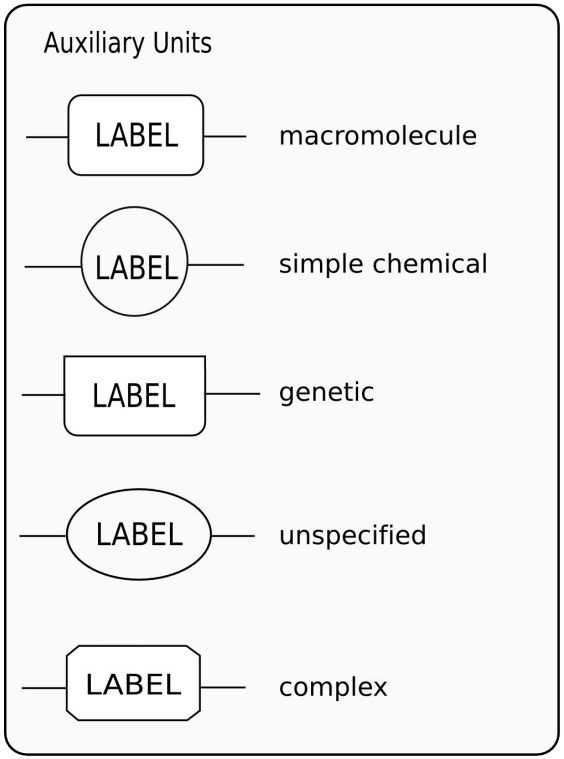
Pending issues

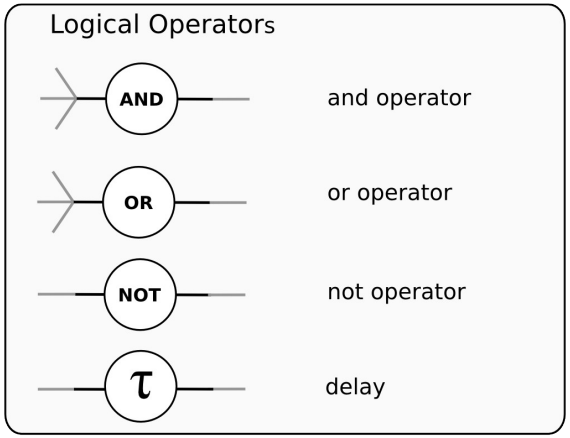
- Internal structure of entities, such as domains, sites, features. (NB: This has been agreed upon for the next version. We will be able to “nest” entities)
- Identification of instances: How to differentiate between several instances of the same entity, differentially involved in a relationships (e.g. trans-phosphorylation)?
- Identification of generics: How to lump together several entities for a given relationships? (e.g. MAPK instead of ERK1 and ERK2).

