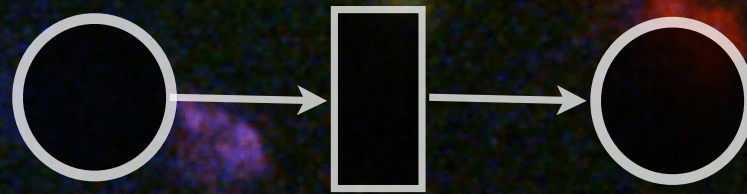
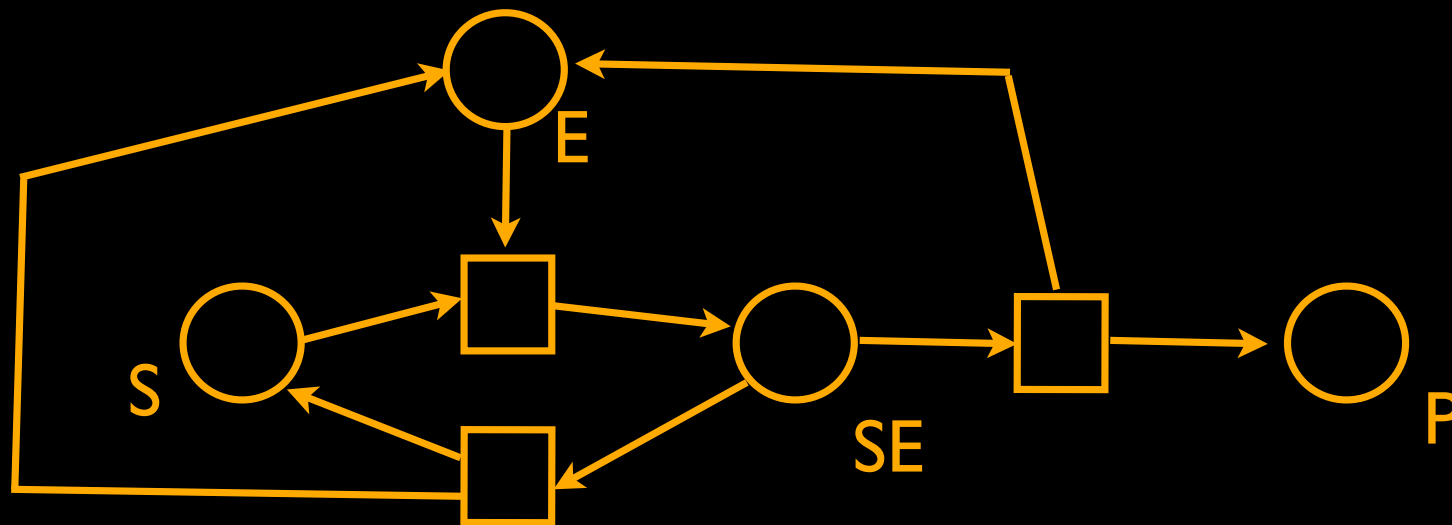


Why aren't Petri nets widely used in biological research ?

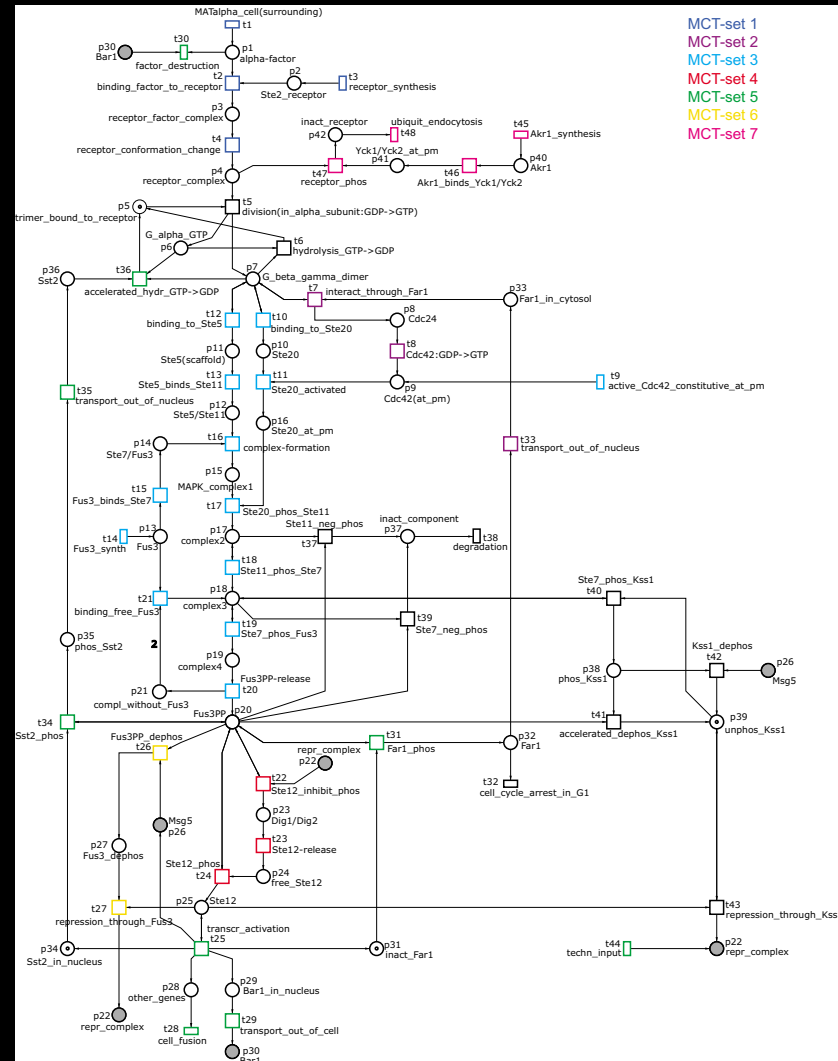
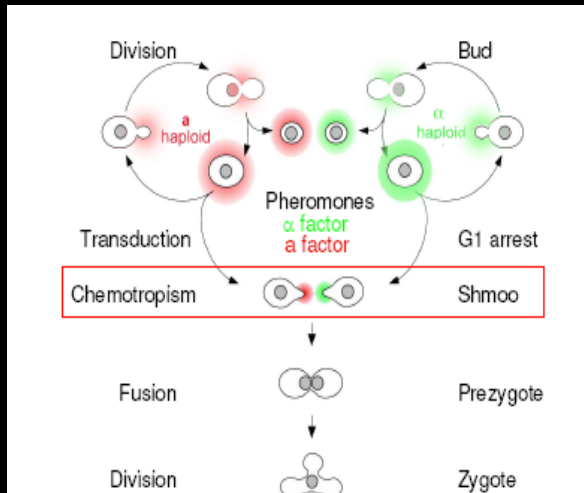


Jorge Carneiro
Instituto Gulbenkian de Ciência, Portugal
<http://qobweb.igc.gulbenkian.pt>

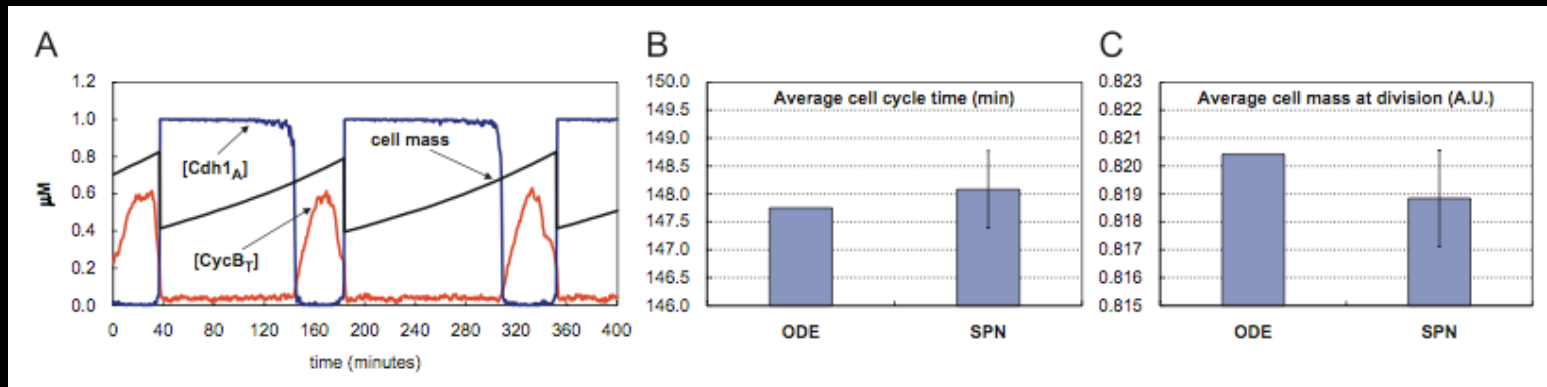
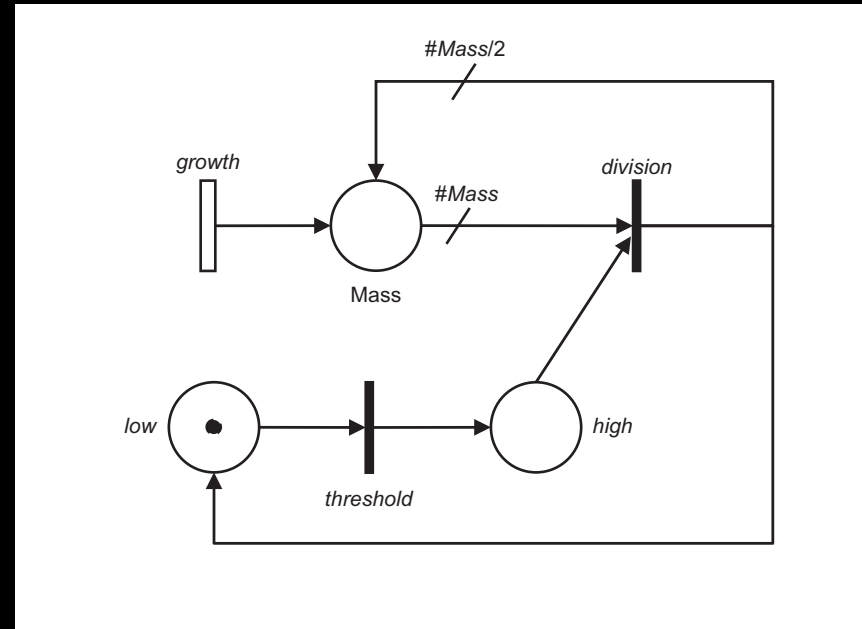
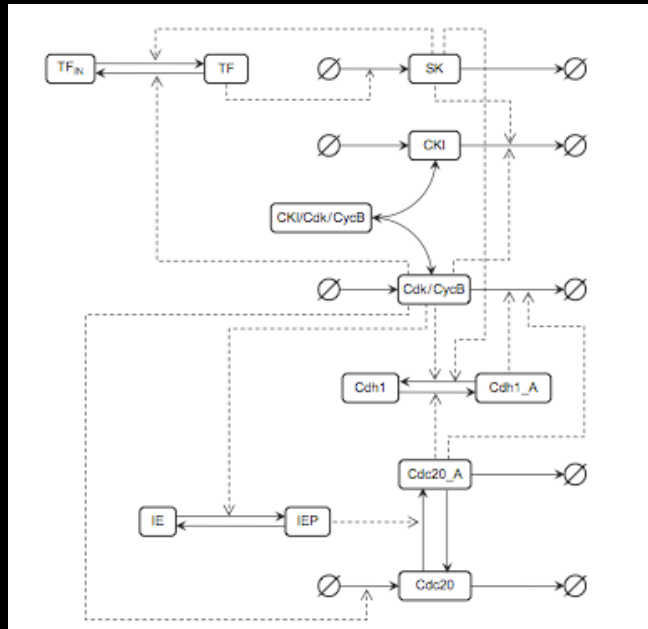
(Stochastic) Petri nets were naturally applied to modelling of **metabolic networks**, signal transduction pathways and gene regulatory networks

