



Workshop

combine

Hackathon

SBGN Process Description

Vasundra Touré

SBGN Workshop 2016
Newcastle upon Tyne, the 24th of September 2016

The SBGN community

The SBGN community is composed of

- Editors
Huaiyu Mi – Alexander Mazein – Augustin Luna – Nicolas Le Novère – Robin Haw
 - Scientific committee
 - SBGN community

_computational
BIOLOGY

PERSPECTIVE

The Systems Biology Graphical Notation

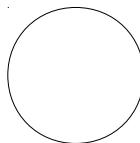
Nicolas Le Novère¹, Michael Hucka², Huaiyu Mi³, Stuart Moodie⁴, Falk Schreiber^{5,6}, Anatoly Sorokin⁷, Emek Demir⁸, Katja Wegner⁹, Mirit I Aladjem¹⁰, Sarala M Wimalaratne¹¹, Frank T Bergman¹², Ralph Gauges¹³, Peter Ghazal^{14,14}, Hideya Kawaji¹⁵, Lu Li¹, Yukiko Matsuo¹⁶, Alice Villéger^{17,18}, Sarah E Boyd¹⁹, Laurence Calzone²⁰, Melanie Courtot²¹, Ugur Dogrusoz²², Tom C Freeman^{14,23}, Akira Funahashi²⁴, Samik Ghosh¹⁶, Akiya Jouraku²⁴, Sohyoung Kim¹⁰, Fedor Kolpakov^{25,26}, Augustin Luna¹⁰, Sven Sahle¹³, Esther Schmidt¹, Steven Watterson^{4,22}, Guanming Wu²⁷, Igor Goryanin⁴, Douglas B Kell^{18,28}, Chris Sander⁸, Herbert Sauro¹², Jacky L Snoep²⁹, Kurt Kohn¹⁰ & Hiroaki Kitano^{16,30,31}

The SBGN standard

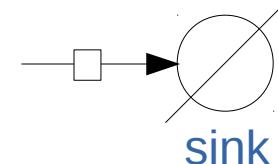
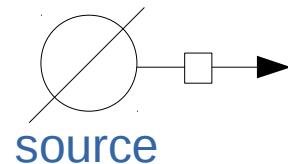
The Systems Biology Graphical Notation is a community effort to standardize visual representation of biological maps



with standardized glyphs and arcs...

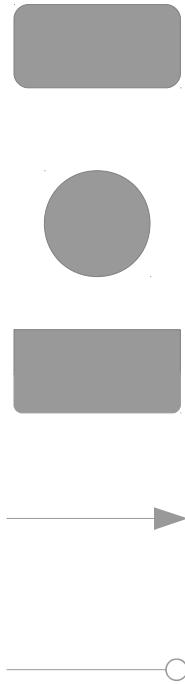


... and well-defined semantics.



The ontology used in SBGN

SBO terms are used in SBGN to distinguish the biological meaning of the symbols

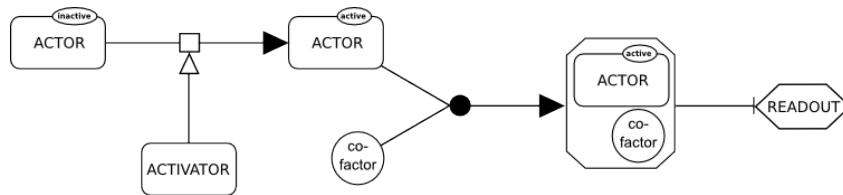


Macromolecule	SBO:0000245
Simple chemical	SBO:0000247
Nucleic Acid Feature	SBO:0000354
Production	SBO:0000393
Catalysis	SBO:0000172

The three SBGN languages

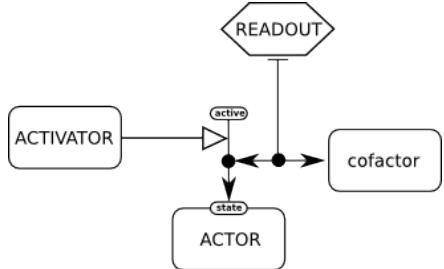
Process Description

Biochemistry



Entity Relationship

Physiology, Genetics



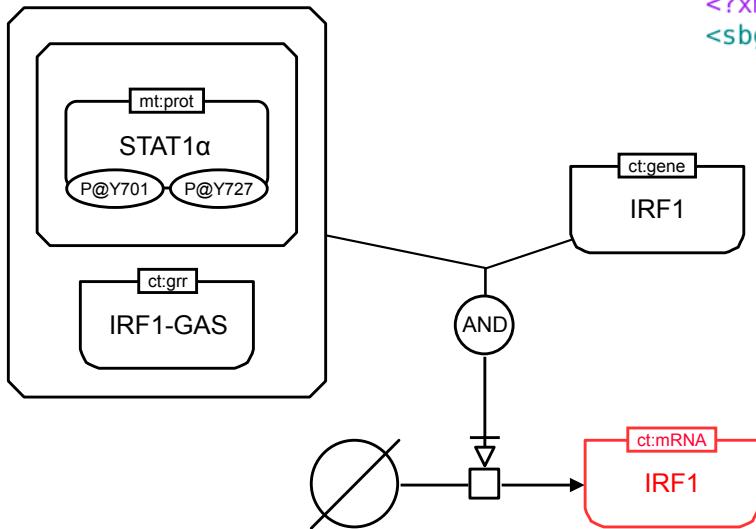
Activity Flow

Molecular biology



The storage format: SBGN-ML

Software support and exchanges are facilitated by libSBGN



```

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    </map>
</sbgn>
    
```

The XML code represents the SBGN diagram. It defines three glyphs: 'glyph7' for a source and sink (rectangle), 'glyph9' for a process (diamond), and 'glyph6' for a nucleic acid feature (rectangle). The 'glyph6' section is highlighted with a red border. The 'ct:mRNA' box is labeled 'IRF1' and has a bounding box of approximately y=313.0, x=415.0, h=60.0, w=120.0. Inside this box is another 'glyph6a' for the 'ct:mRNA' unit, with a bounding box of approximately y=304.0, x=443.5, h=18.0, w=63.0.