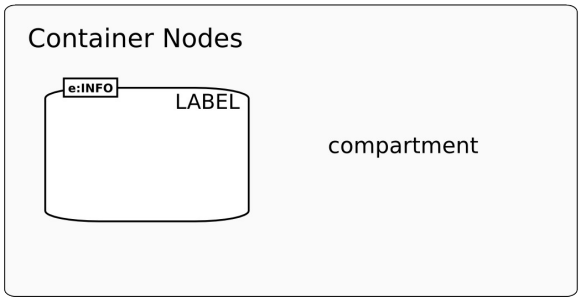
SBGN Activity Flows L1 reference card



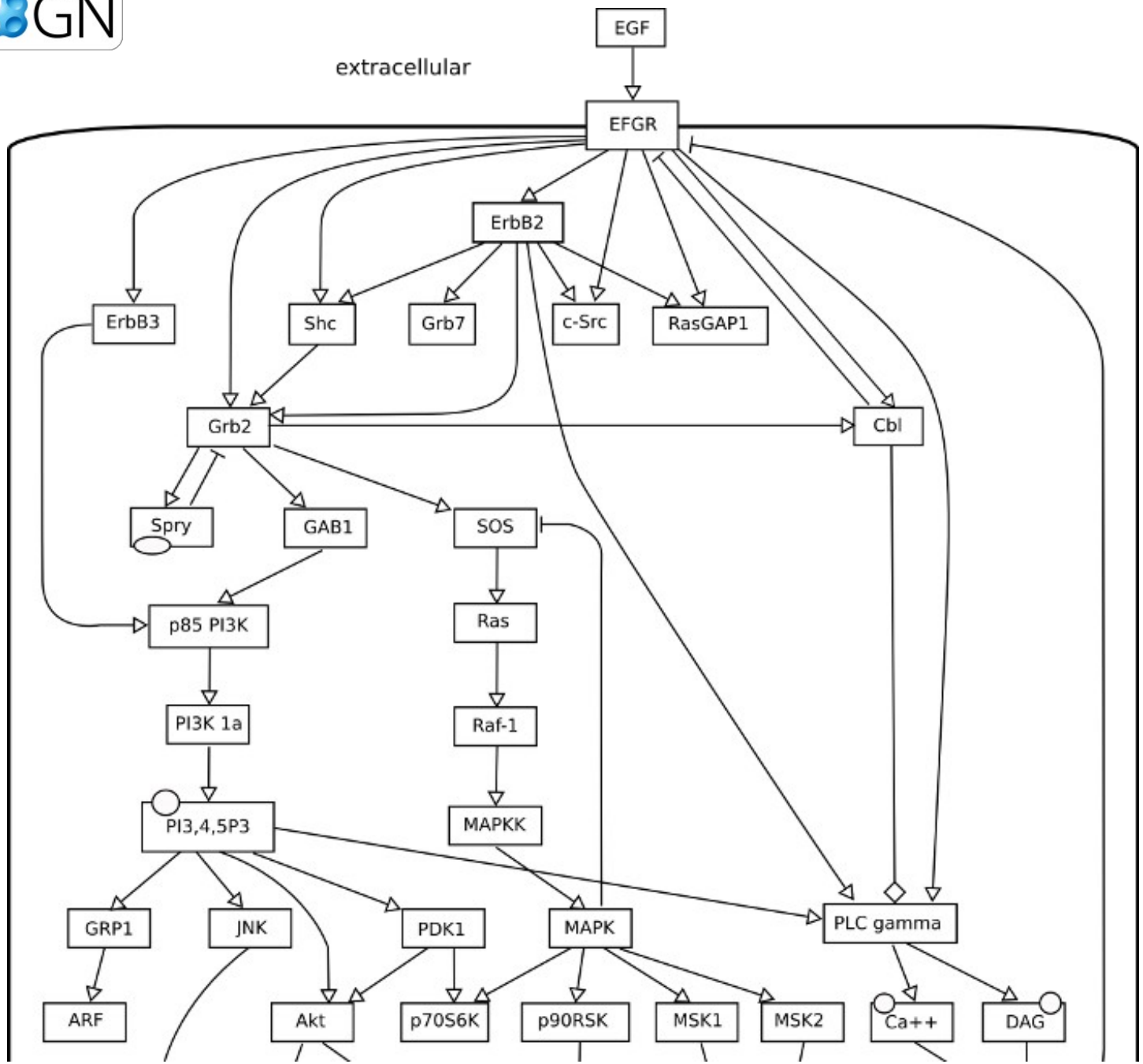




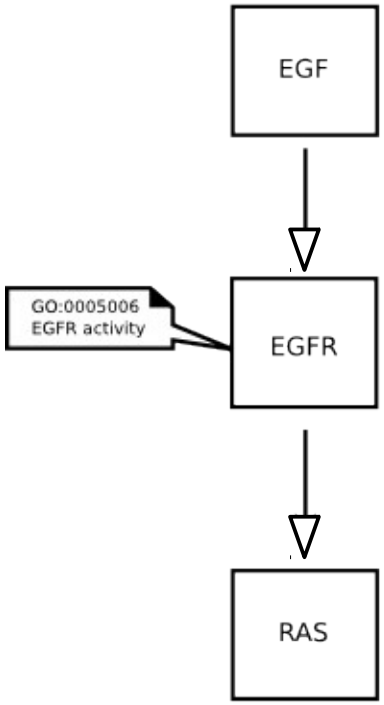