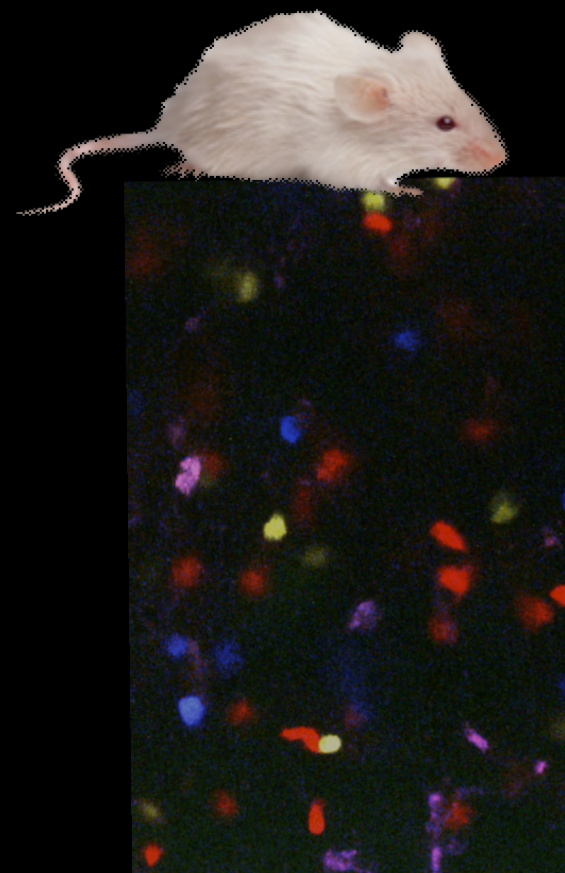
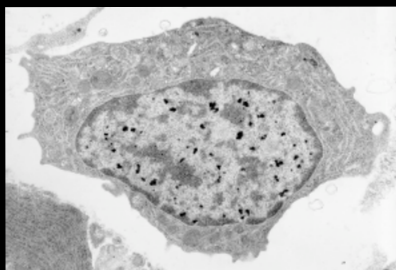


Application of Petri net based analysis techniques to signal transduction pathways



Stochastic Petri Net extension of a yeast cell cycle model



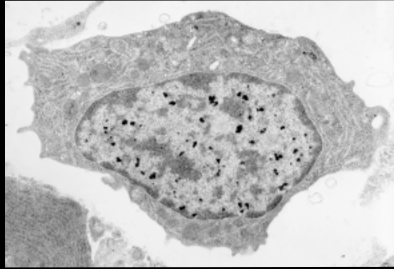


A few examples of biological processes that I am trying
to model by Stochastic Petri Nets

V(D)J recombination

Ion channel dynamics

Cell population dynamics



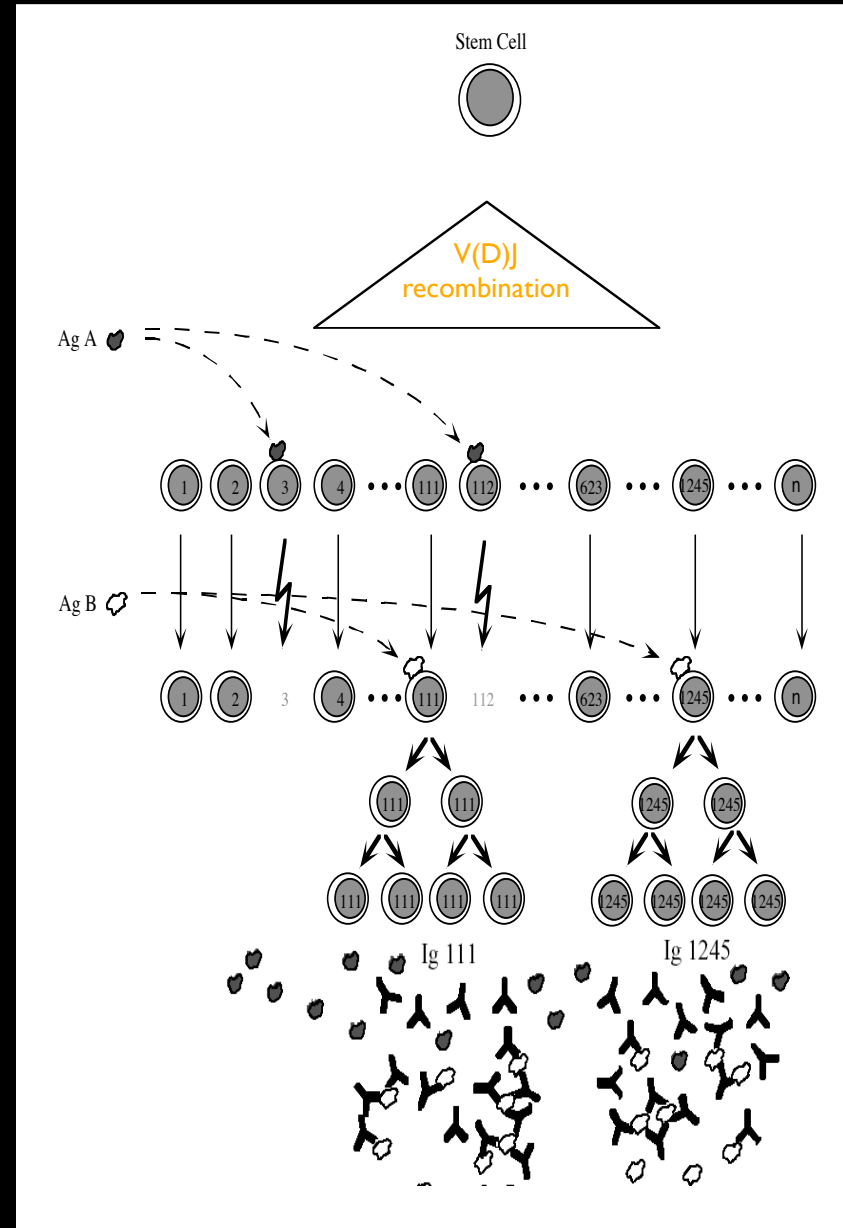
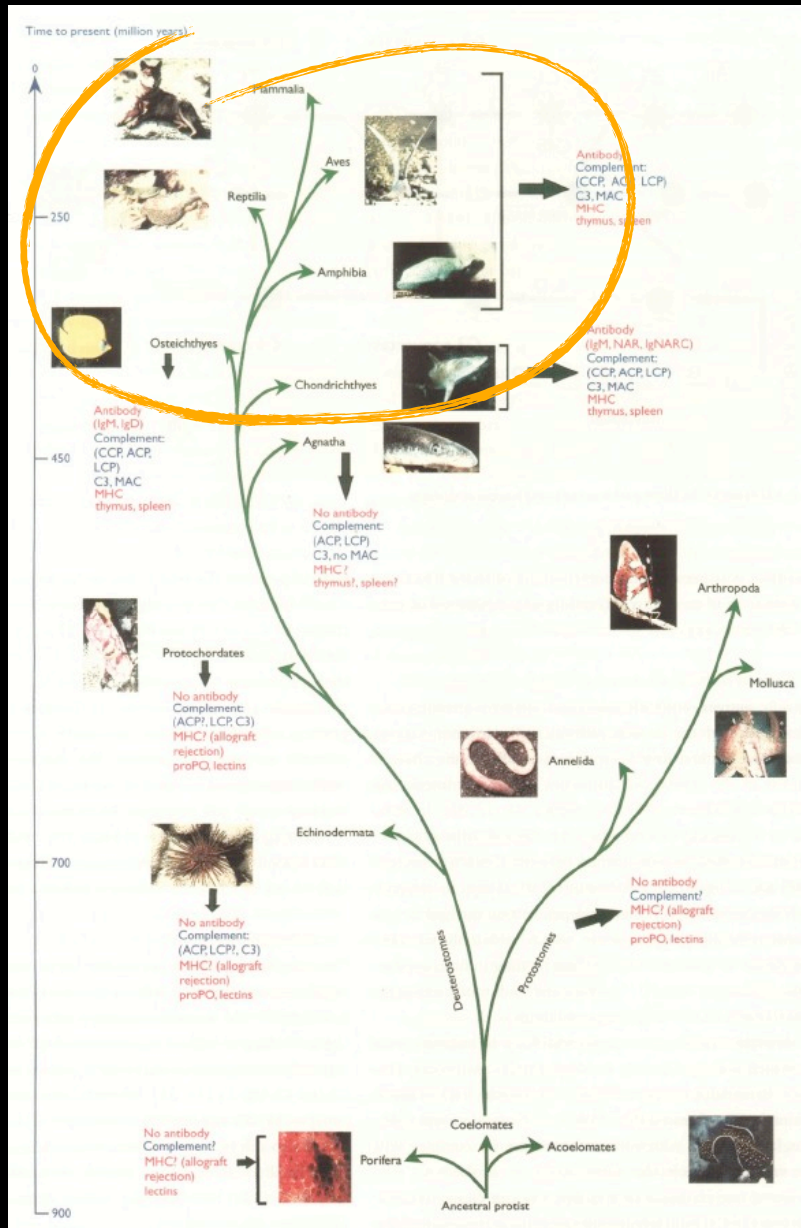
V(D)J recombination

a.k.a.

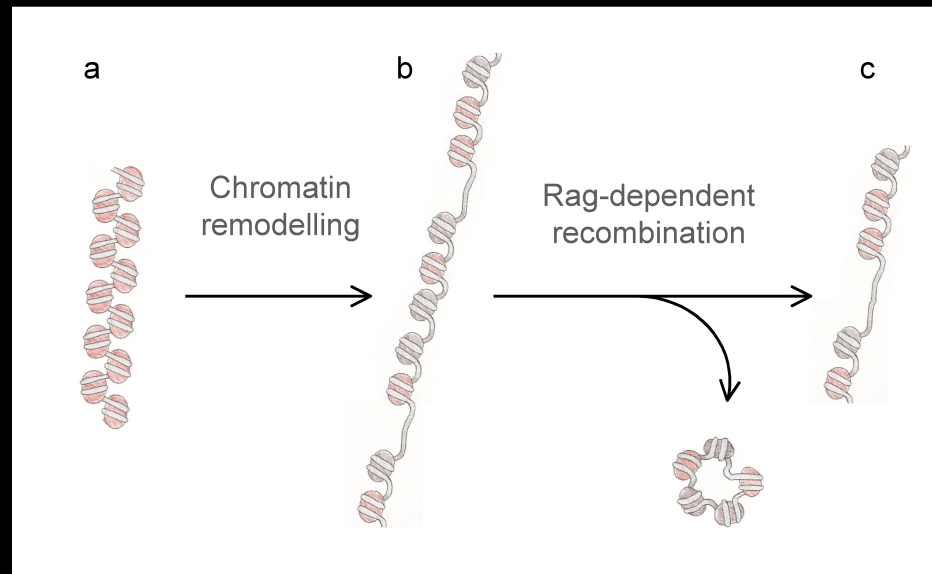
Making an antibody gene

a.k.a.

