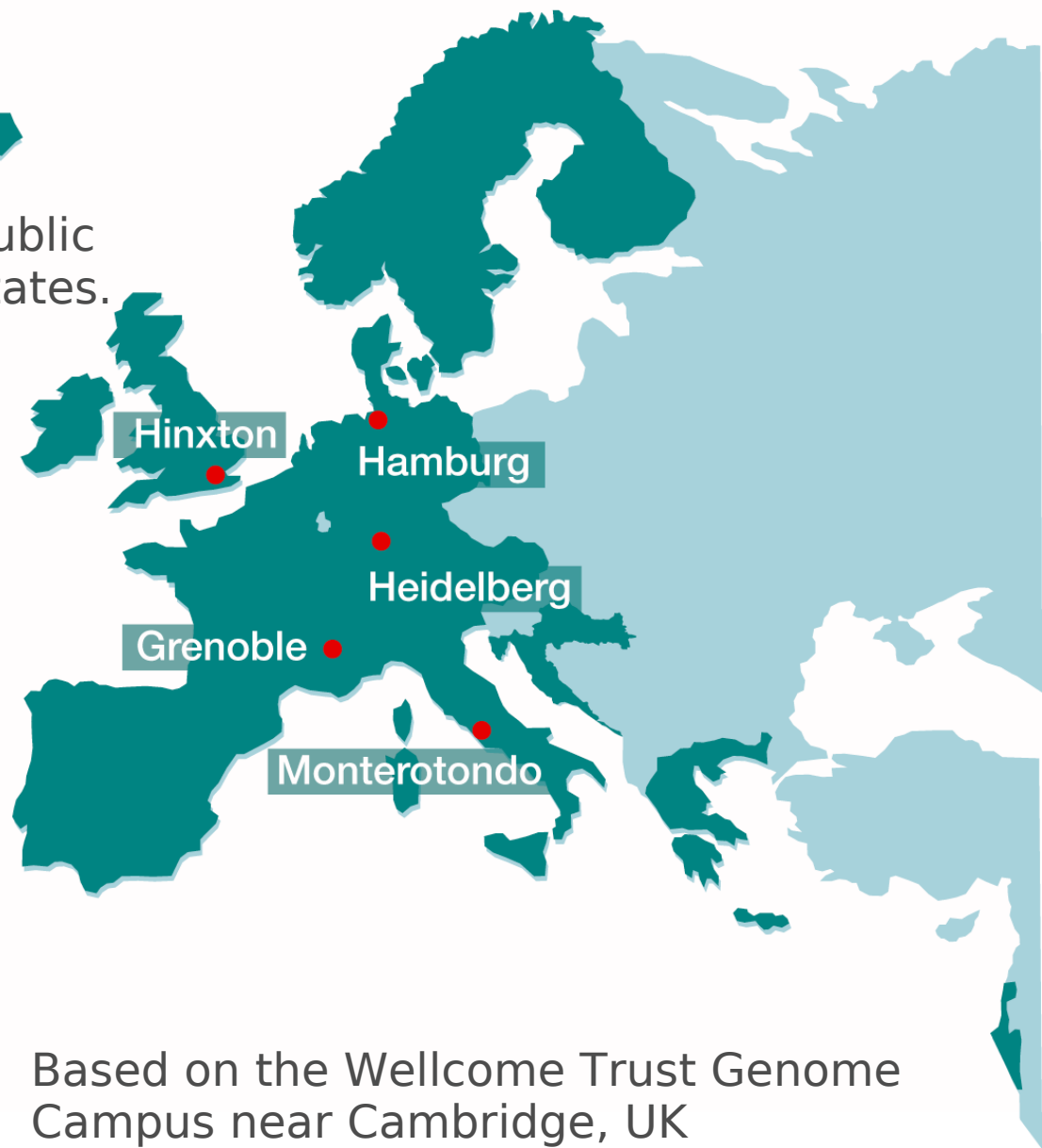


The Systems Biology Graphical Notation

Nicolas Le Novère, EMBL-EBI

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

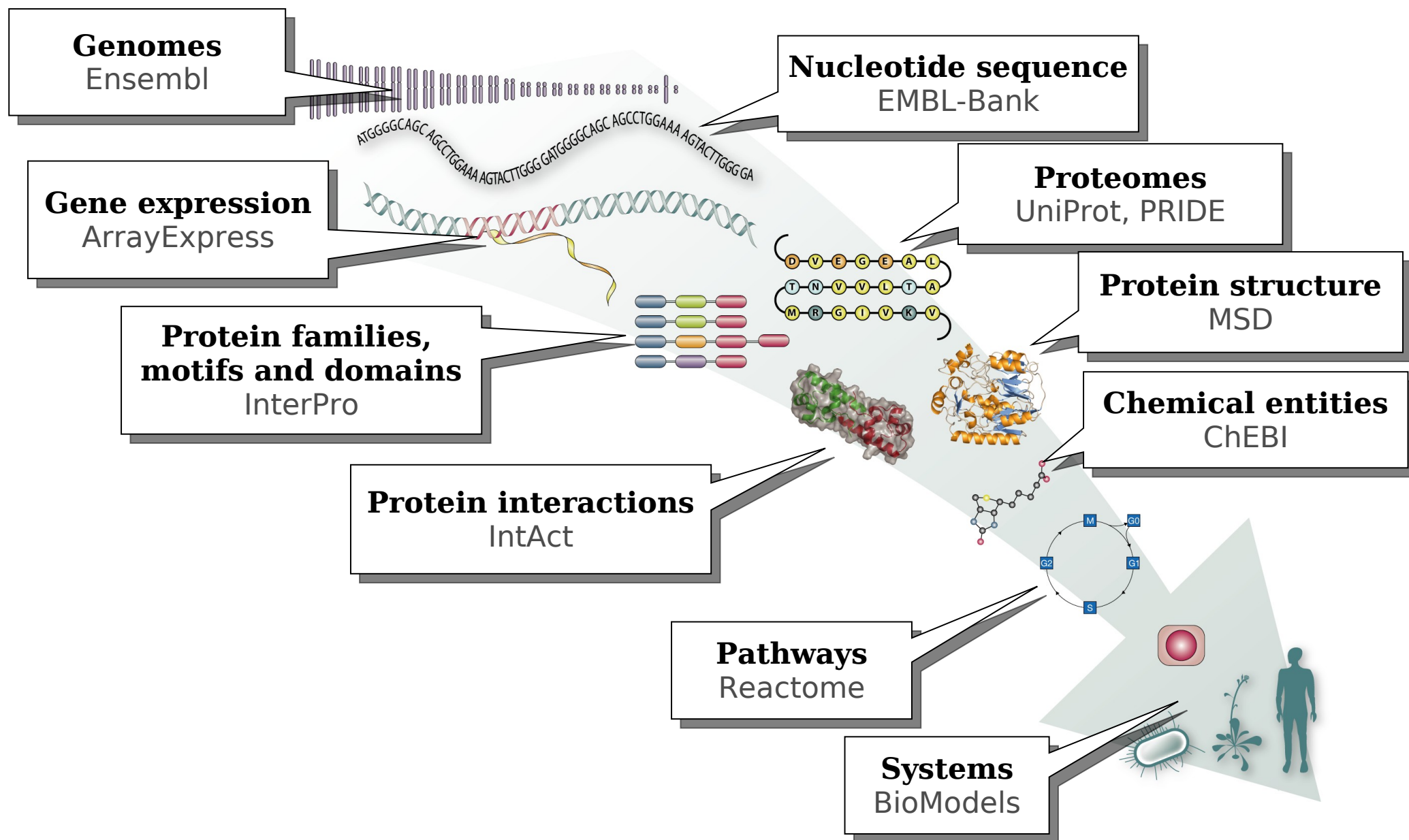
- Non-profit organization
- Part of the European Molecular Biology Laboratory (EMBL), a basic research institute funded by public research monies from 19 member states.

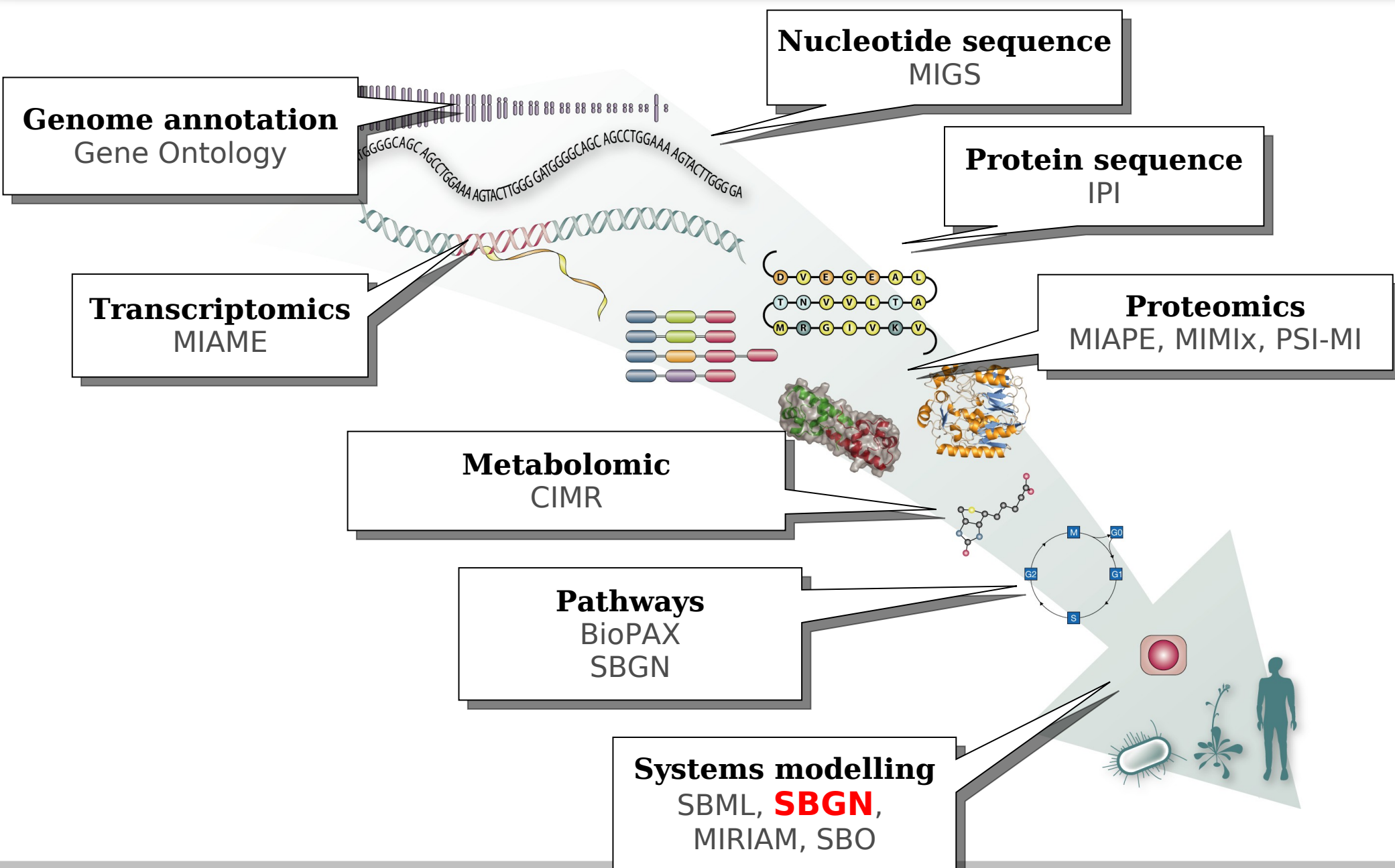


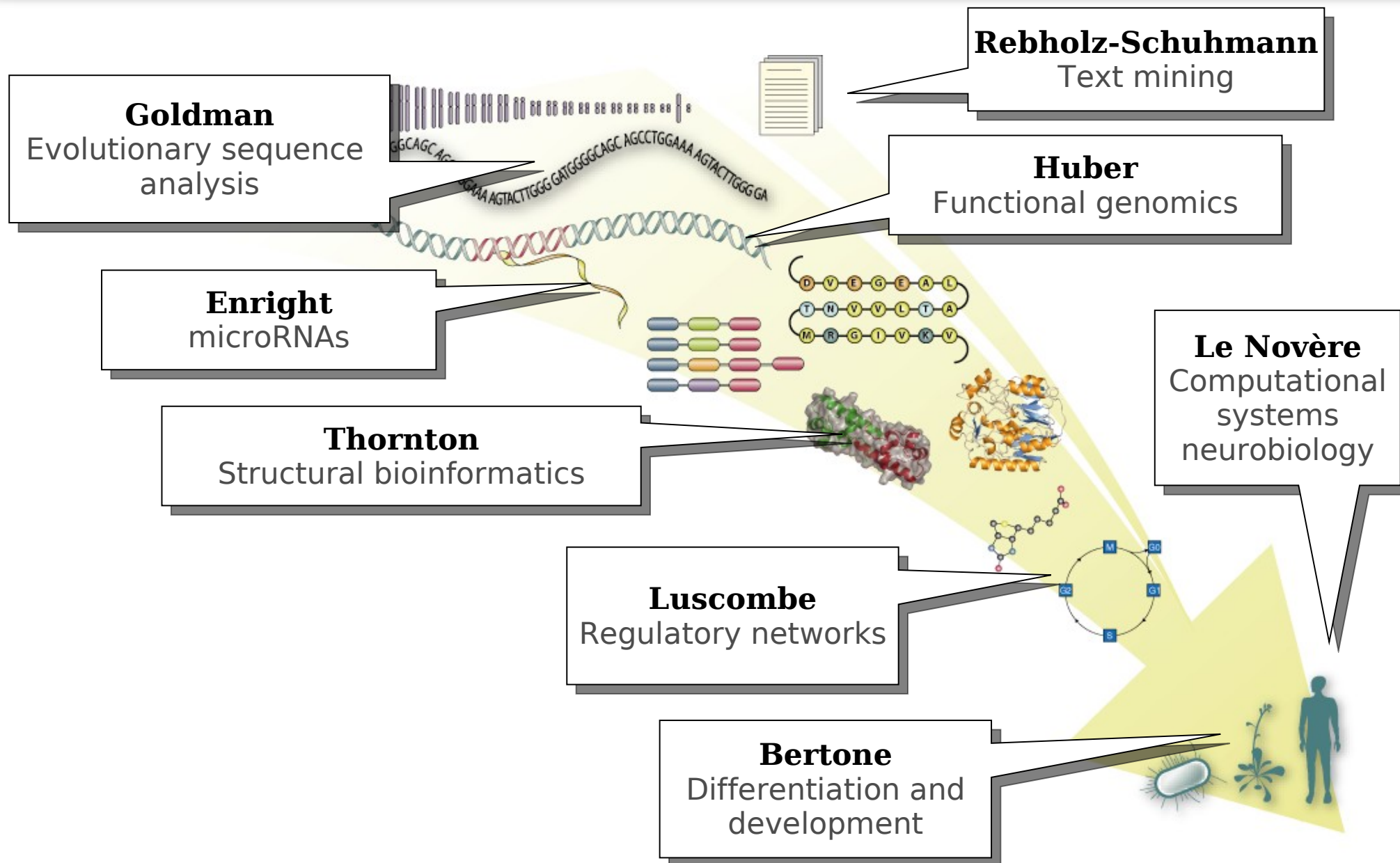
- Based on the Wellcome Trust Genome Campus near Cambridge, UK

- To provide freely available **data** and bioinformatics **services** to all facets of the scientific community in ways that promote scientific progress
- To contribute to the advancement of biology through basic investigator-driven **research** in bioinformatics
- To provide advanced bioinformatics **training** to scientists at all levels, from PhD students to independent investigators
- To help disseminate cutting-edge technologies to **industry**

- **Accessibility** – all data and tools freely available without restriction
- **Compatibility** – we develop and promote the use of standards in bioinformatics
- **Comprehensive data sets** – agreements with other data providers ensure that our resources contain comprehensive and up-to-date data; agreements with publishers ensure that published data are placed in a public repository at the earliest opportunity
- **Portability** – data and software can be downloaded and installed locally
- **Quality** – Our databases are enhanced through annotation and cross-referencing

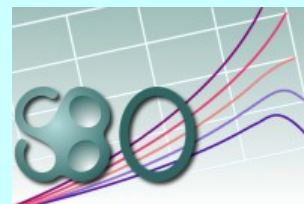
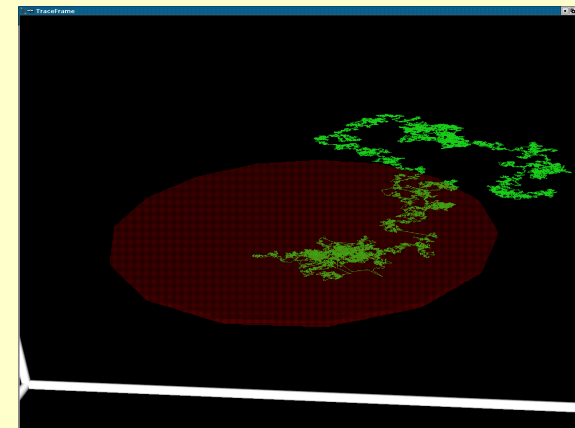
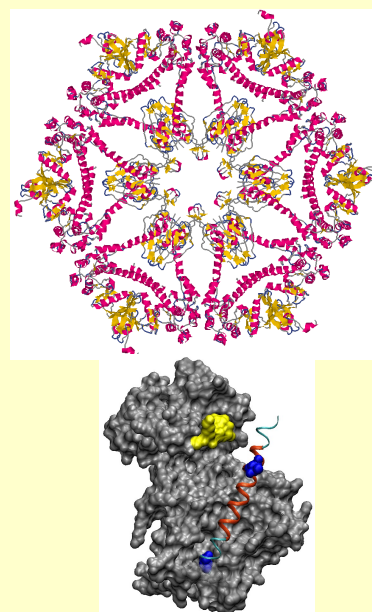
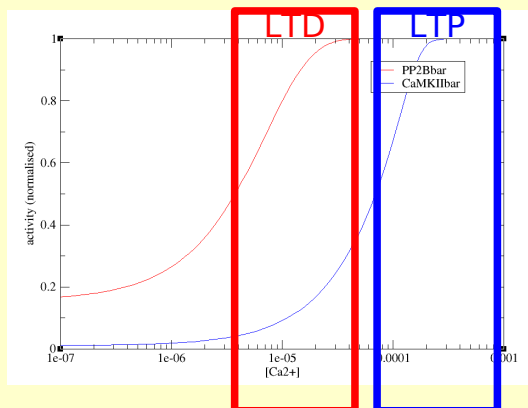
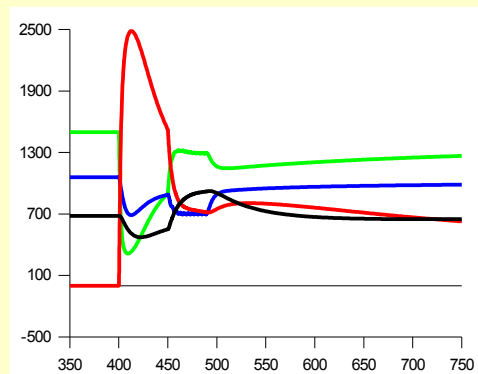




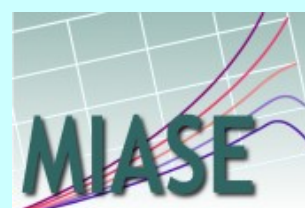


- ~3.4 million web requests per day
- >300 000 unique hosts served per month
- ~3 million files downloaded per month
- ~150 TB data downloaded in 2007
- Millions of cross-references

Computational Neurobiology



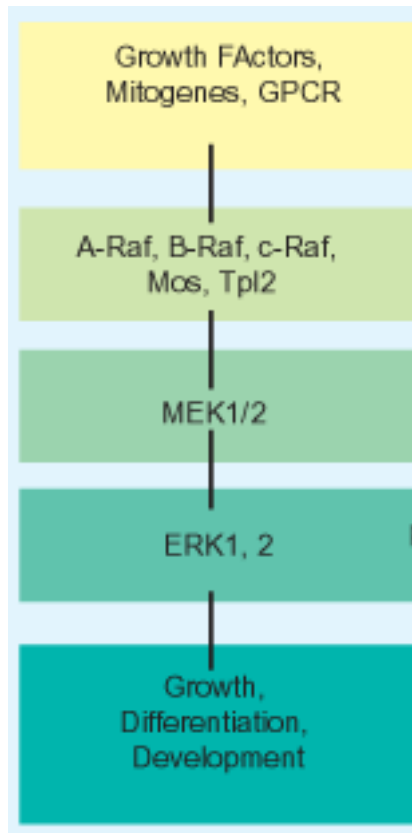
Systems Biology



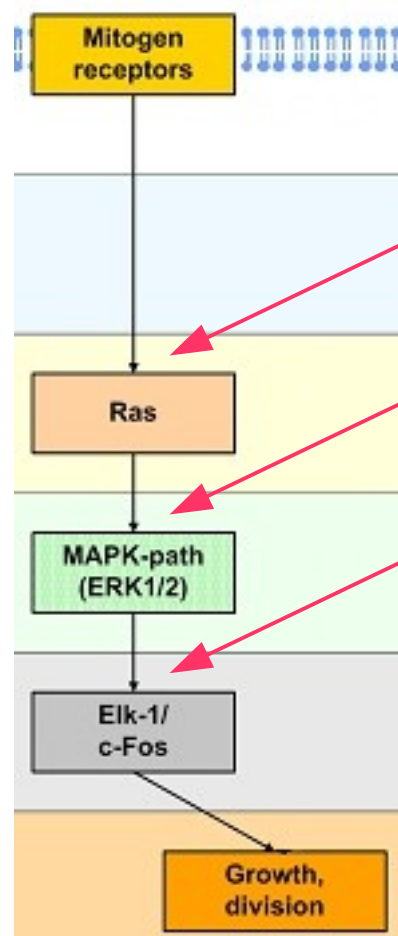
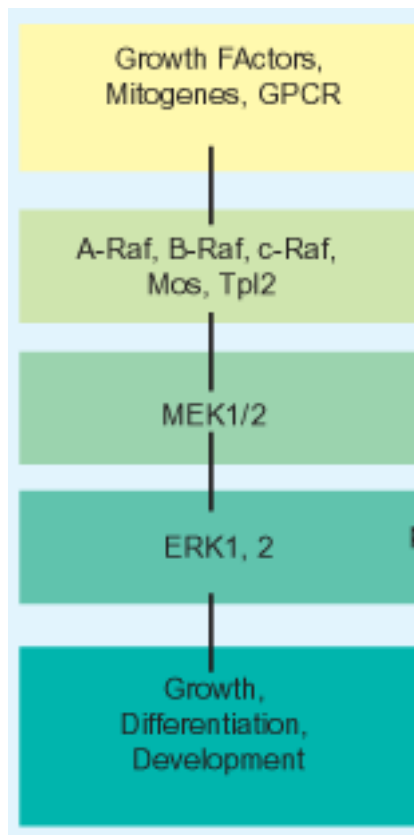
The Systems Biology Graphical Notation

Nicolas Le Novère, EMBL-EBI

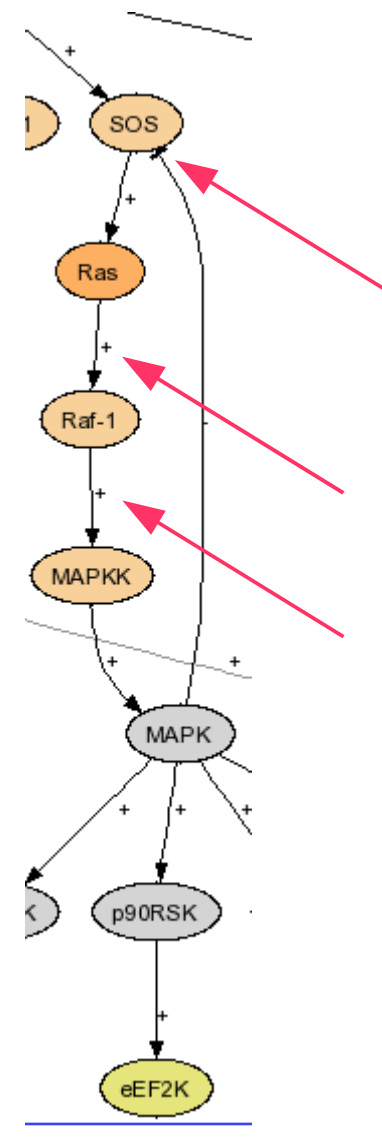
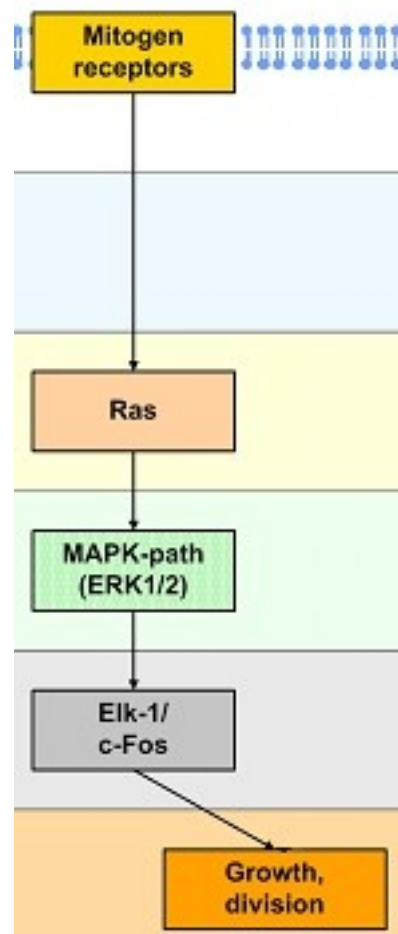
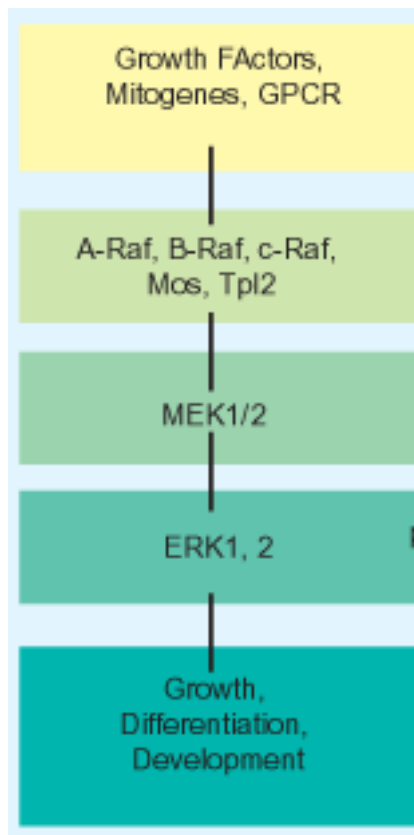
(on the behalf of SBGN editors, authors and contributors)