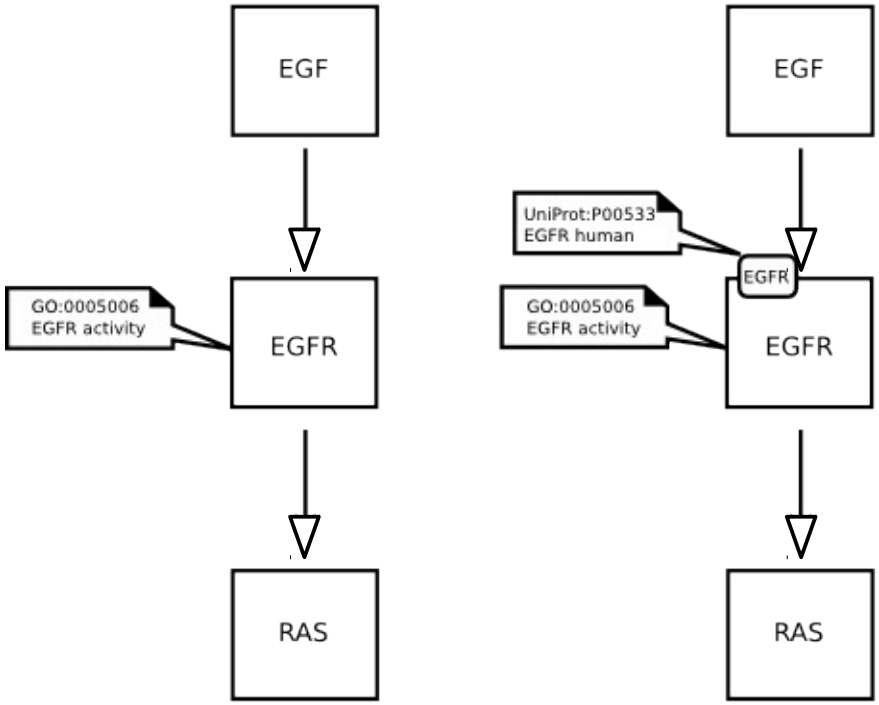


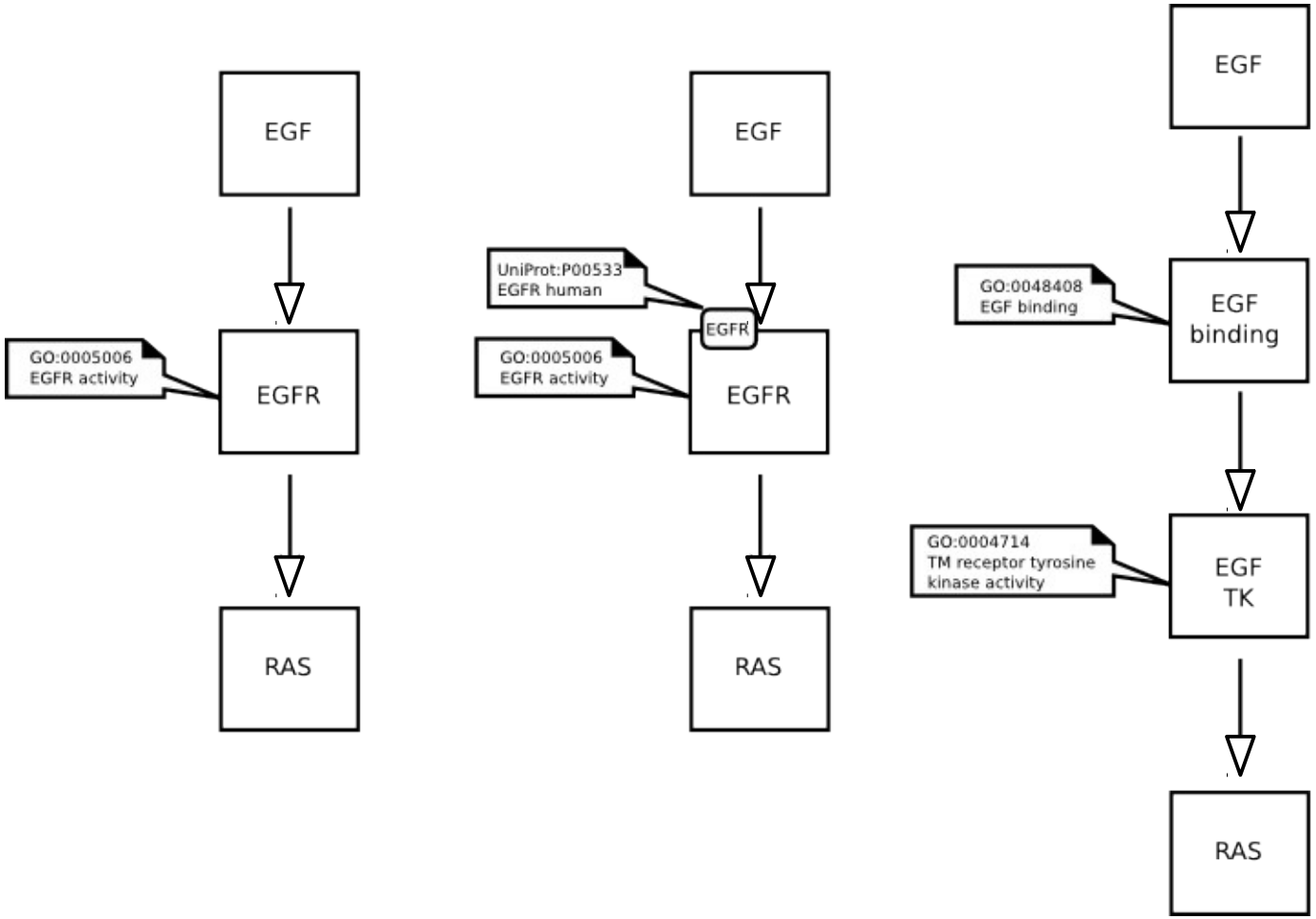
Example of Activity Flow map

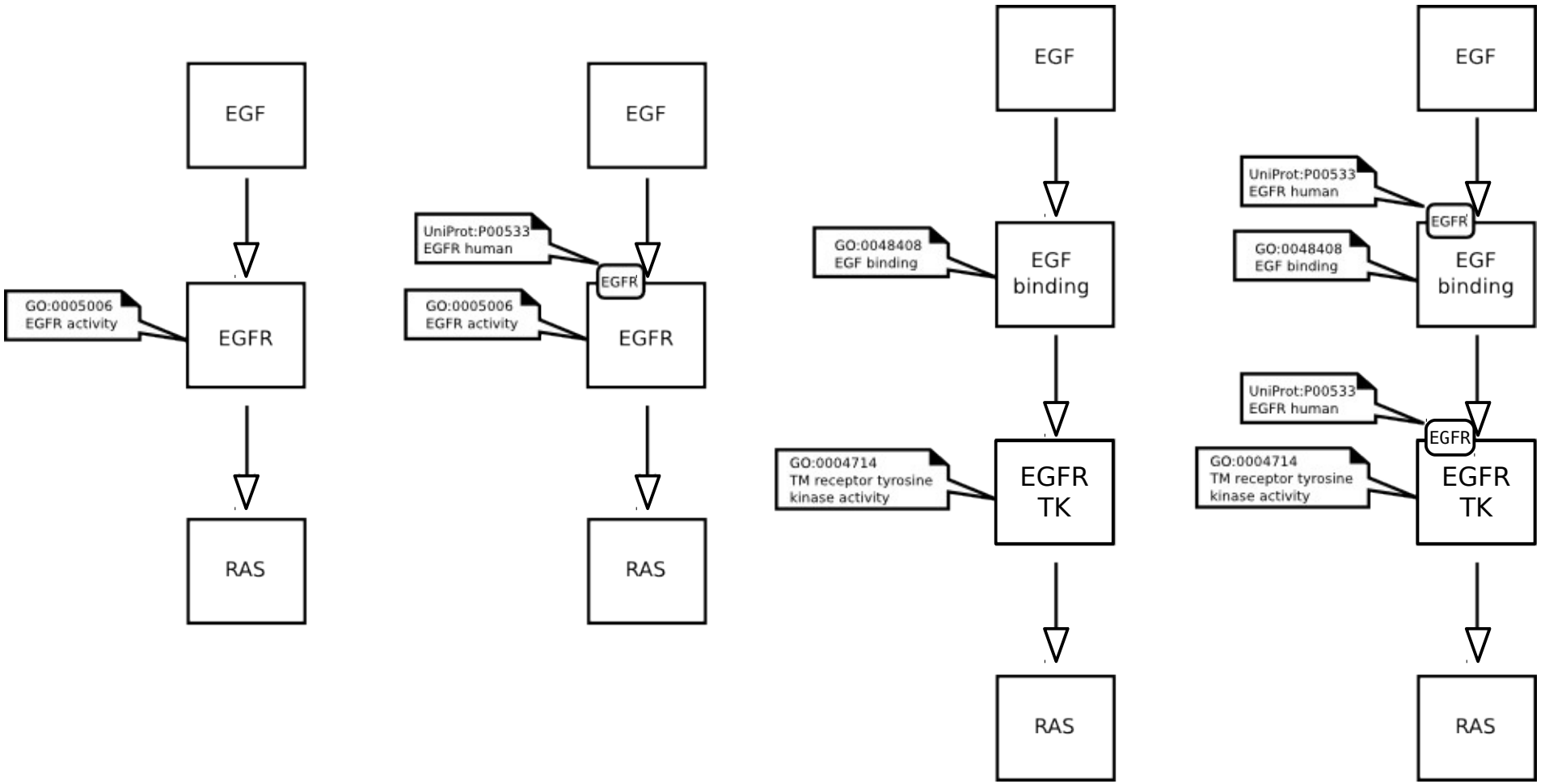


There Is More Than One Way To Do It (TIMTOWDI)