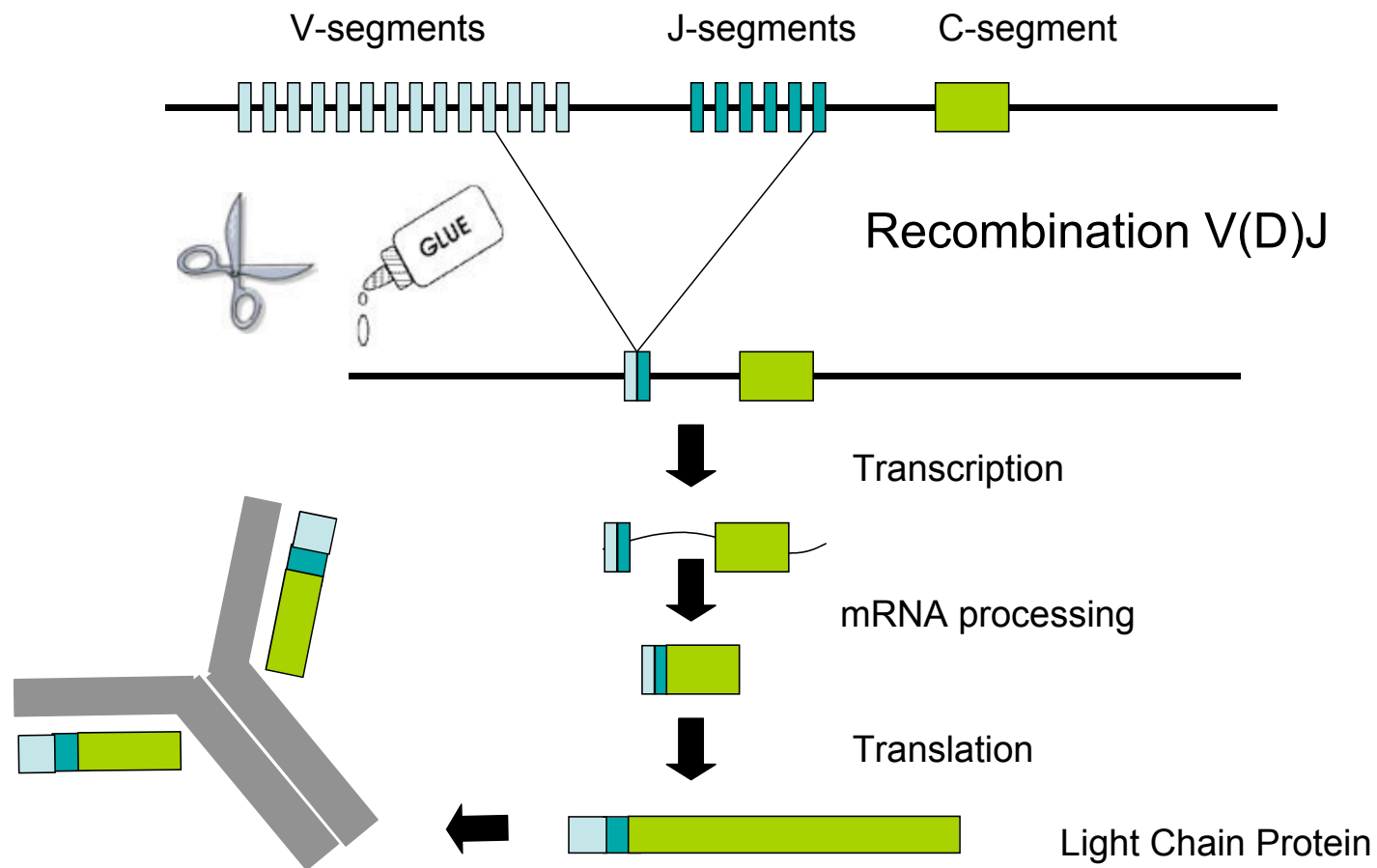
Random cutting and pasting of DNA



V(D)J recombination



A Cartoon of V(D)J recombination

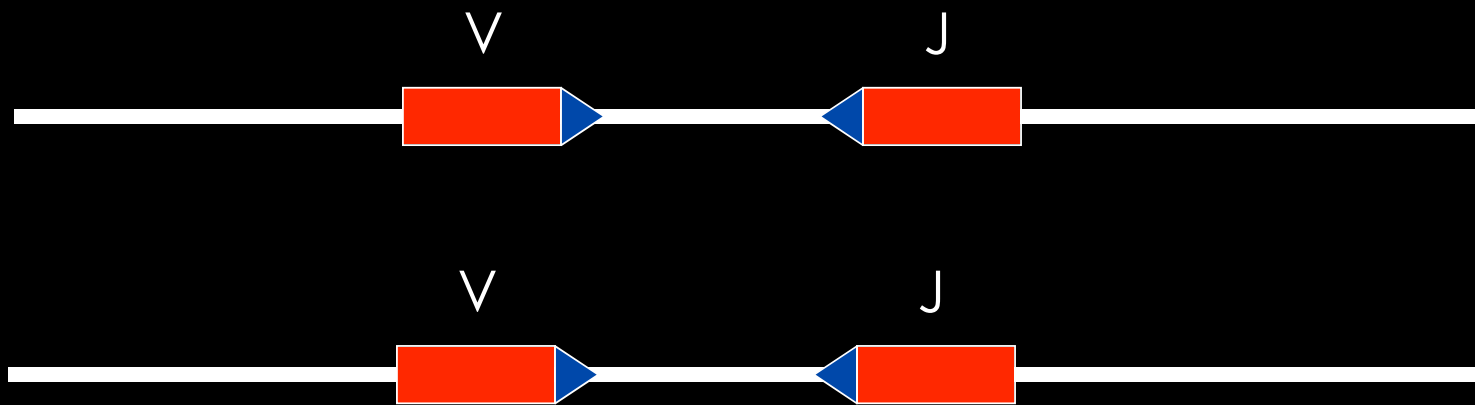


Lymphocytes must have only one antigen receptor

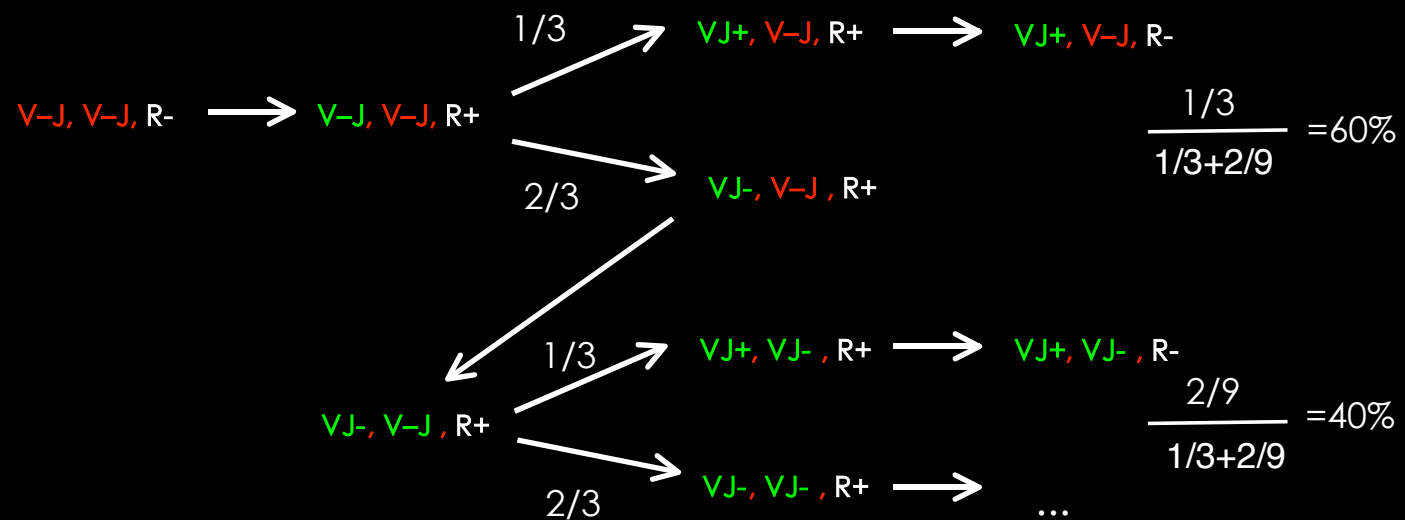
Yield and allelic exclusion constrain the kinetics of V(D)J recombination