SBGN

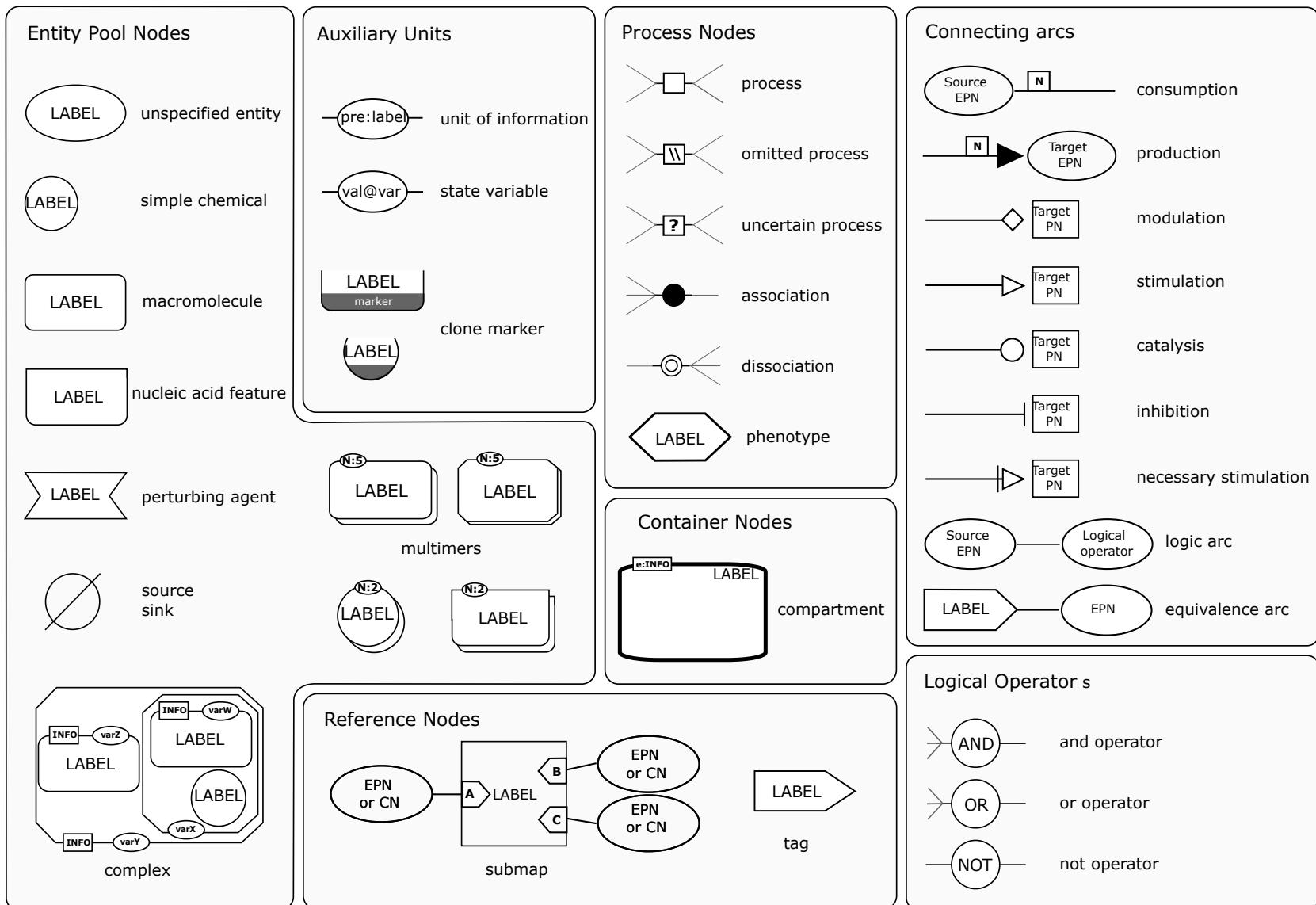
SBGN-ML

- SBGN-ED: Viewer / Editor
- SBGNViz: Viewer / Editor for PD
- PathVisio: Viewer / Editor

List of tools available:

http://sbgn.github.io/sbgn/software_support

The SBGN Process Description



The Entity Pool Nodes

EPNs indicate the chemical structure of the entity

Material entities

simple chemical

macromolecule

nucleic acid feature

multimer simple chemical

multimer macromolecule

multimer nucleic acid feature

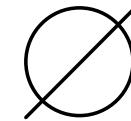
complex

multimer complex

unspecified entity

Conceptual entities

perturbing agent



Source and sink

The Entity Pool Nodes

EPNs indicate the chemical structure of the entity

Material entities

simple chemical

macromolecule

nucleic acid feature

multimer simple chemical

multimer macromolecule

multimer nucleic acid feature

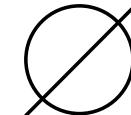
complex

multimer complex

unspecified entity

Conceptual entities

perturbing agent

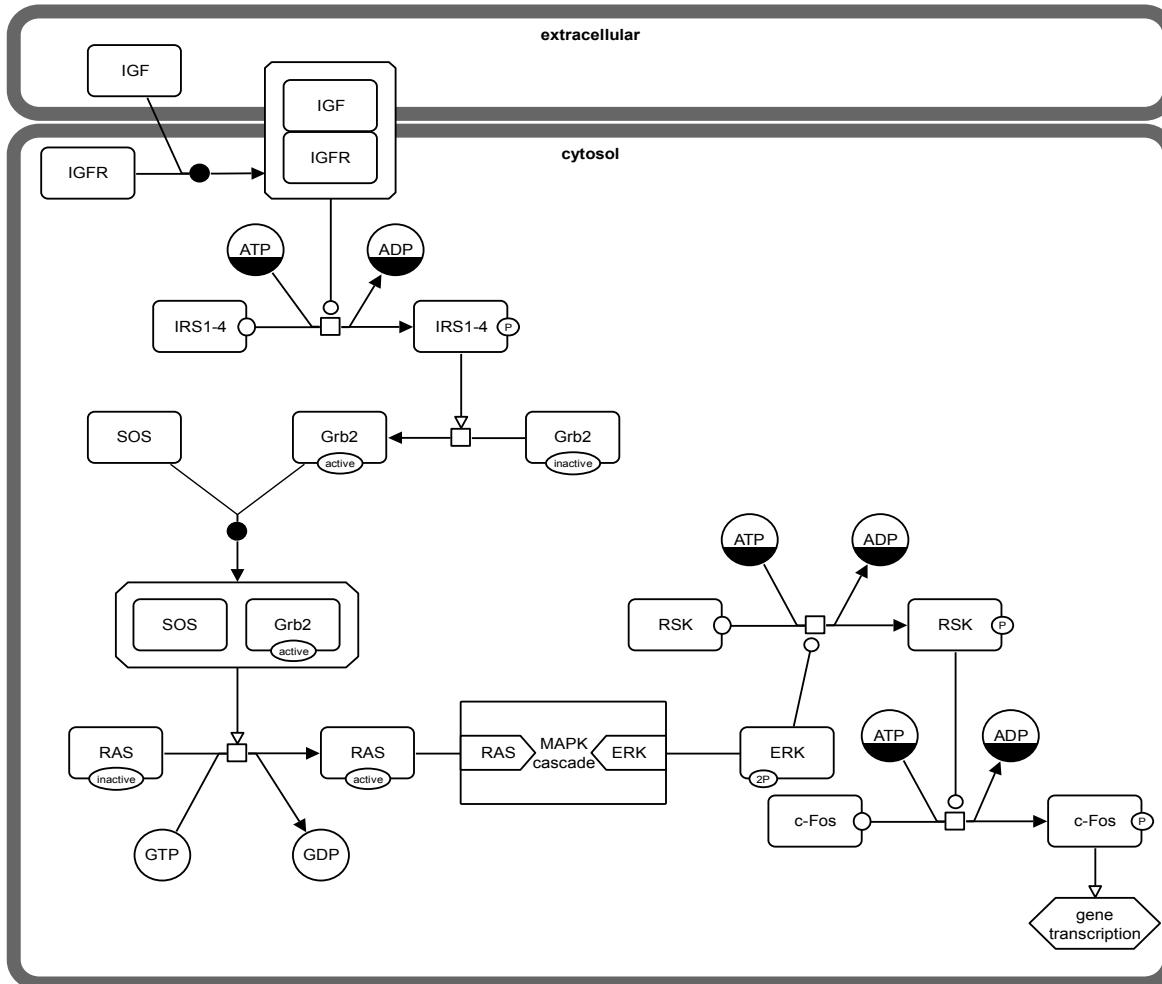


Source and sink

Generic entity used
if no SBO terms

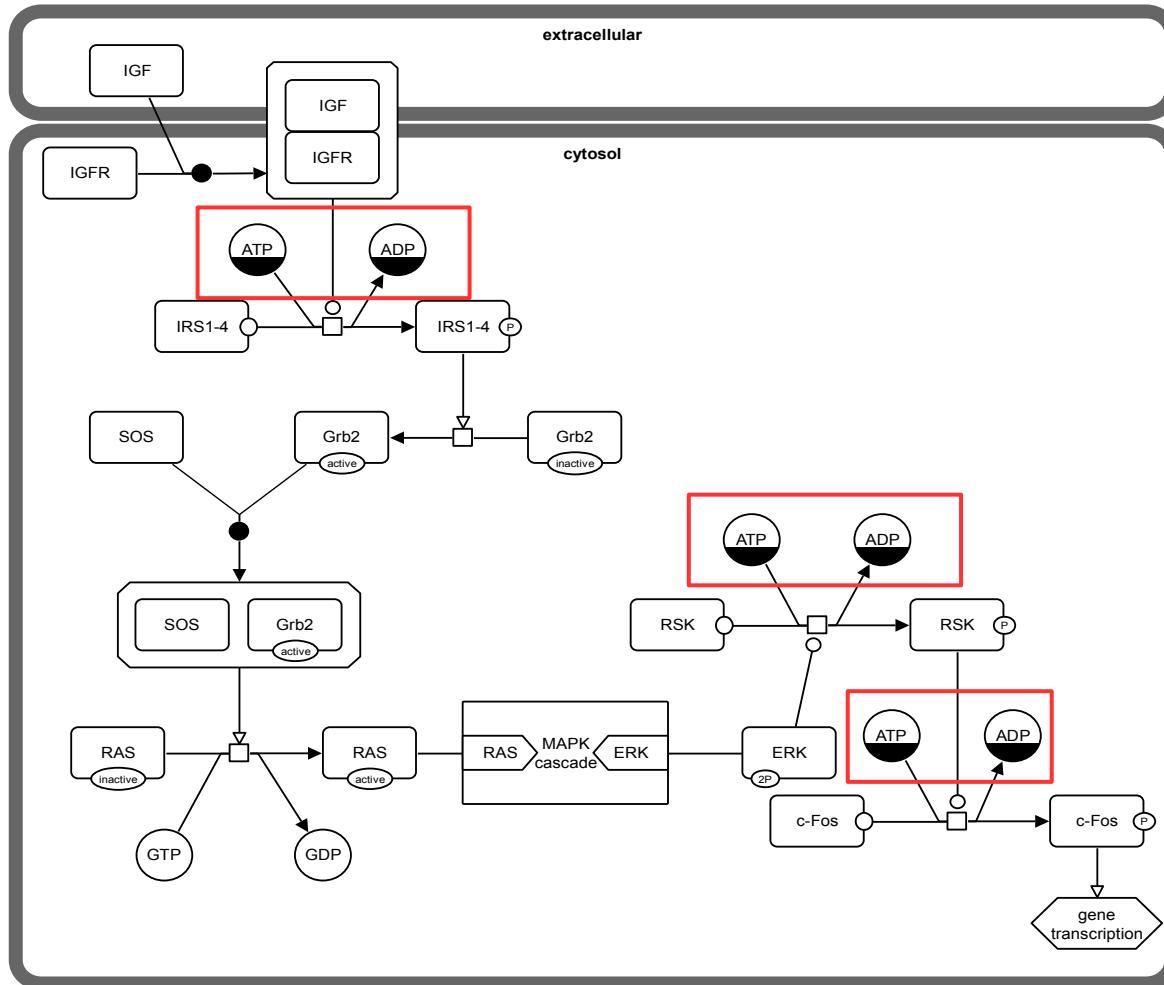
The Clone Markers

Identify identical EPNs in a given network



The Clone Markers

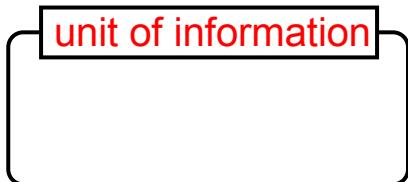
Identify identical EPNs in a given network



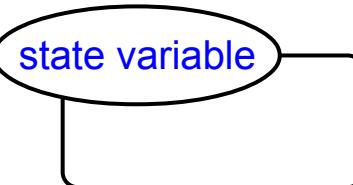