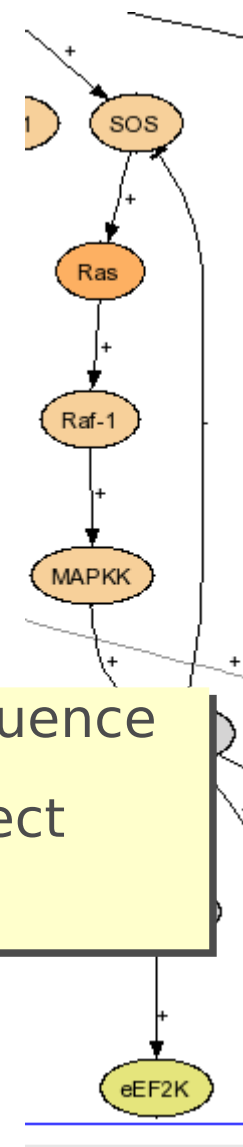
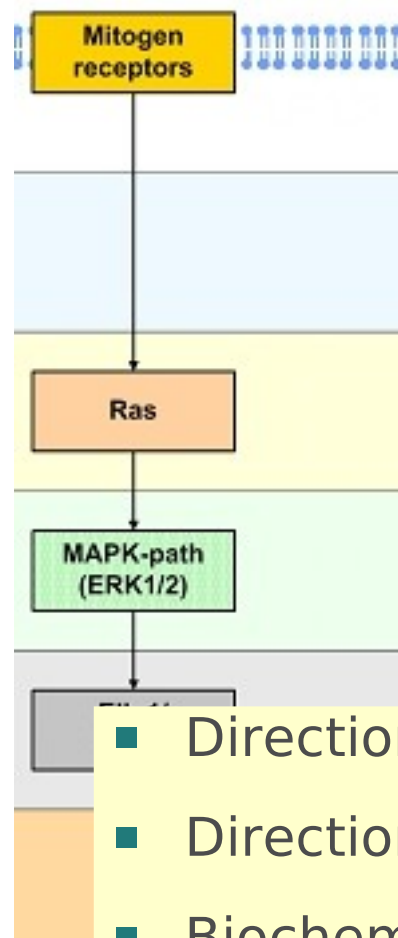
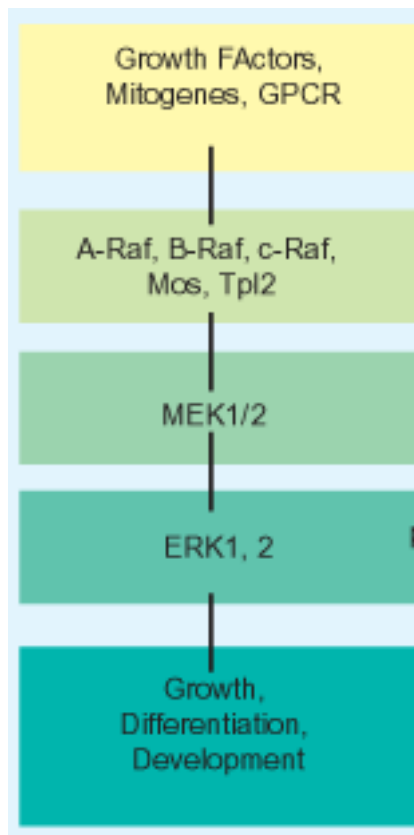
- No temporal sequence
- No directionality
- No biochemical effects
- No mechanistic descriptions



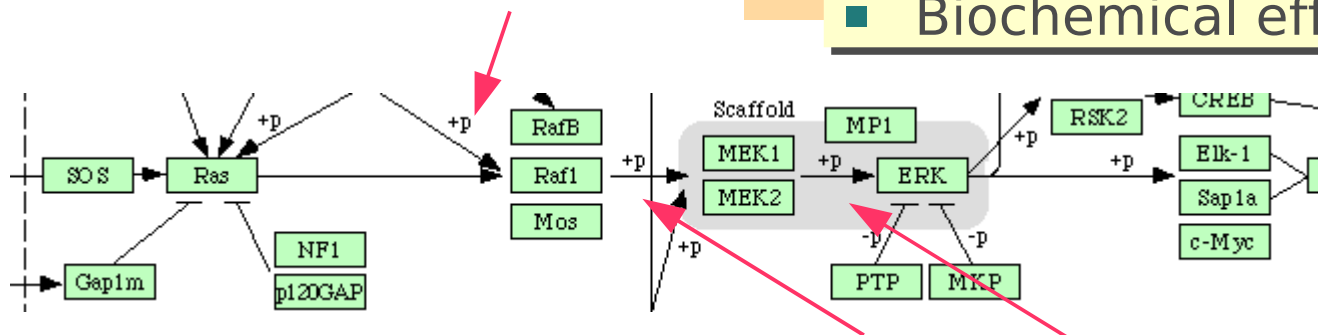
■ Directionality of influence

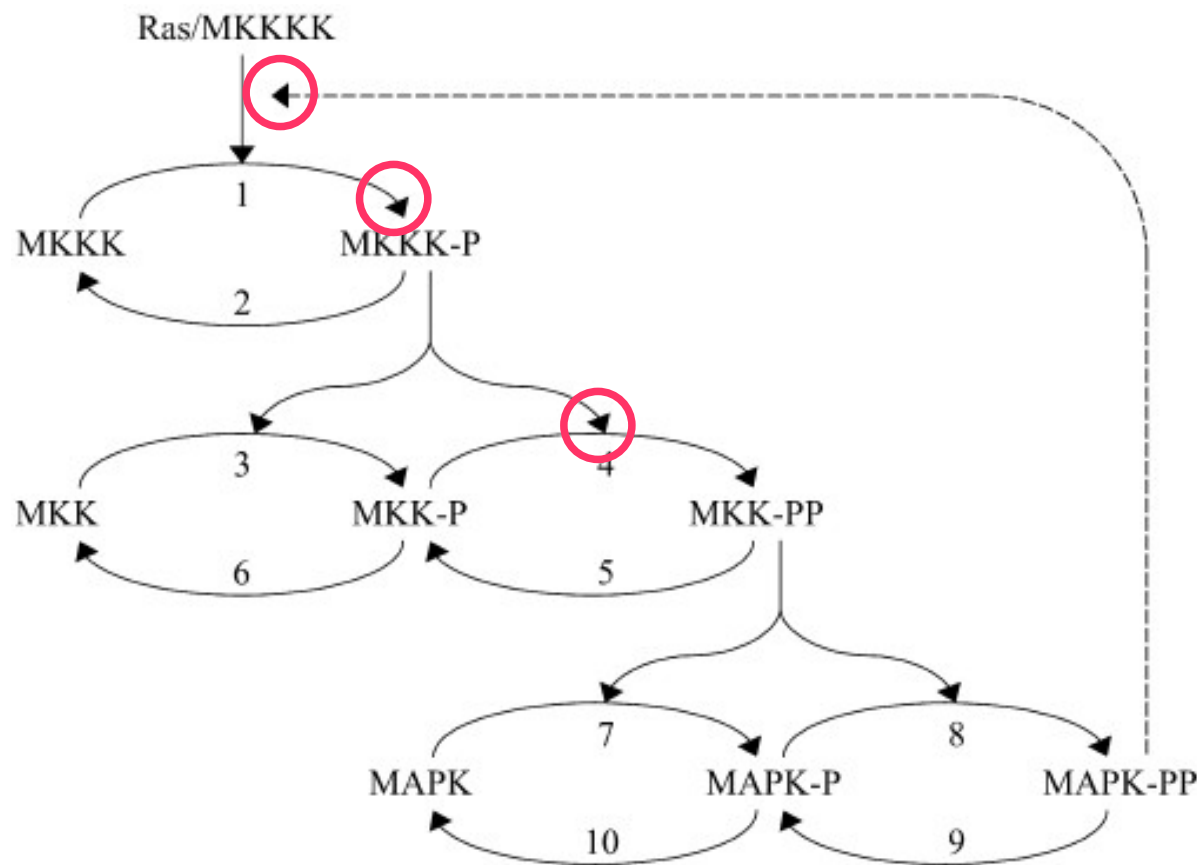


- Directionality of influence
- Directionality of effect



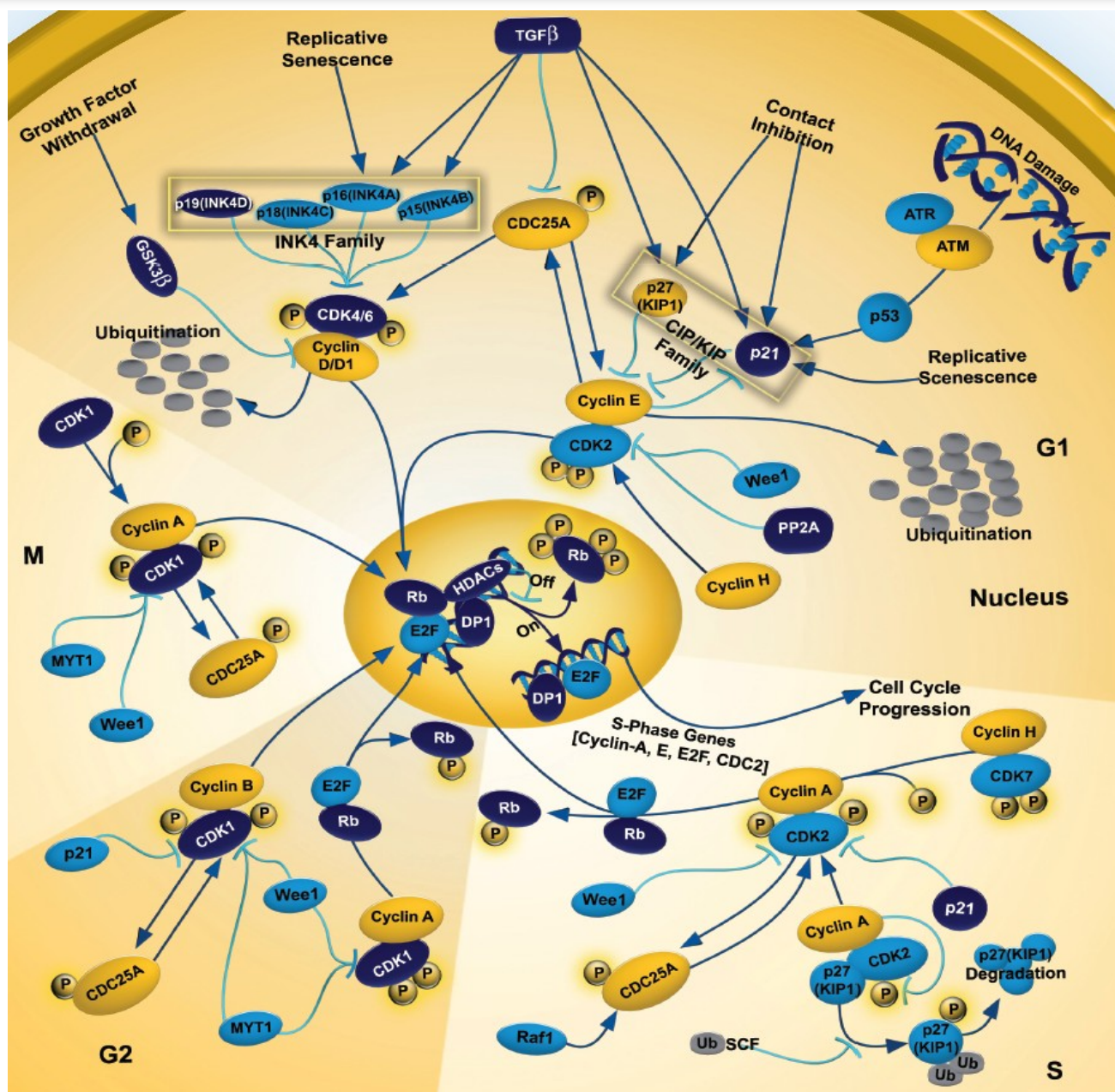
- Directionality of influence
- Directionality of effect
- Biochemical effect

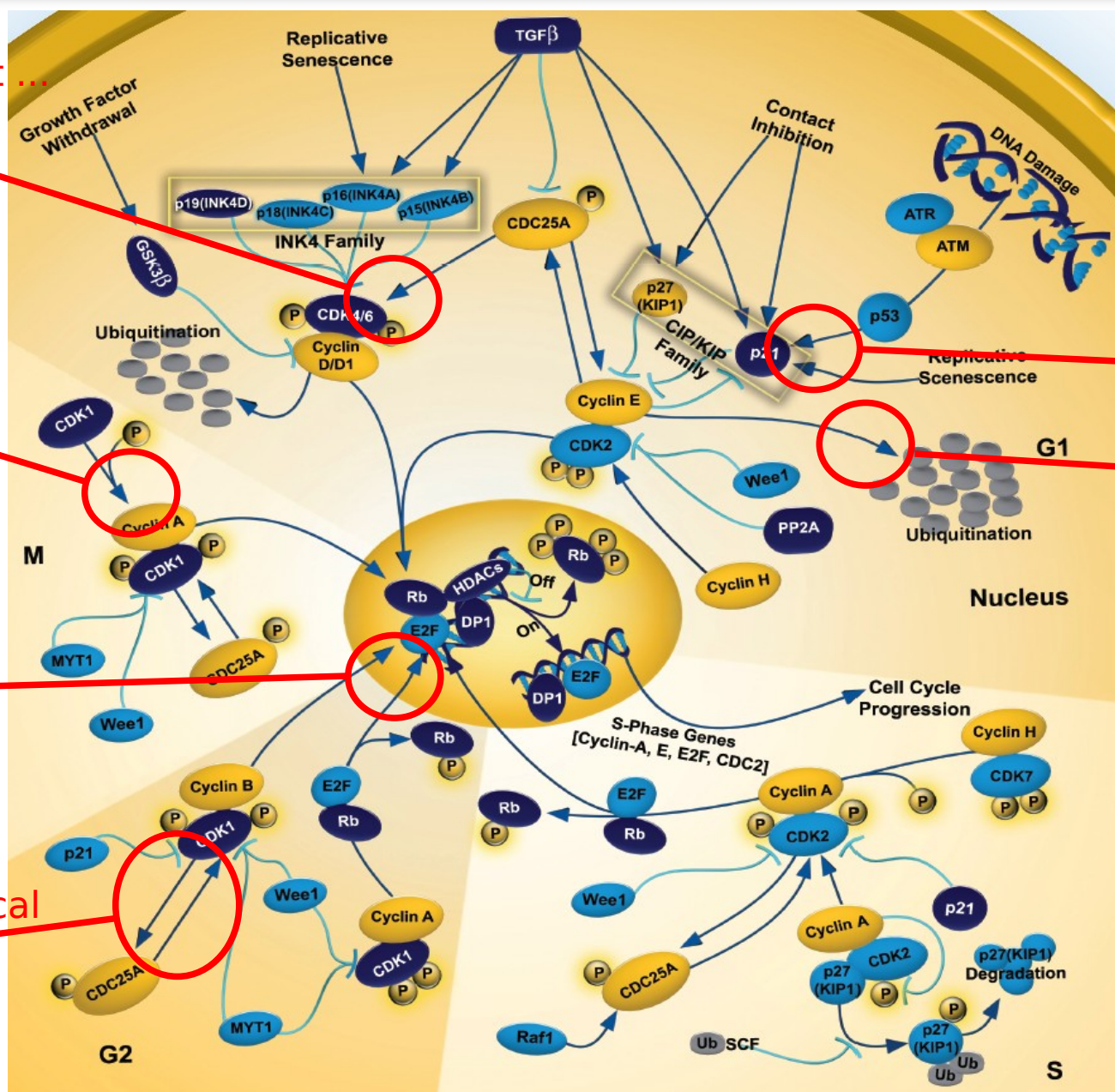




THREE *different* meanings
for ONE symbol!

- Transition
- catalysis
- inhibition





Stimulates? but ...
what exactly?

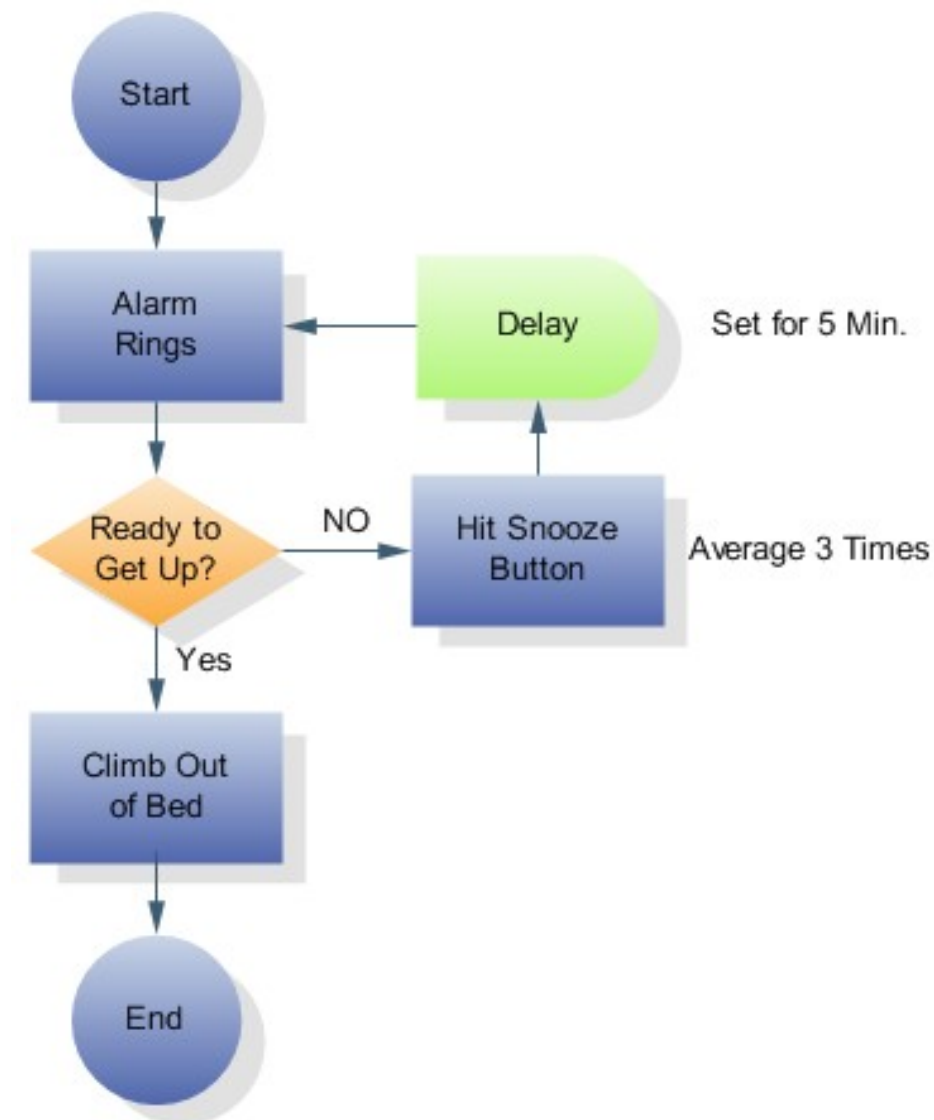
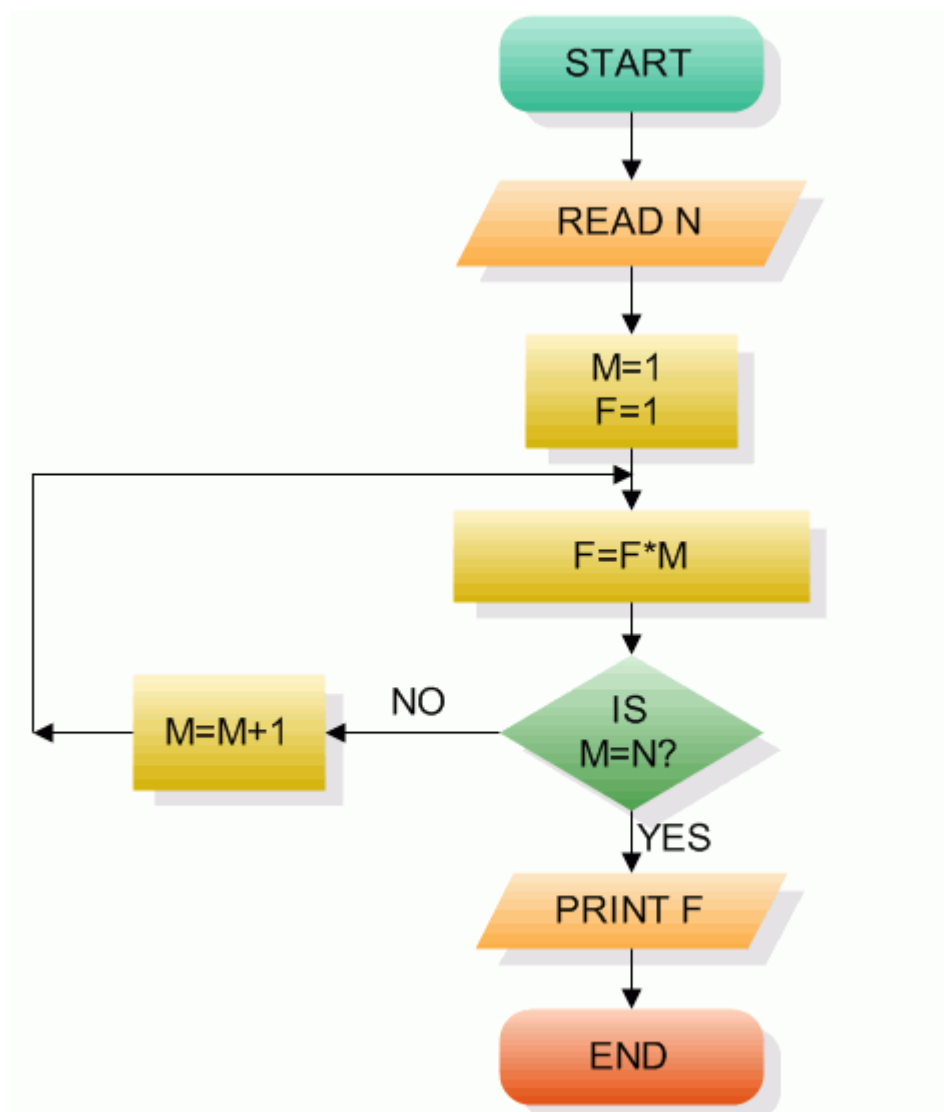
Associates into?

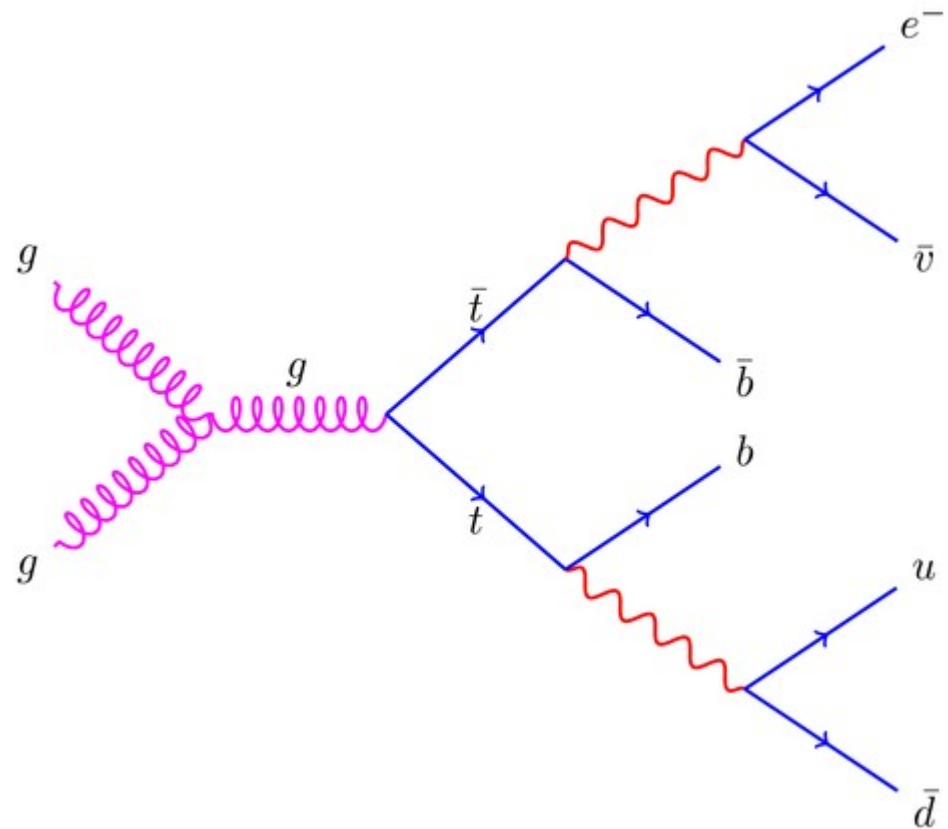
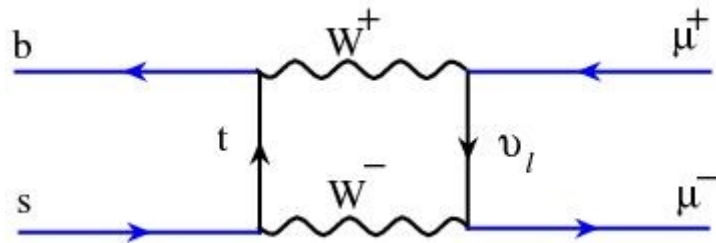
Stimulates gene
transcription?

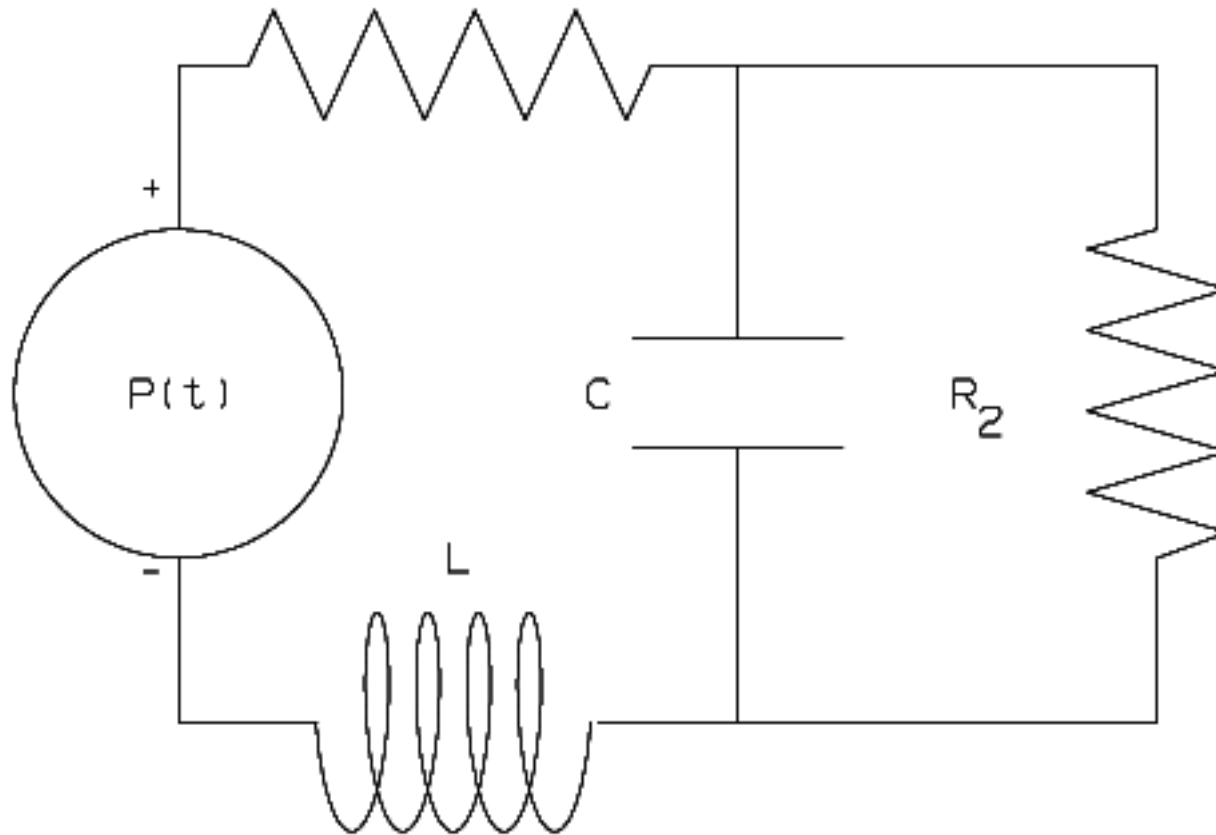
Is degraded?