Maximize diversity and allelic exclusion in the output of the reaction

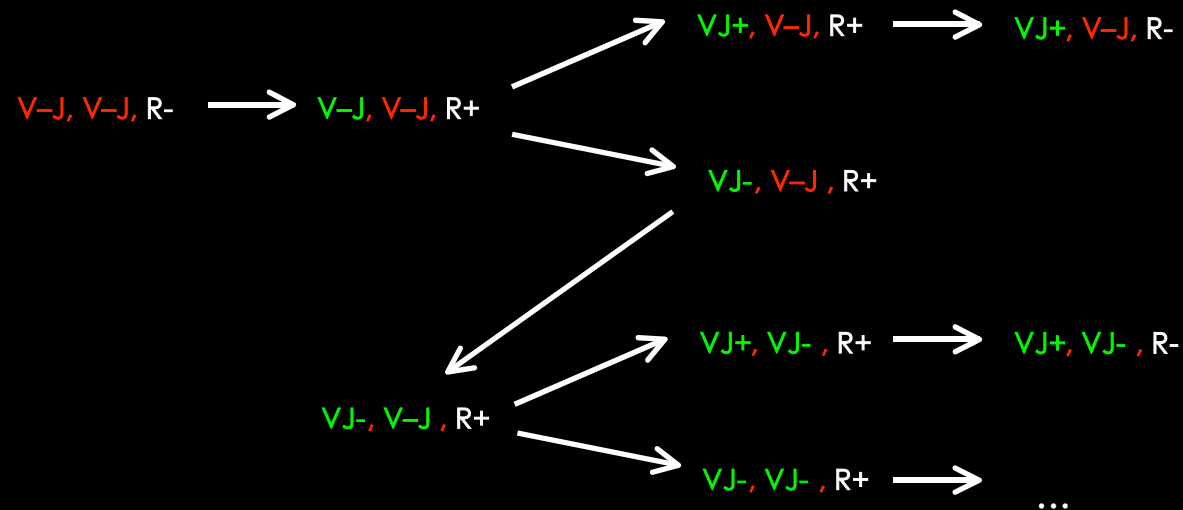
A toy VJ locus model



A toy VJ locus model

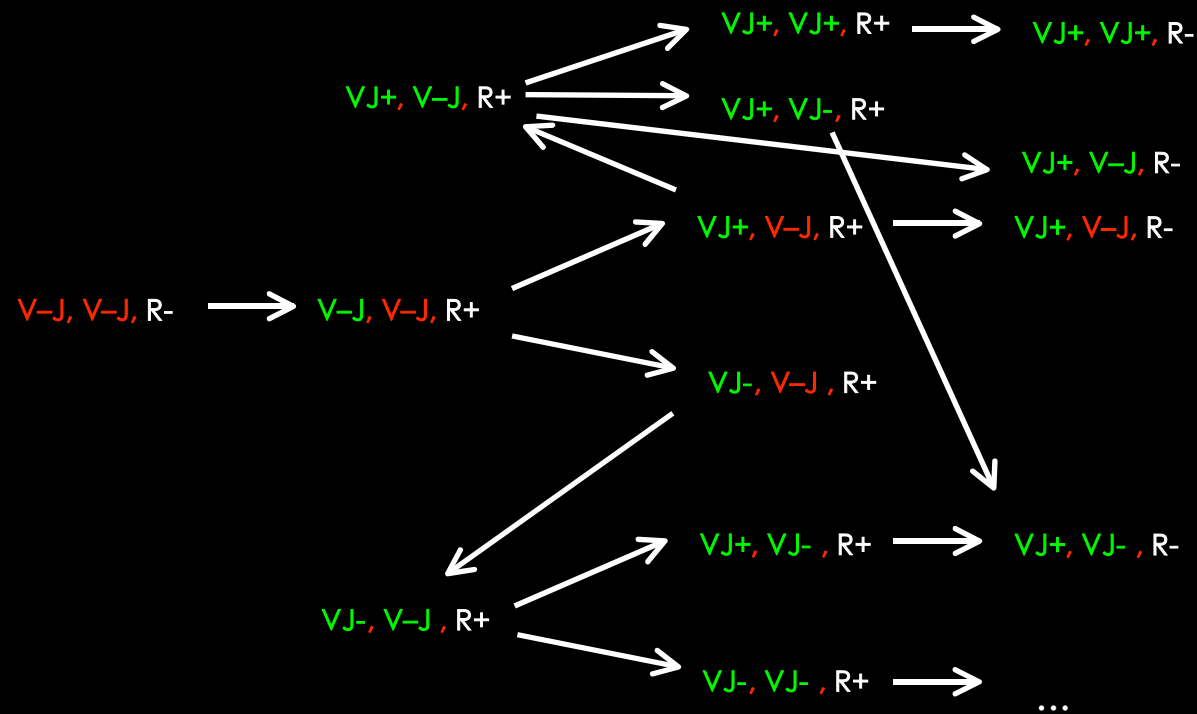


A toy VJ locus model



[Rajewsky]

A toy VJ locus model



Boucontet et al. *J. Immunol.* (2005) **234**: 153
 Sepúlveda et al. *J.Theor. Biol.* (2005) **174**: 3912

Continuous time Markov chain (CTMC)

$$S_t = S_0 \cdot \text{Exp}(Qt)$$

$$Q = \{q_{i,j}\}$$

0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
d	-d	0	0	0	0	0	0	0	0	0	0	0	0	0
0	2W	-2o-2W	0	0	2o	0	0	0	0	0	0	0	0	0
2c	0	0	-2c	0	0	0	0	0	0	0	0	0	0	0
0	2c	0	2d	-2c-2d-2r	0	0	0	2(1-f)r	0	0	0	0	2fr	0
0	0	2c	0	2W	-2c-2o-2r-2W	0	0	2o	0	2(1-f)r	0	0	0	0
0	0	0	2c	0	0	-2c	0	0	0	0	0	0	0	0
0	0	0	0	2c	0	d	-2c-d-2r	0	0	0	0	0	0	0
0	0	0	0	0	0	0	W	-2r-W	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	-2c-2d	0	2c	0	0	0
0	0	0	0	0	0	0	0	0	2W	-2c-2o-2W	0	2c	0	0
0	0	0	0	0	0	0	0	0	0	0	-2d	0	0	0
0	0	0	0	0	0	0	0	0	0	2o	2W	-4o-2W	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	-2d	0
0	0	0	0	0	0	0	0	0	0	0	0	0	2(w+W)	0
0	0	0	0	0	0	0	0	0	2c	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	2c	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	2c	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Boucontet et al. *J. Immunol.* (2005) **234**: 153
 Sepúlveda et al. *J.Theor. Biol.* (2005) **174**: 3912

