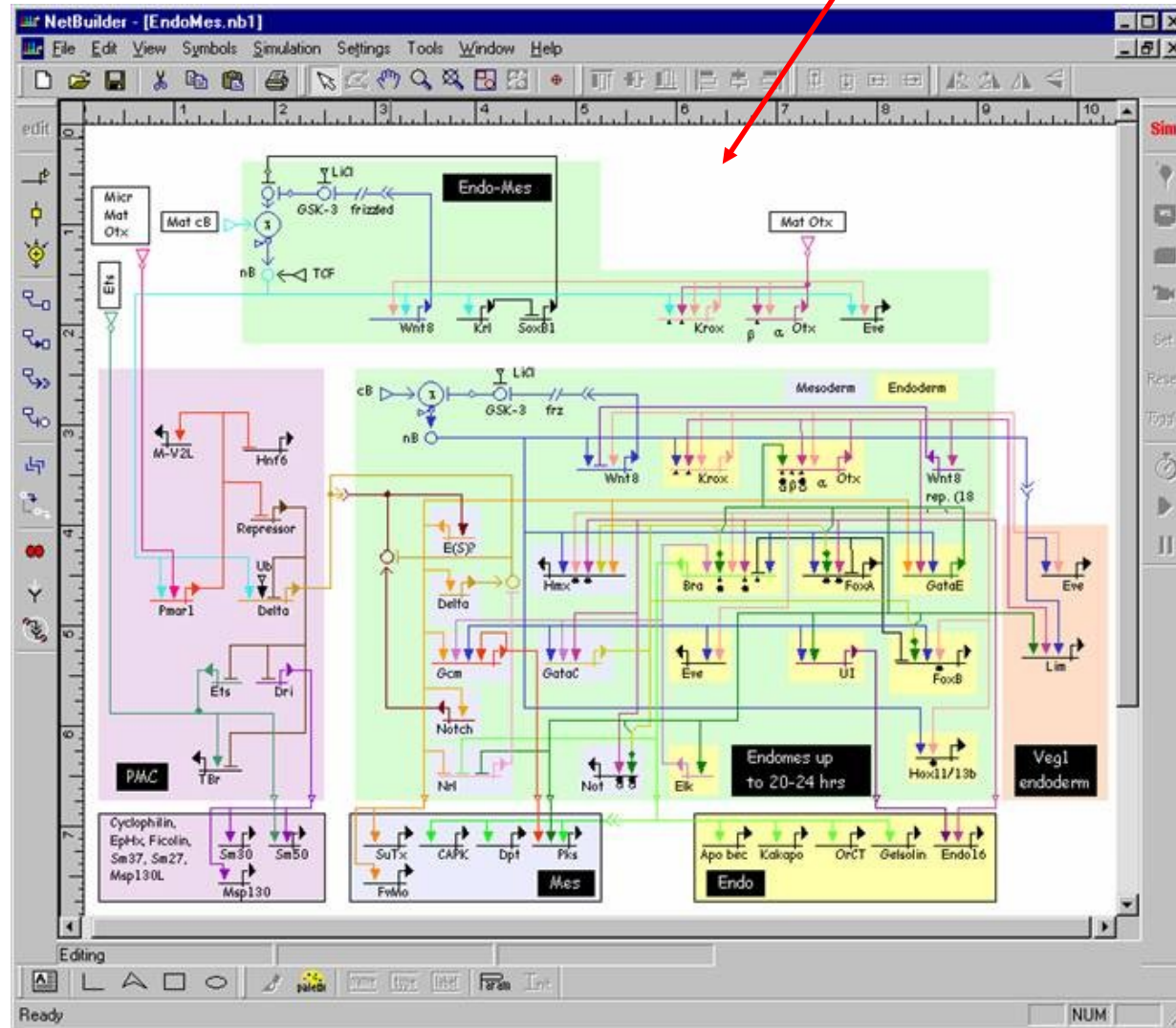


NetBuilder'