EGF
GO:0005006
EGFR activity
EGFR
RAS


EGF
GO:0005006
EGFR activity
EGFR
RAS
EGF
UniProt:P00533
EGFR human
EGFR
GO:0005006
EGFR activity
EGFR
RAS


EGF
GO:0005006
EGFR activity
EGFR
RAS
EGF
UniProt:P00533
EGFR human
EGFR
GO:0005006
EGFR activity
EGFR
RAS
EGF
GO:0048408
EGF binding
EGF
binding
GO:0004714
TM receptor tyrosine
kinase activity
EGF
TK
RAS


EGF
GO:0005006
EGFR activity
EGFR
RAS
EGF
UniProt:P00533
EGFR human
EGFR
GO:0005006
EGFR activity
EGFR
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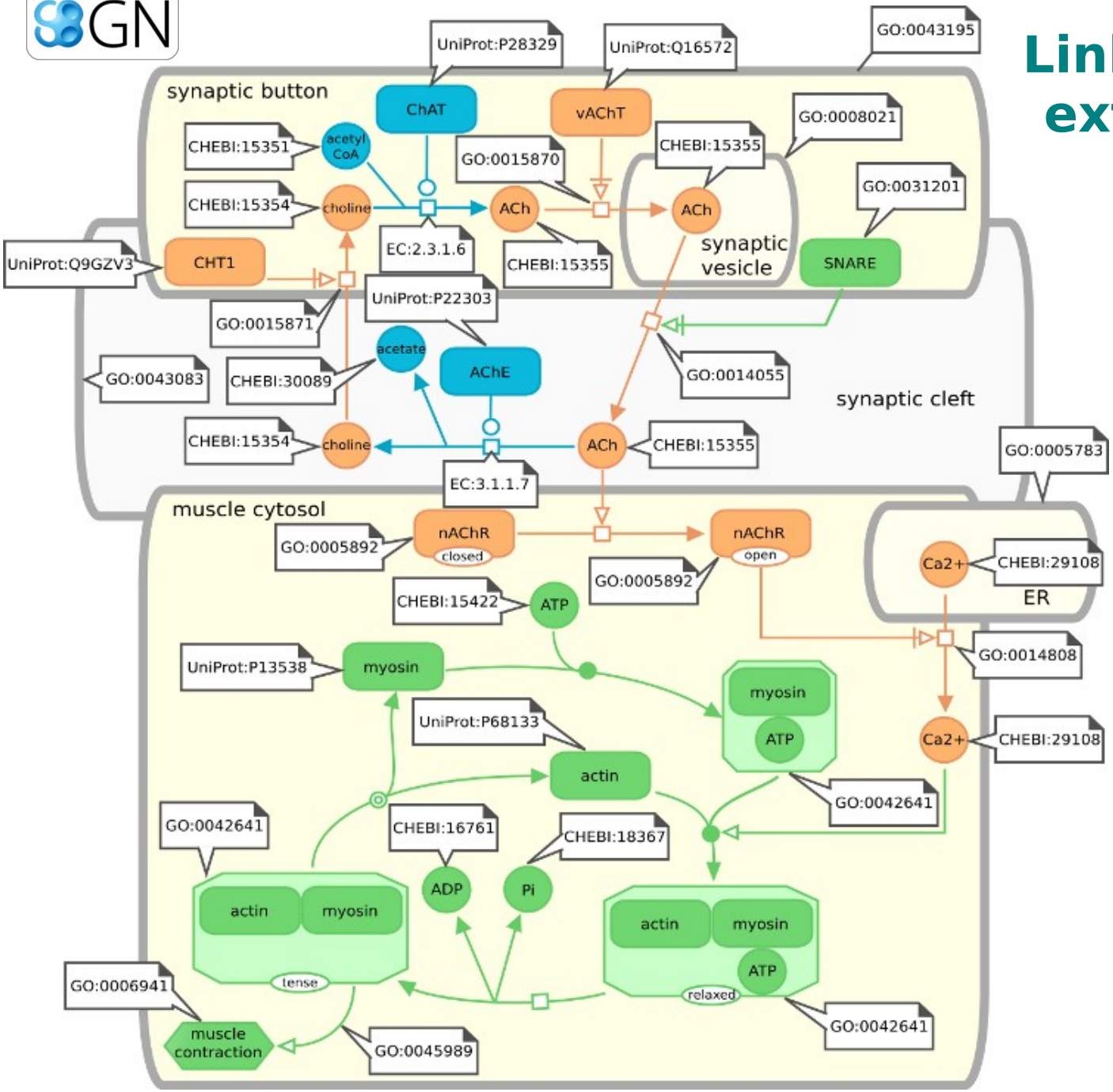
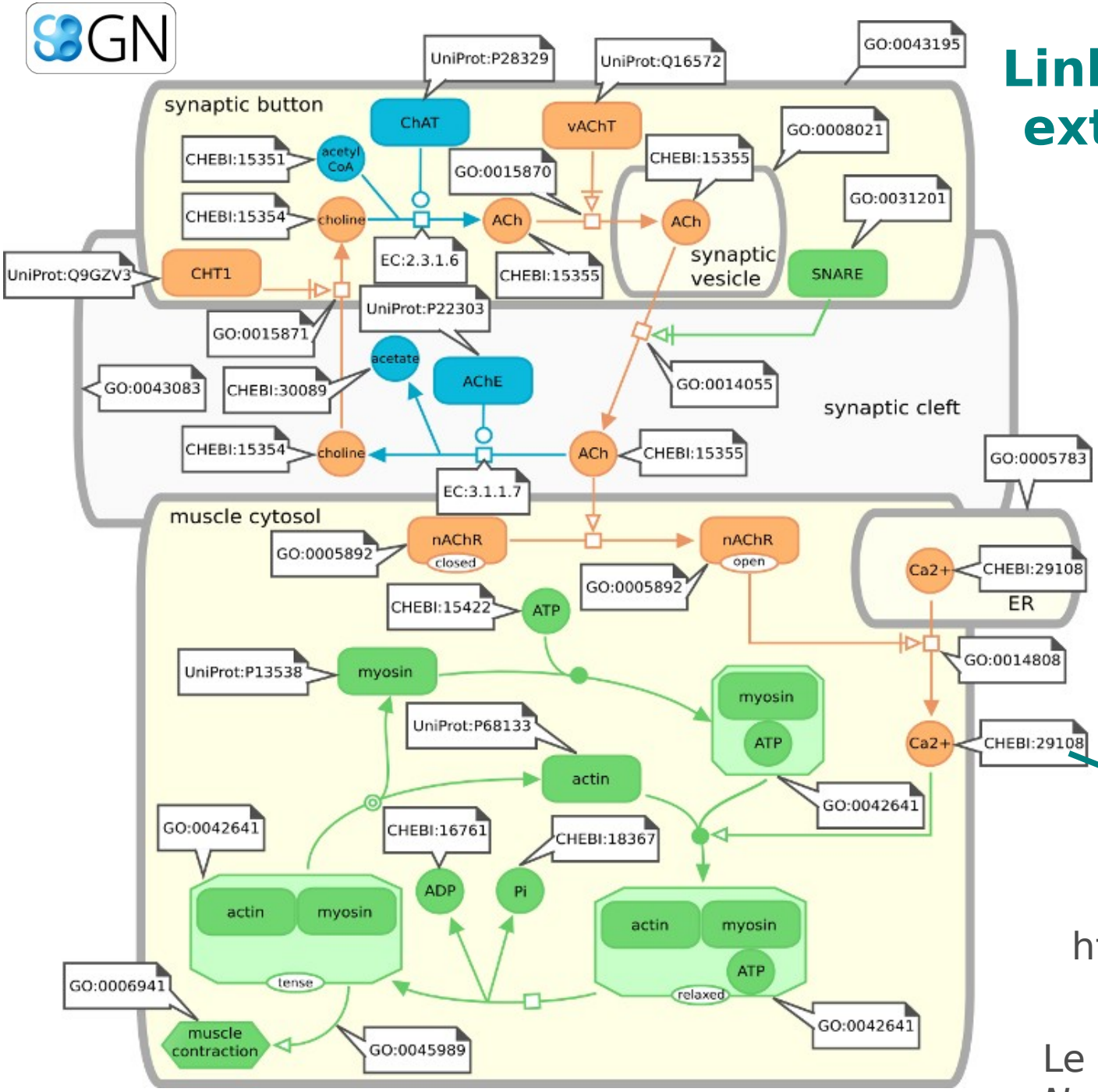
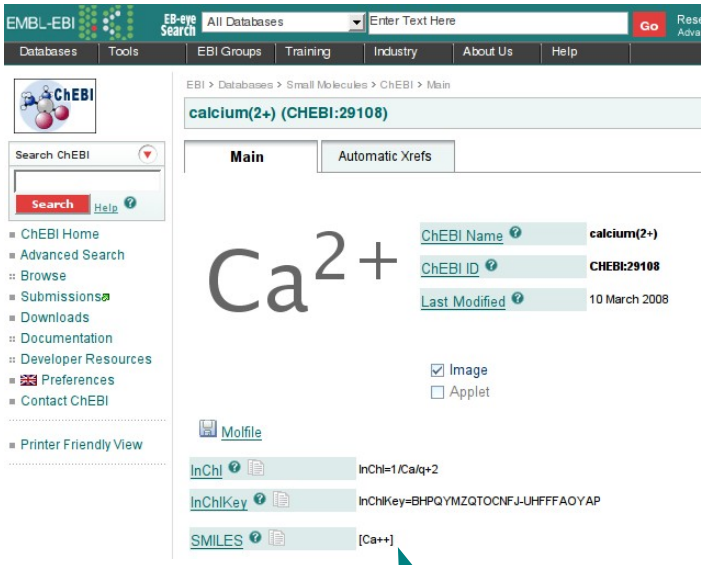
EGF
GO:0048408
EGF binding
EGF
binding
GO:0004714
TM receptor tyrosine
kinase activity
EGFR
TK
RAS
EGF
UniProt:P00533
EGFR human
EGFR
GO:0048408
EGF binding
EGF
binding
UniProt:P00533
EGFR human
EGFR
GO:0004714
TM receptor tyrosine
kinase activity
EGFR
TK
RAS