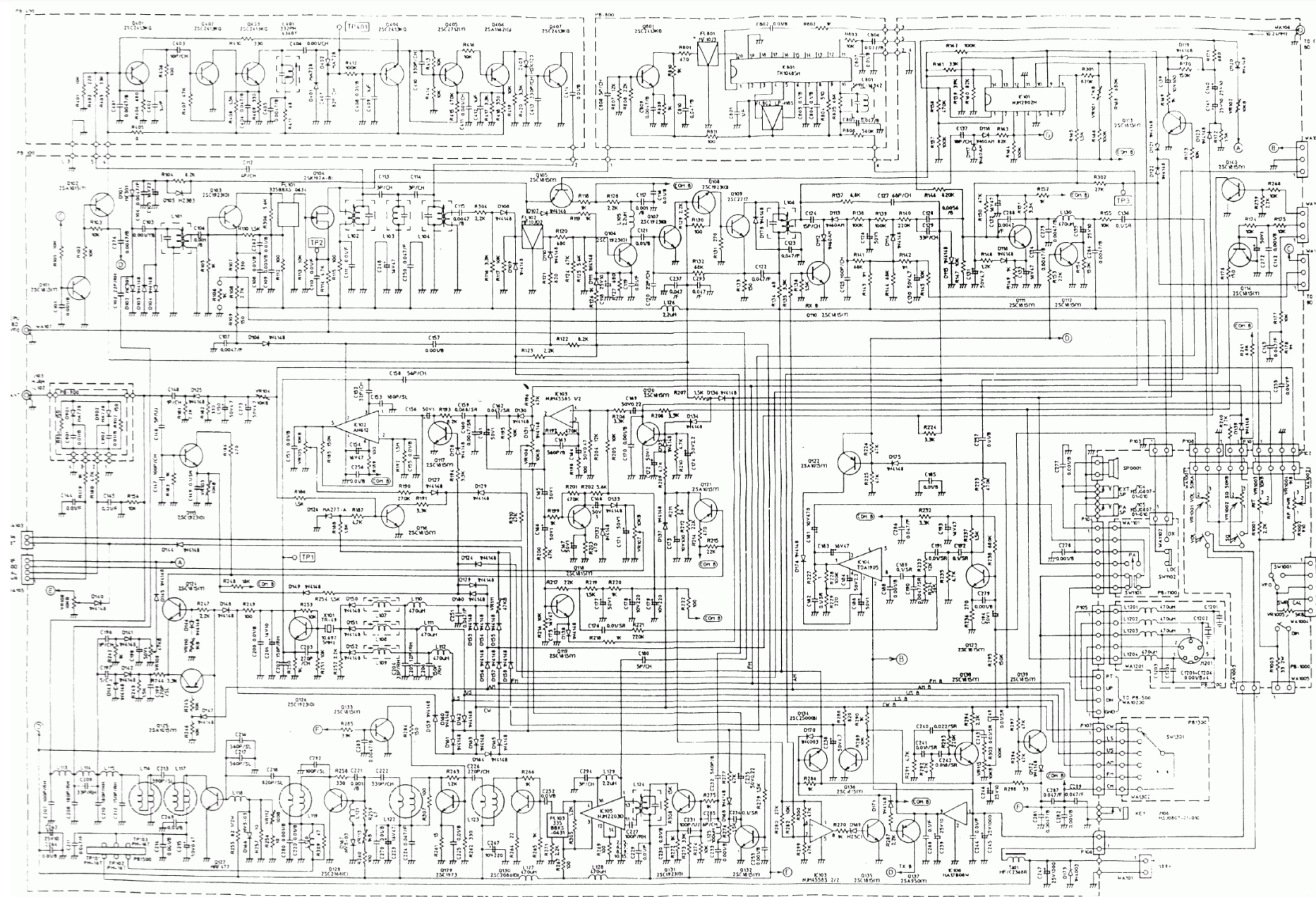
Translocates?

No idea. Reciprocal
stimulation?









What did those diagram bring?





Basic science

Systems of Life

Systems Biology



Technology



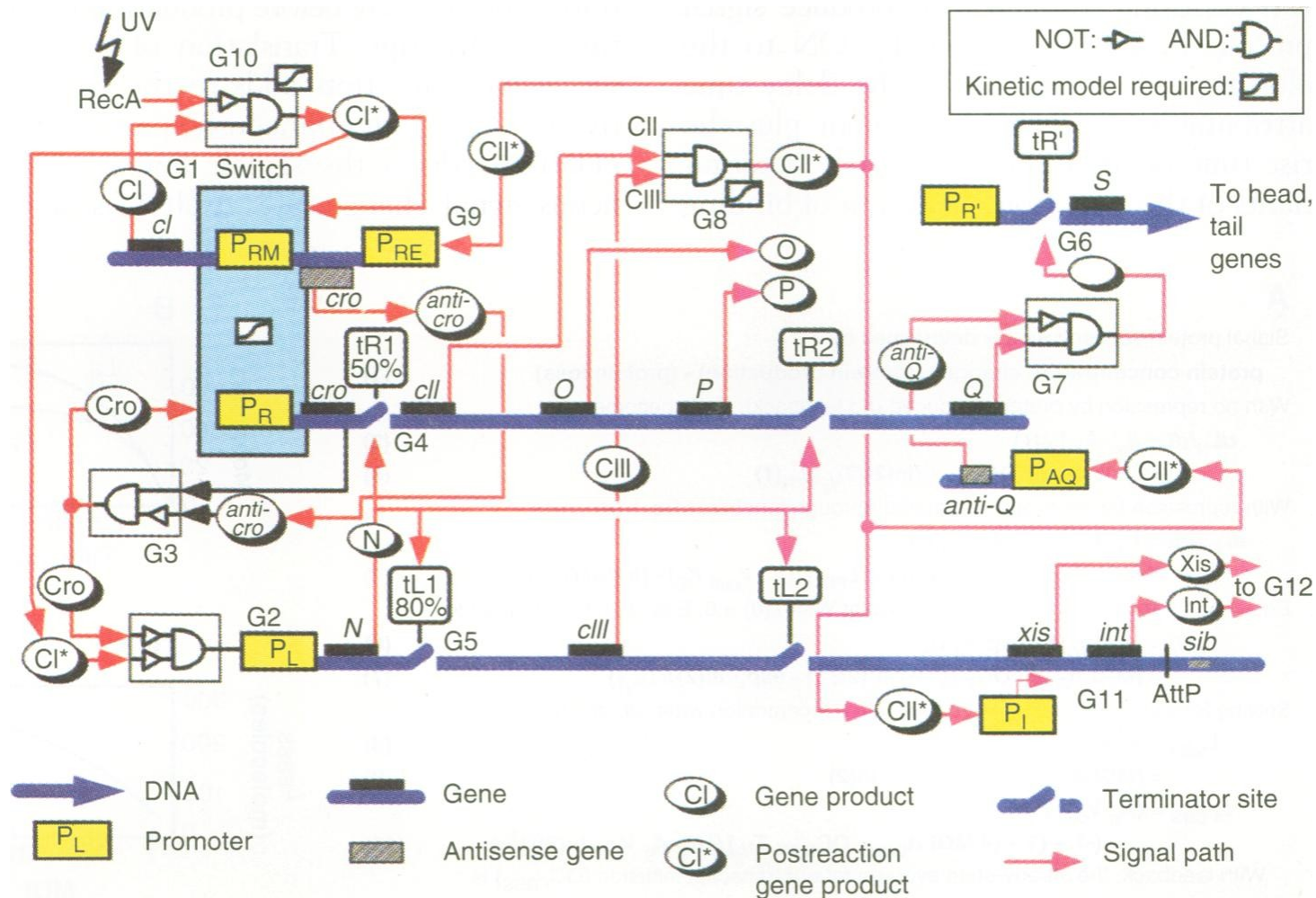
EXTREME GENETIC ENGINEERING

An Introduction to Synthetic Biology

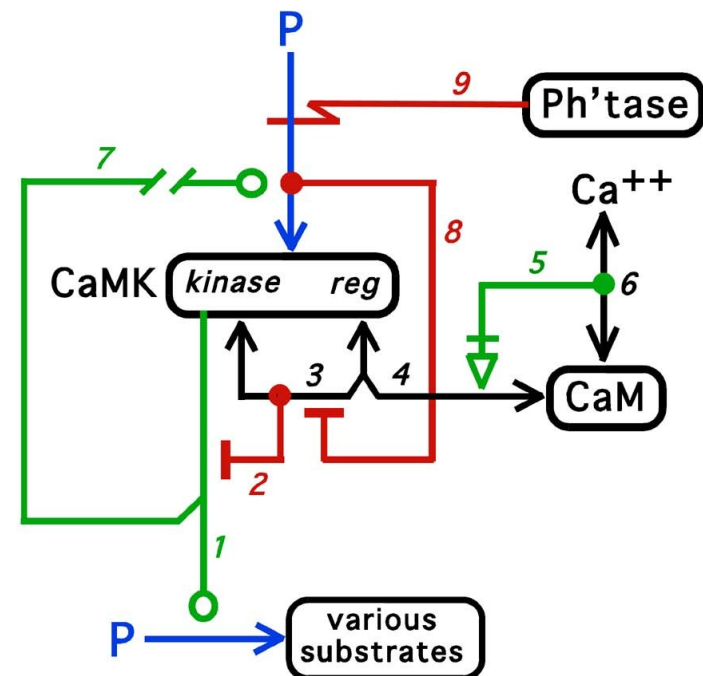
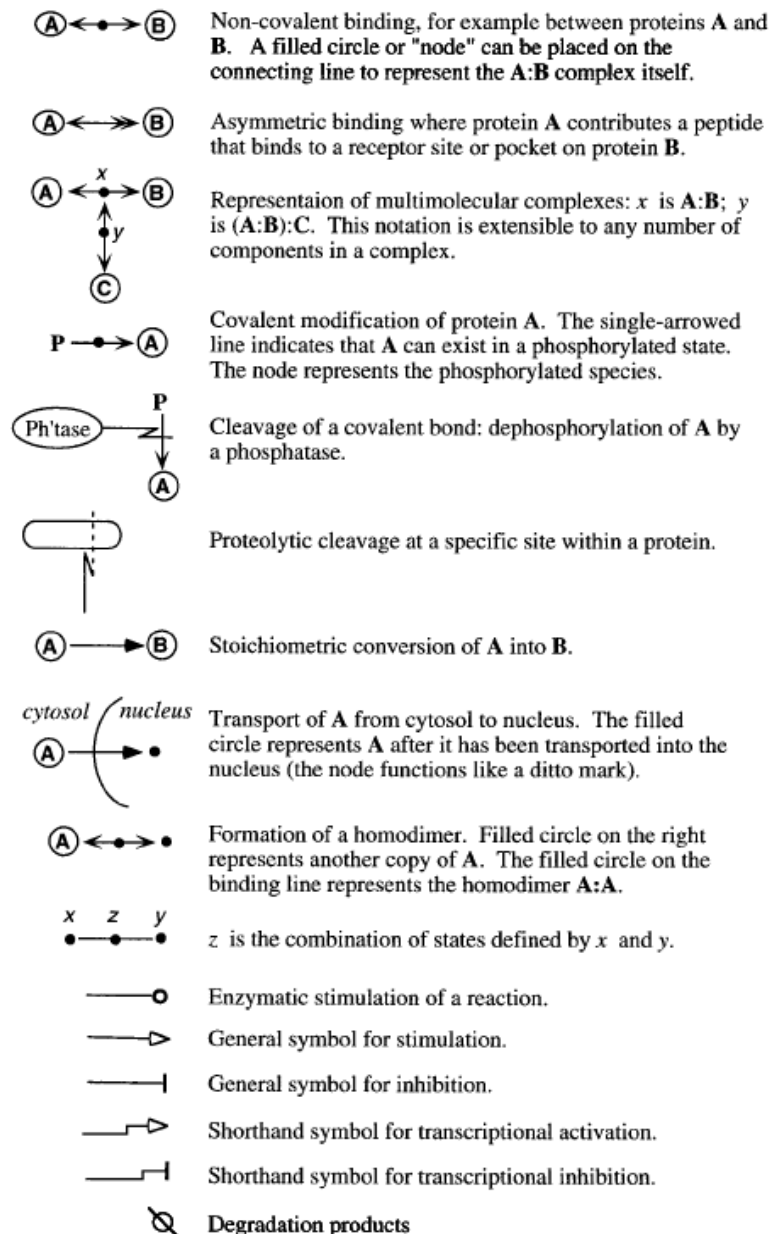
January 2007



- 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



- McAdams and Shapiro (1995) Science, 269: 650-657



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

- Non-sequential interactions between entities
- Each *entity* appears only once
- Complexes are defined by interactions
- Modulations of relationships possible
- Order of interactions is meaningful (only binary ones)
- Angles between edges are meaningful
- ...
- Designed manually

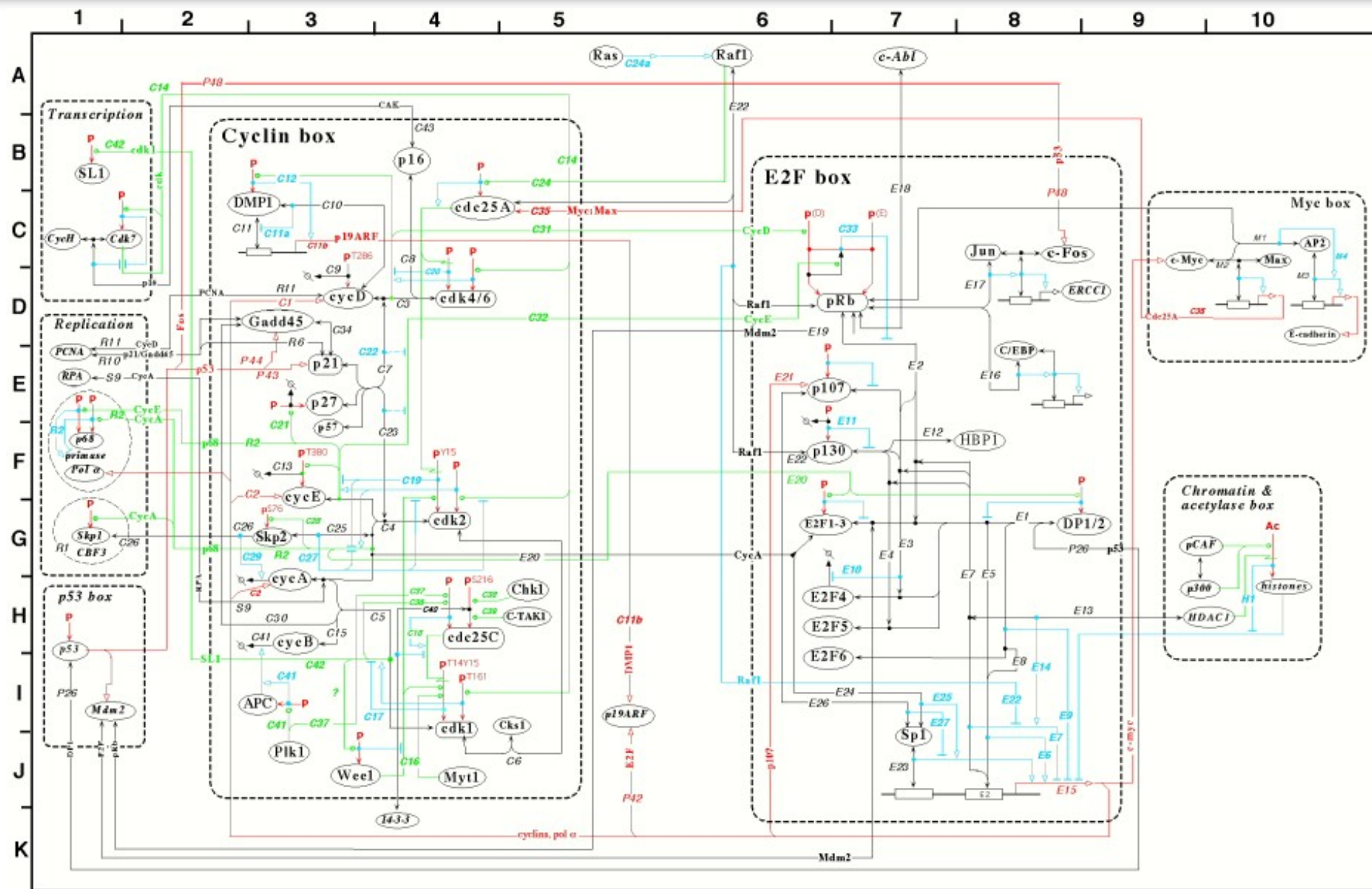
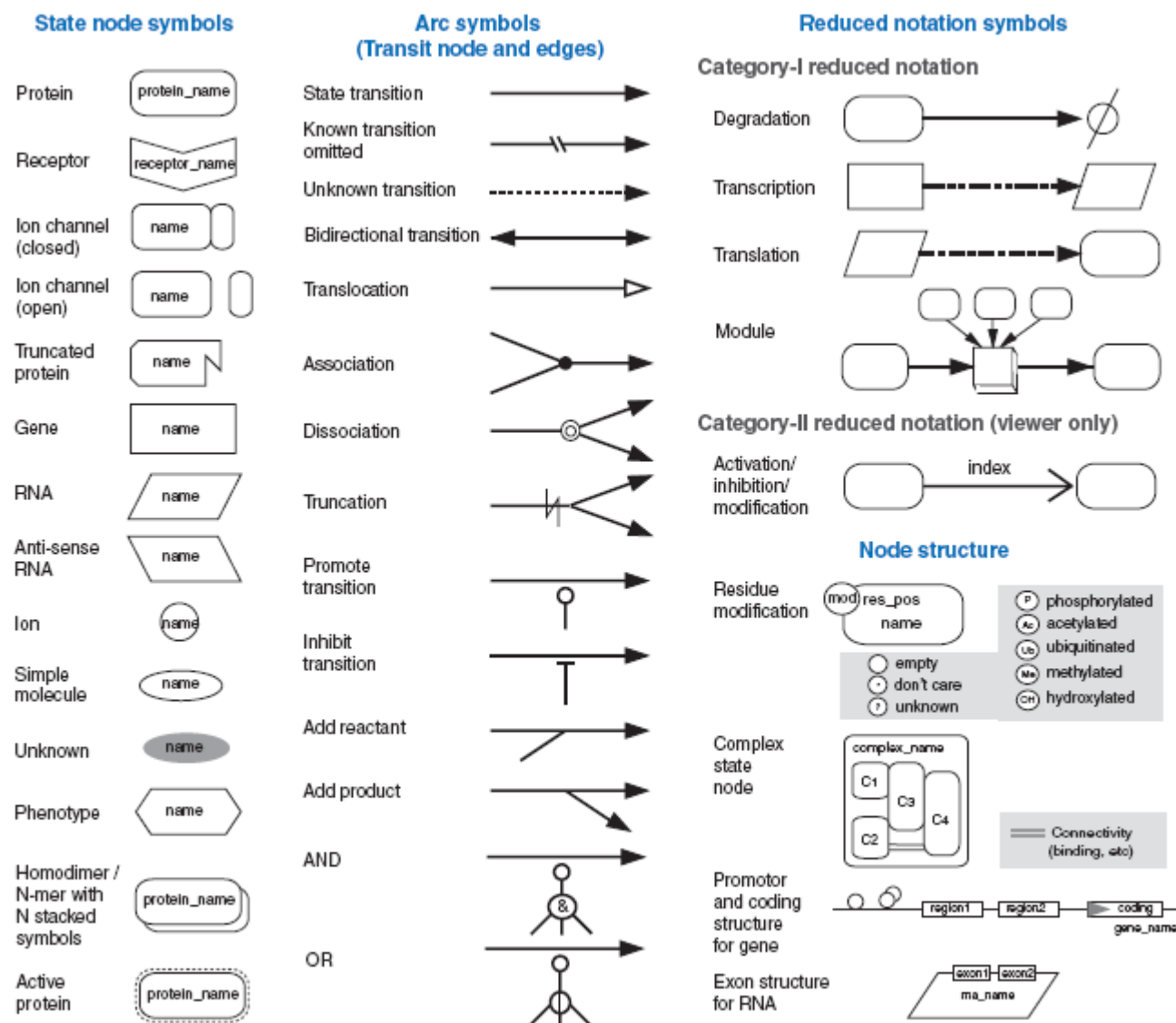


Figure 6A: The Cyclin - E2F cell cycle control system (version 3a - June 8, 1999)

MIM-Cell 20



■ Kitano (2003)
Biosilico, 1: 169-170

■ Kitano et al (2005)
Nat Biotech, 23:
961-966

- Causal sequence of molecular processes and their results
- Each *state* appears only once
- Complexes are defined as independent entity nodes
- Correspondence with *pathway* descriptions and reaction-based *models*
- Some software support (CellDesigner)

- 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
- No software support (except Cell Designer 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

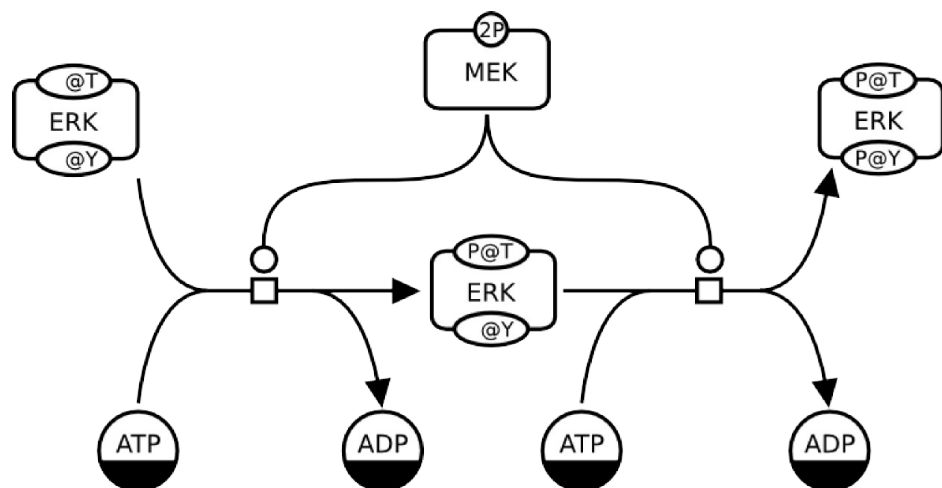
Enters The Systems Biology Markup Language



<http://www.sbgn.org/>

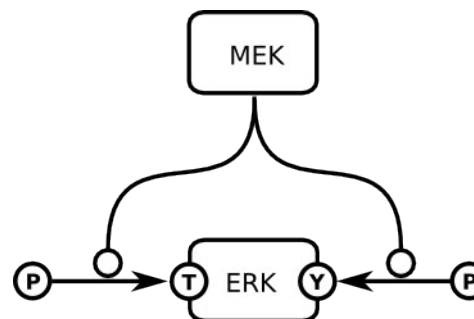
- A way to unambiguously describe biochemical and cellular events in graphs
- Limited amount of symbols (32) ➡ Smooth learning curve
- Can graphically represent quantitative models, biochemical pathways, at different levels of granularity
- Developed over three years by a growing community
- Three languages
 - Process Diagrams ➡ one state = one glyph, biochemical level
 - Entity Relationships ➡ one entity = one glyph, biochemical level
 - Activity Flow ➡ conceptual level

Process diagrams



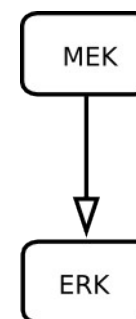
- Unambiguous
- Mechanistic
- Sequential
- Combinatorial explosion

Entity Relationships diagrams



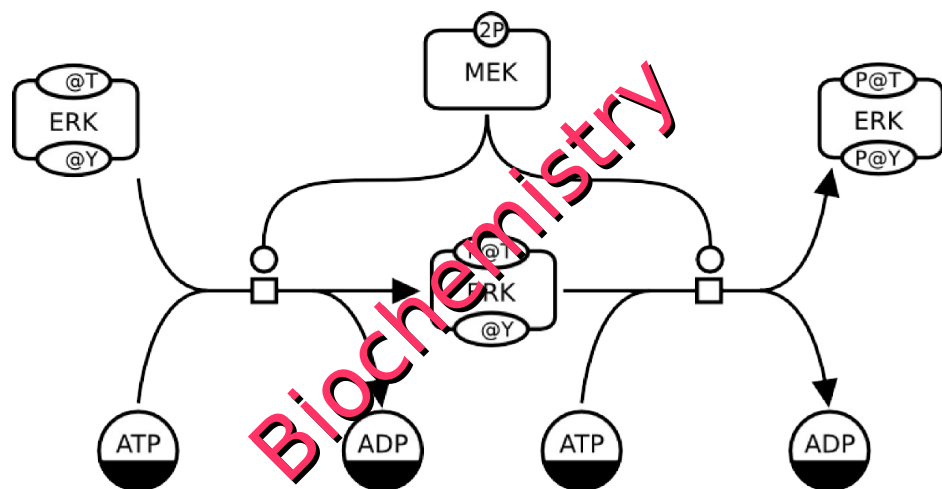
- Unambiguous
- Mechanistic
- Non-sequential