Modelling V(D)J recombination using CTMC

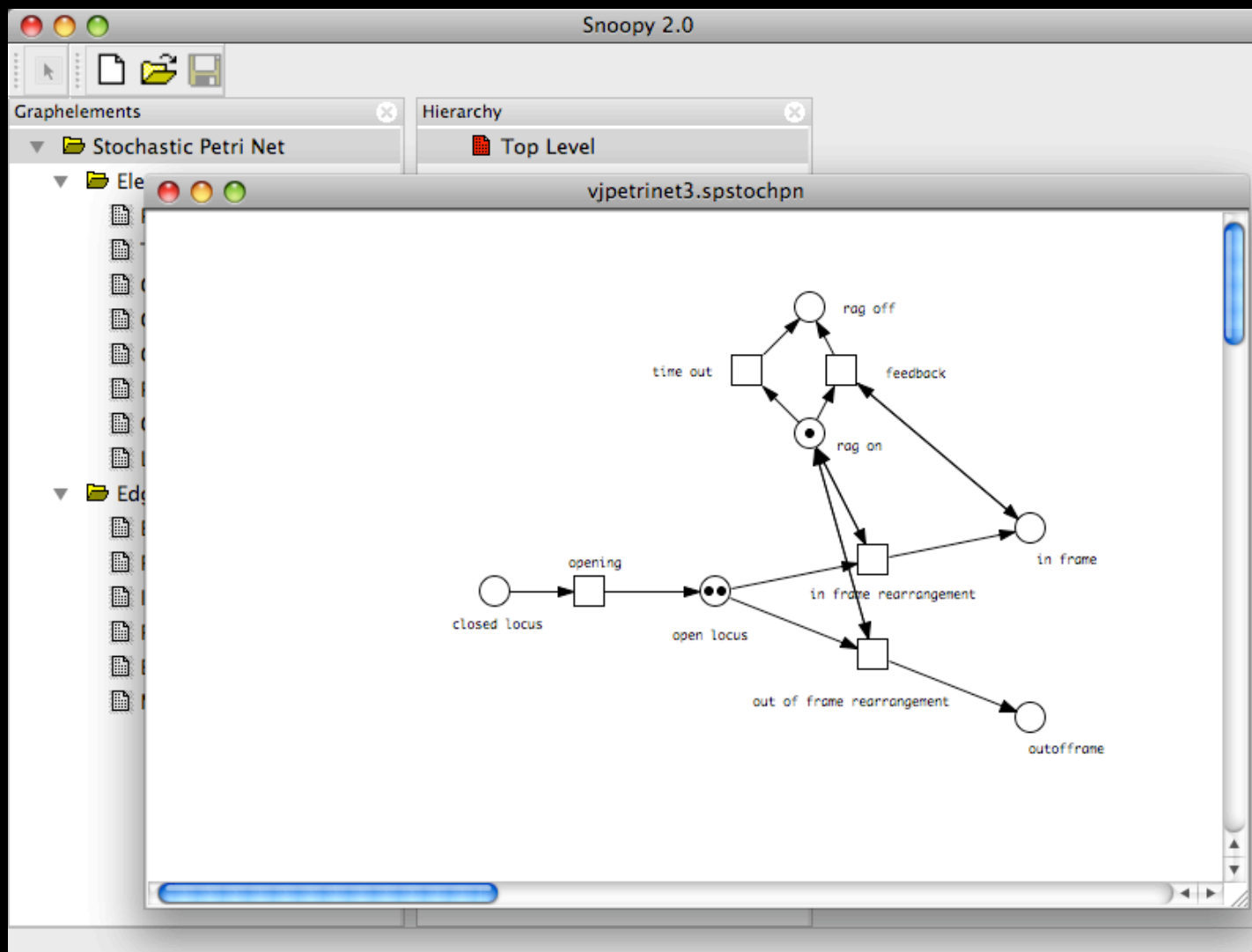
Theoretically sound but,

Hard to handle

Entering terms in large transition matrices is error prone

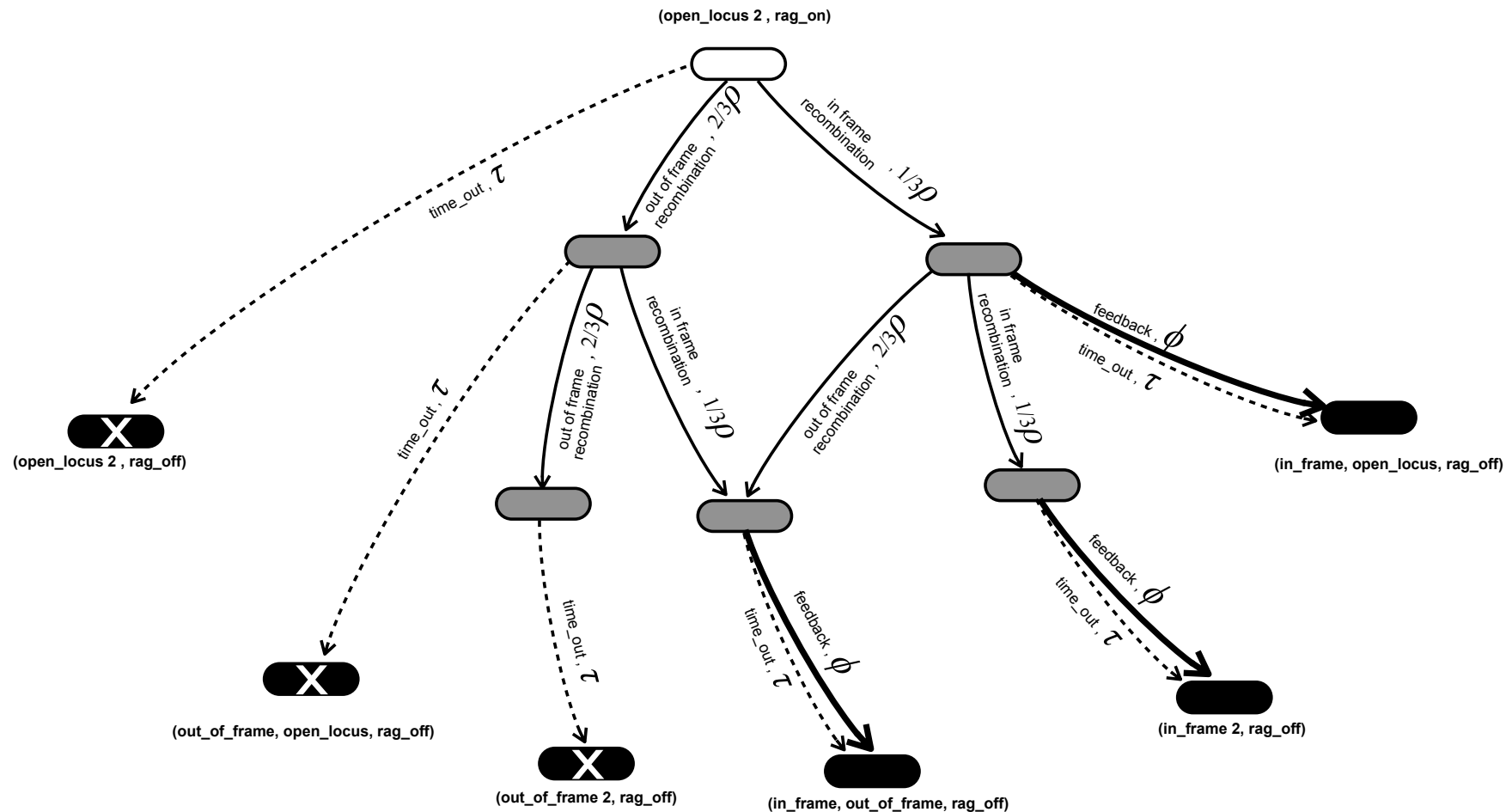
Model (re)design is painful

CTMC equivalent stochastic Petri net



Petri net editor and simulator

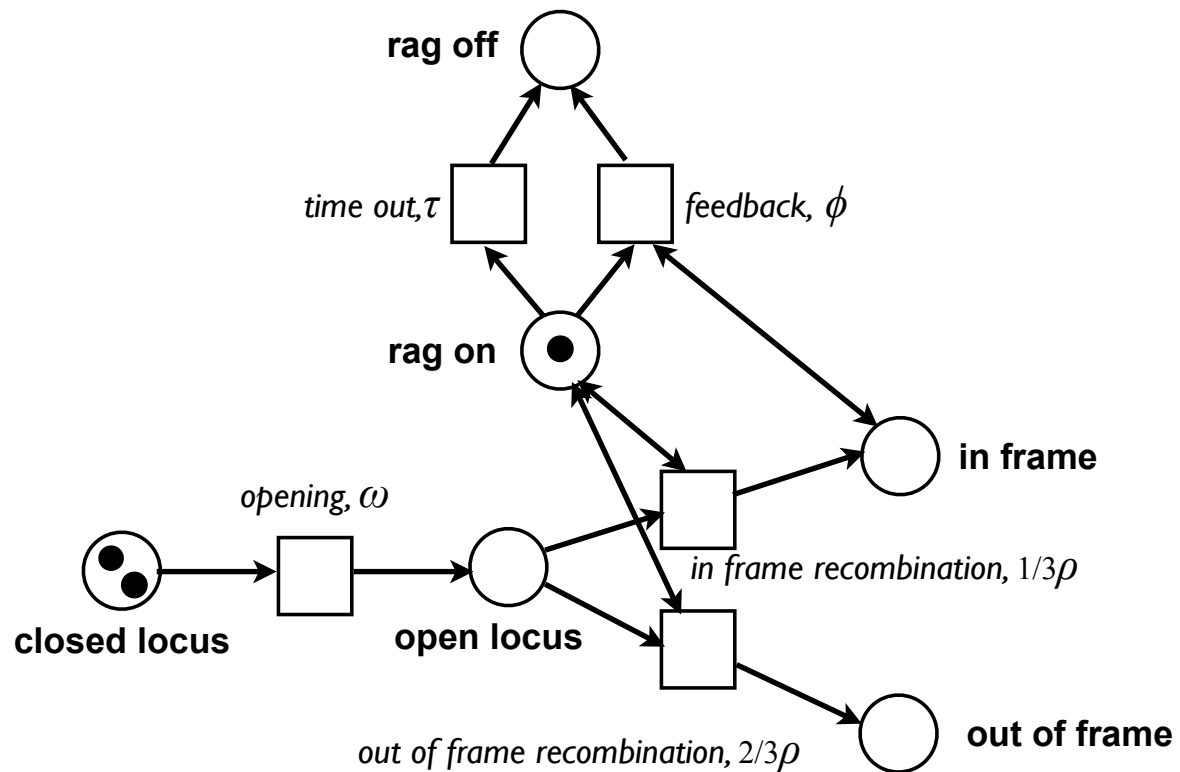
Snoopy 2.0: <http://www-dssz.informatik.tu-cottbus.de/software/snoopy.html>



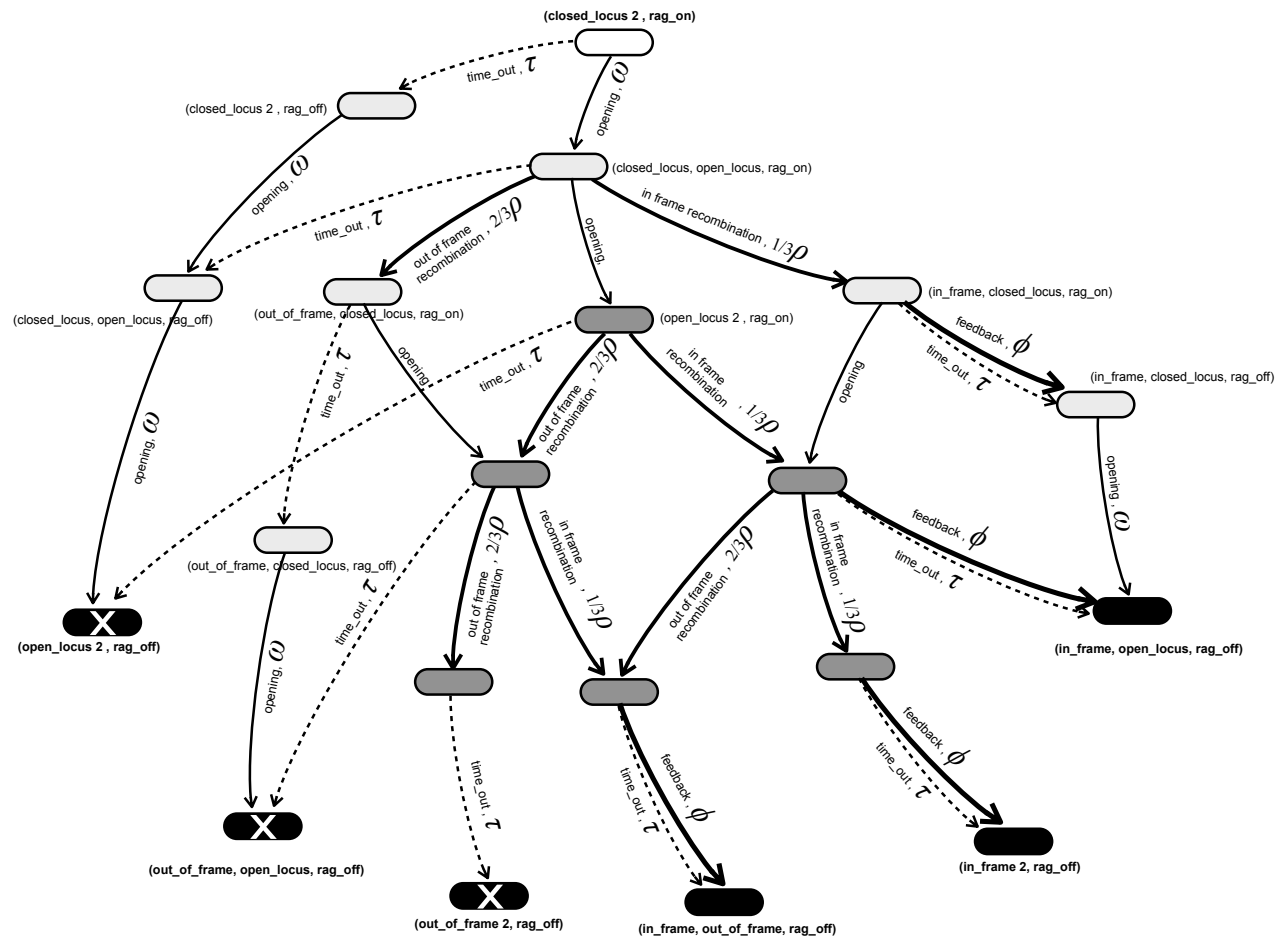
Petri net analyser

Charlie: <http://www-dssz.informatik.tu-cottbus.de/software/charlie.html>

Asynchronous allele accessibility with feedback



A toy VJ locus model



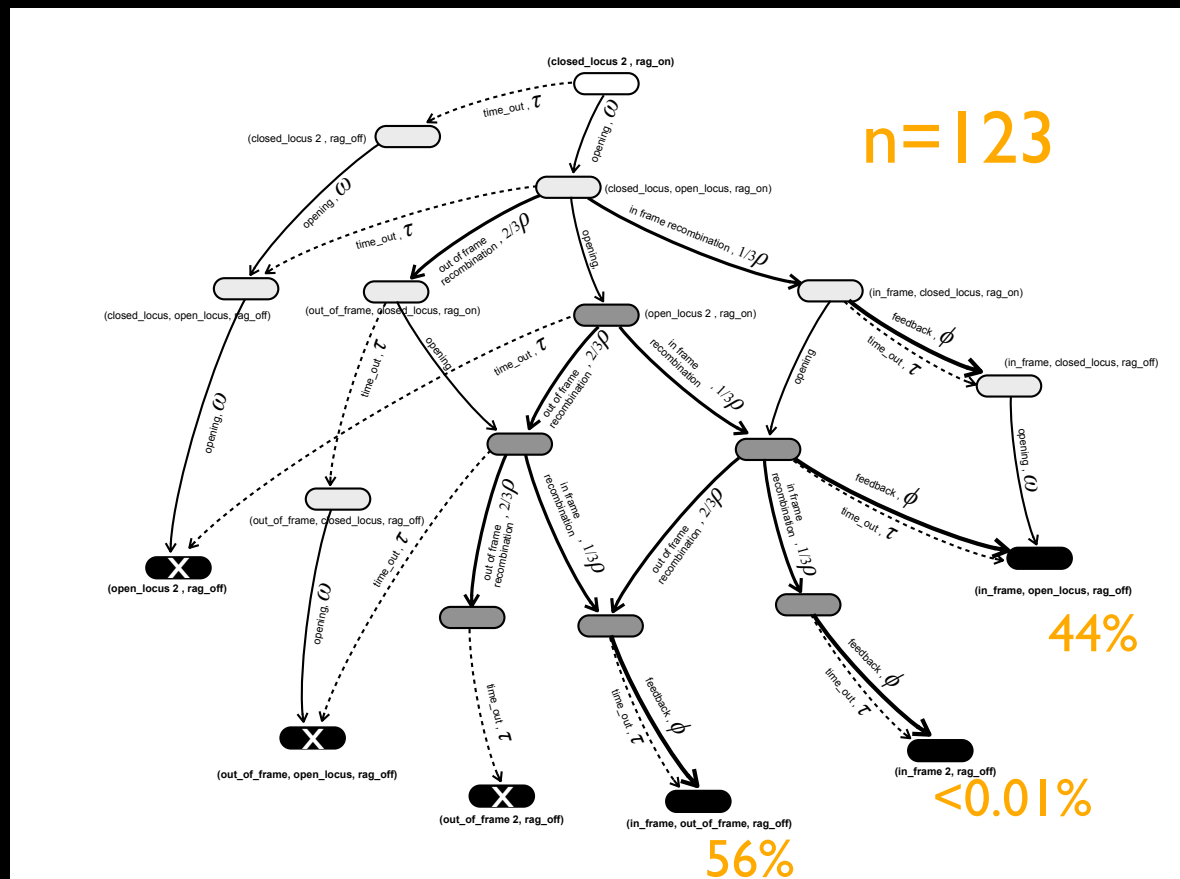
Reachability is excellent,

but ...

How can we estimate the parameters that explain the experimentally observed output of the $V(D)J$ reaction ?

How can we estimate the parameters that explain the experimentally observed output of the V(D)J reaction ?

Locus configuration in $\gamma\delta$ thymocytes



How likely are these experimental values given the model ?