Linking SBGN maps to external information



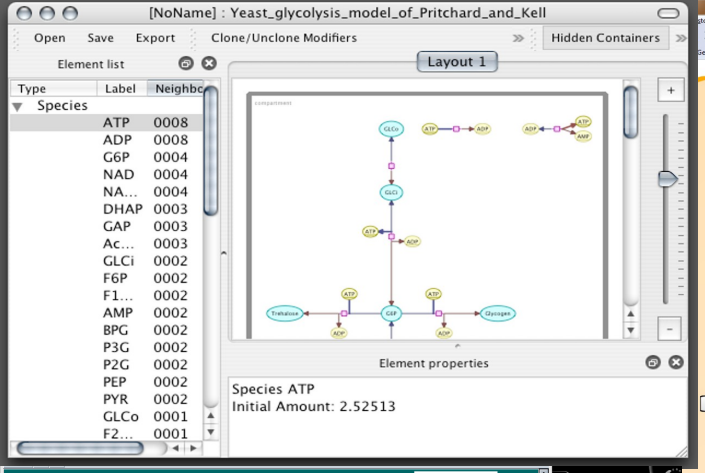
Linking SBGN maps to external information

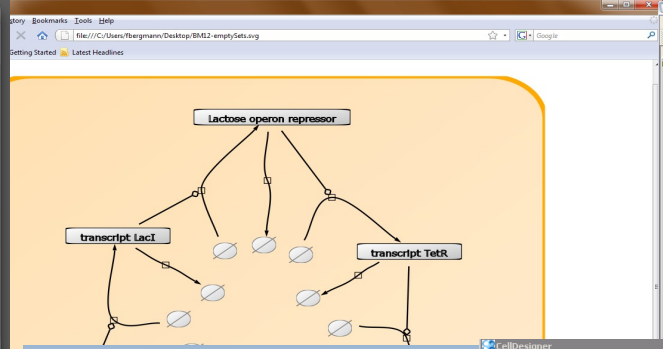


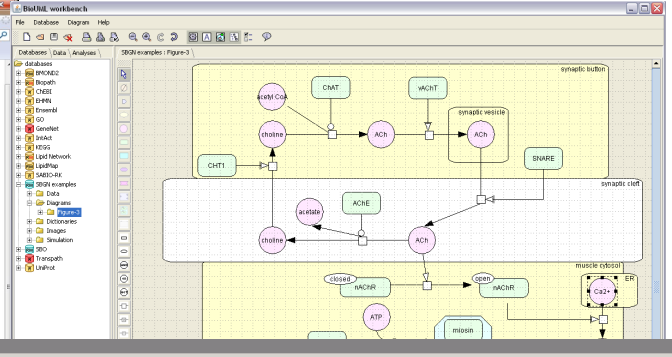


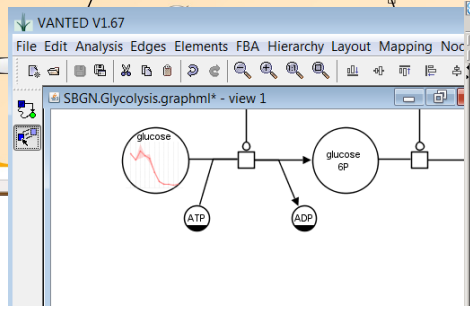
http://www.ebi.ac.uk/miriam/

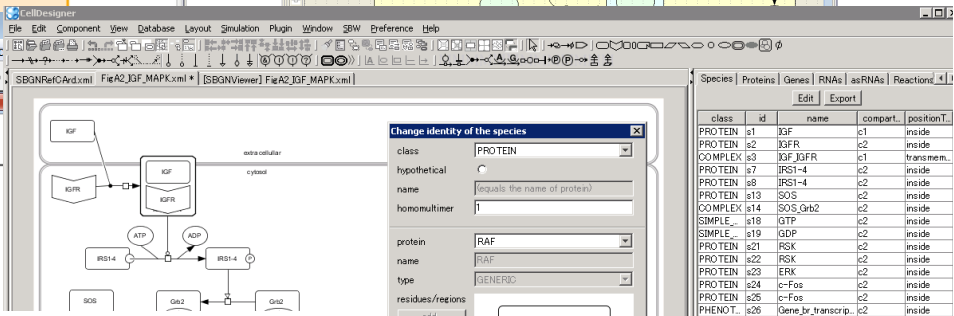
Le Novère *et al* (2005)
Nat Biotechnol, 23: 1509-1515.

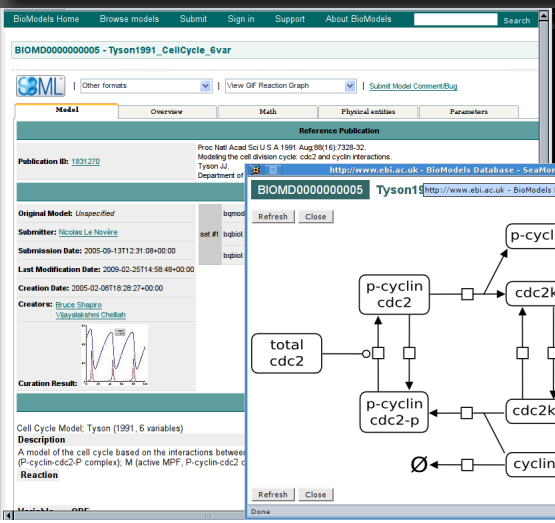

[NoName] : Yeast_glycolysis_model_of_Pritchard_and_Kell
Open
Save
Export
Clone/Unclone Modifiers
Hidden Containers
Element list
Layout 1
Type
Label
Species
ATP 0008
ADP 0008
G6P 0004
NAD 0004
DHAP 0003
GAP 0003
GLCi 0002
F6P 0002
PEP 0002
PYR 0002
GLCo 0001
Element properties
Species ATP
Initial Amount: 2.52513