Activity Flow diagrams



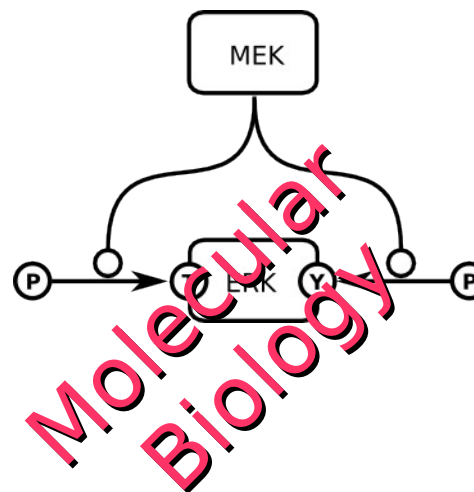
- Ambiguous
- Conceptual
- Sequential

Process diagrams



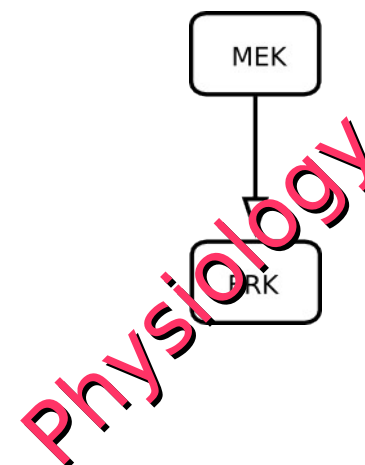
- Unambiguous
- Mechanistic
- Sequential
- Combinatorial explosion

Entity Relationships
diagrams

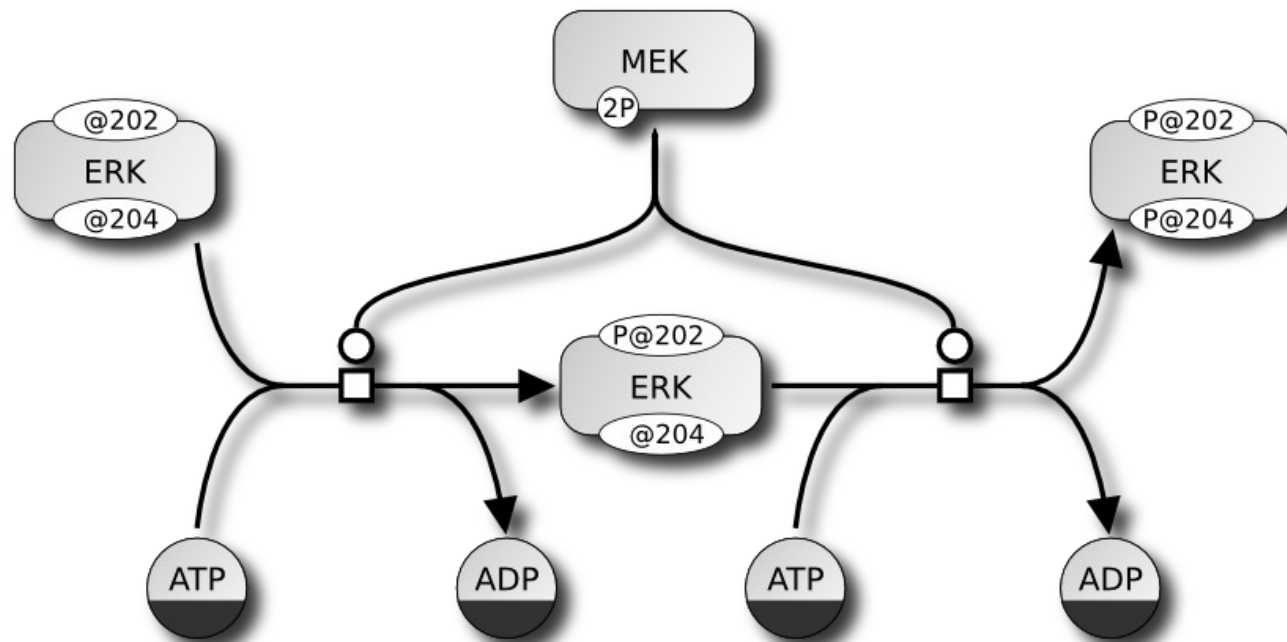


- Unambiguous
- Mechanistic
- Non-sequential

Activity Flow
diagrams

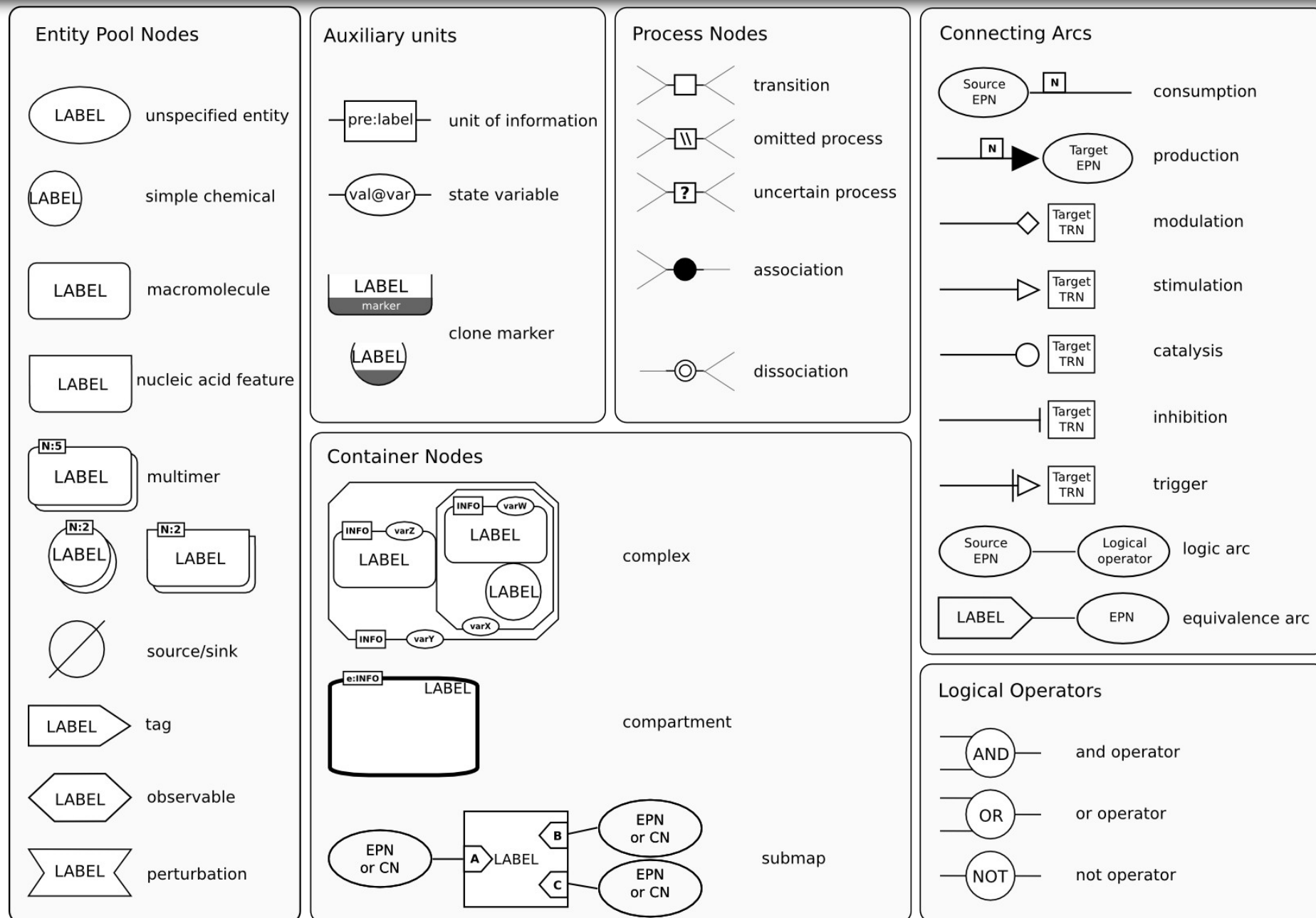


- Ambiguous
- Conceptual
- Sequential



Le Novère, Moodie, Sorokin, Hucka, Schreiber, Demir, Mi, Matsuoka, Wegner, Kitano
Systems Biology Graphical Notation: Process Diagram Level 1 (2008)
Available from *Nature Precedings* <<http://hdl.handle.net/10101/npre.2008.2320.1>>

SBGN Process Diagram L1 reference card

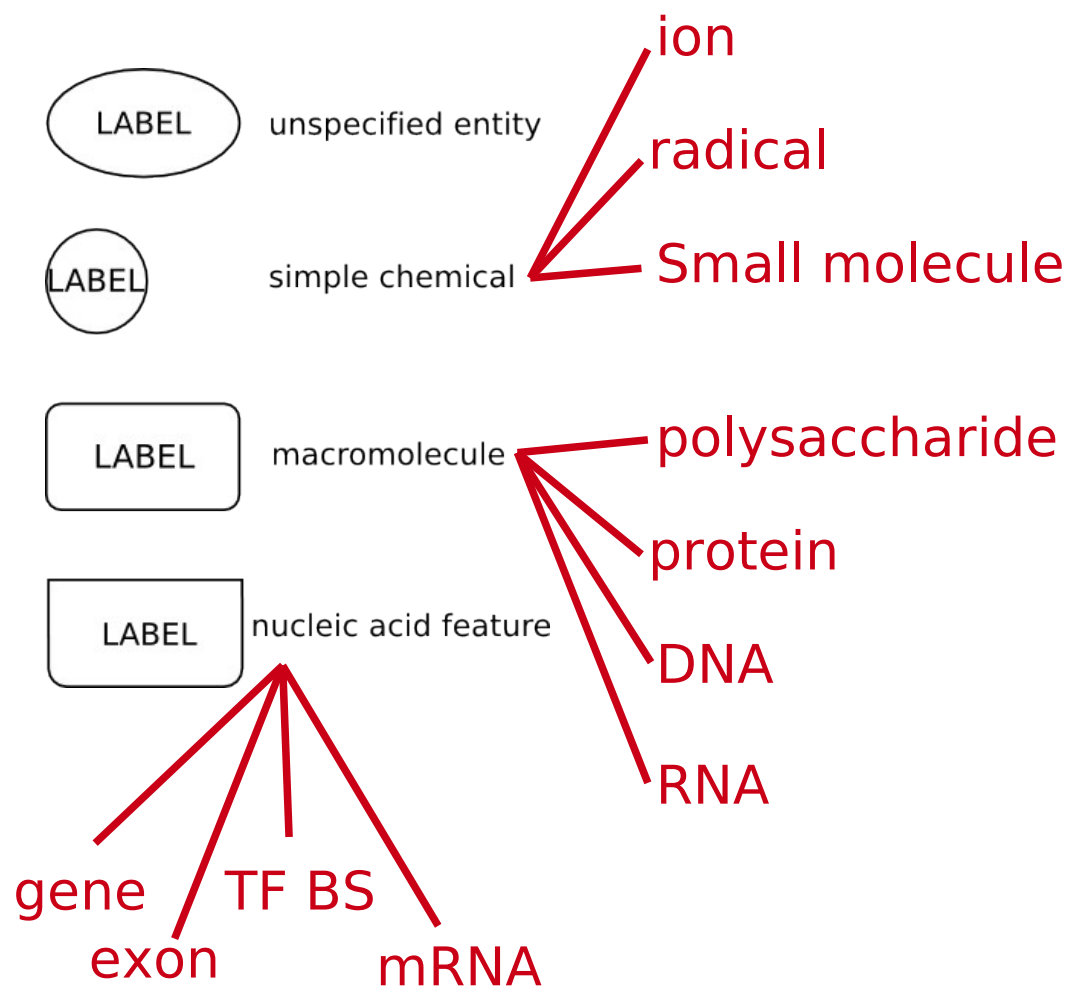


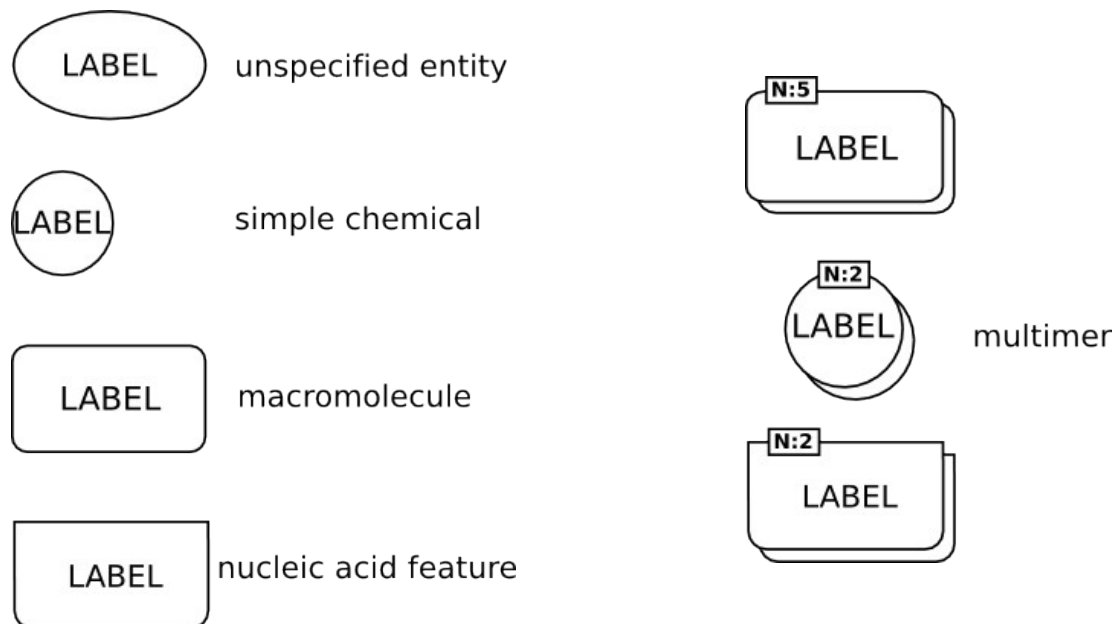
 LABEL unspecified entity

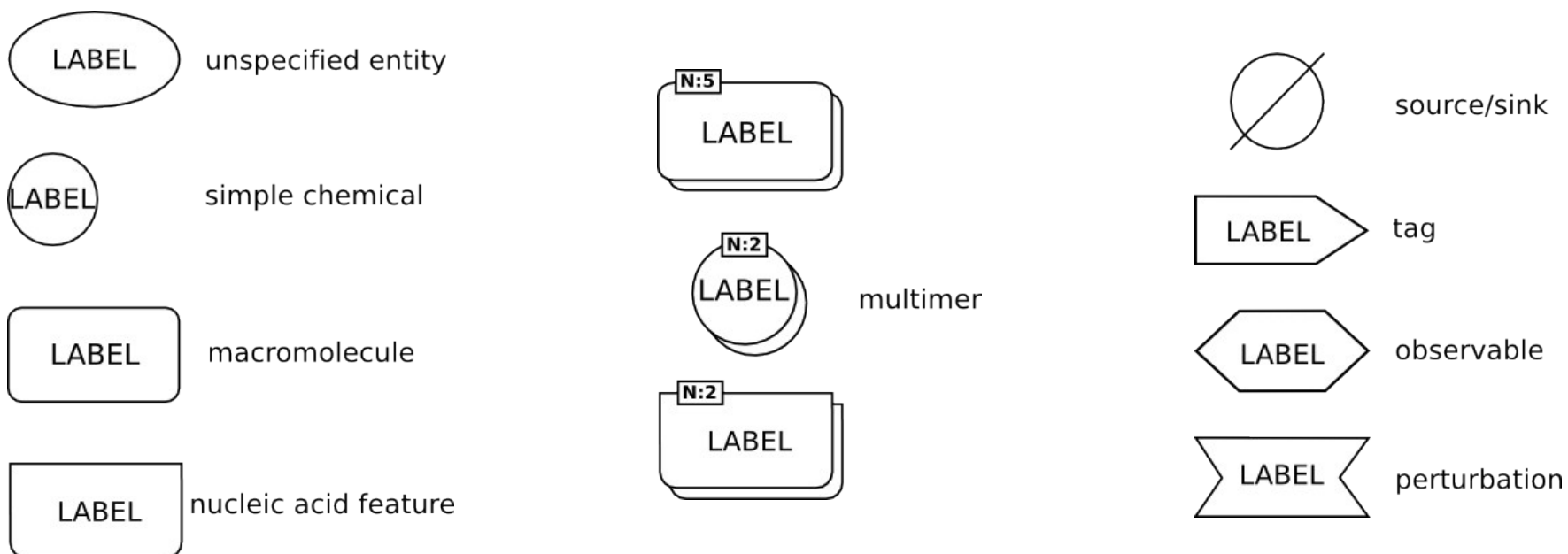
 LABEL simple chemical

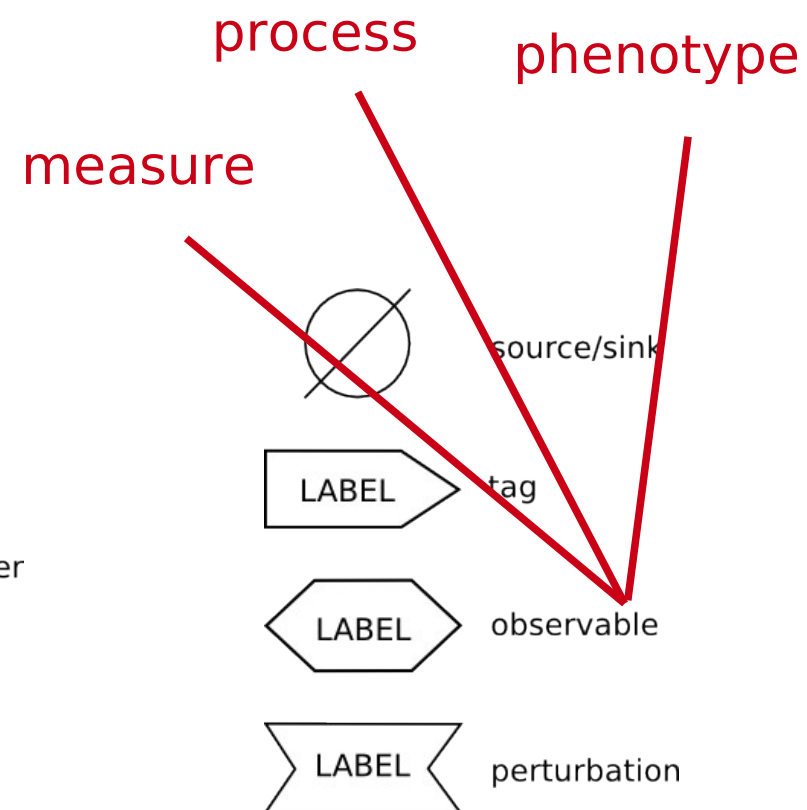
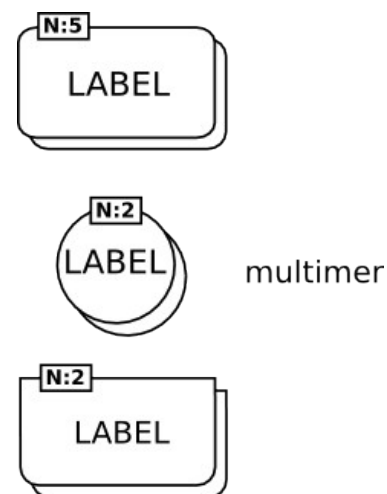
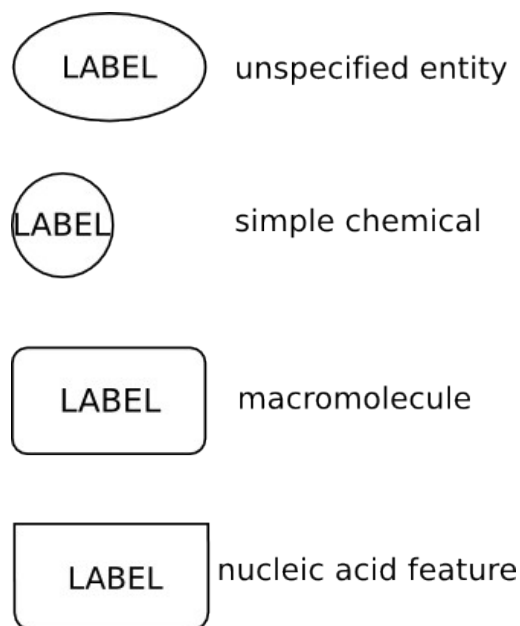
 LABEL macromolecule

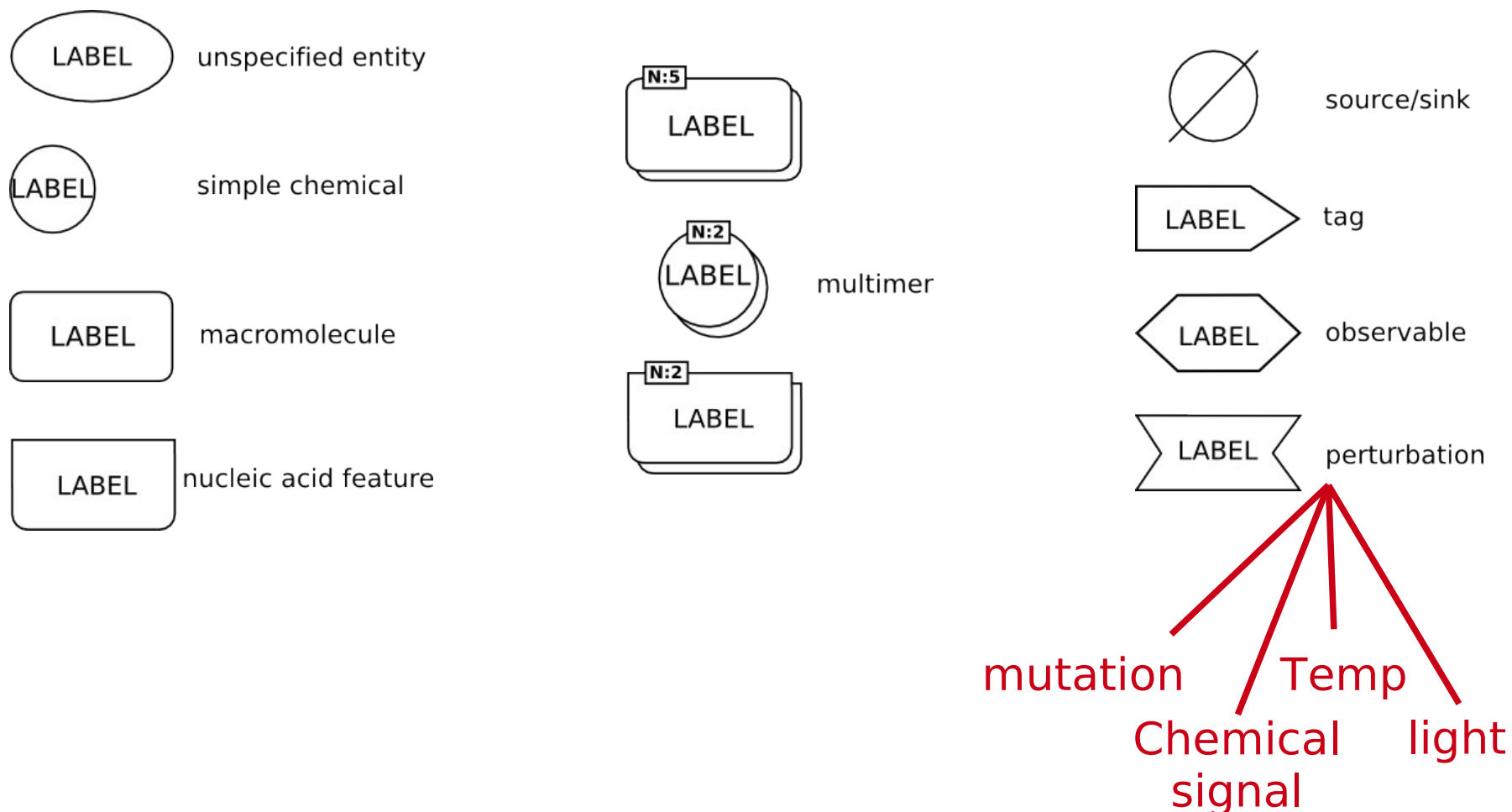
 LABEL nucleic acid feature

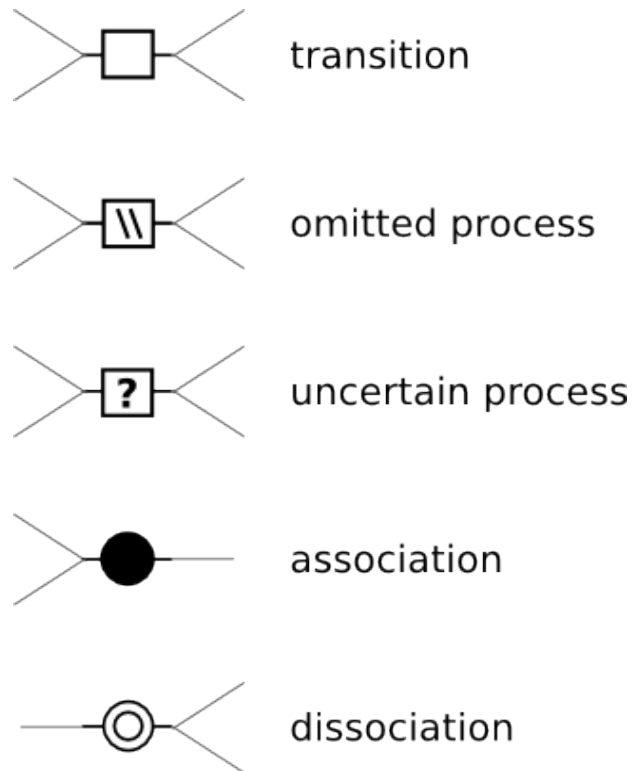


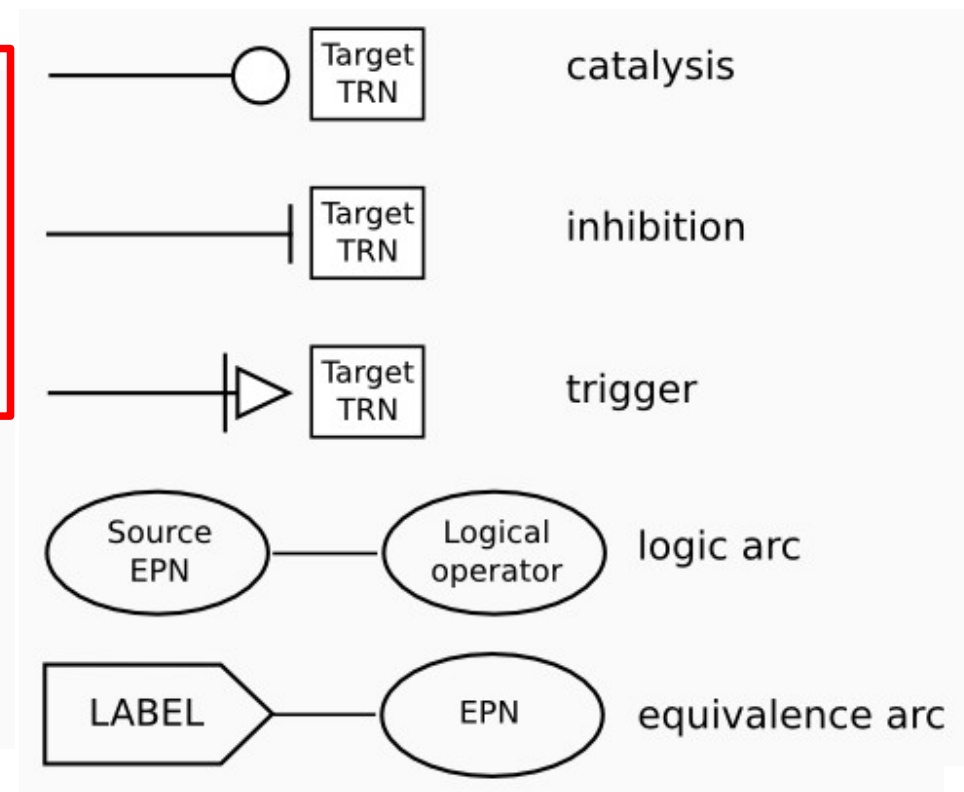
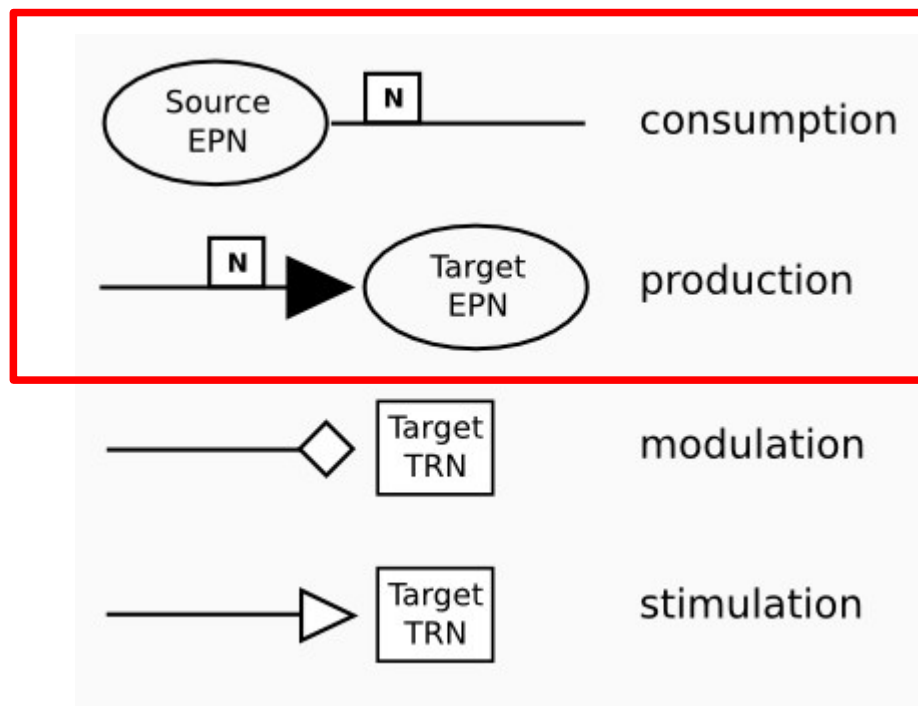