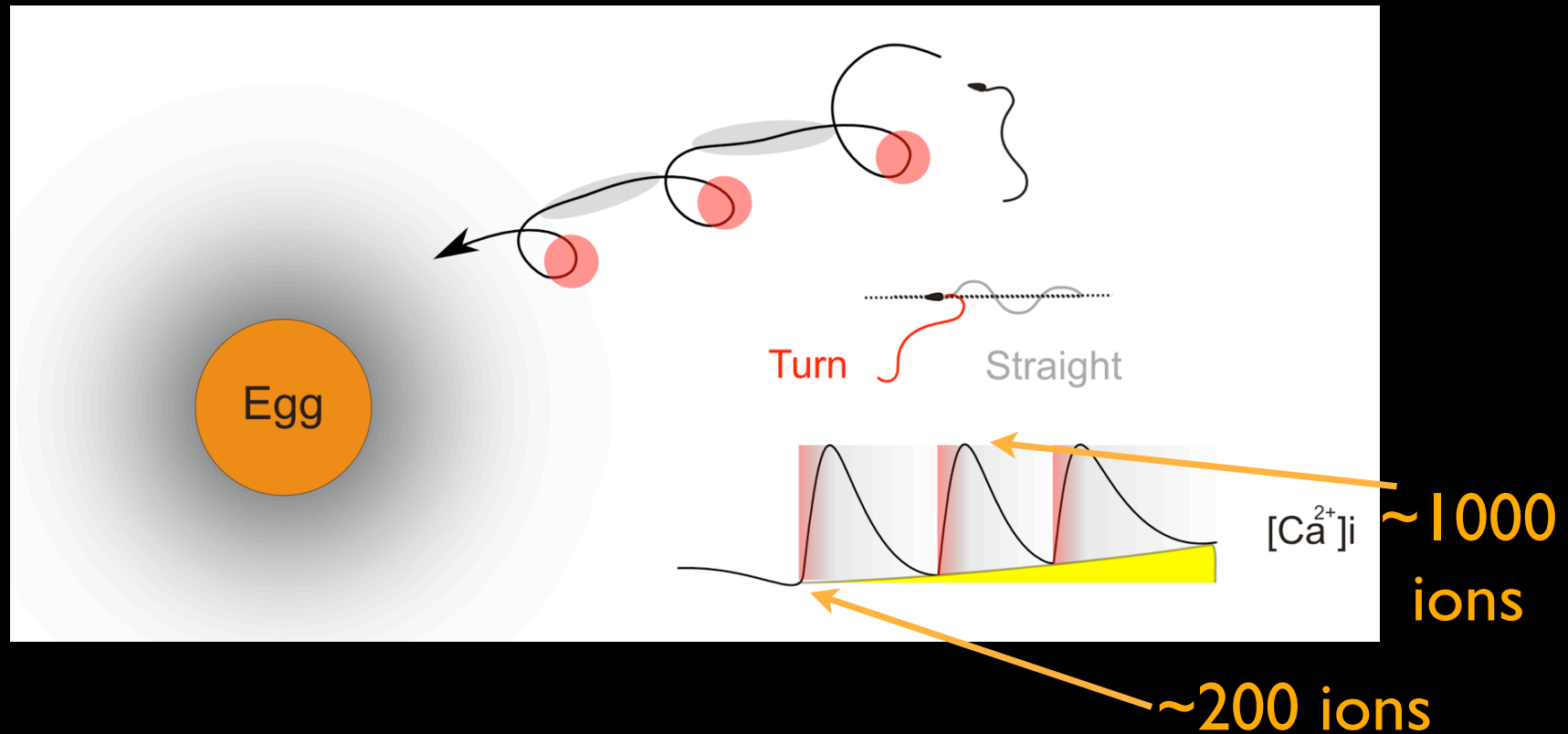
Parameter estimation **based on data** is not available
(or is not straightforward) in none of the Petri net
tools I tried



Ion channel dynamics

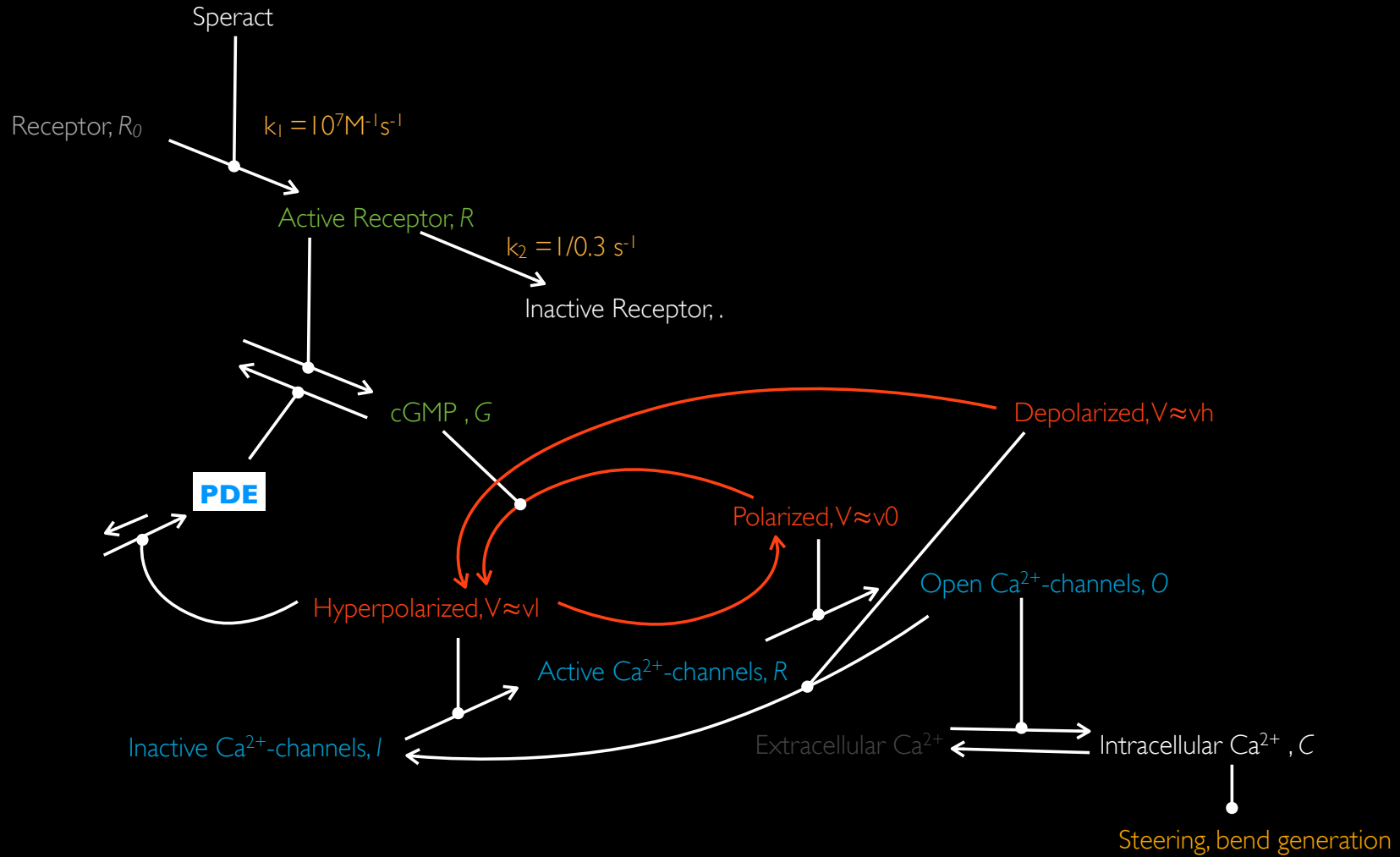


Ion (Ca^{2+}) channel dynamics controls sperm chemotaxis

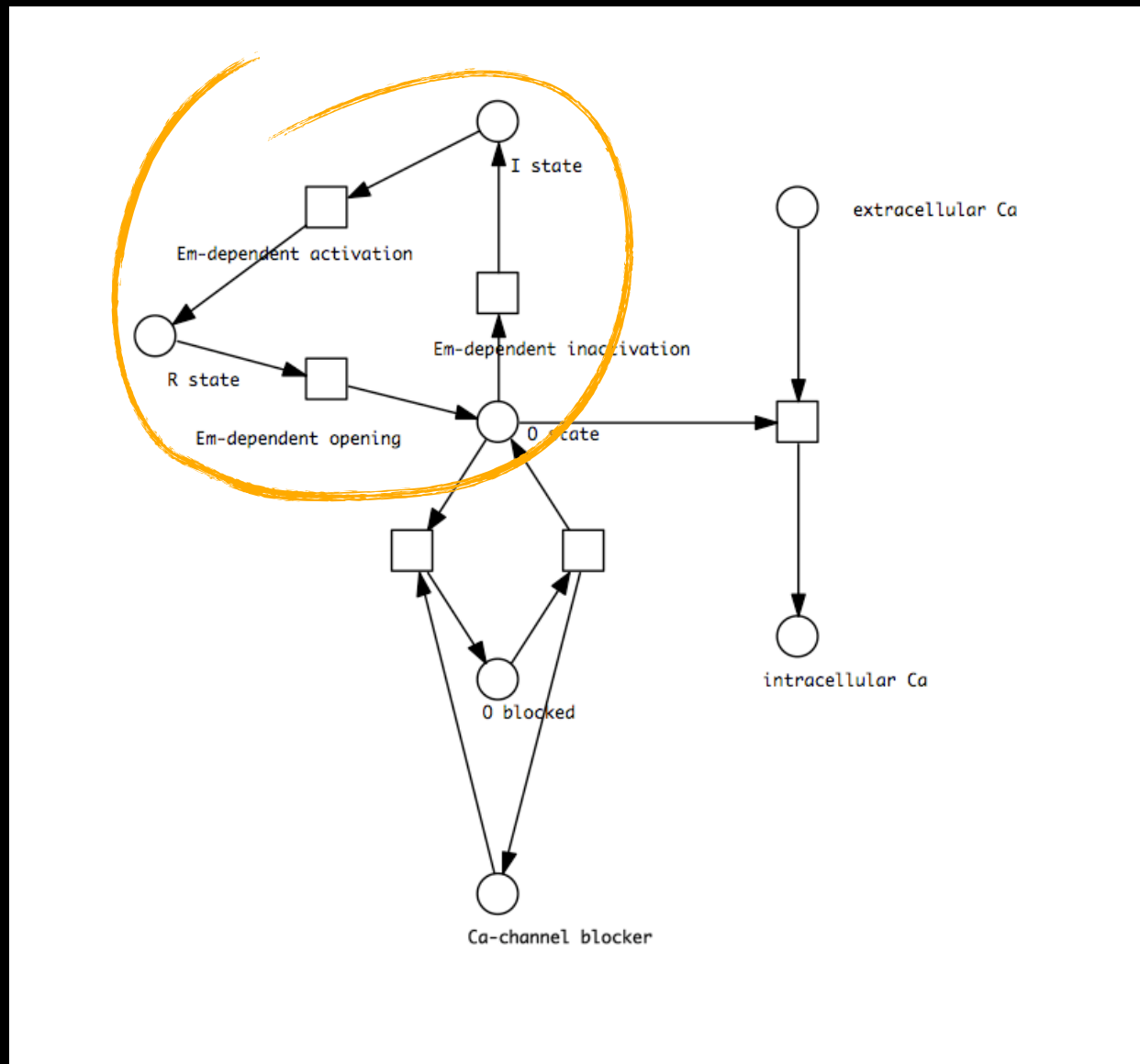


Guerrero et al. *Biochem. Soc. Trans.* (2010) in press

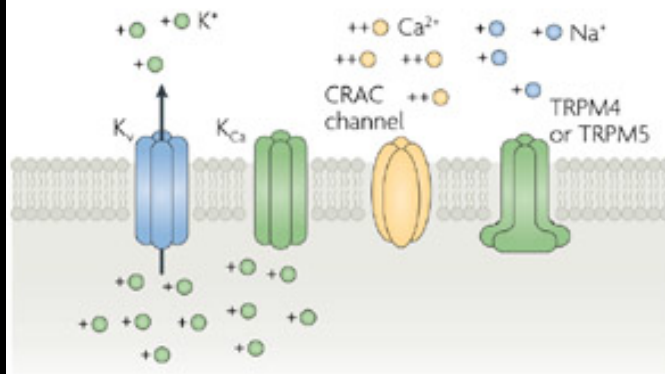
Ion (Ca^{2+}) channel dynamics controls sperm chemotaxis