Lactose operon repressor
transcript LacI
transcript TetR

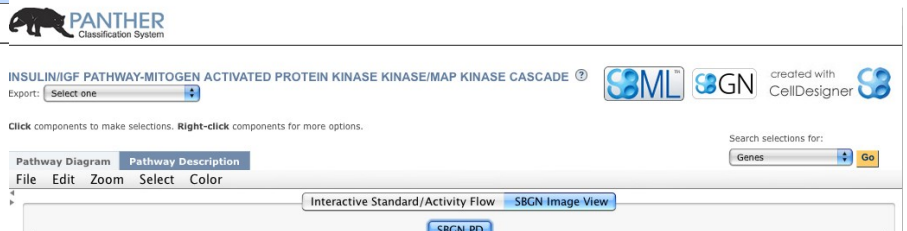

BioUML workbench
synaptic button
synaptic vesicle
synaptic cleft
muscle cytosol

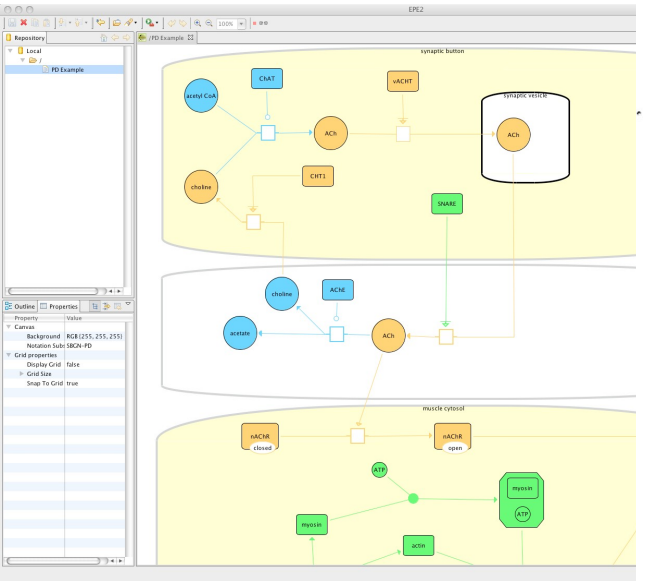

VANTED V1.67
File Edit Analysis Edges Elements FBA Hierarchy Layout Mapping
SBGN.Glycolysis.graphml* - view 1
glucose
glucose 6P
ATP
ADP

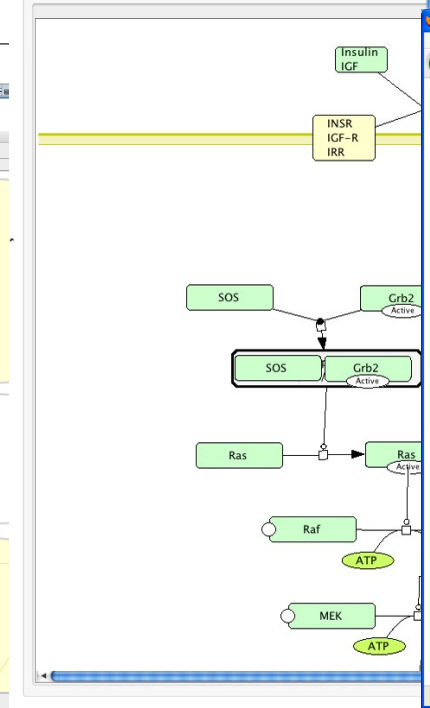

CellDesigner
File Edit Component View Database Layout Simulation Plugin Window SBW Preference Help
Change identity of the species
class
PROTEIN
hypothetical
name
homomultimer
protein
RAF
type
GENERIC
residues/regions
modification
state
empty
text input
Apply
Reset
Cancel

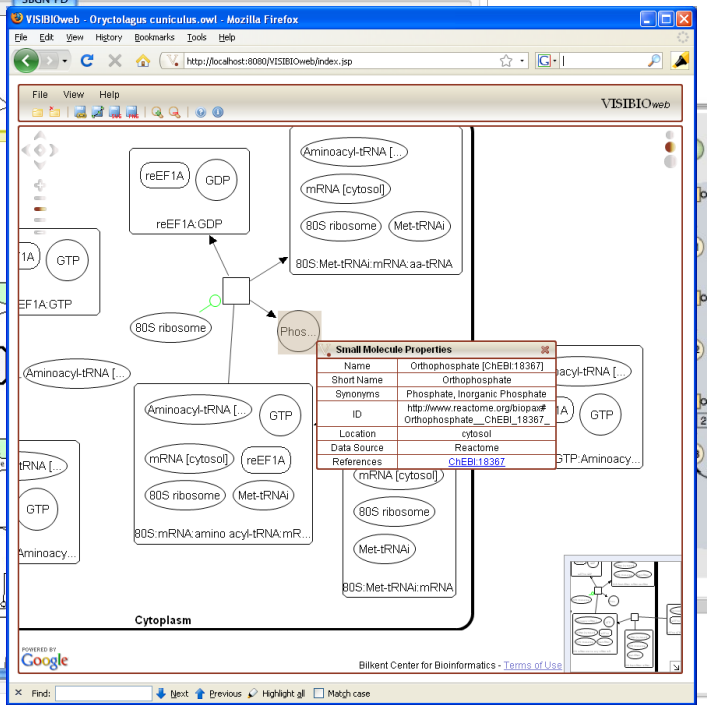

BioModels Home
Browse models
Submit
Sign in
Support
About BioModels
BIOMD0000000005 - Tyson1991_CellCycle_6var
Reference Publication
Cell Cycle Model; Tyson (1991, 6 variables)
Description
Reaction

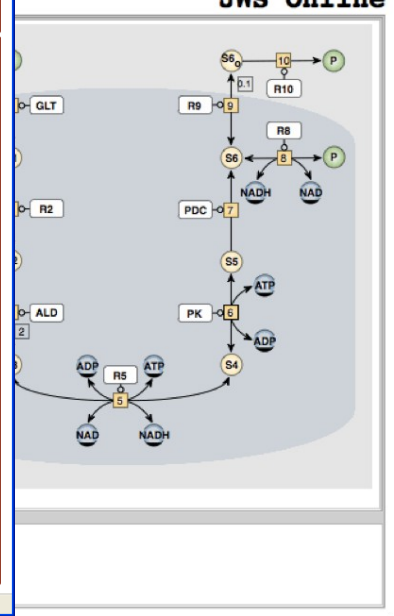
BIOMD0000000005
Refresh
Close
p-cyclin
p-cyclin cdc2
cdc2k
total cdc2
p-cyclin cdc2-p
cdc2k-P
cyclin


PANTHER
Classification System
INSULIN/IGF PATHWAY-MITOGEN ACTIVATED PROTEIN KINASE KINASE/MAP KINASE CASCADE
Export:
Select one
created with CellDesigner
Click components to make selections. Right-click components for more options.
Search selections for:
Genes
Go
Pathway Diagram
Pathway Description
File Edit Zoom Select Color
Interactive Standard/Activity Flow
SBGN Image View