Katja Wegner
STRI, University of Hertfordshire, UK

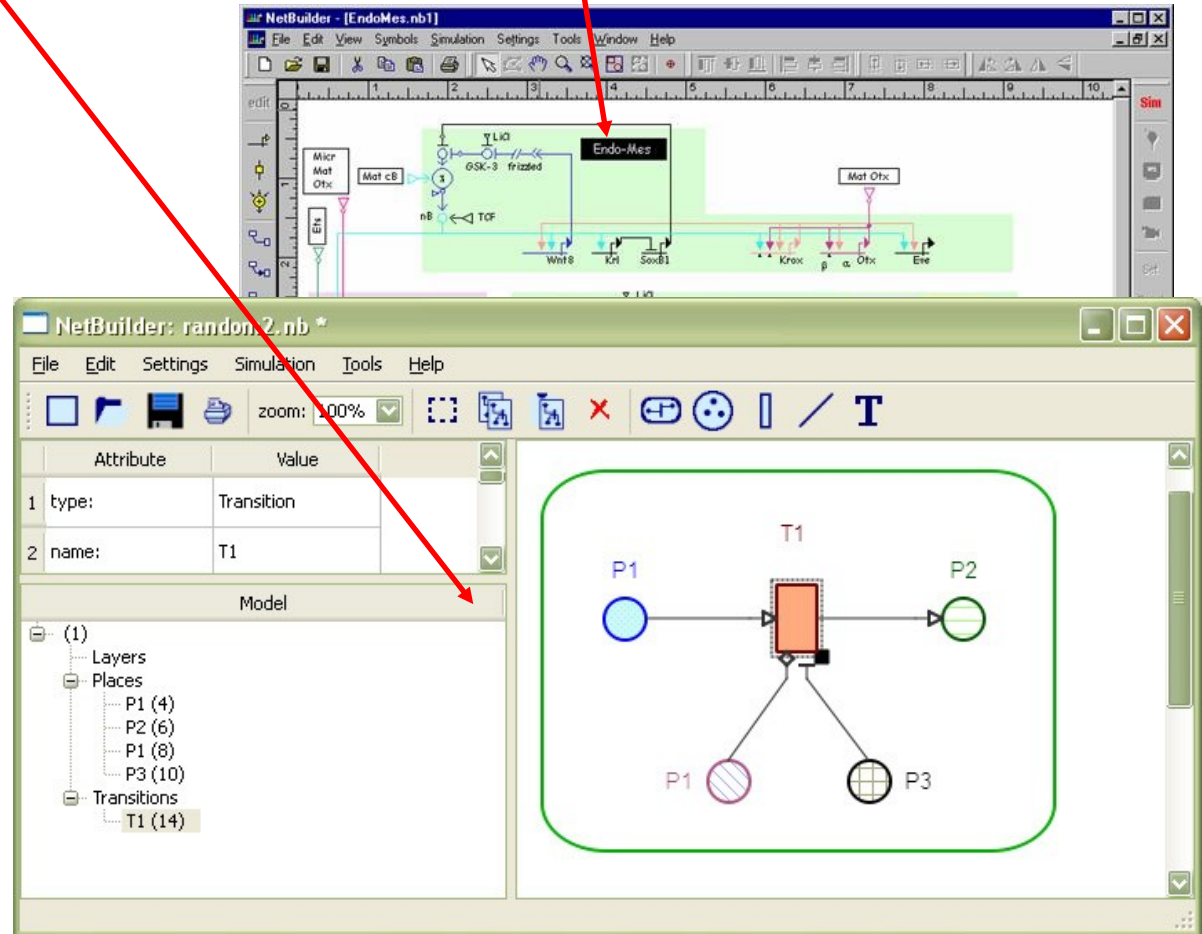
<http://strc.herts.ac.uk/bio/aria/Apostrophe/>

NetBuilder' ≠ NetBuilder



NetBuilder' ≠ NetBuilder

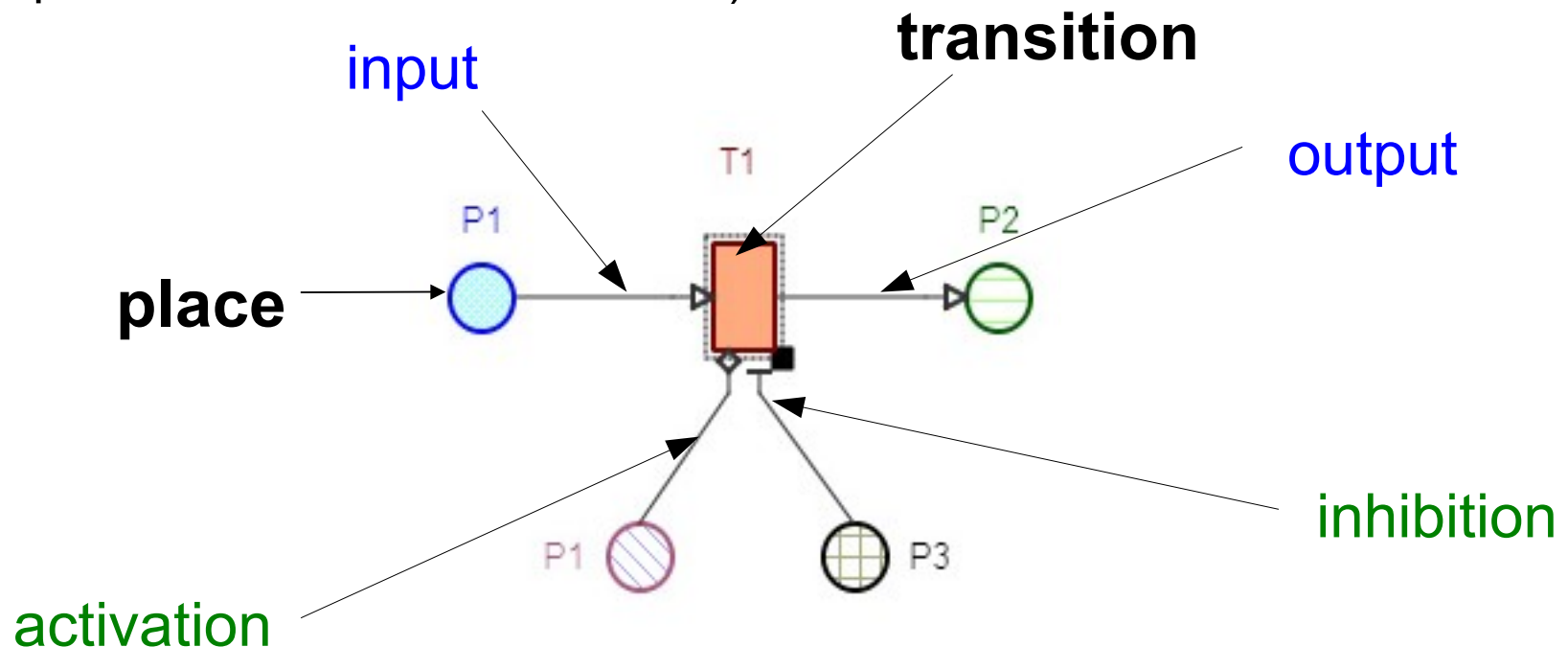
- NetBuilder':
 - completely overhauled version
 - different model visualisation
 - more simulation and analysis methods