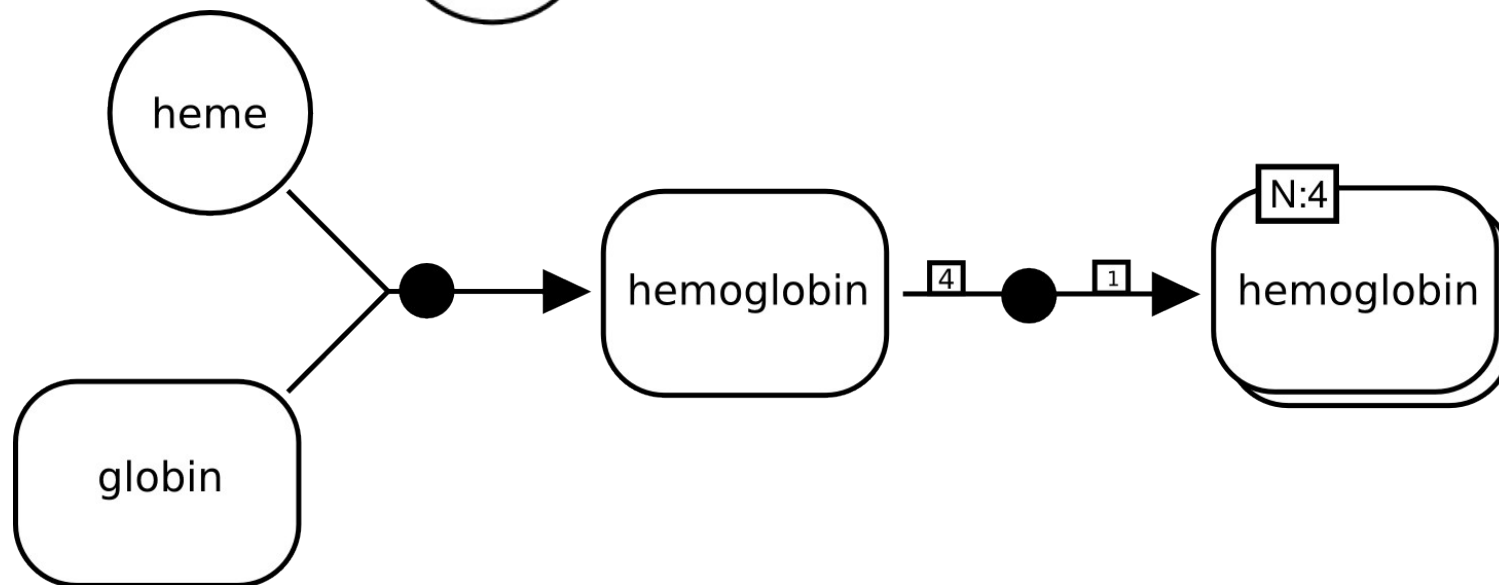
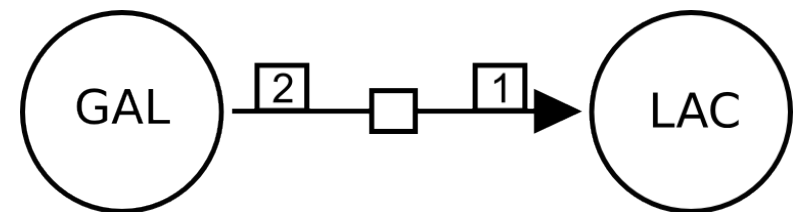
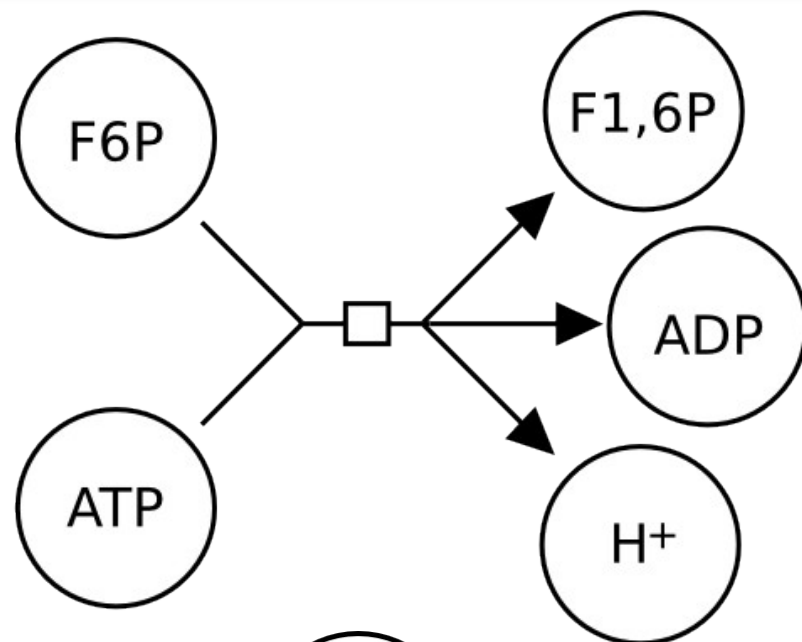


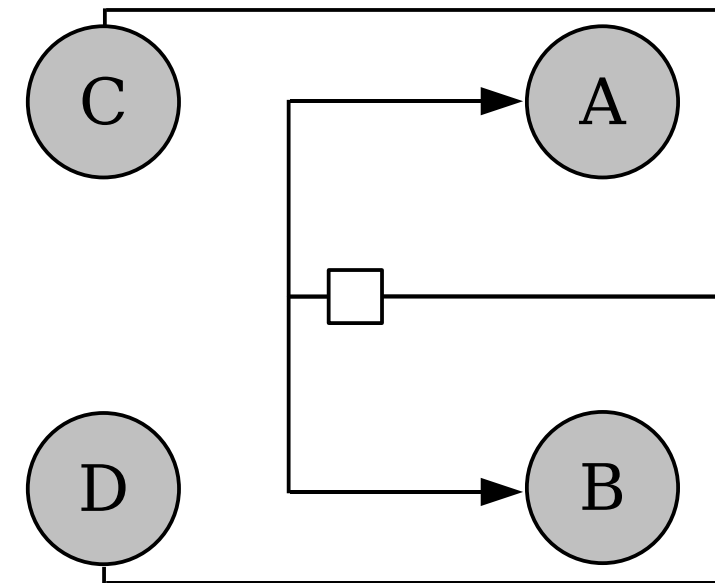
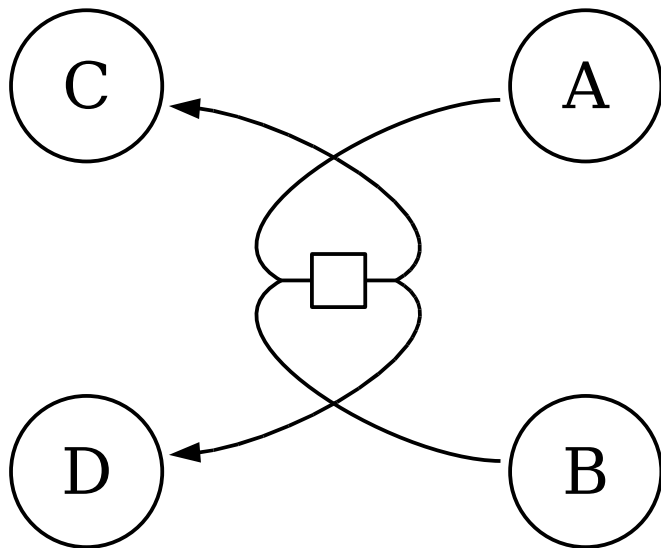
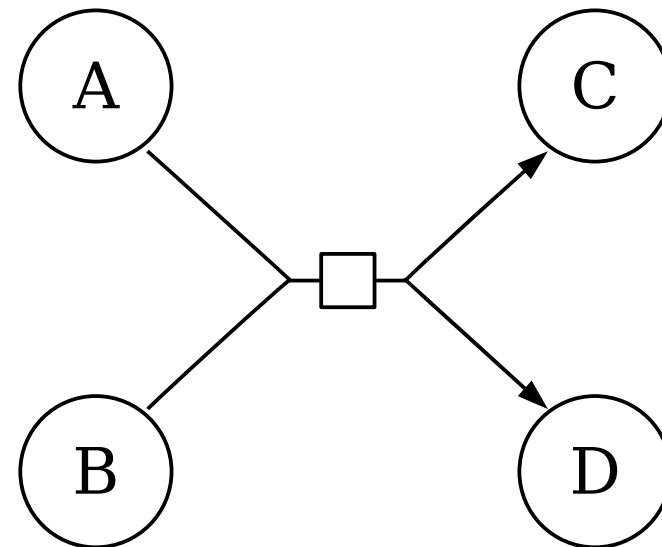
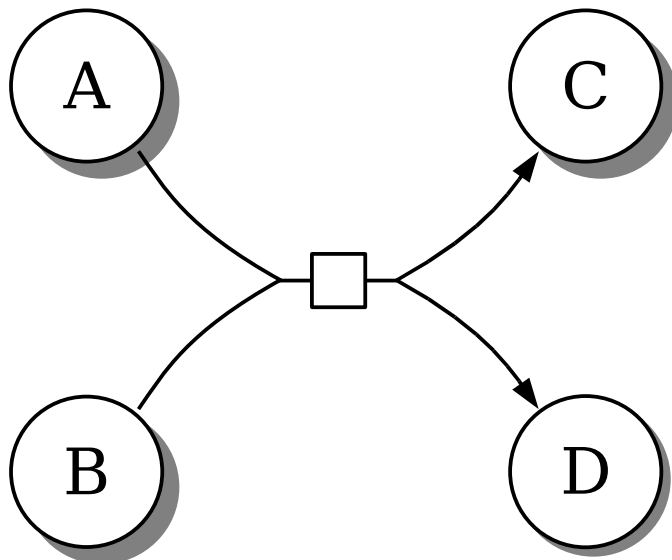


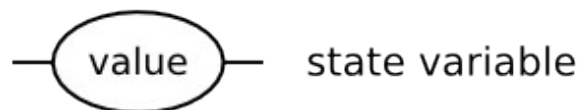
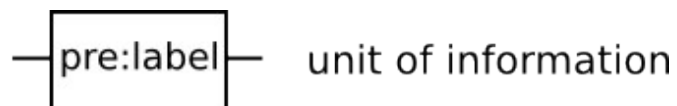




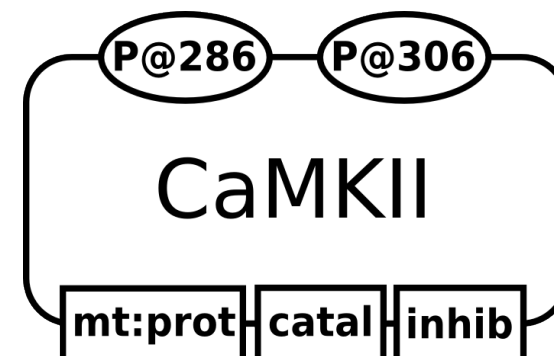


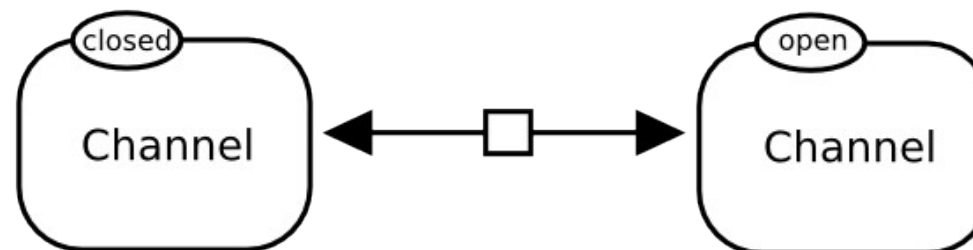
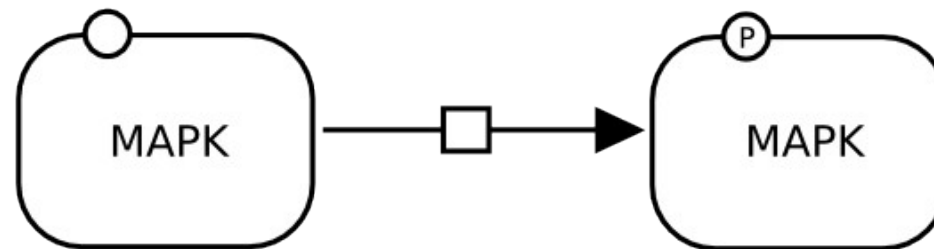


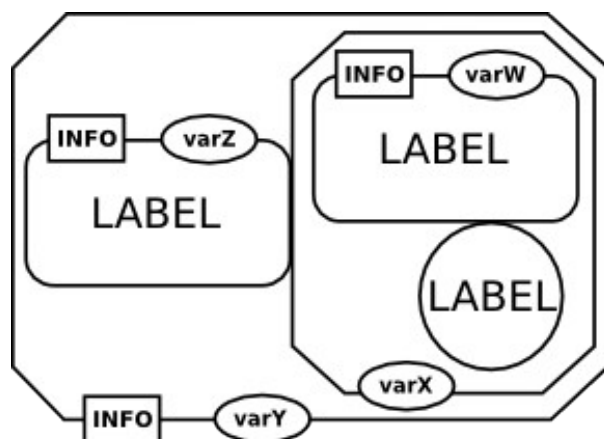




clone marker



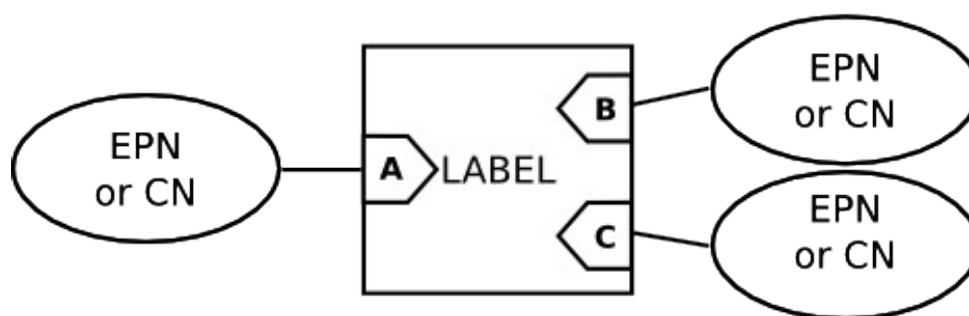




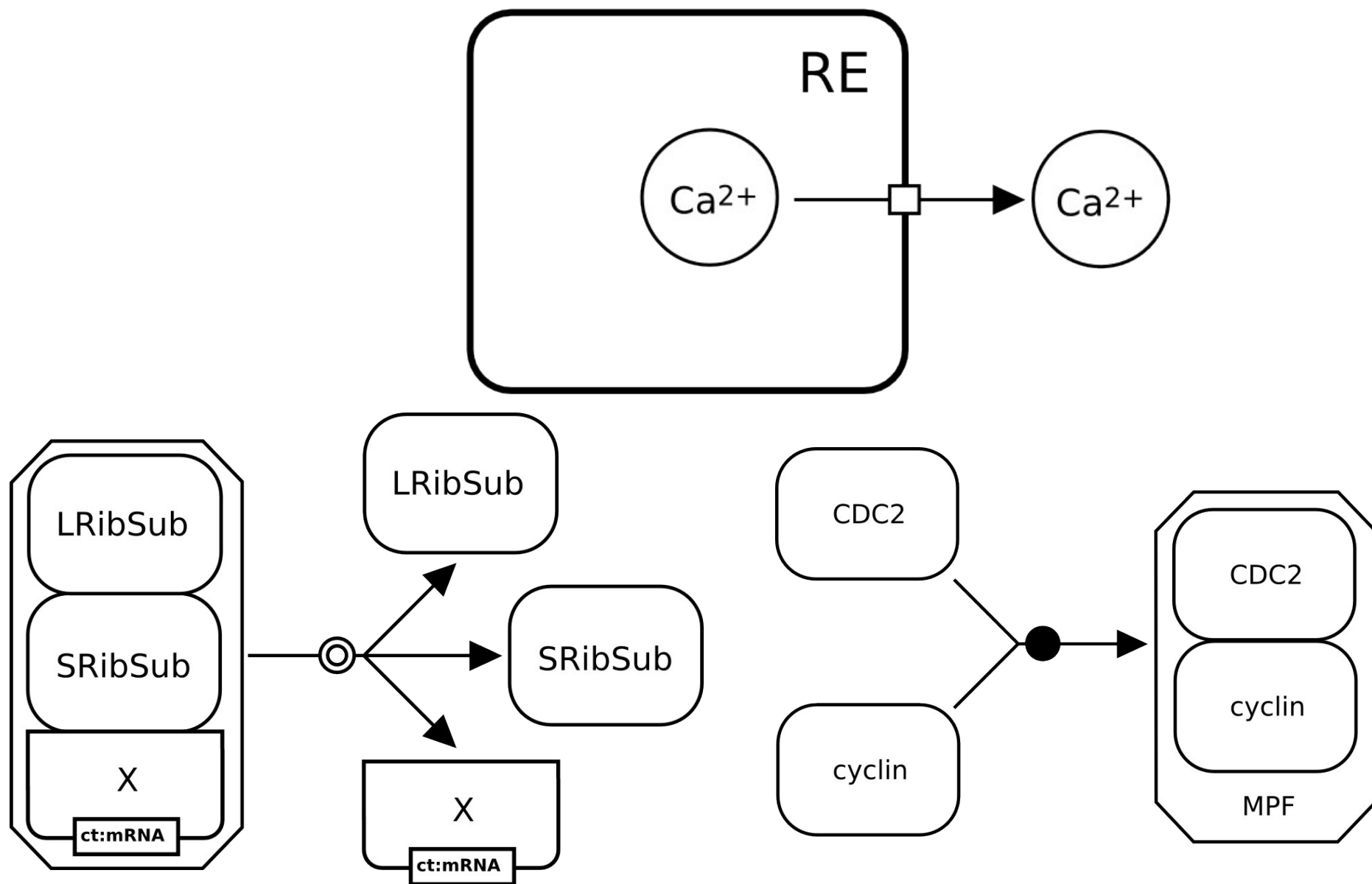
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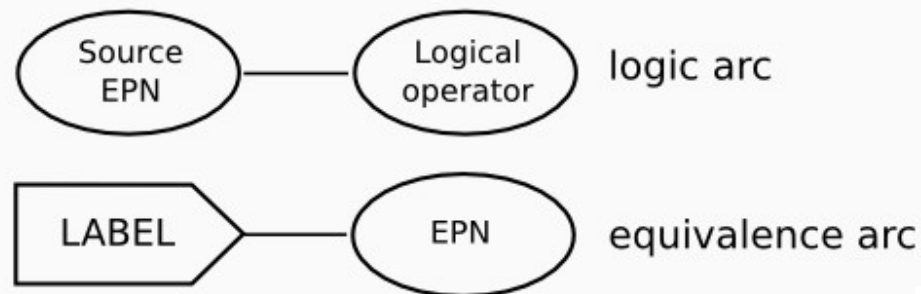
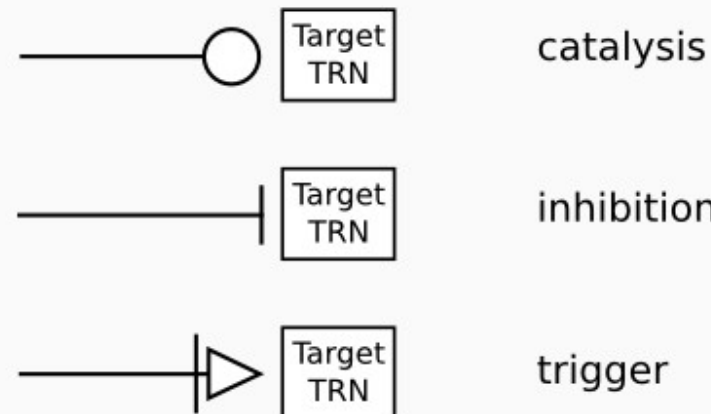
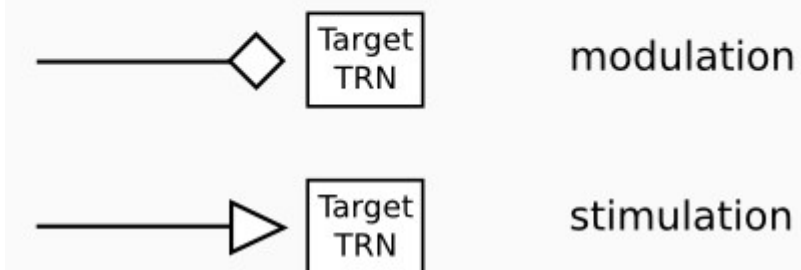
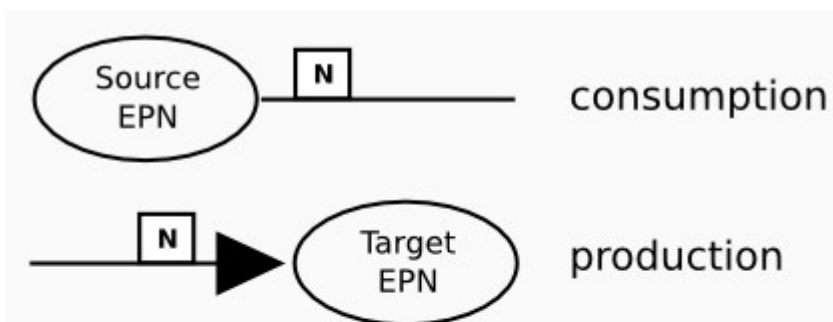