The Auxiliary Units

Additional information that can be part of glyphs

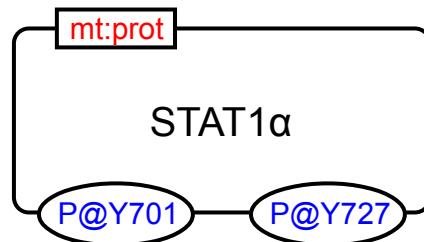
1.



2.



Example



The Container Node

Encloses Entity Pool Nodes – also called Compartment

Compartment

Specificity:

- border is thicker than EPNs
- can hold units of information

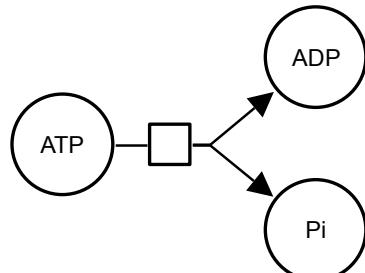
Reminder from EPNs

macromolecule

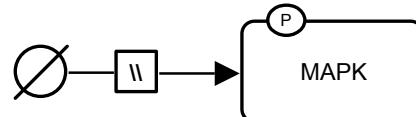
The Process Nodes

Represent processes that transforms biochemicals (EPNs) into the same or other biochemicals

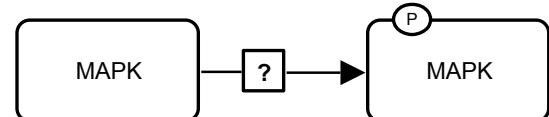
process



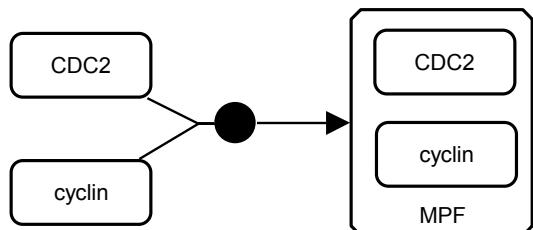
omitted process



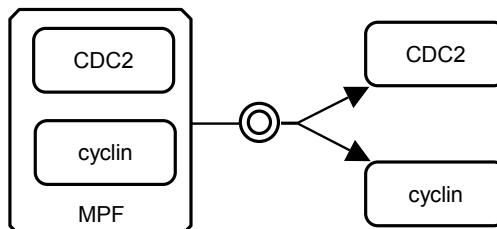
uncertain process



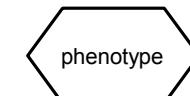
association



dissociation



phenotype



Link between entity pools and processes



consumption



production



necessary
stimulation



modulation



catalysis



stimulation



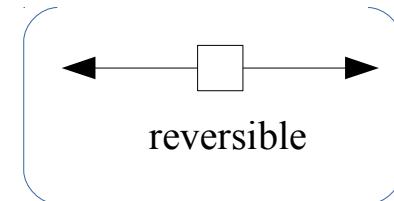
inhibition



logic arc

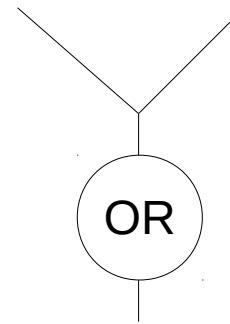
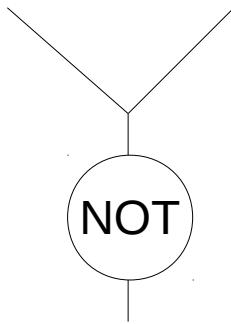
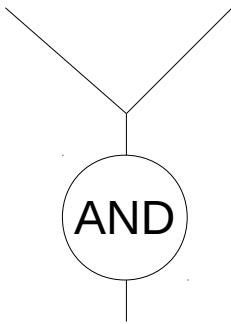