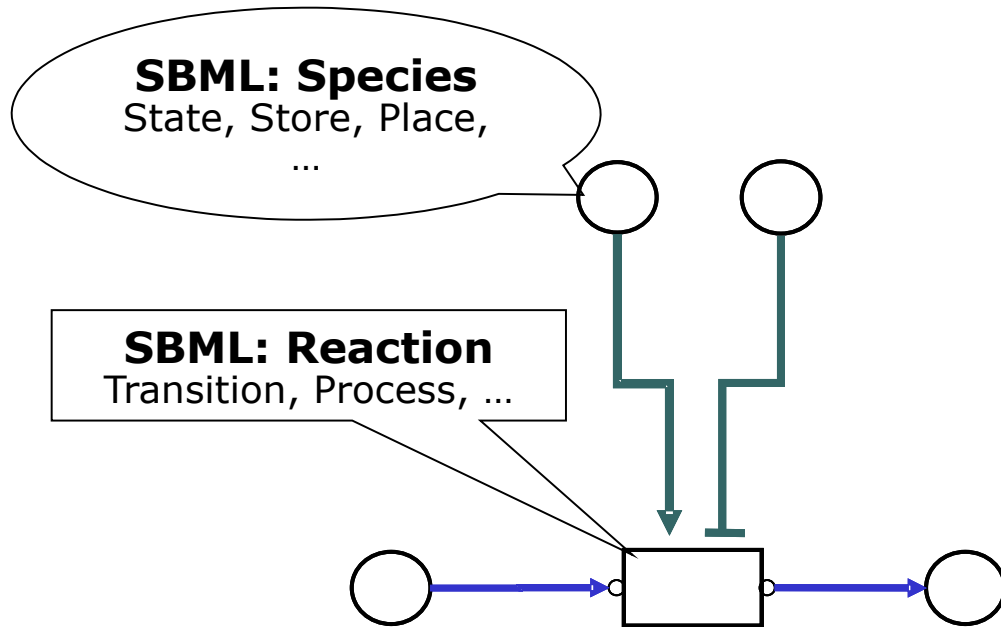
NetBuilder' - Petri net

- bipartite graph

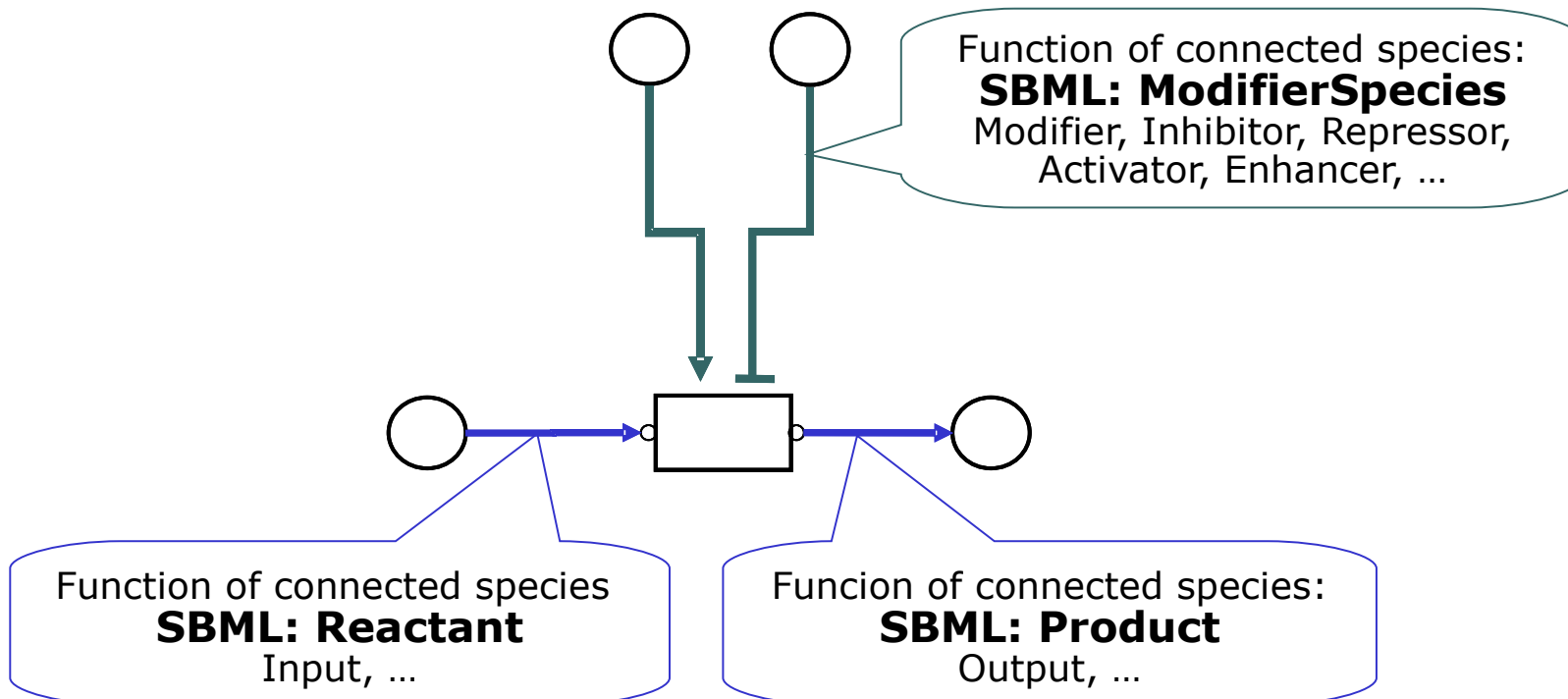
- place – e.g. proteins (**circle**)
- transition – e.g. reaction, gene (**rectangle**)
- **arc** - connection between a place and a transition (what is consumed to produce what or what **modifies**)