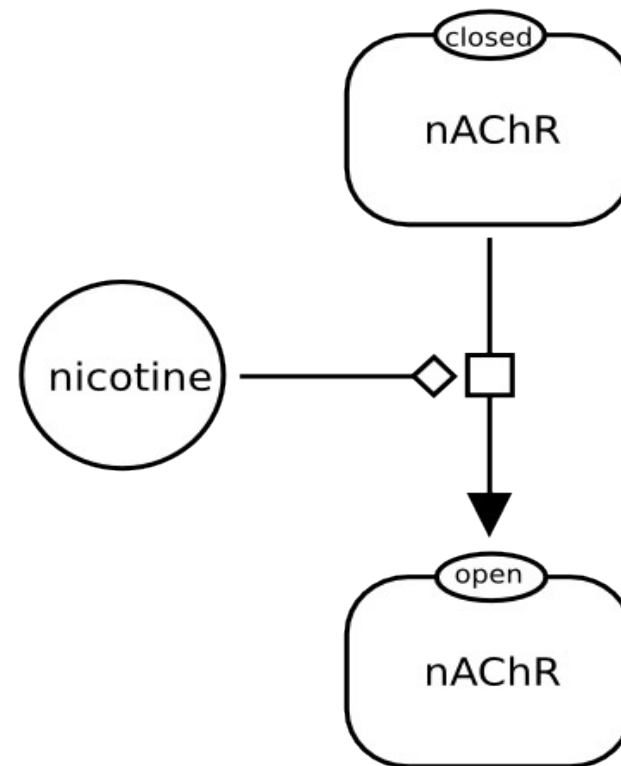
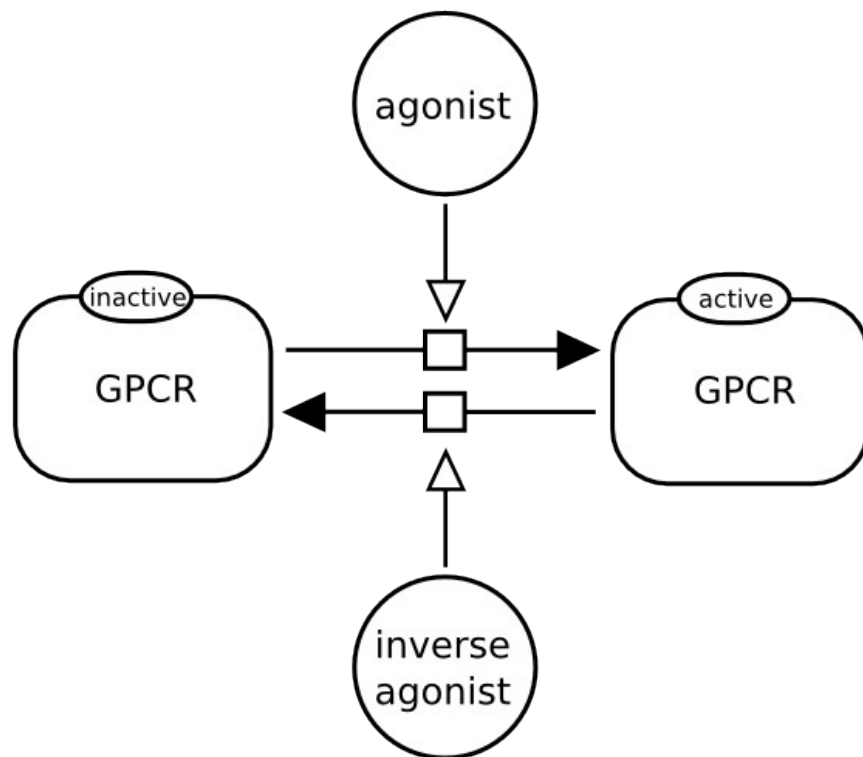
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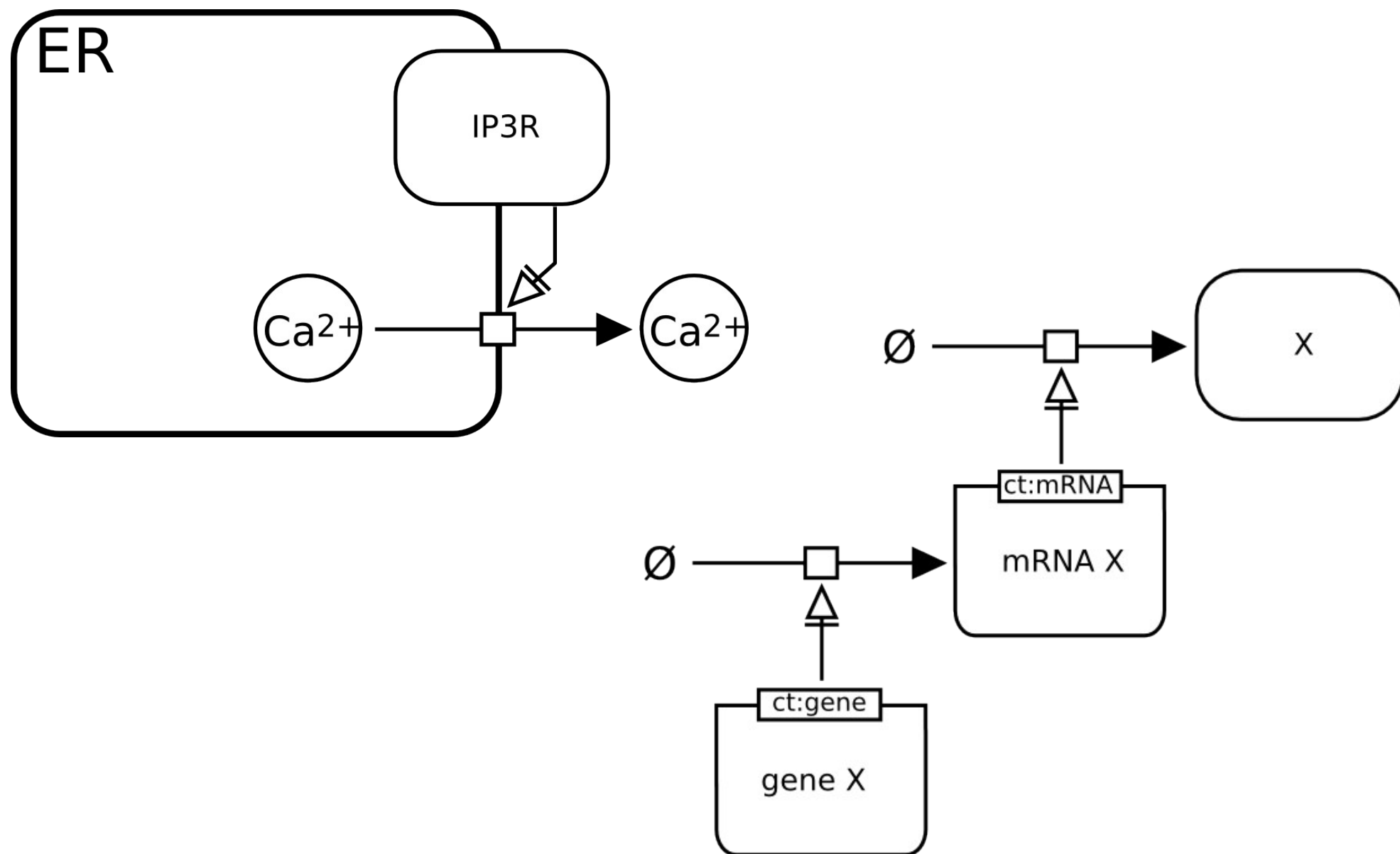


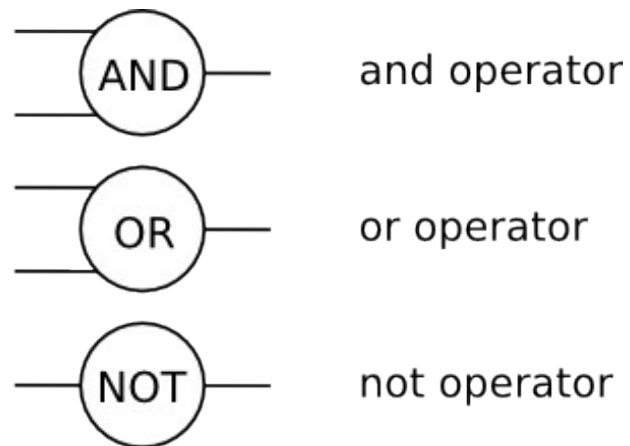
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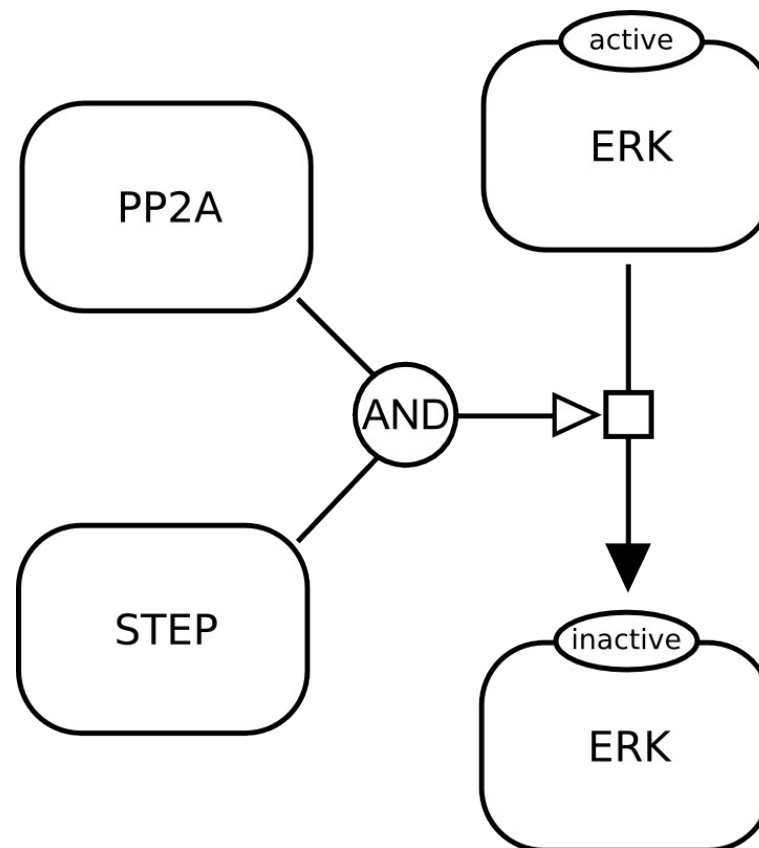


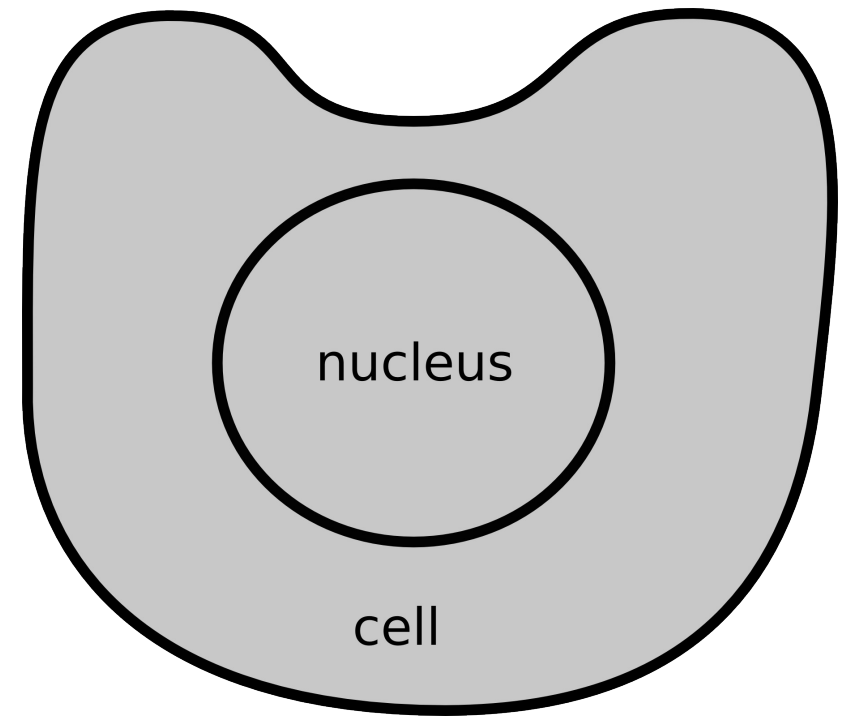
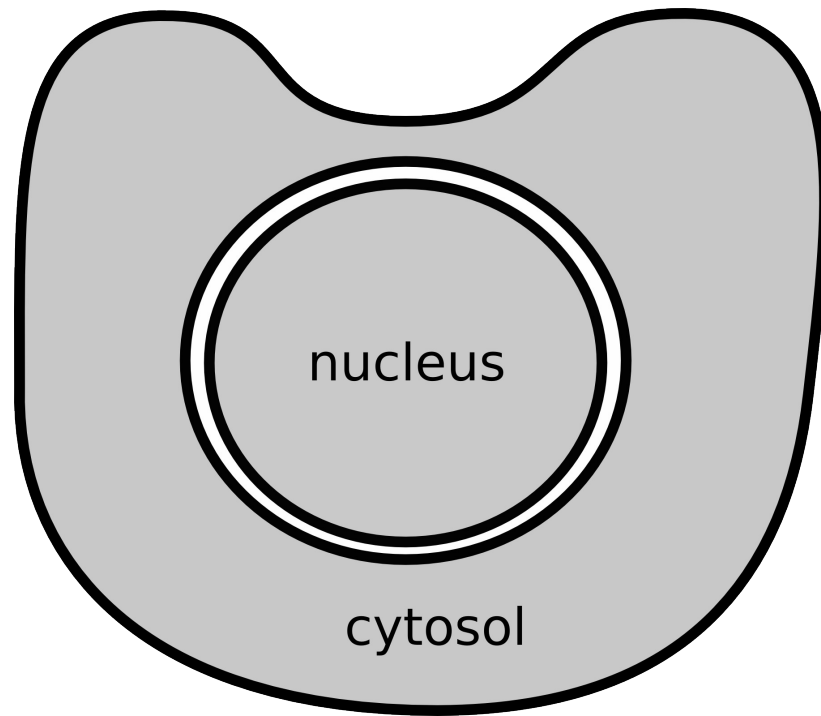


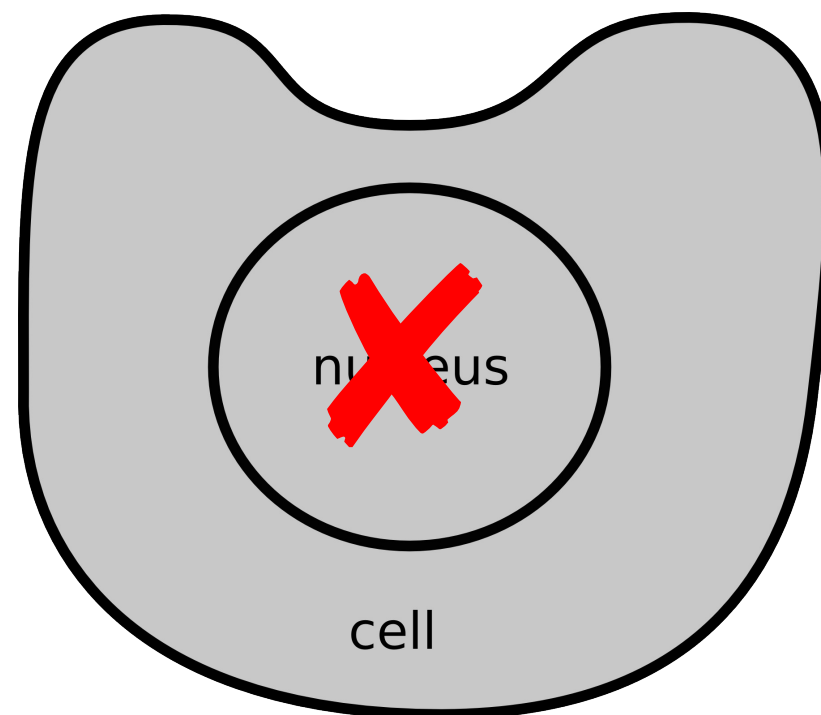
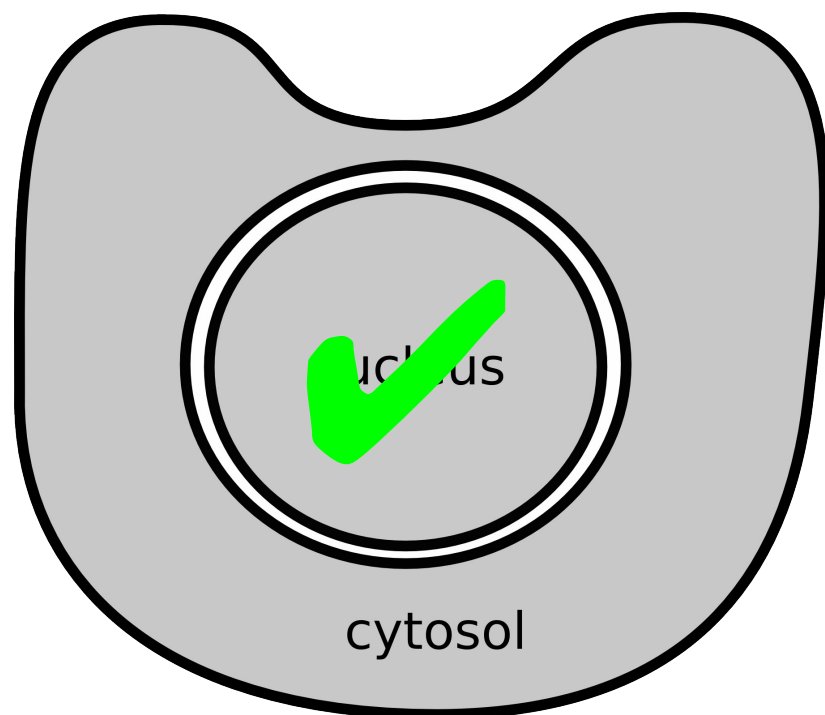


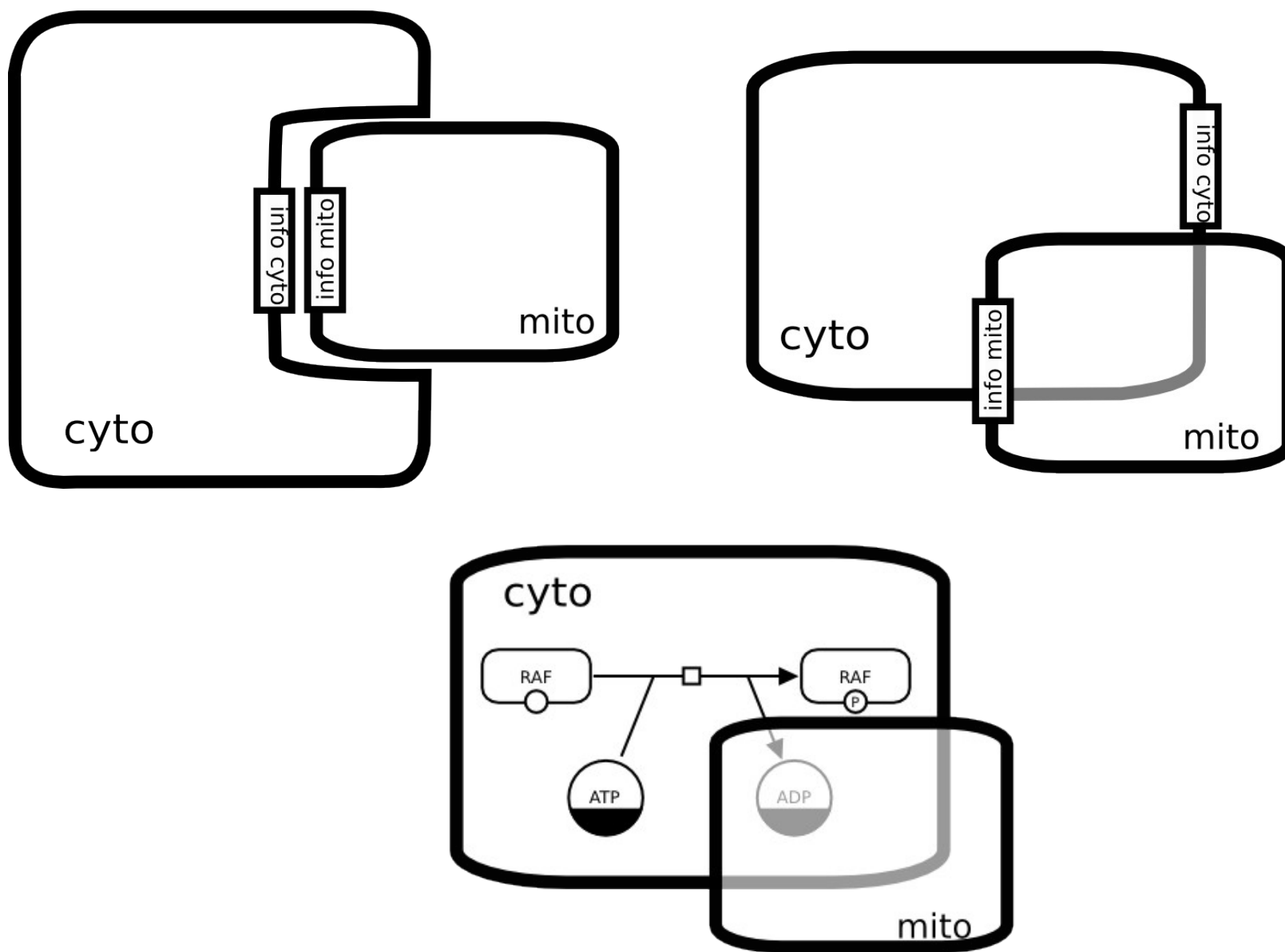


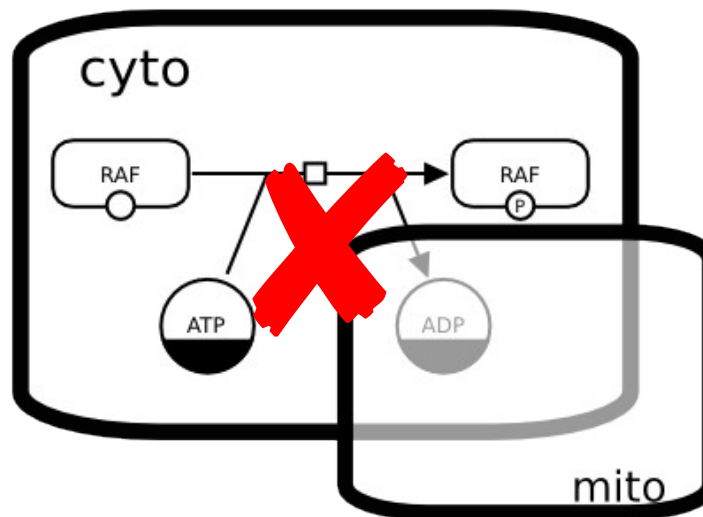
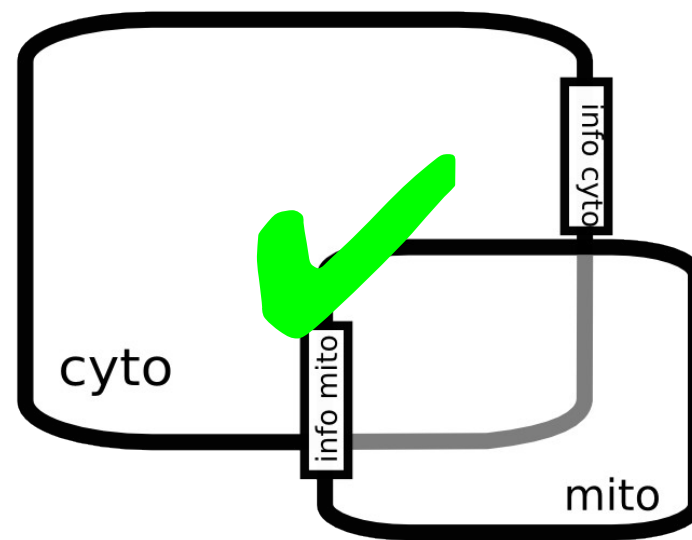
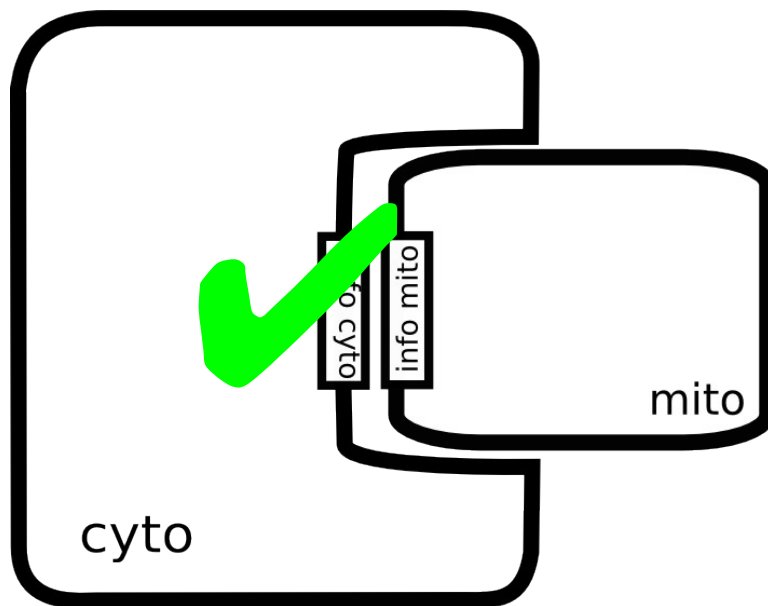