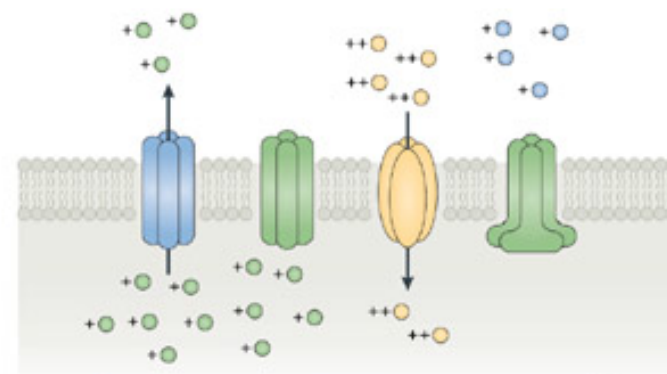
SPN representation of ion (Ca^{2+}) channel dynamics



a Resting

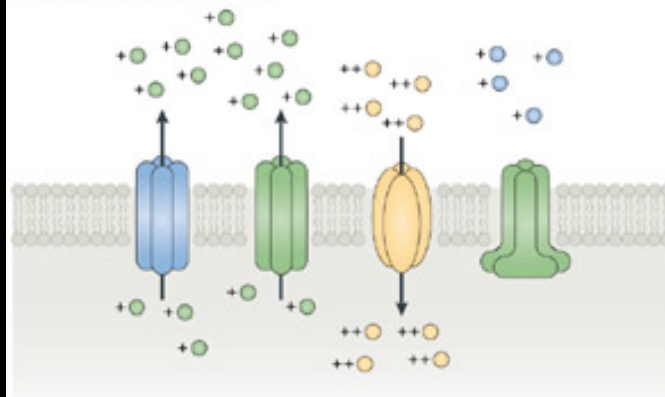


b Activated SOCE

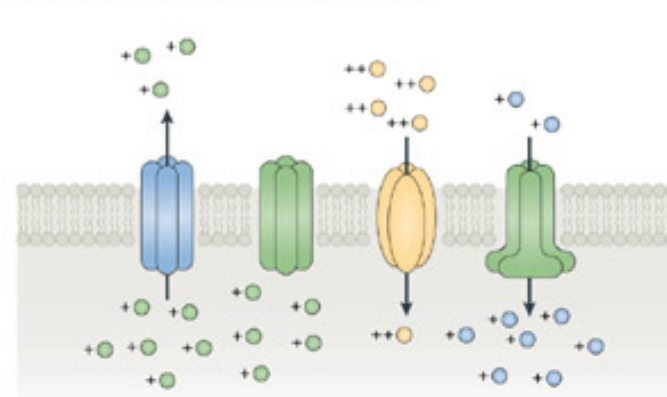


- GPCR signalling
- Integrin activation and cell adhesion
- Subset/differentiation-dependent expression

c K_{Ca} hyperpolarization



d TRPM4 and/or TRPM5 depolarization

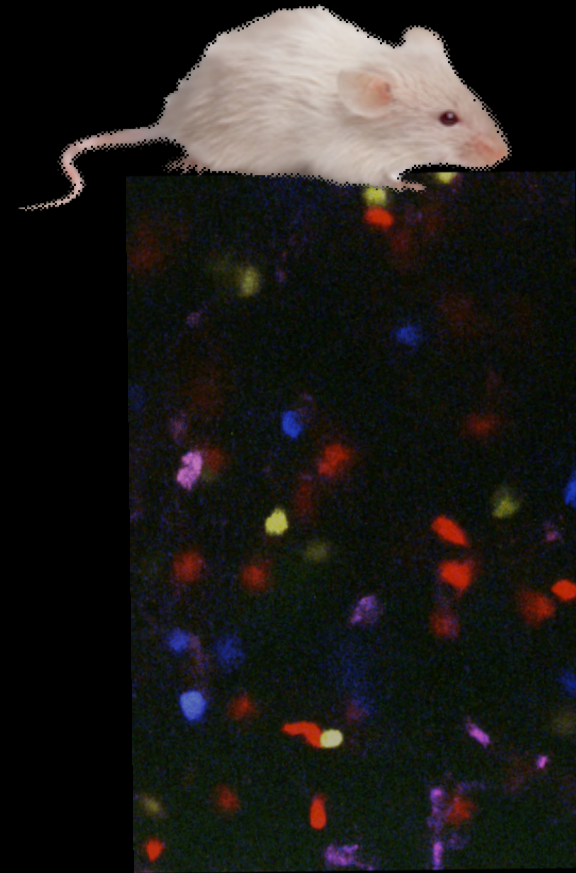


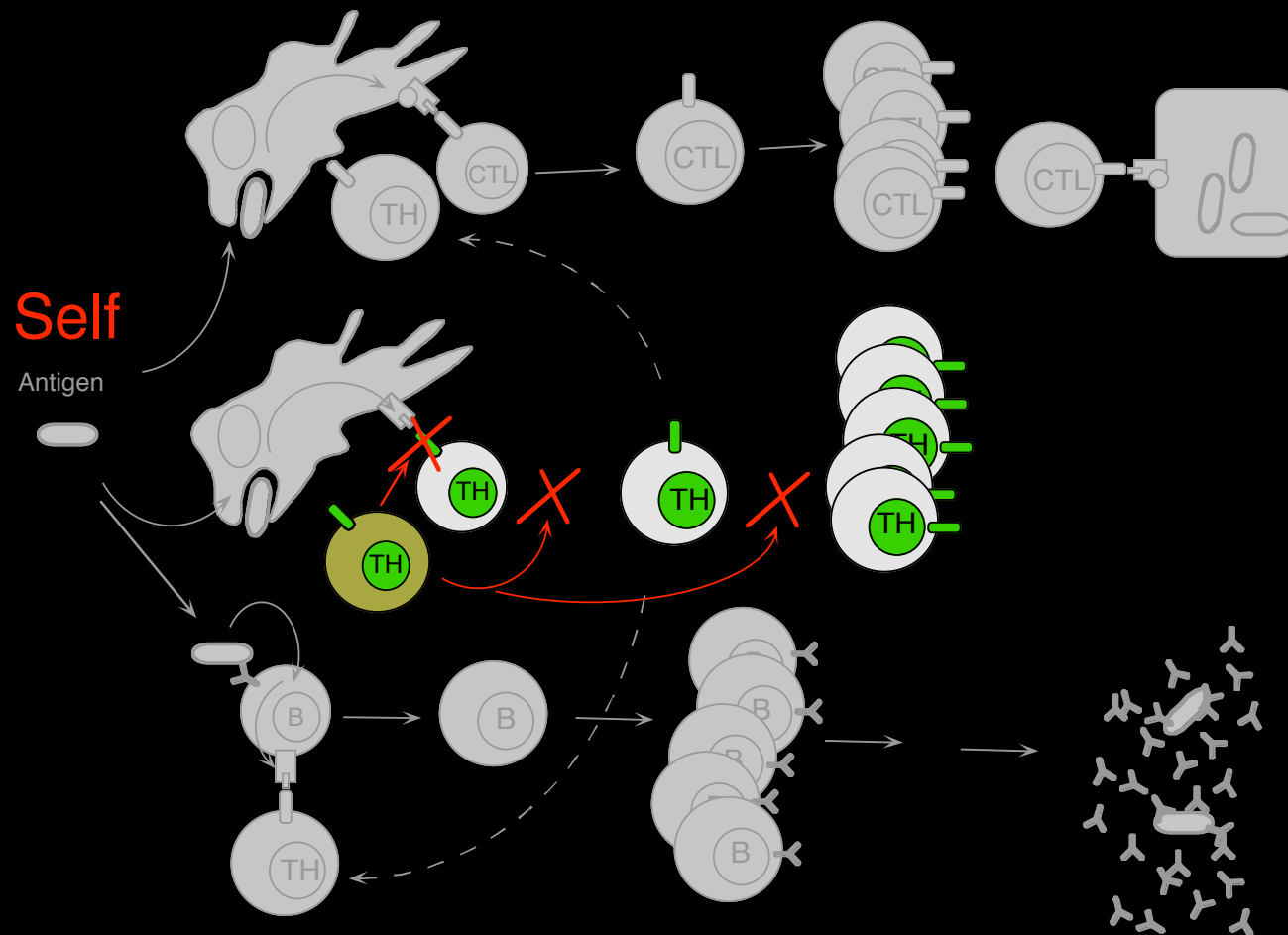
How can one estimate the model parameters based on experimental data ?

How can E_m be represented in a SPN framework ?

One would like to avoid representing all the ions...

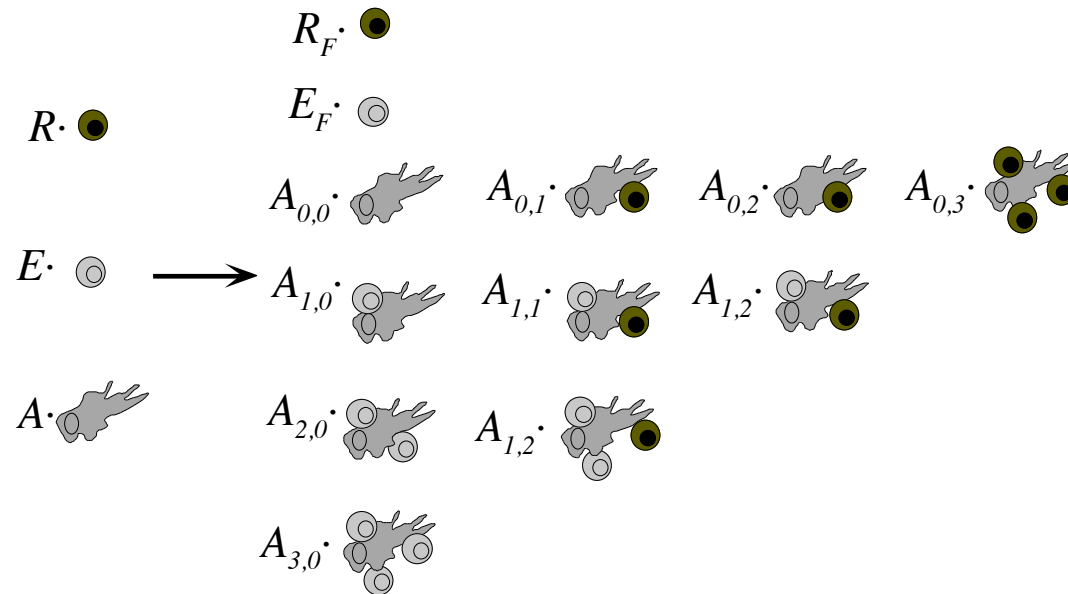
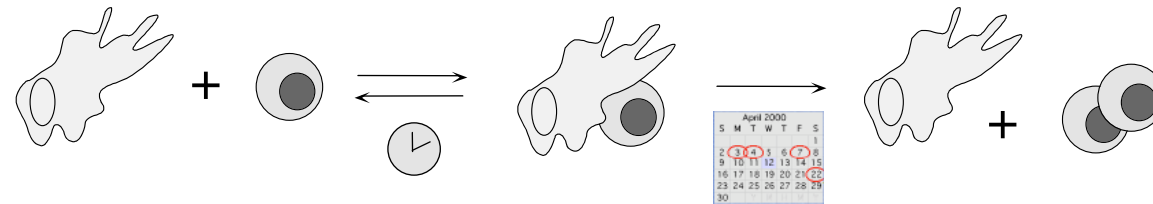
Modelling T-cell interactions and dynamics involved in autoimmunity