Petri net notation: Nodes



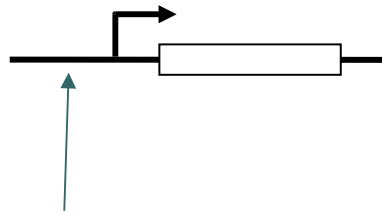
Petri net notation: Arcs



GRNs – Common notation

Single gene:

Promoter:
Starting point for transcription

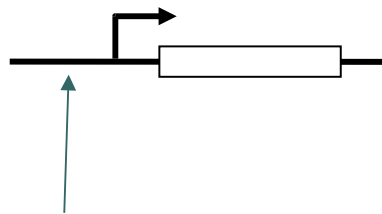


“Upstream” region:
Often contains interaction points for
Transcription Factors: proteins that
repress or activate transcription

GRNs – Common notation

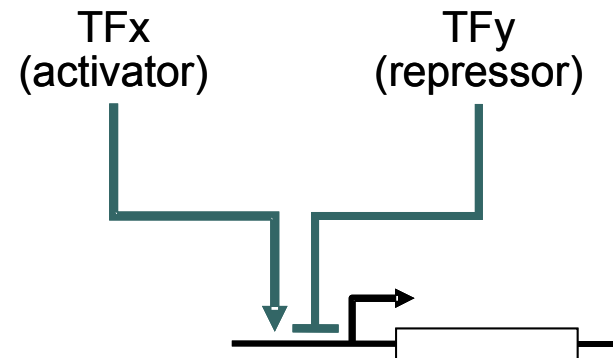
Single gene:

Promoter:
Starting point for transcription



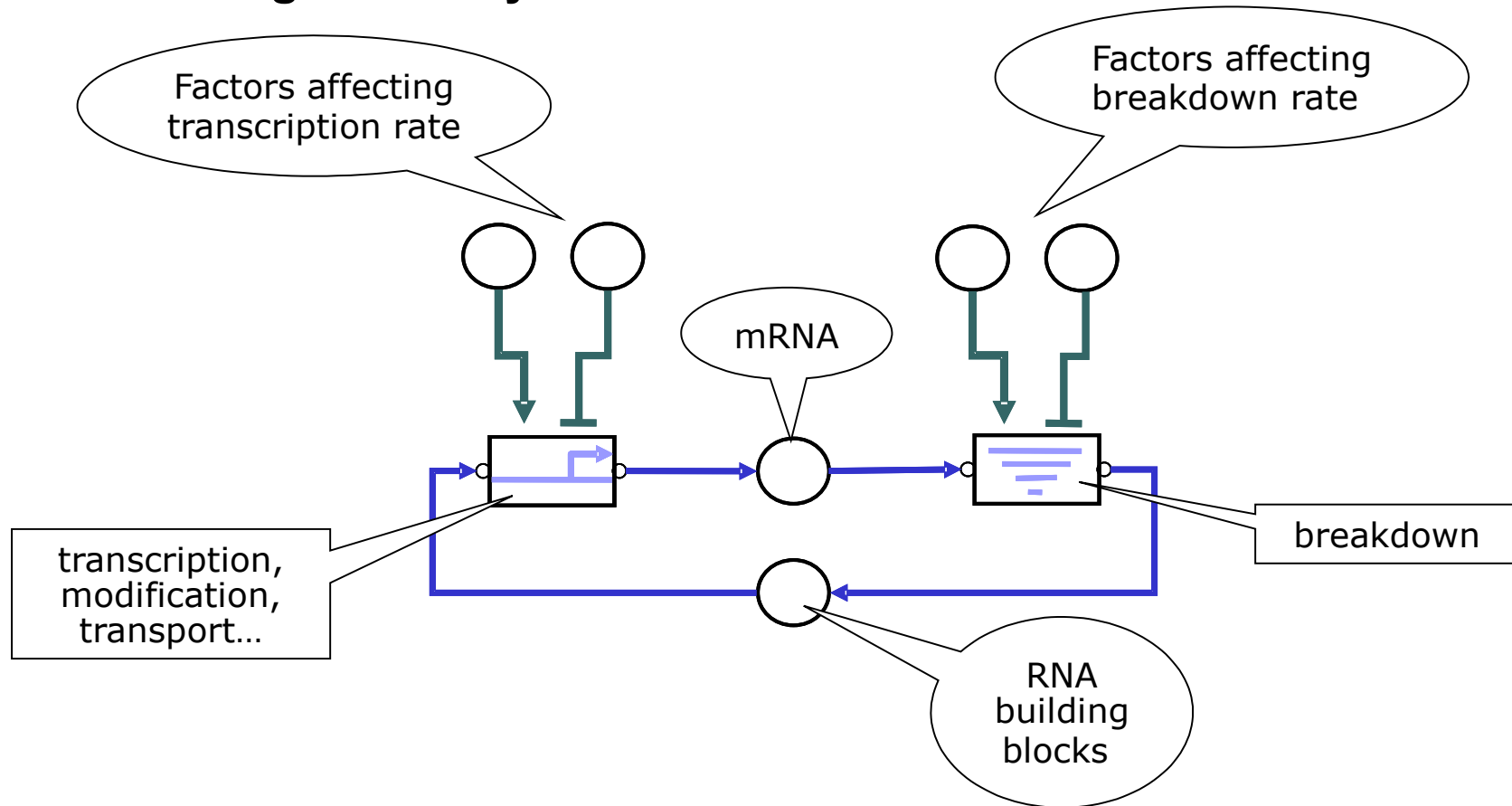
“Upstream” region:
Often contains interaction points for
Transcription Factors: proteins that
repress or activate transcription