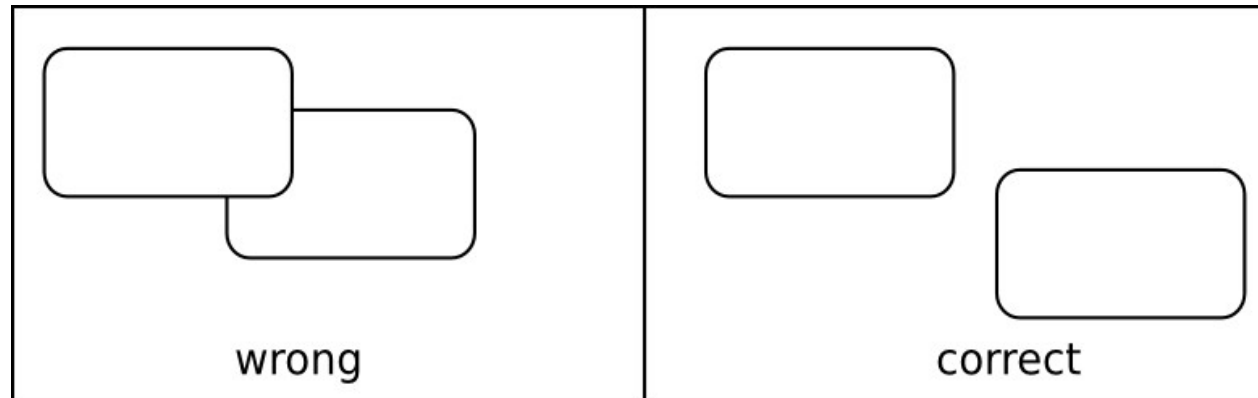


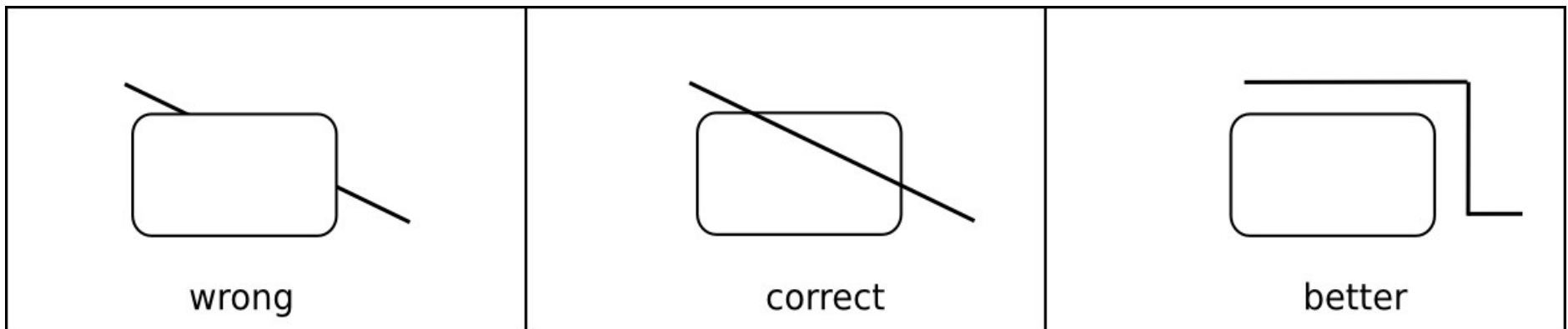


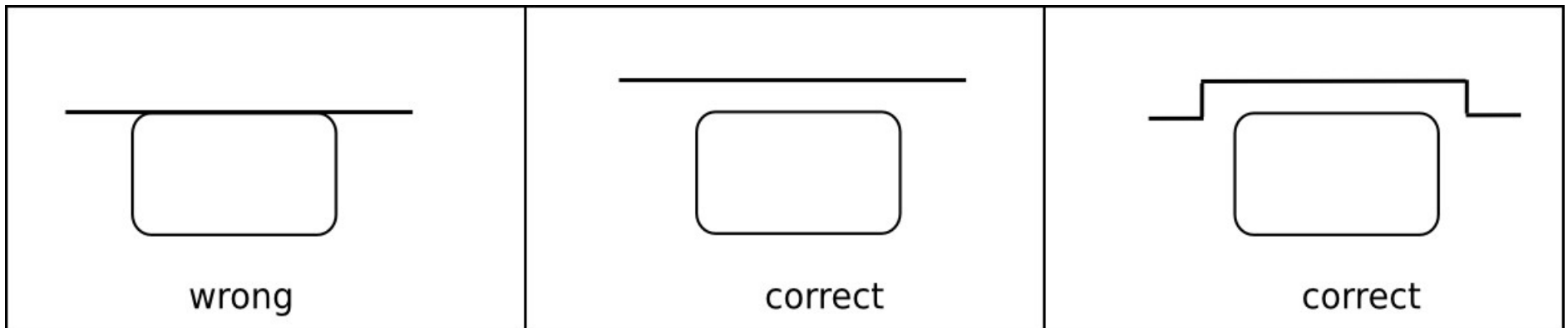


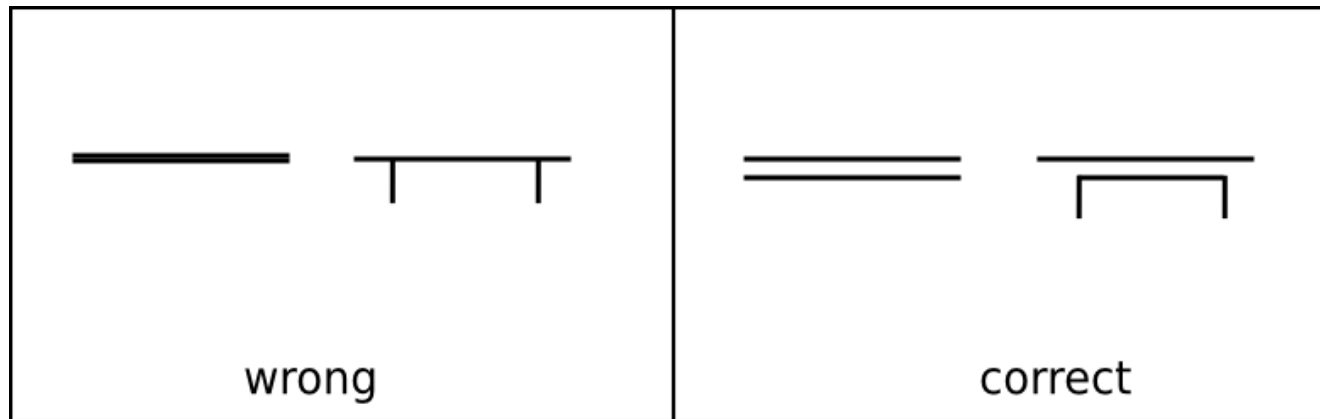


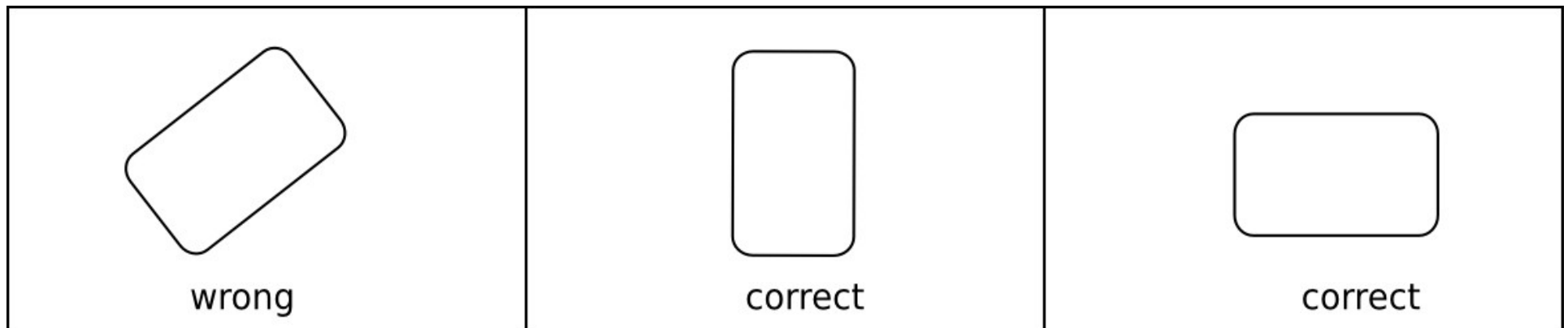


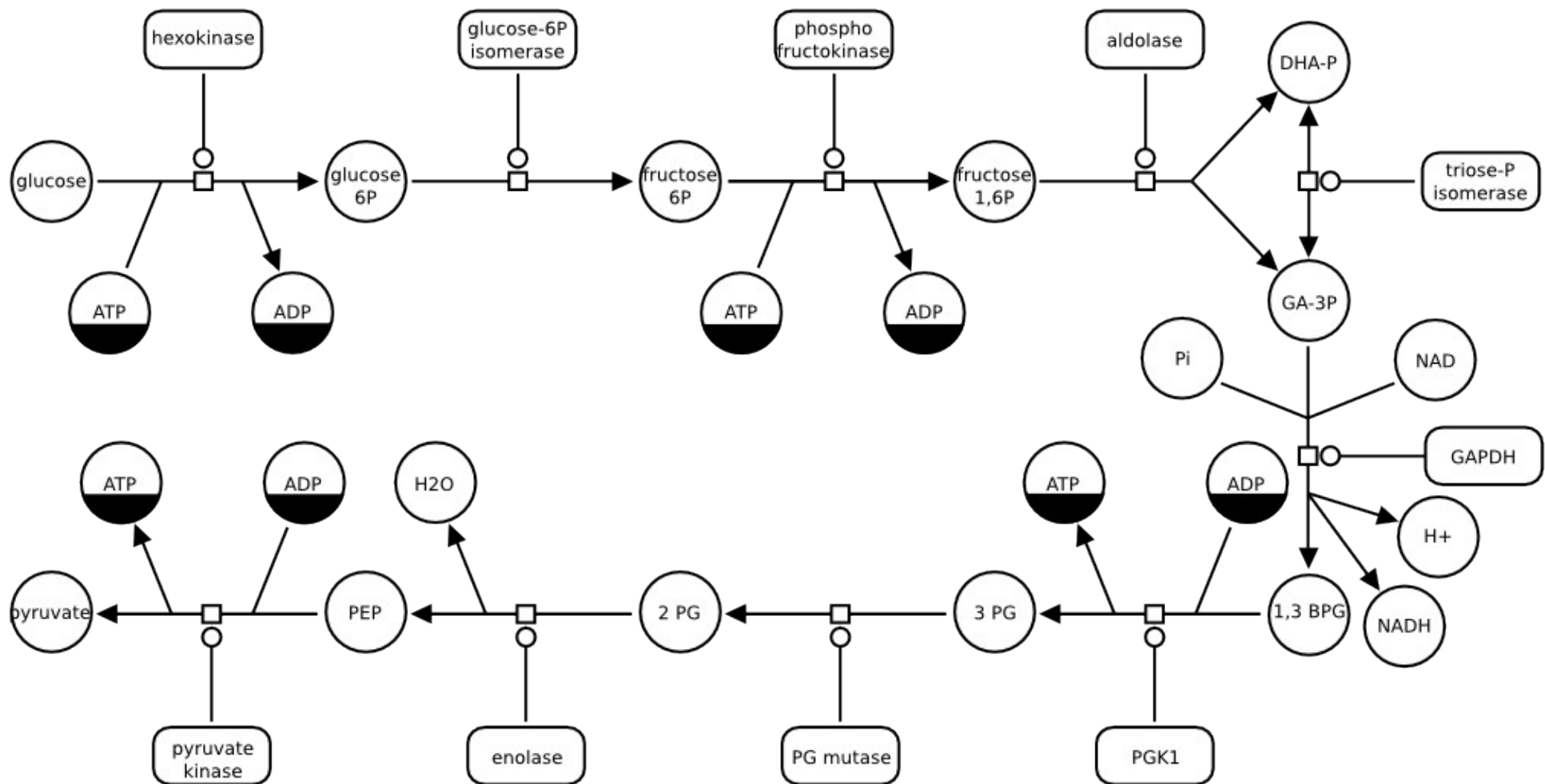


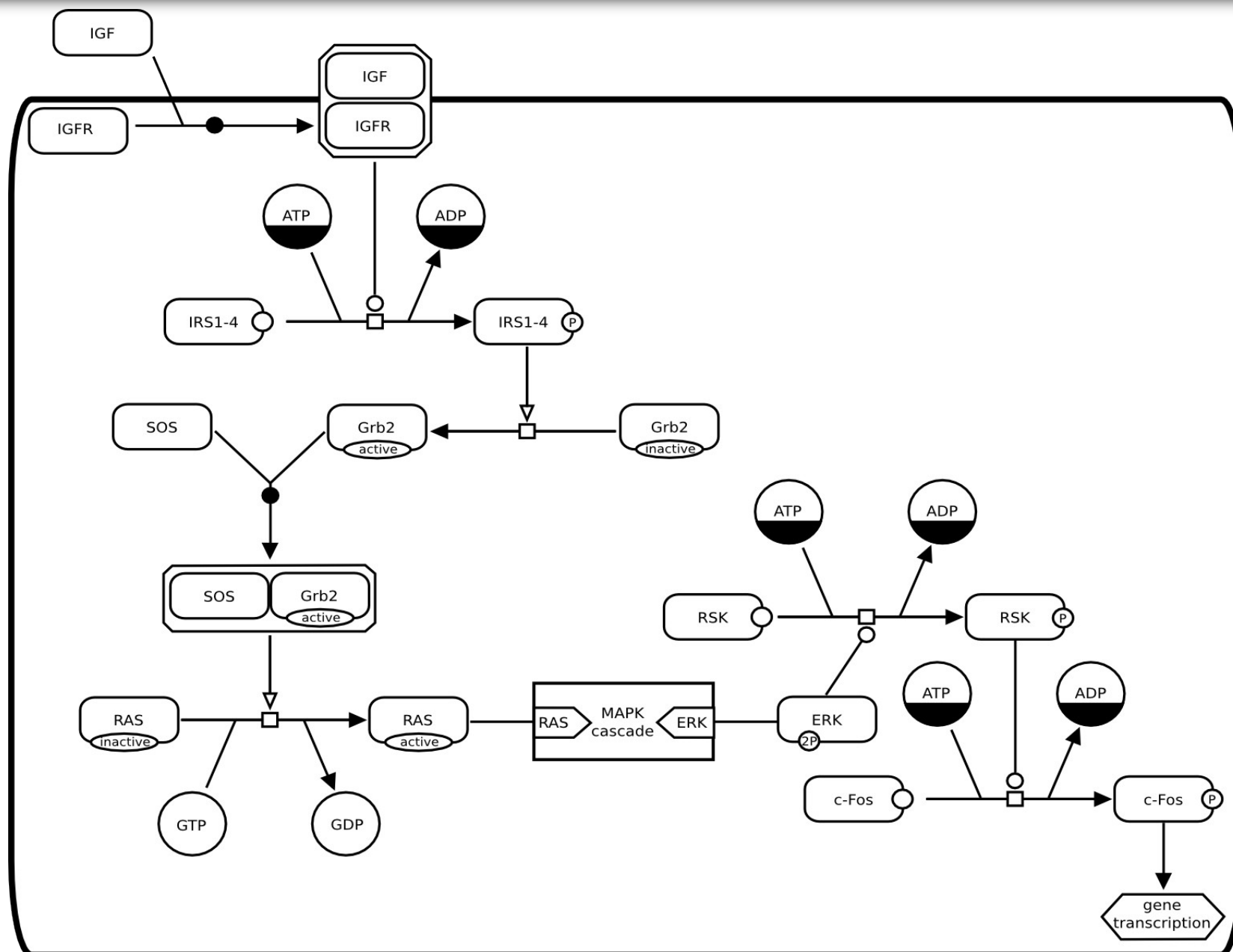


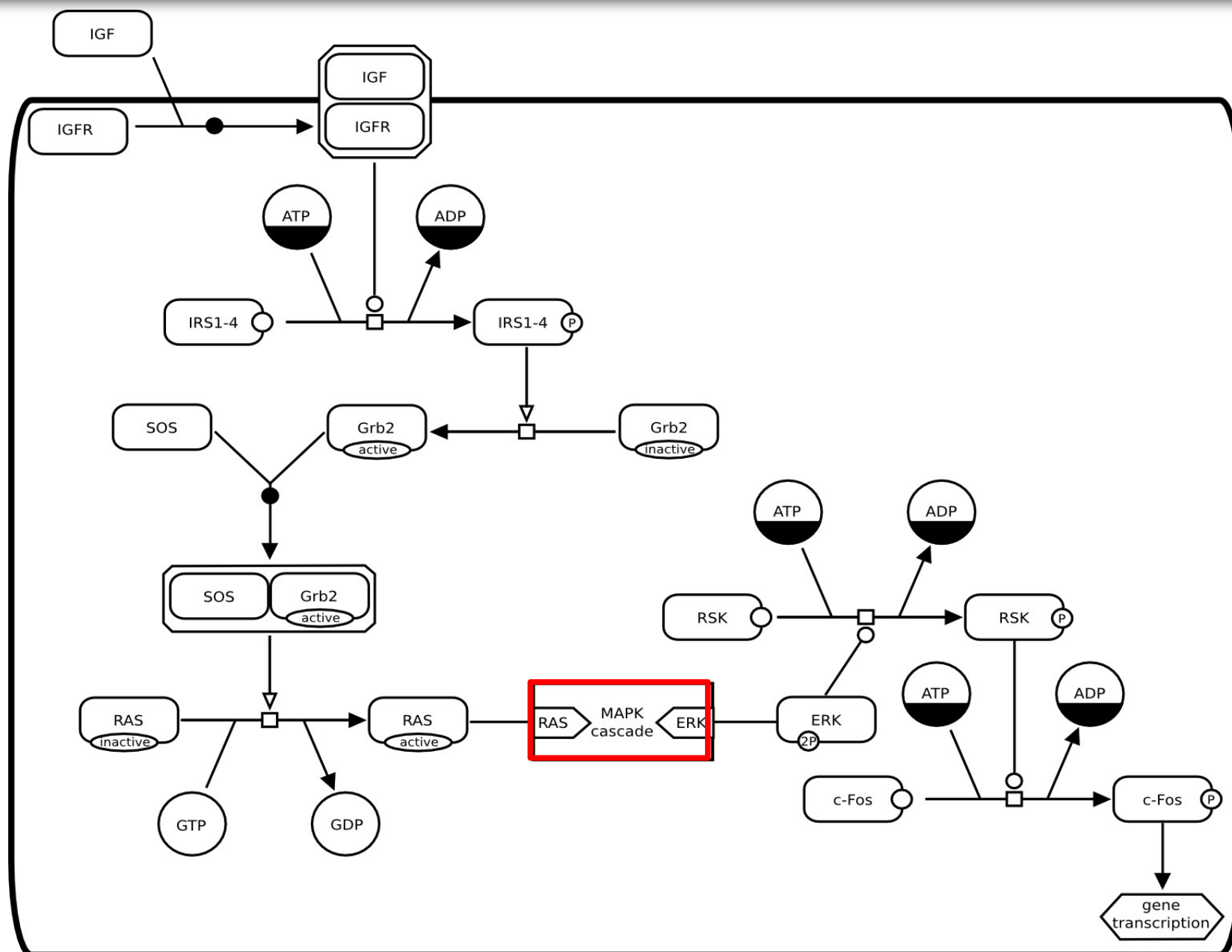


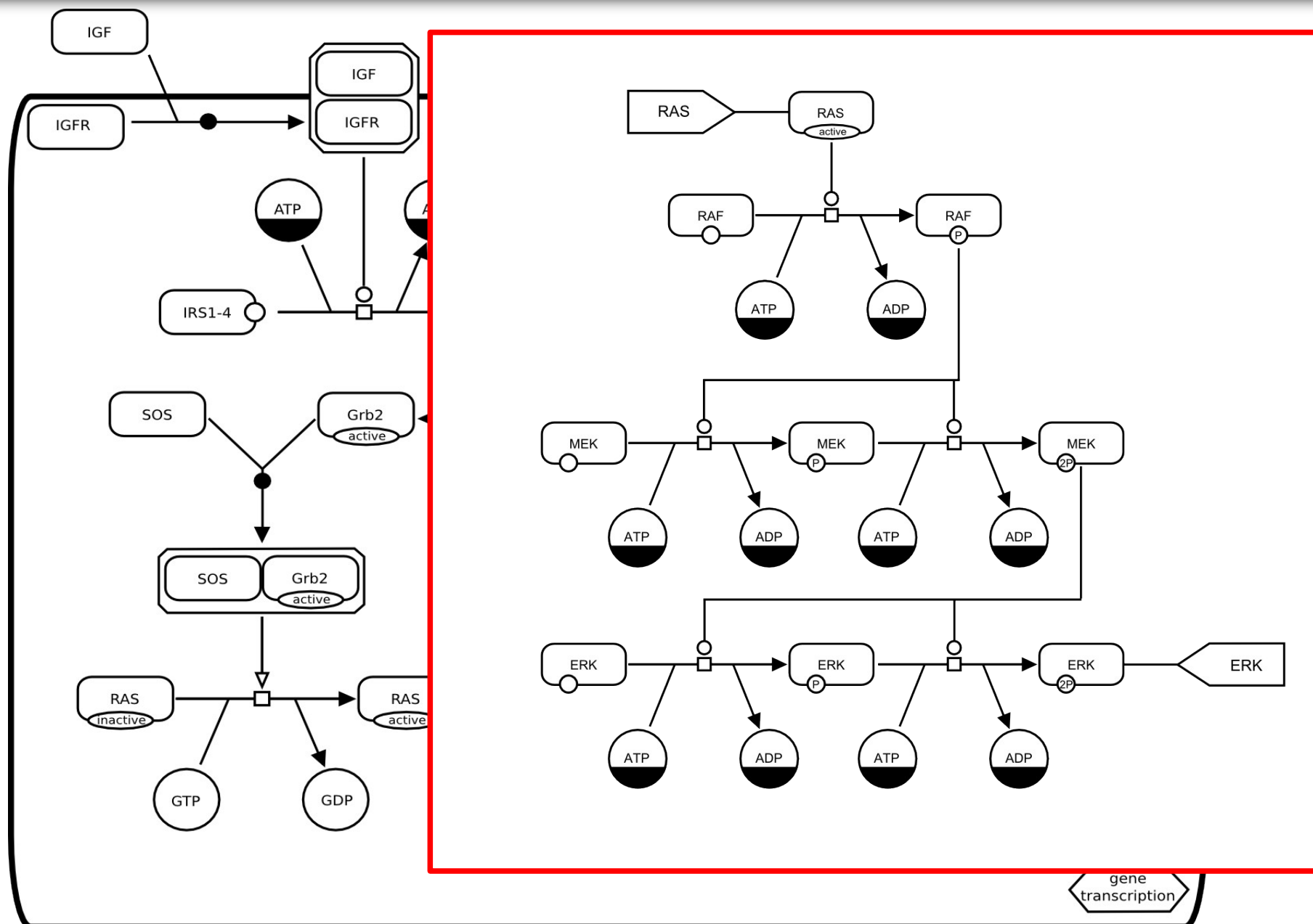


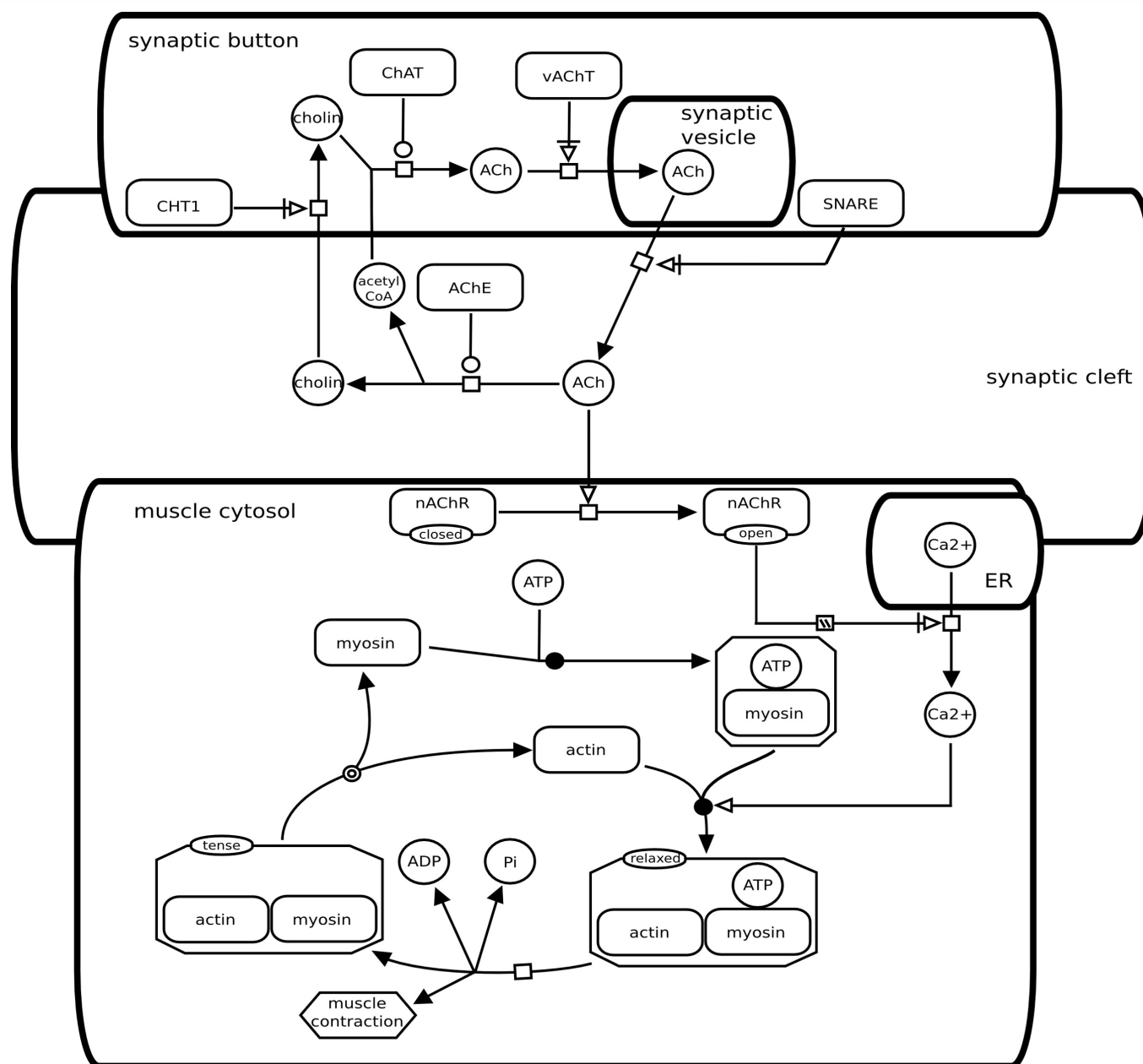


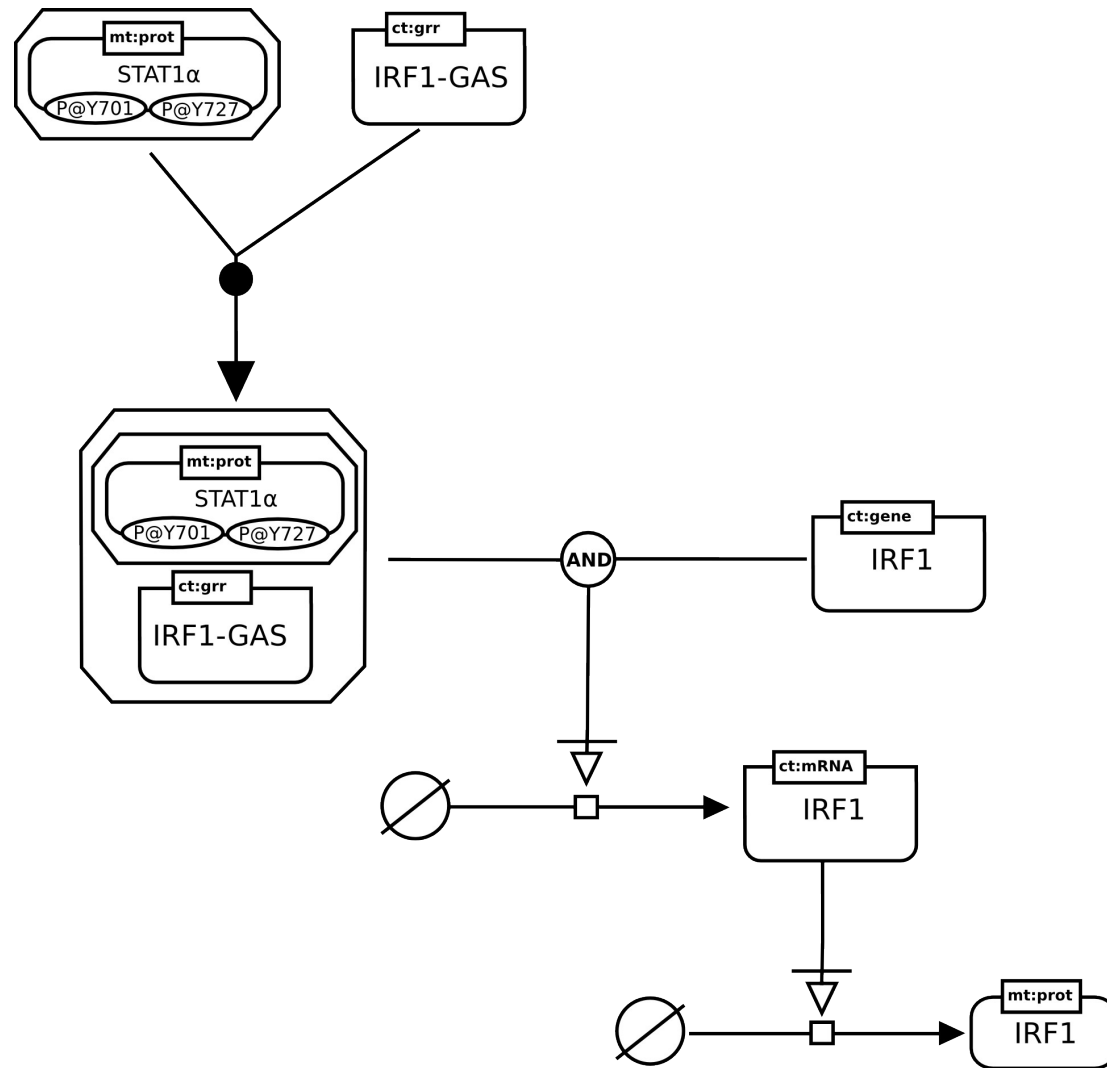




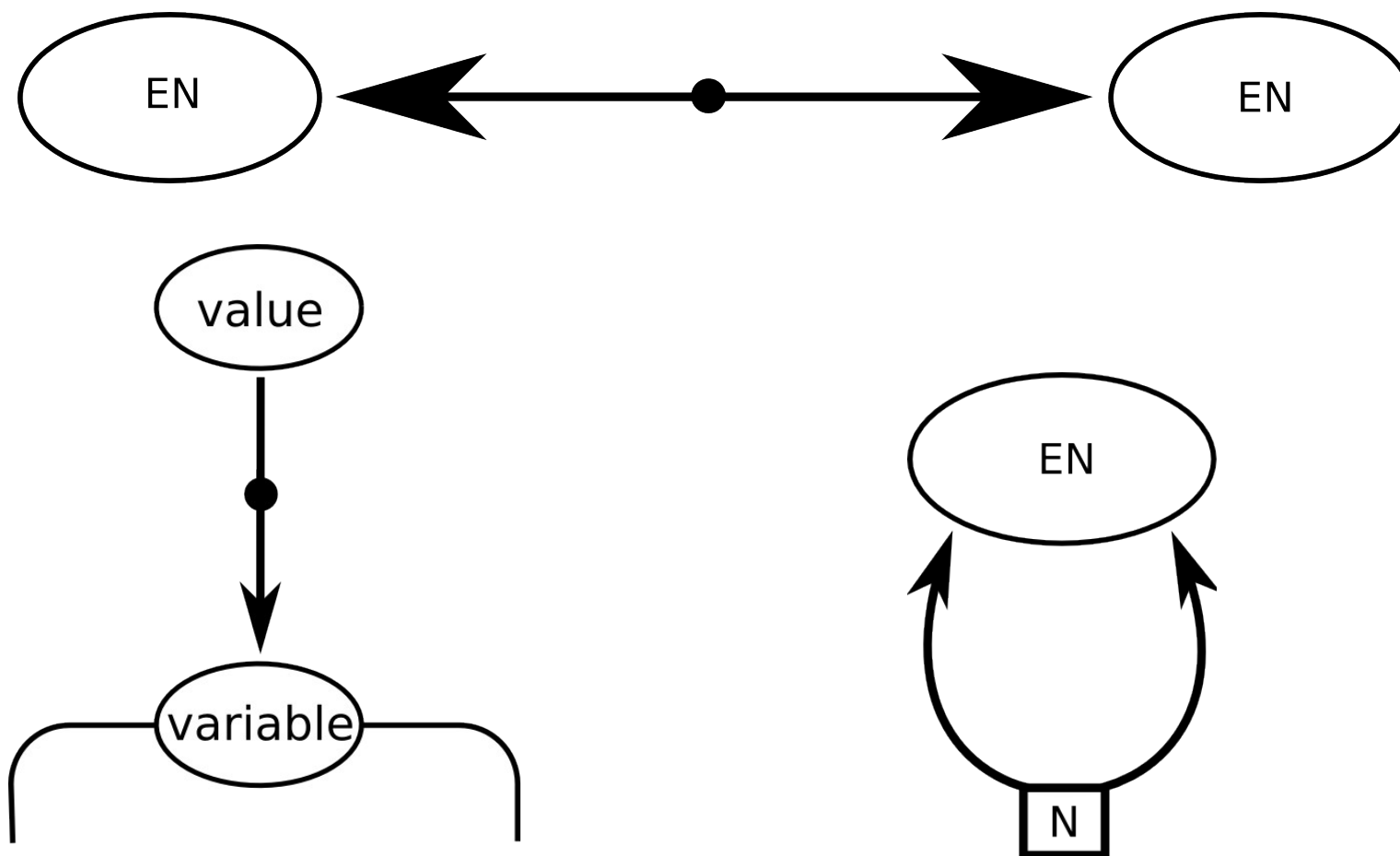


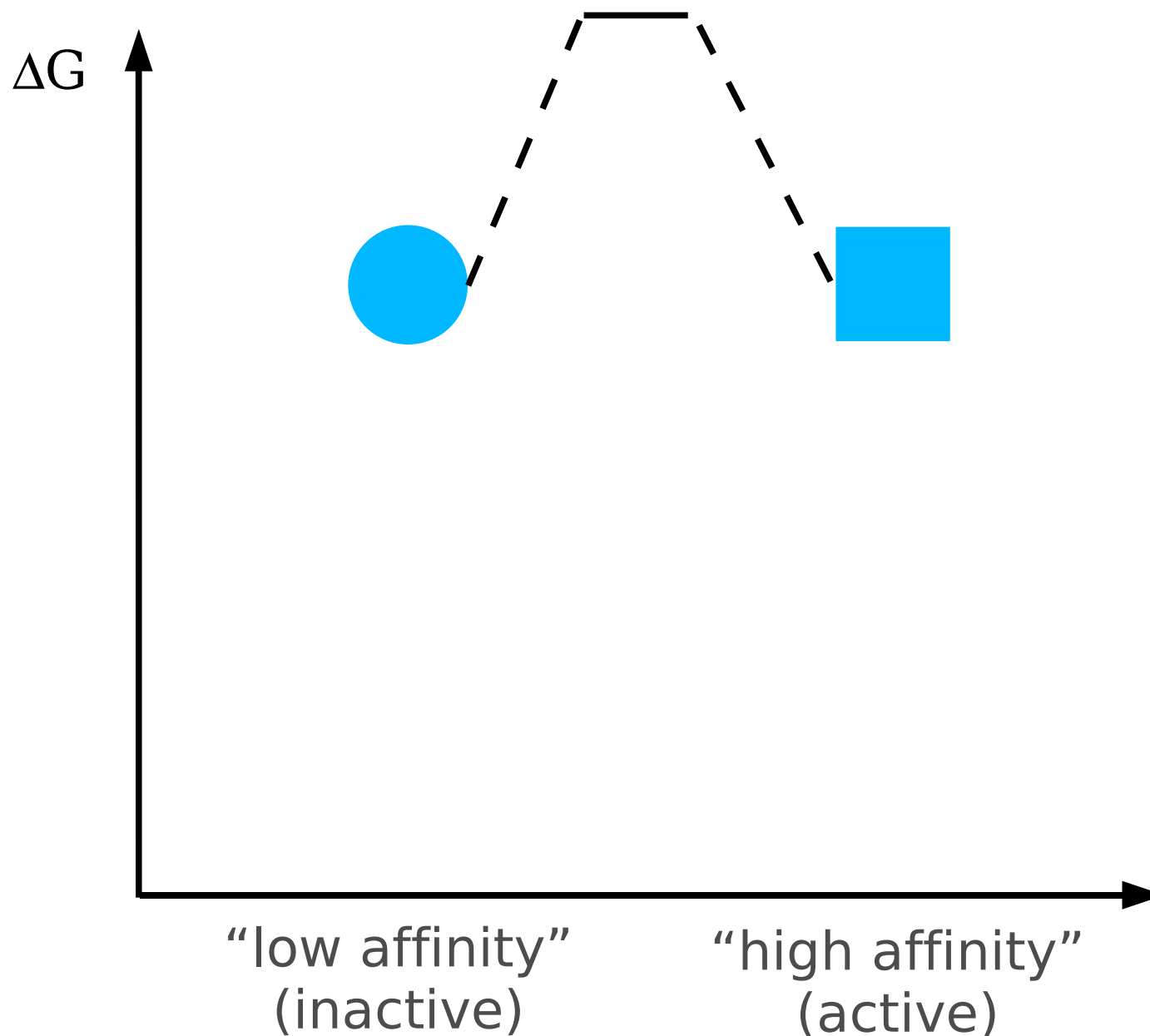


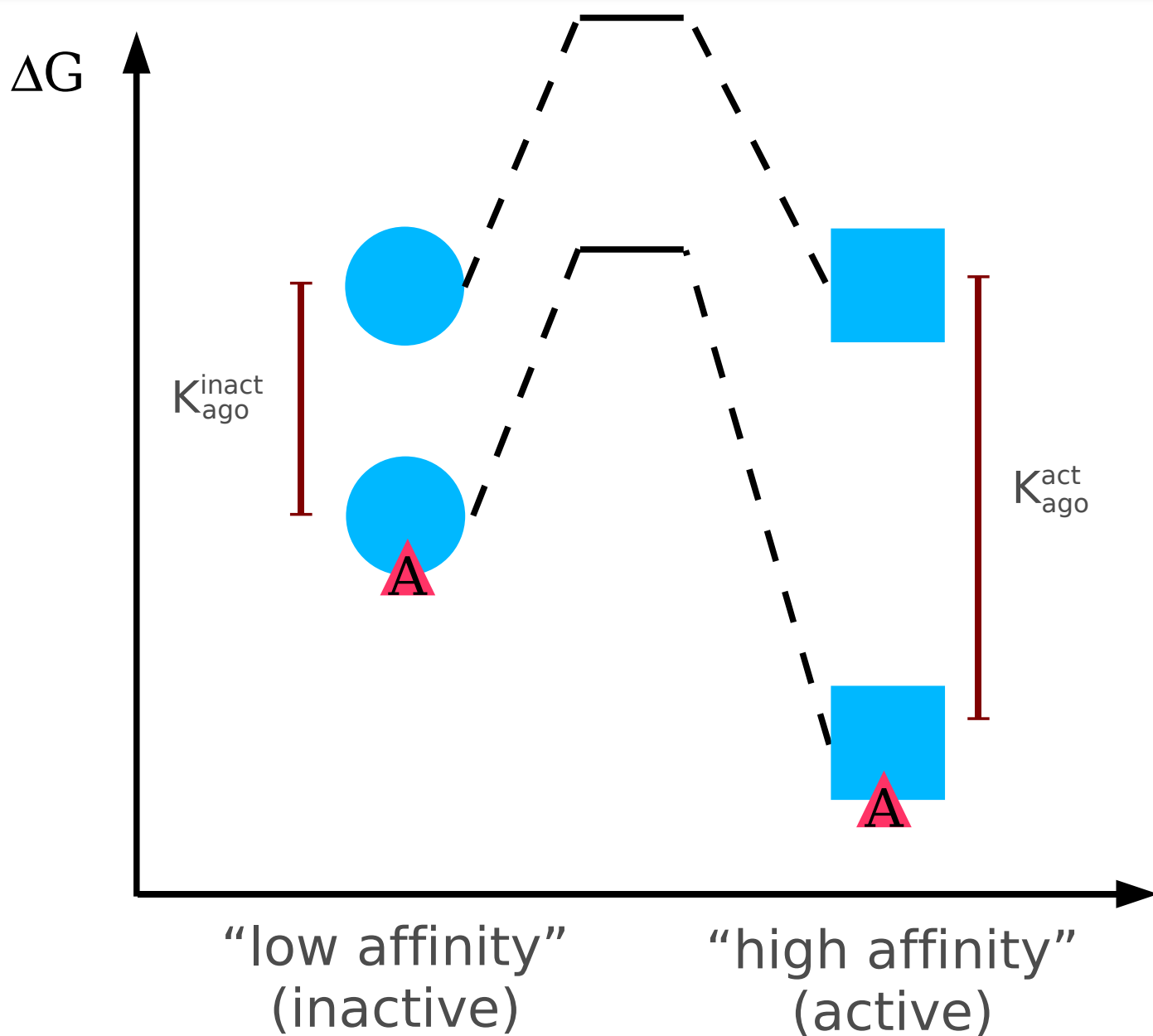


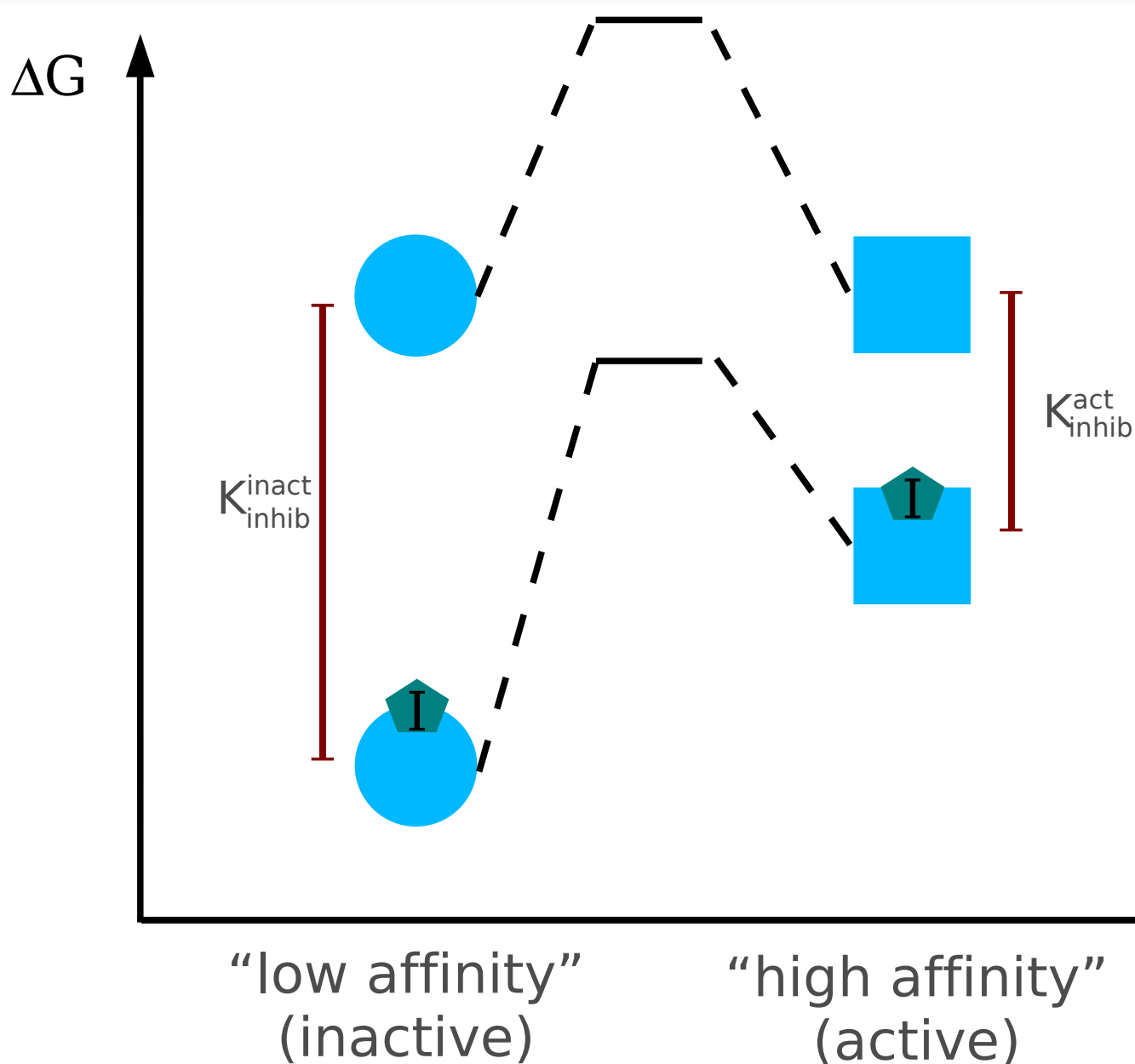


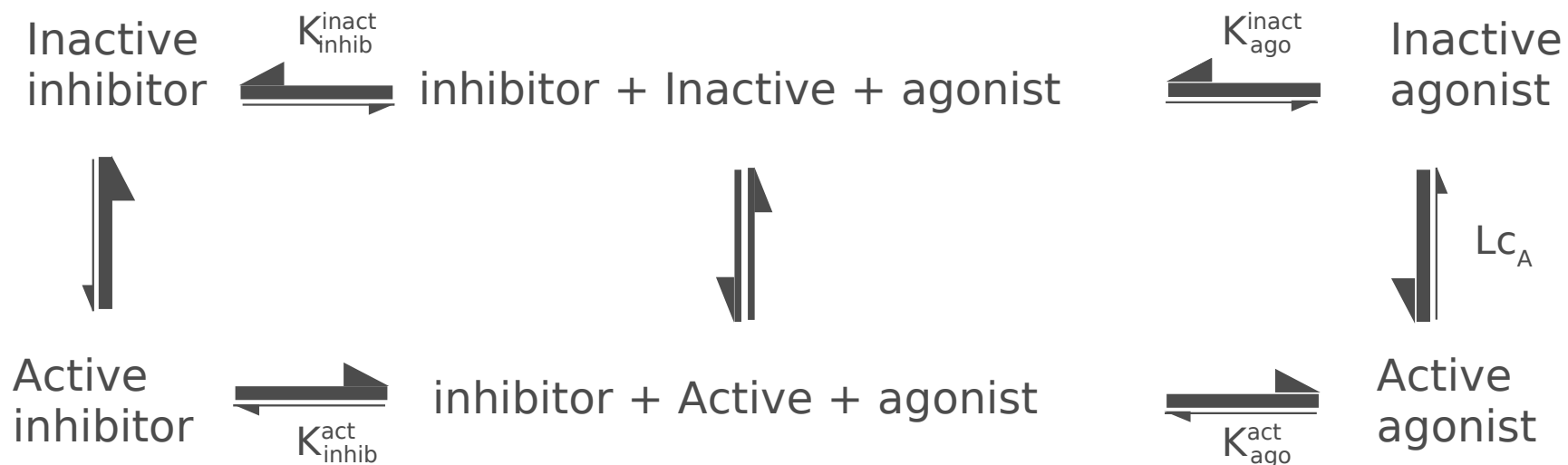
- **Arcadia** - <http://personalpages.manchester.ac.uk/staff/Alice.Villeger/arcadia.html>
- **CellDesigner** - <http://www.celldesigner.org/>
- **Edinburgh Pathway Editor** - <http://www.bioinformatics.ed.ac.uk/epe/>
- **BioModels Database** - <http://www.ebi.ac.uk/biomodels/>
- **Reactome** - <http://www.reactome.org/>
- **Vanted** - <http://vanted.ipk-gatersleben.de/>
- **Athena** - <http://www.codeplex.com/athena>
- **Netbuilder** - <http://strc.herts.ac.uk/bio/maria/Apostrophe/index.htm>



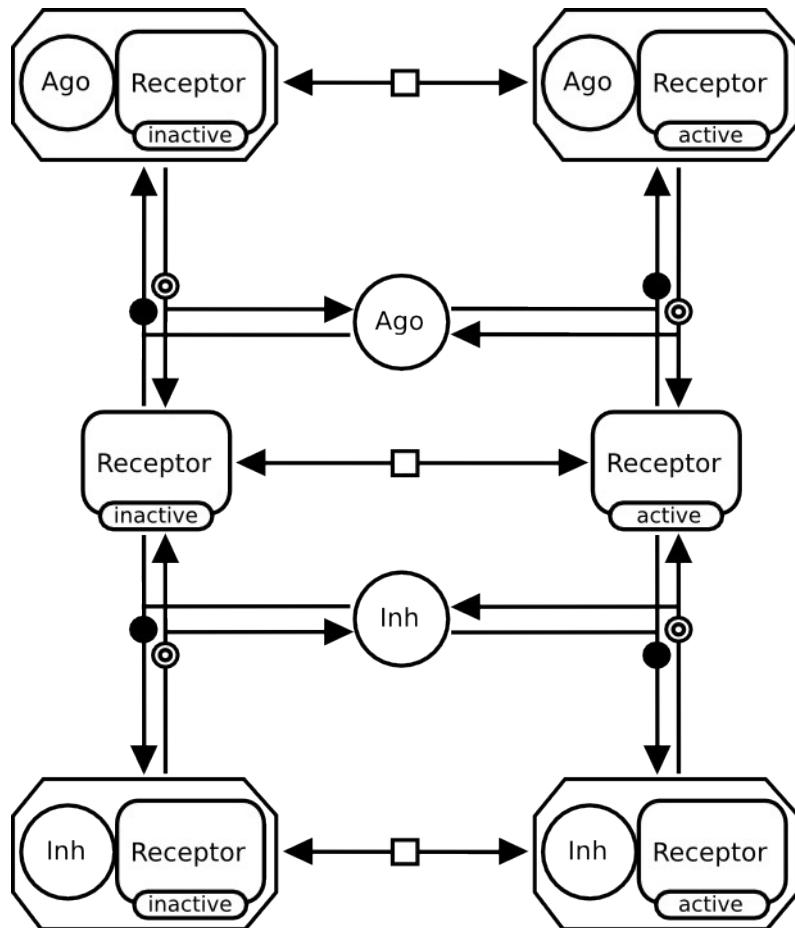




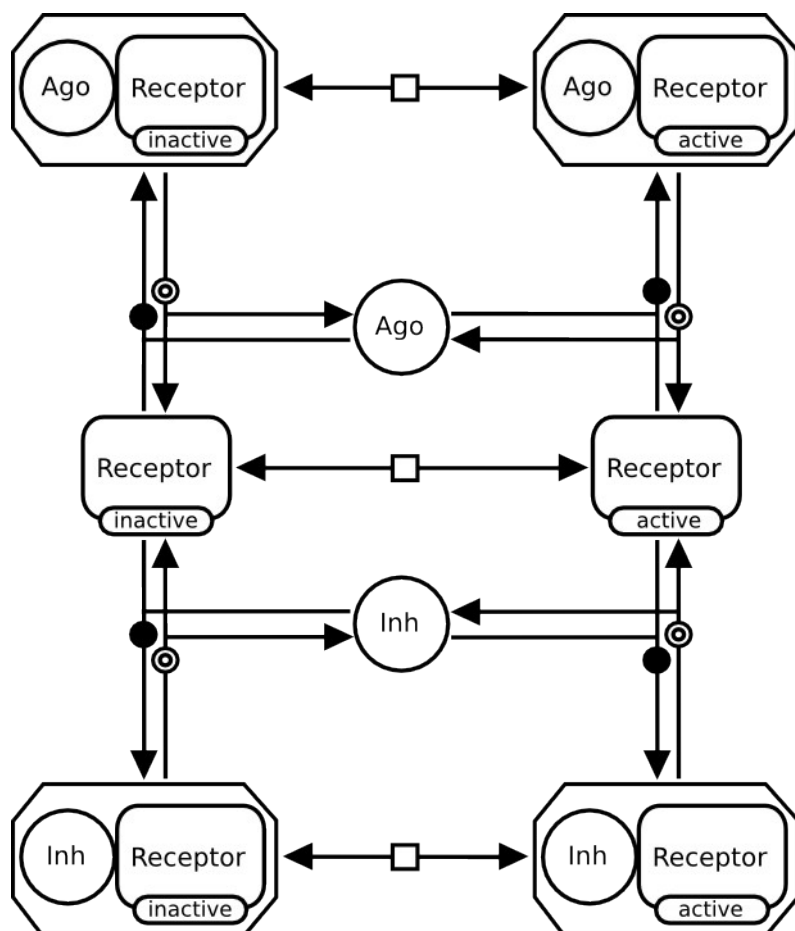




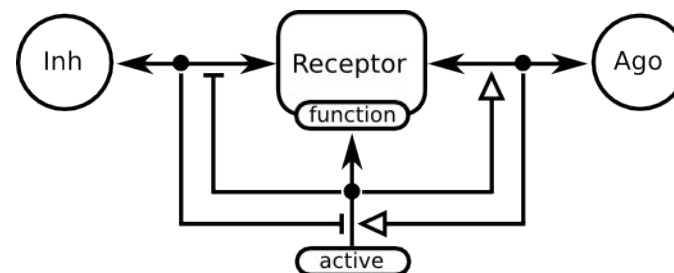
Process Diagram notation

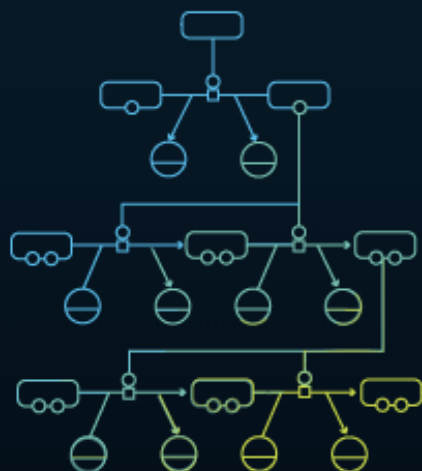


Process Diagram notation



Entity Relationships notation





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 diagrams of biochemical and cellular processes studied in systems biology.

Standardizing the diagrammatic notation is crucial for more efficient and accurate transmission of biological knowledge between different research communities in the expanding field of systems biology. Notations traditionally used by researchers and software have been informal, idiosyncratic and highly variable. Until SBGN, there has been no standard agreed-upon convention defining precisely how to draw biochemical interaction diagrams in a regular and systematic way that helps readers interpret them consistently and unambiguously.