EPE2
synaptic button
synaptic vesicle
muscle cytosol


SBGN PD
Insulin
IGF
INSR
IGF-R
IRR
SOS
Grb2
Ras
Raf
MEK
ATP


VISIBIOweb - Oryctolagus cuniculus.owl - Mozilla Firefox
VISIBIOweb
reEF1A
GDP
reEF1A:GDP
80S ribosome
Met-tRNAi
80S:Met-tRNAi:mRNA:aa-tRNA
Small Molecule Properties
Name
Orthophosphate [ChEBI:18367]
Short Name
Orthophosphate
Synonyms
Phosphate, Inorganic Phosphate
ID
Location
cytosol
Data Source
Reactome
References
ChEBI:18367
mRNA [cytosol]
80S:mRNA:amino acyl-tRNA:mR...
80S:Met-tRNAi:mRNA
Cytoplasm
Bilkent Center for Bioinformatics - Terms of Use


JWS Online
GLT
R9
R8
S6
NADH
NAD
R2
PDC
S5
ALD
PK
ATP
ADP
S4
R5

Status of Specifications

- SBGN Process Descriptions
  - Level 1 Version 1.0 released on August 23rd 2008
  - Level 1 Version 1.1 released on September 1st 2009
  - Level 1 Version 2 under discussion
- SBGN Entity Relationships
  - Level 1 Version 1.0 released on September 1st 2009
- SBGN Activity Flows
  - Level 1 Version 1.0 released on September 1st 2009

Future SBGN meetings

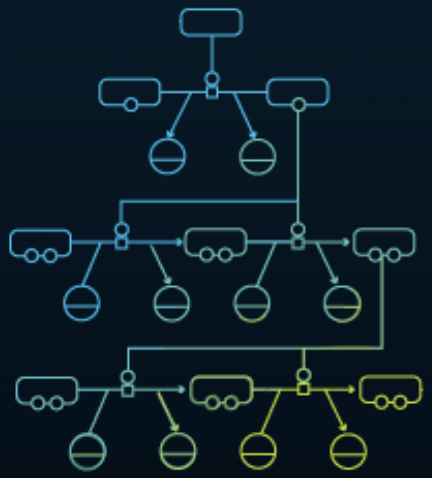
- 4rd SBGN hackathon (SBGN 5.5)
  - 21-23 April 2010
  - Wittenberg
- 6th SBGN forum (provisional)
  - October 2010
  - Edinburgh
  - Satellite of ICSB 2010

- Future hackathons and forums
  - part of HARMONY and COMBINE meetings
  - SBML (model), SED-ML (simulation), SBO (semantics), MIRIAM (metadata), SBGN (graphical), BioModels DB (distribution), ?

http://sbgn.org/

SBGN Systems Biology Graphical Notation

Home | News | Documents | Lists | Community | Events | About | Google Site Search.



A Visual Notation for Network Diagrams in Biology

SBGN.org is the global portal for documentation, news, and other information about the Systems Biology Graphical Notation (SBGN) project, an effort to standardize the graphical notation used in maps of biochemical and cellular processes studied in systems biology.

Standardizing the visual representation is crucial for more efficient and accurate transmission of biological knowledge between different communities in research, education, publishing, and more. When biologists are as familiar with the notation as electronics engineers are familiar with the notation of circuit schematics, they can save the time and effort required to familiarize themselves with different notations, and instead spend more time thinking about the biology being depicted.

SBGN is made up of [I three orthogonal languages], representing different visions of biological systems. Each language defines a comprehensive set of symbols with precise semantics, together with detailed syntactic rules how maps are to be interpreted.

On this site, you can browse some example maps to get a feeling for SBGN, read the SBGN specification documents , join online discussions, see current working documents and software support in the SBGN wiki, and much more.

SBGN is the work of many people. It would not have been possible without the generous support of multiple organizations over the years, for which we are very thankful.

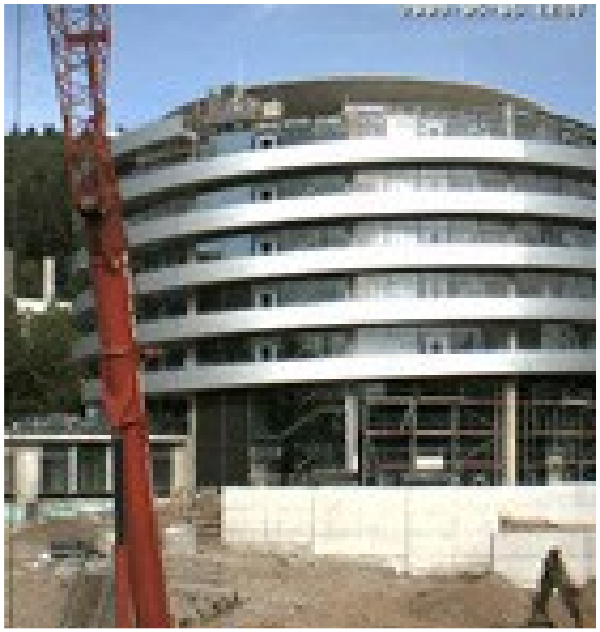
To quote SBGN as a whole, please use:

Le Novère N, Hucka M, Mi H, Moodie S, Schreiber F, Sorokin A, Demir E, Wegner K, Aladjem MI, Wimalaratne SM, Bergman FT, Gauges R, Ghazal P, Kawaji H, Li L, Matsuoka Y, Villéger A, Boyd SE, Calzone L, Courtot M, Dogrusoz U, Freeman TC, Funahashi A, Ghosh S, Jouraku A, Kim S, Kolpakov F, Luna A, Sahle S, Schmidt E, Watterson S, Wu G, Goryanin I, Kell DB, Sander C, Sauro H, Snoep JL, Kohn K, Kitano H. The Systems Biology Graphical Notation. Nat Biotechnol. 2009 27(8):735-41.

SBGN News

(02 Sep.'09) The first specifications for SBGN Entity Relationships and SBGN Activity Flows] are out.

What happens if one can read the blueprint



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Special contributors

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The whole community participating to SBGN meetings, and mailing-lists

NEDO bbsrc biotechnology and biological sciences research council NIGMS EMBL