Control (modifiers):



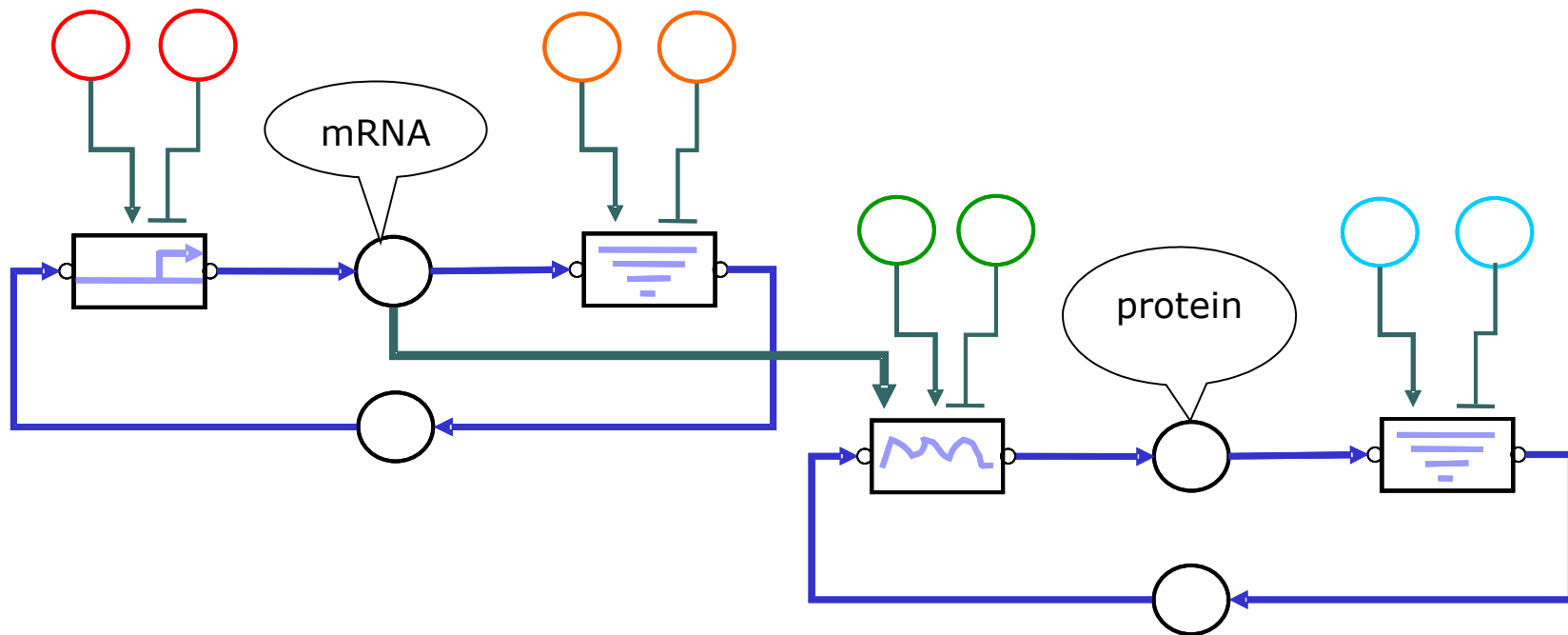
Petri net notation - Example

Messenger RNA dynamics



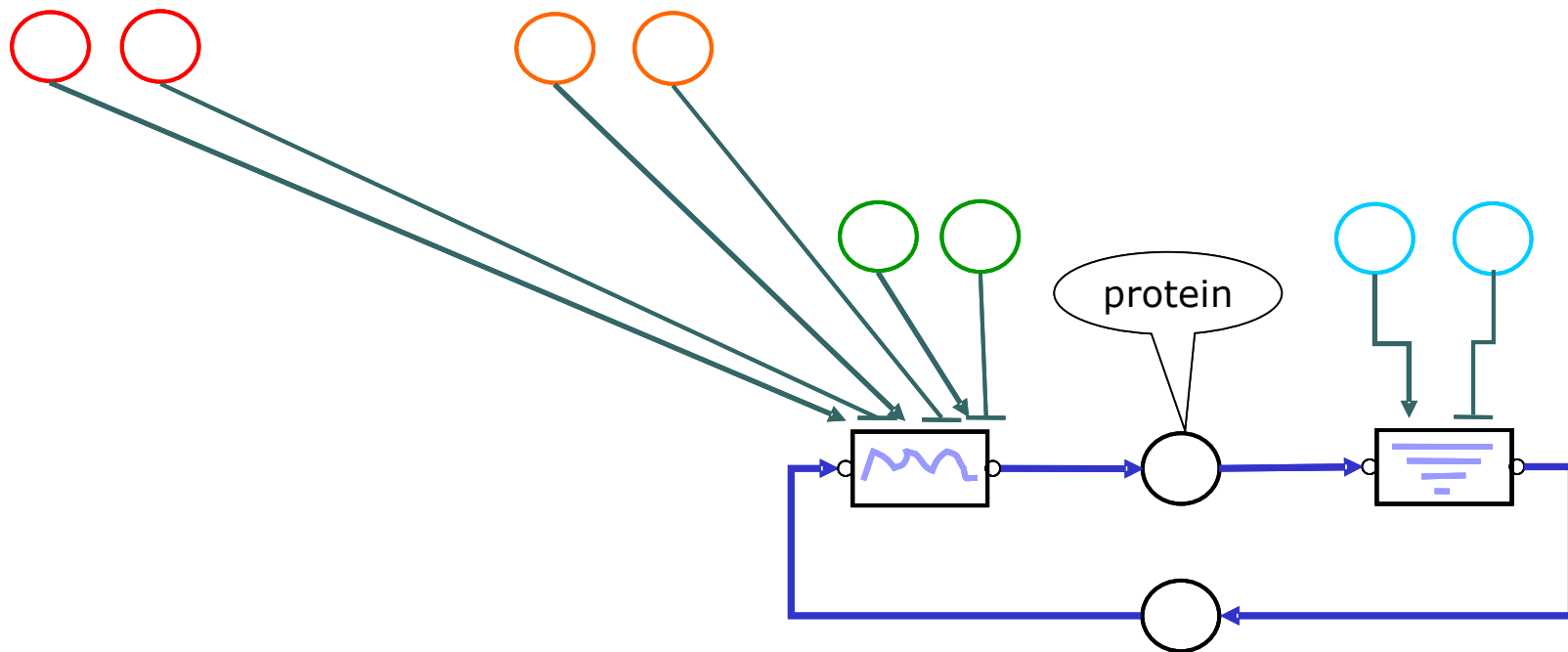
Petri net notation - Example

Messenger RNA and protein product dynamics

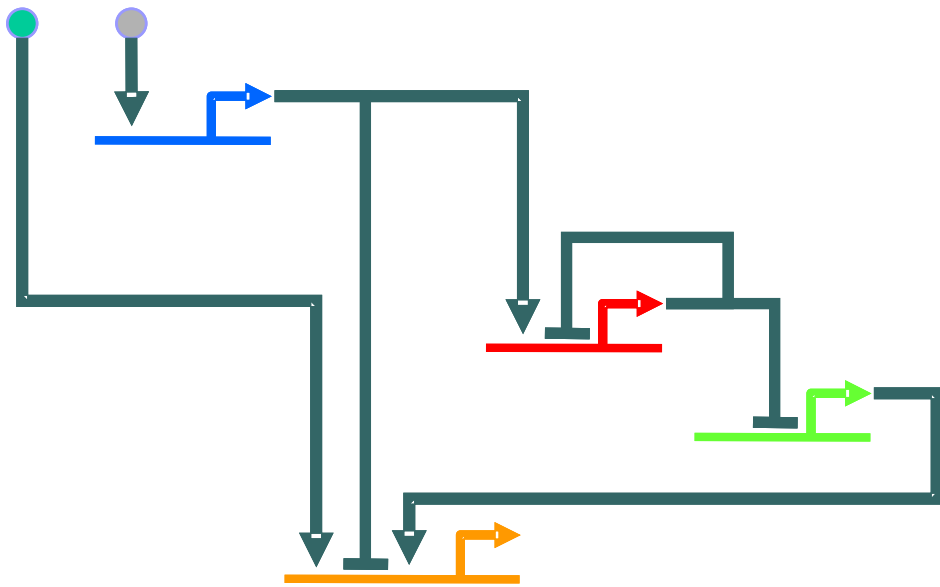