equivalence
arc



Logical Operators

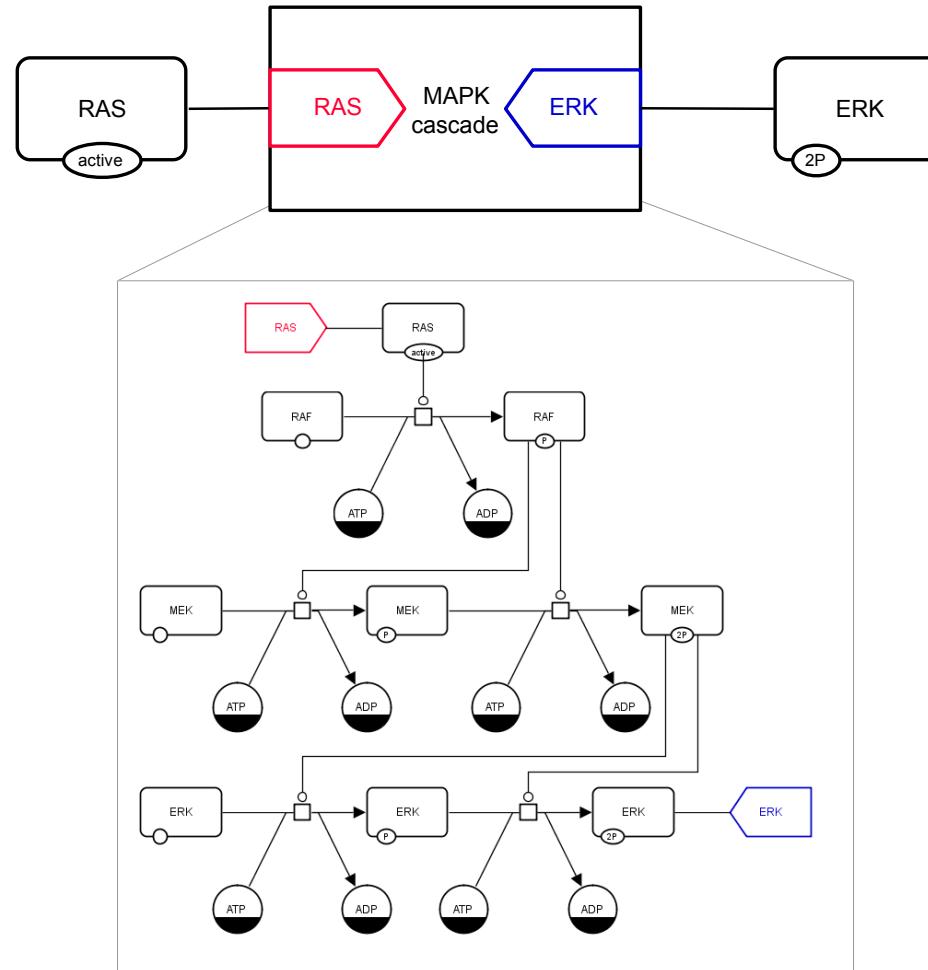
Logical connection involving two or more inputs