SBGN defines a comprehensive set of symbols with precise semantics, together with detailed syntactic rules defining their use and how diagrams are to be interpreted. By standardizing the visual notation, SBGN can serve as a bridge between different communities in research, education, publishing, and more. The real payoff will come when researchers are as familiar with the notation as electronics engineers are familiar with the notation of circuit schematics. If researchers are saved the time and effort required to familiarize themselves with different notations, they can spend more time thinking about the biology being depicted.

On this site, you can browse some [example diagrams](#) to get a feeling for SBGN, read the SBGN [specification documents](#), join [online discussions](#), see current working documents 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.

SBGN News

(23 Aug. '08) The first **SBGN Process Diagrams Level 1** specification is out! [Download the specification](#) and [tell us](#) what you think!

EVENTS

As part of our efforts to develop and establish SBGN, in 2006 we initiated a workshop series to bring together individuals from around the world who are interested in discussing SBGN, its implementation and its evolution.

This page provides access to meeting pages, agendas, notes and other information about upcoming as well as past events.



[SBGN 4](#)

Rostock, Germany

16–17 Oct. 2008

SBGN 4 will be a satellite of the *The 6th Conference on Computational Methods in Systems Biology (CMSB)*.



[SBGN 3.5](#)

Okinawa, Japan

28 Jan.–2 Feb. 2008

SBGN 3.5 was part of the super-hackathon on "standards and ontologies for systems biology", held in Okinawa, Japan.



[SBGN 3](#)

Long Beach, California, USA

30 Sep. 2007

SBGN 3 was held the day before the ICSB 2007 conference in Long

- 4th SBGN forum
 - 15-16 October 2008
 - Rostock (Warnemunde), Germany
 - Satellite of CMSB 2008
- 3rd SBGN hackathon (SBGN 4.5)
 - 5-9 April 2009
 - Auckland (Waiheke island), New Zealand
 - Coupled with CellML workshop
- 5th SBGN forum (provisional)
 - September 2009
 - San Francisco (Stanford)
 - Satellite of ICSB 2009

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- Anatoly Sorokin (UK)
- Michael Hucka (US)
- Falk Schreiber (DE)
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- Huaiyu Mi (US)
- Yukiko Matsuoka (JP)
- Katja Wegner (UK)
- Hiroaki Kitano (JP)

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- Sarala Dissanayake (NZ)
- Ralph Gauges (DE)
- Peter Ghazal (UK)
- Lu Li (UK)

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