Petri net notation - Example

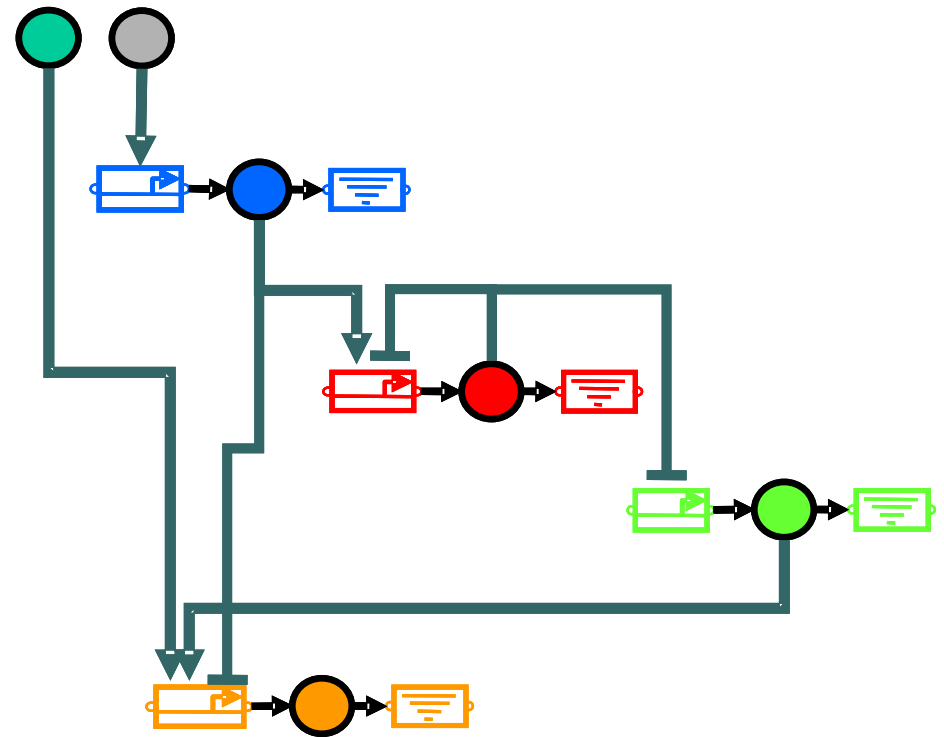
Messenger RNA and protein product dynamics



Basic GRN network



common



NetBuilder'

Rate equations

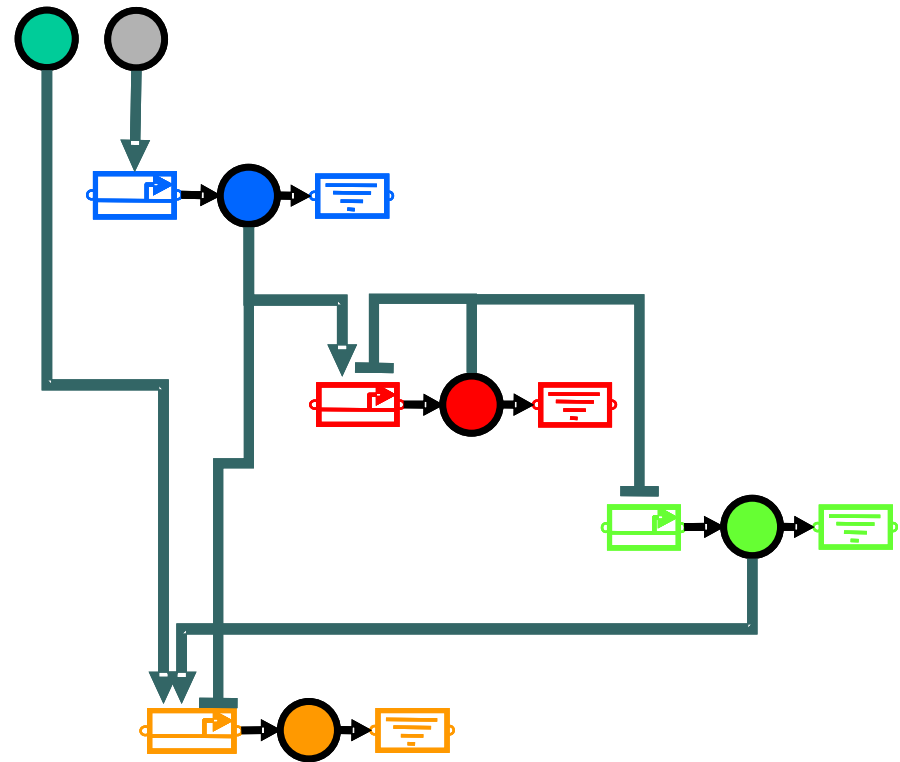
Product production rate:

$$v_p = k_p \times f(\text{modifiers})$$

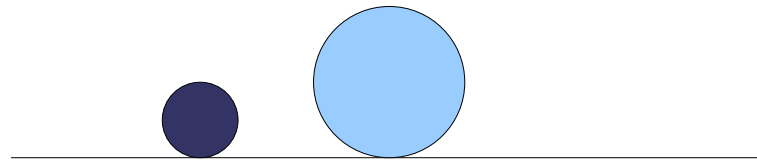
Product breakdown rate:

$$v_b = k_b \times [P]$$

k_p , k_b : production and breakdown rate constants
 $[P]$: concentration or amount of species P
 P : gene product