Reference Nodes

Submaps are supported in SBGN PD

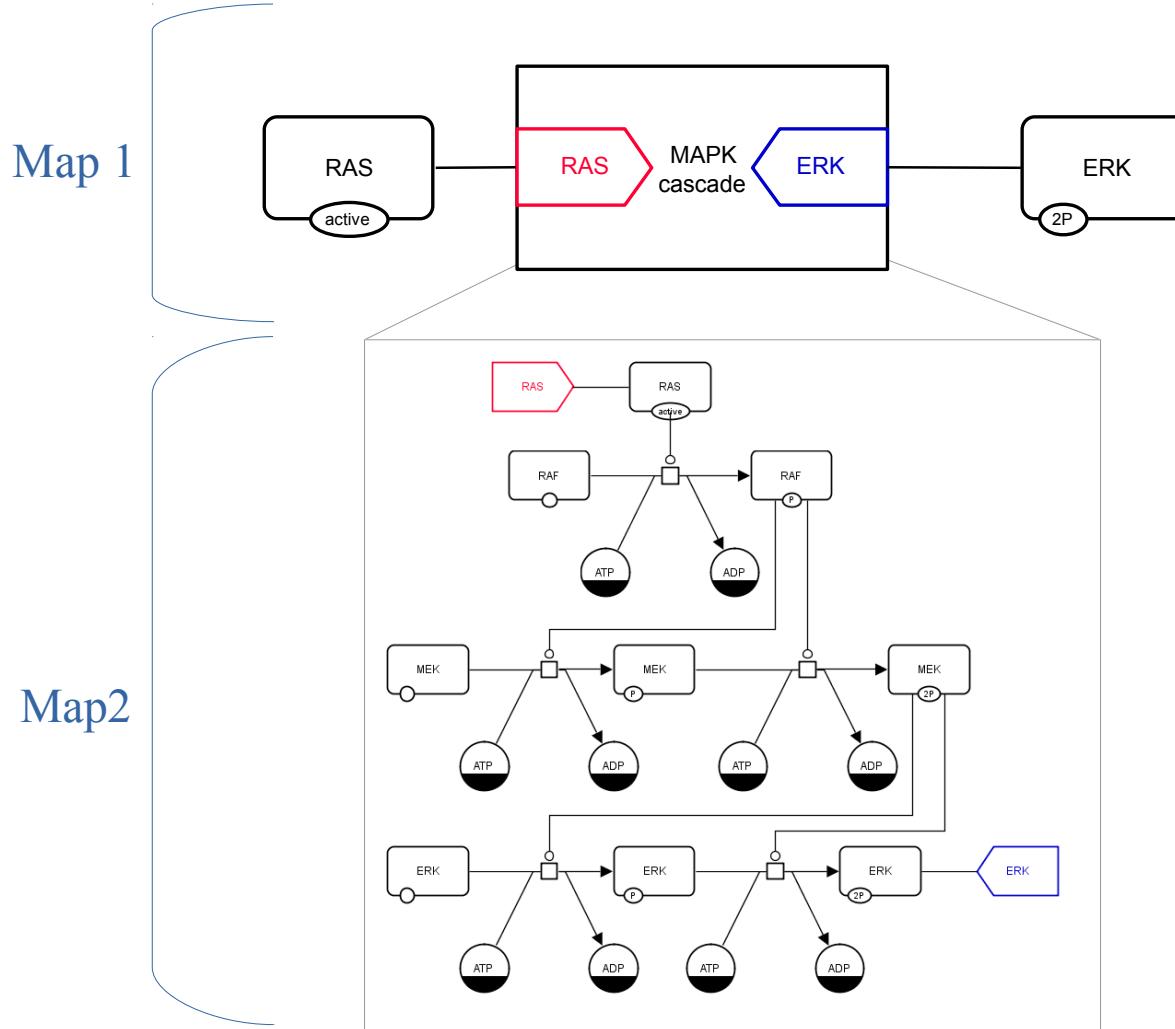
Tag



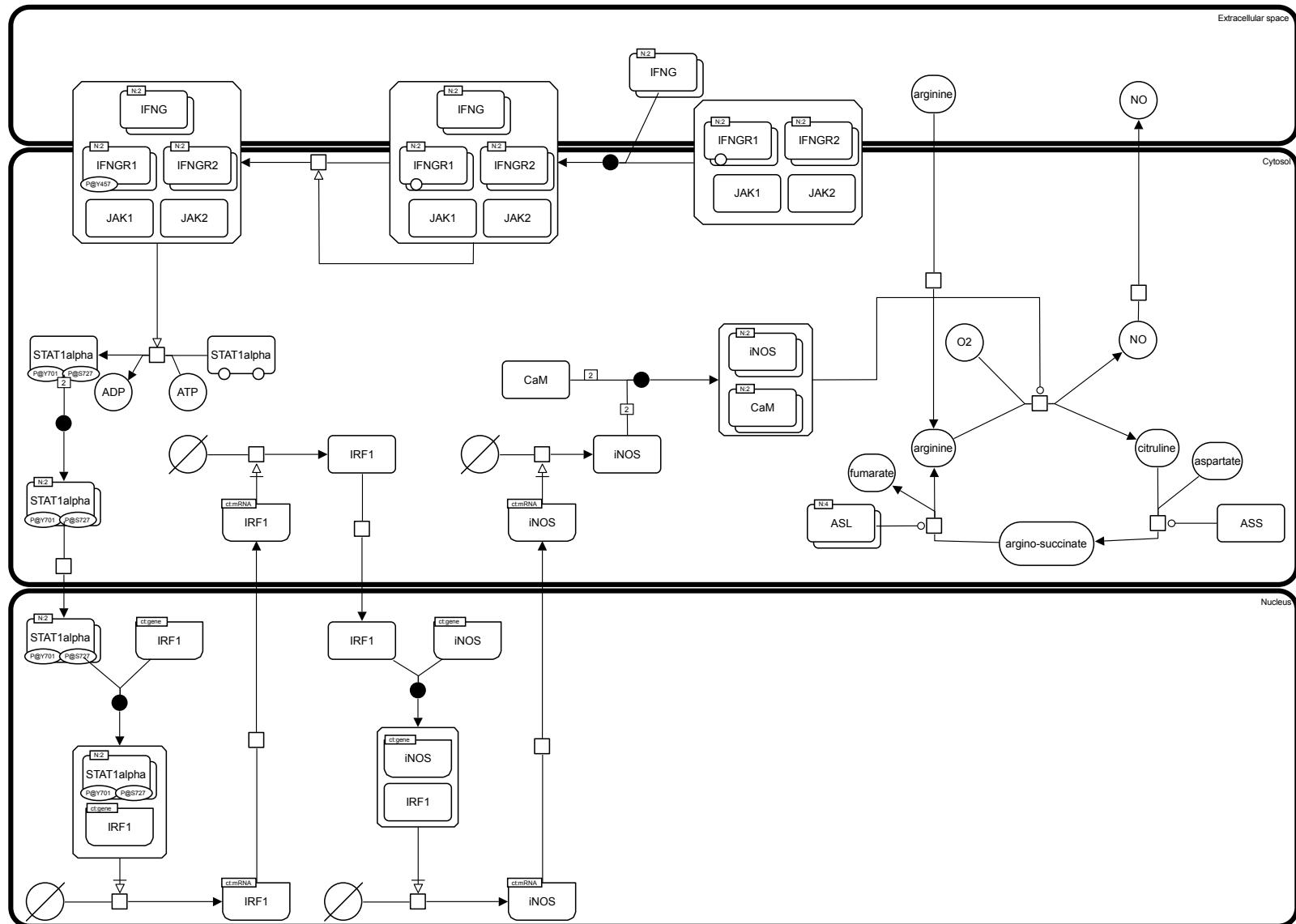
Reference Nodes

Submaps are supported in SBGN PD

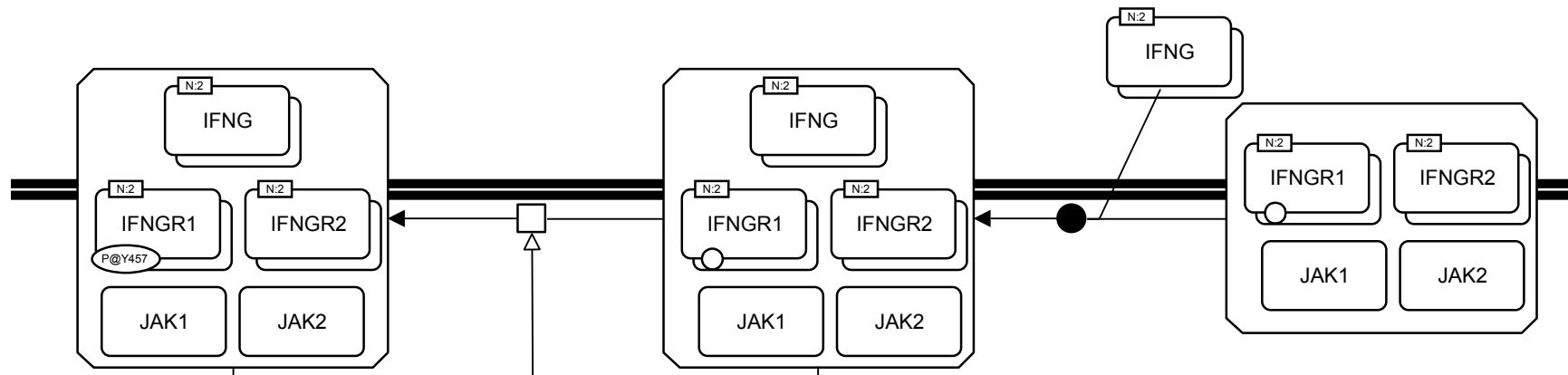
Tag



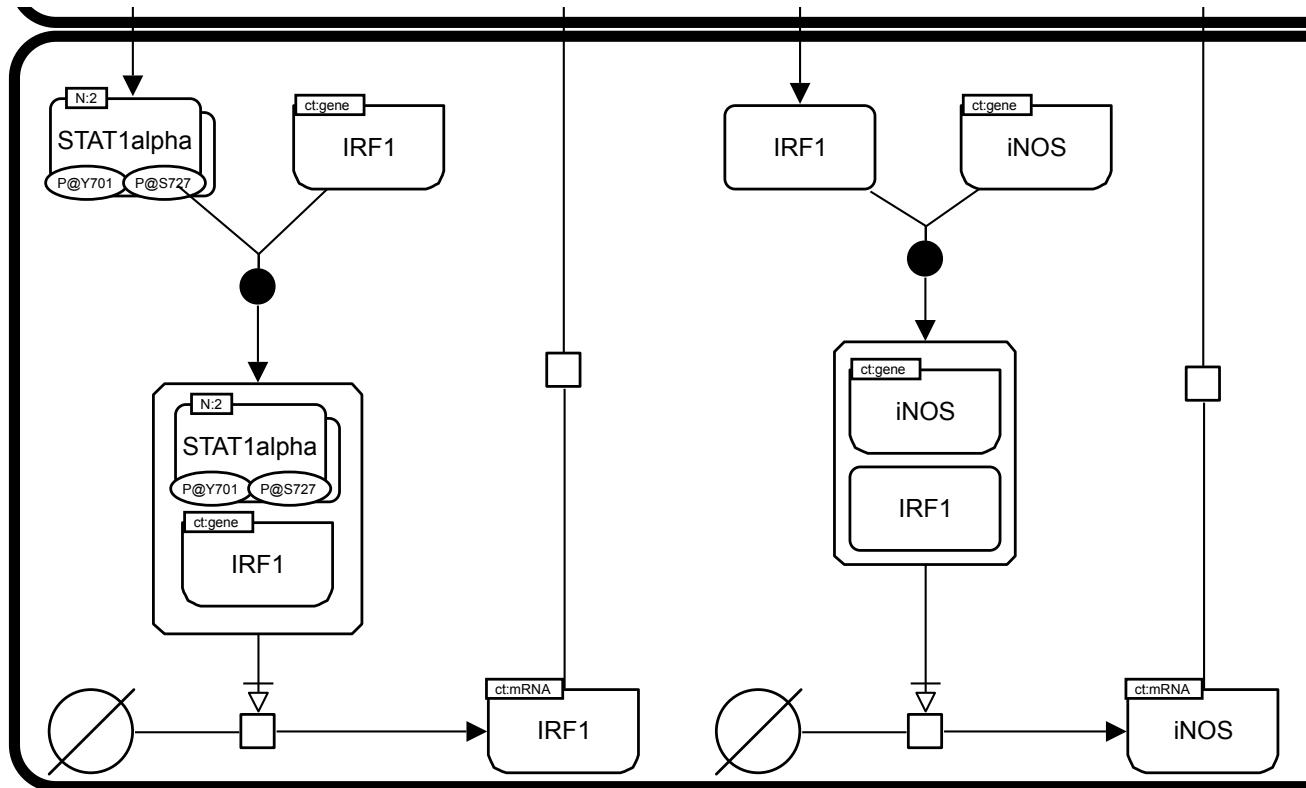