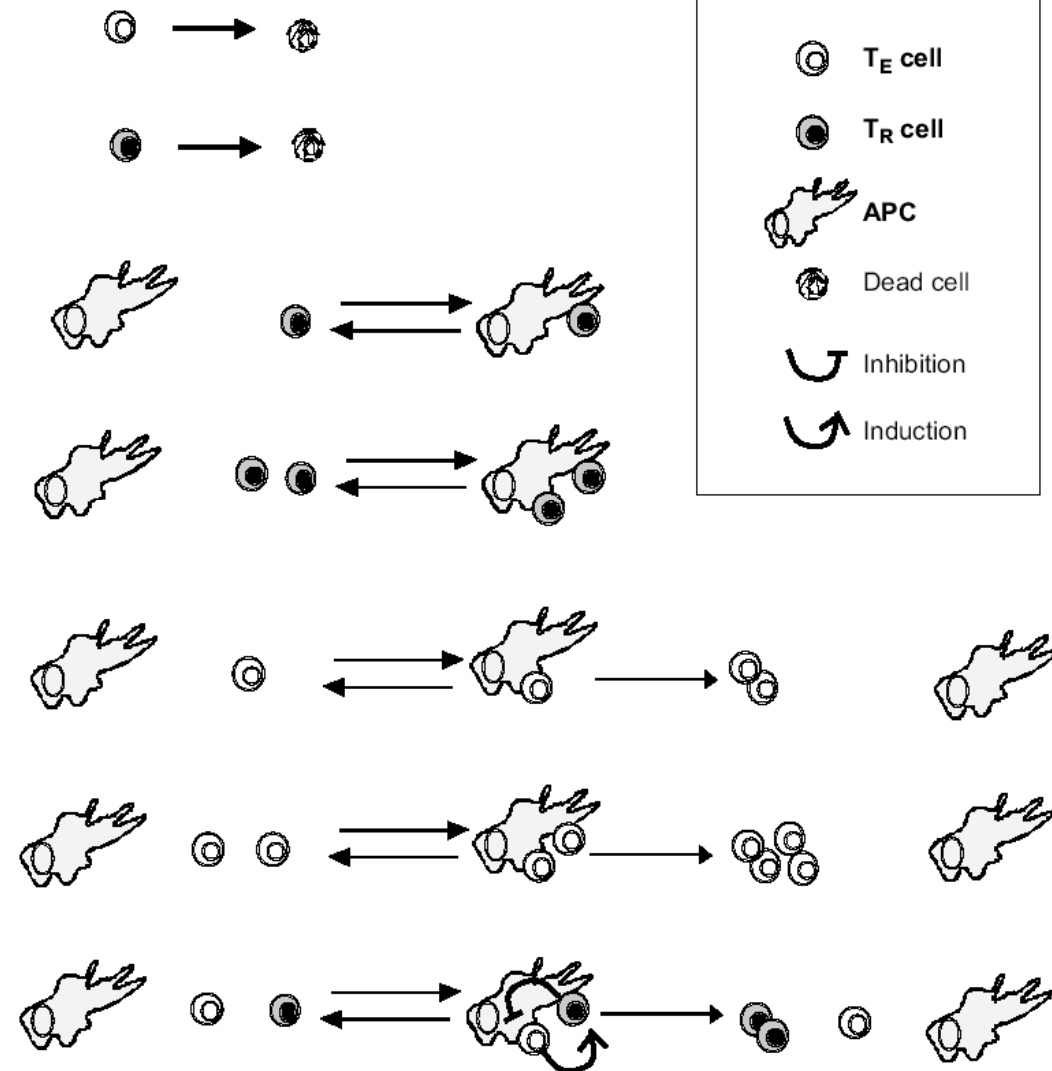


Sakaguchi et al. *Annu. Rev. Immunol.* (2004) 22: 531

Carneiro et al. *Immunol. Reviews* (2007) 216: 48



Crossregulation Model



The crossregulation model was formulated in terms of ordinary differential equations

$$\frac{dE}{dt} = p_E \cdot E_A - d_E \cdot E$$

$$\frac{dR}{dt} = p_R \cdot R_A - d_R \cdot R$$

$$C = \frac{1 + K(A+T) - \sqrt{(1 + K(A+T))^2 - 4ATK^2}}{2K}$$

$$E_C = \frac{E}{T} C, \quad R_C = \frac{R}{T} C$$

$$\varepsilon = \frac{E_C}{A}, \quad \rho = \frac{R_C}{A}$$

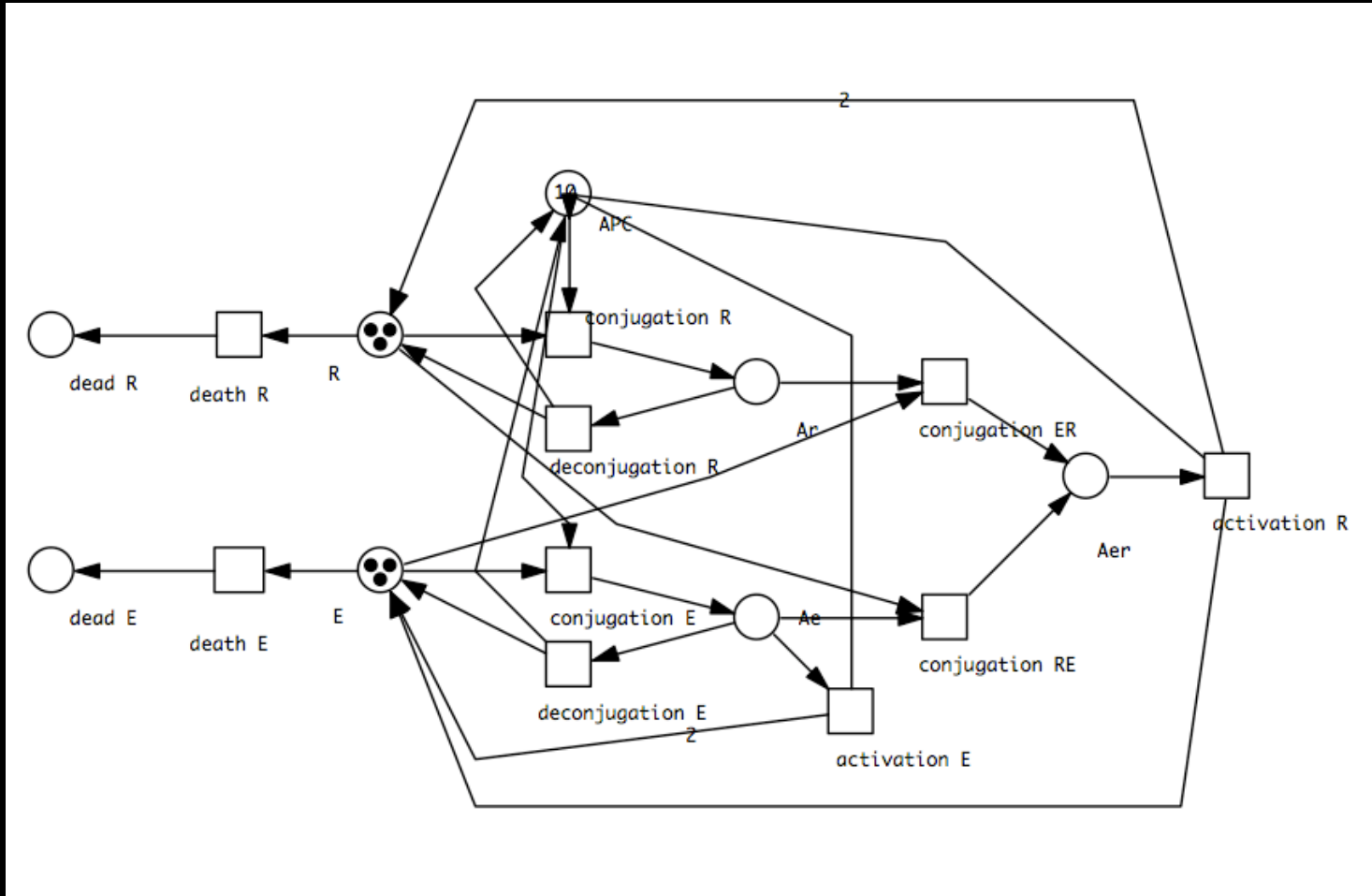
$$E_A = E_C \left(1 - \frac{2\rho}{2 - \varepsilon} \right)$$

$$R_A = R_C \left(\frac{2\varepsilon}{2 - \rho} \right)$$

Carneiro et al. *Immunol. Reviews* (2007) **216**: 48

How much would stochasticity and discreteness affect the results ?

The crossregulation model formulated as a SPN

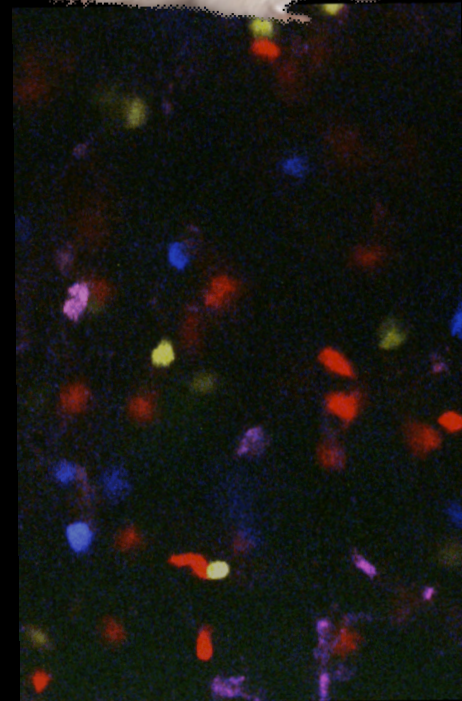
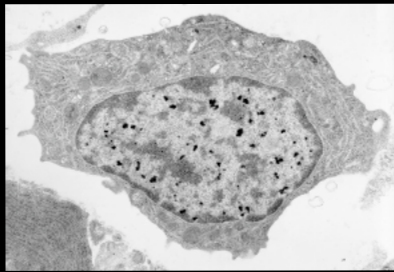


SPN representation for two sites per APC is cumbersome !

The crossregulation model formulated as a SPN

How to study the dependence on number of sites
without redrawing the structure ?

Why aren't Petri nets widely used in biological research ?



Difficulties in adopting SPN framework

A personal experience

V(D)J recombination ~ how to estimate parameters ?

Ion channel dynamics ~ how to represent E_m ?

T-cell population dynamics ~ SPN is too complex !

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Kalet Leon

Pablo Pereira, Laurent Boucontet
Pasteur Institute



Lisa Bergman, Jocelyne Demengeot
(IGC, Portugal)

Email: jcarneir@igc.gulbenkian.pt
URL: <http://qobweb.igc.gulbenkian.pt>

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