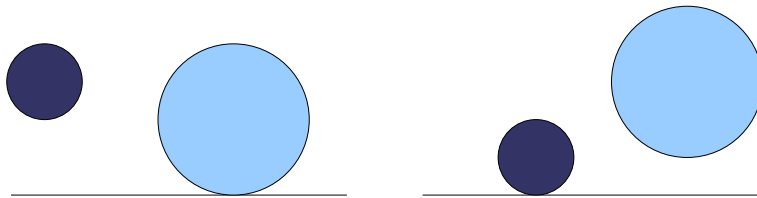
Modifier binding mechanisms



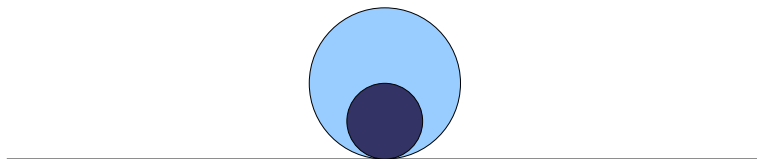
Independent



Compulsory order



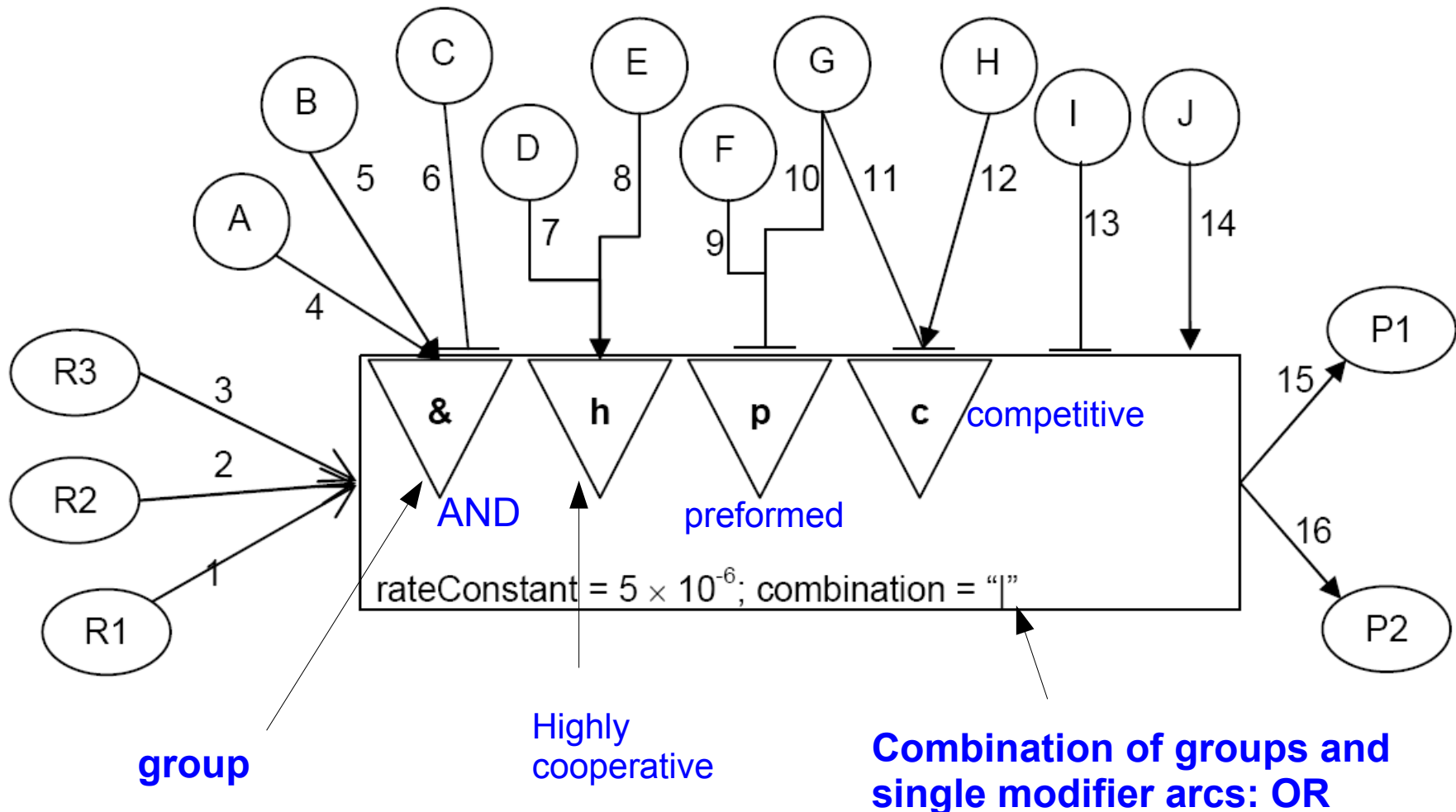
Competitive



Highly competitive
Preformed complex

Abstract grouping example

Maria J. Schilstra & C. L. Nehaniv (2008) *Artificial Life* 14, 121-133



NetBuilder' - Summary

- Graphical editor (Im-/Export SBML with layout)
- Equations describing process dynamics
 - Mass-action type rate equations automatically generated
 - Define own kinetics
- Rules for (combined) effects of regulatory interactions (grouping)
- Numerical representation of component values
 - Continuous and/or discrete places
- Evaluation methods:
 - Stochastic (based on Gibson & Bruck)
 - Deterministic (LSODA and Euler)
 - Hybrid
- **Beta version online available (open source)**
- **Developers: Maria Schilstra, Johannes Knabe, Attila Egri-Nagy**

<http://strc.herts.ac.uk/bio/maria/Apostrophe/>