Example of network: the INOS pathway



Example of network: the INOS pathway



Example of network: the iNOS pathway

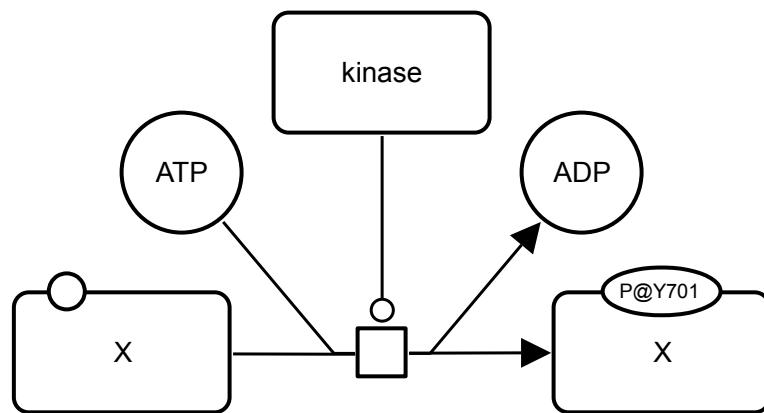


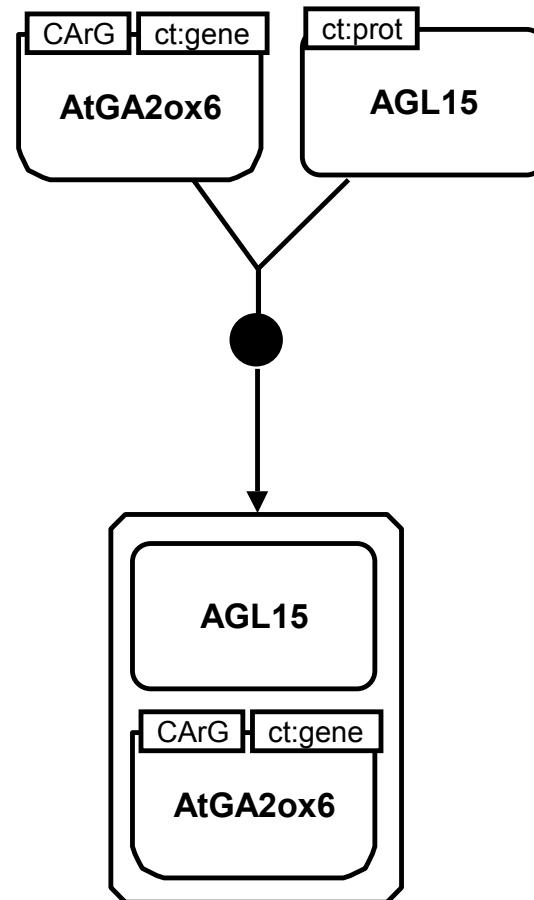


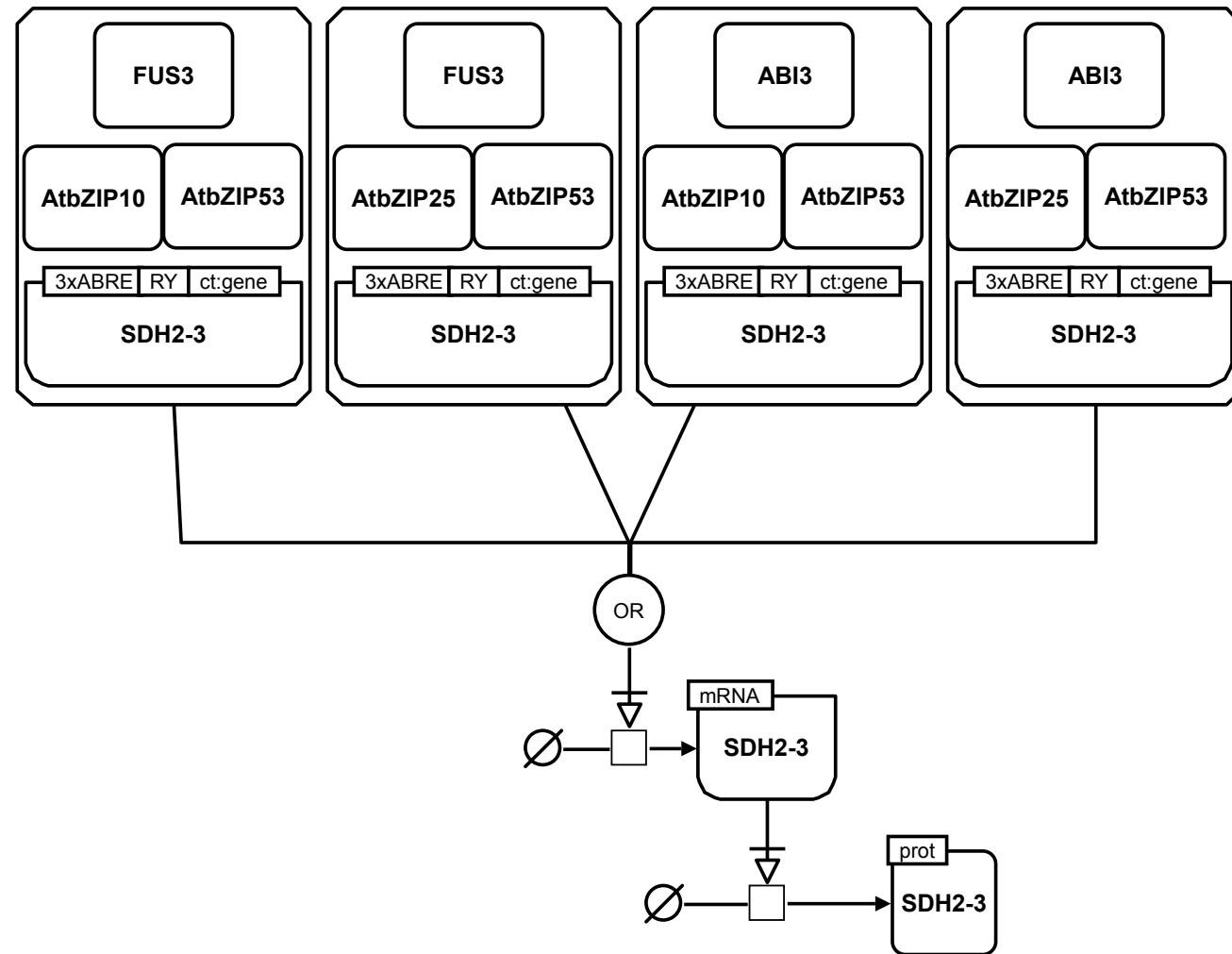
Now it's your turn!



Interpret the examples on following slides







- SBGN website:
 - <http://sbgn.github.io/sbgn>
- SBGN discussion
 - <https://groups.google.com/forum/#!forum/sbgn-discuss>
- SBGN core-related projects
 - <https://github.com/sbgn>