
Why I'm always late!

Dagstuhl Seminar

Jeremy Bradley

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Department of Computing, Imperial College London

Produced with prosper and L^AT_EX

With thanks to...

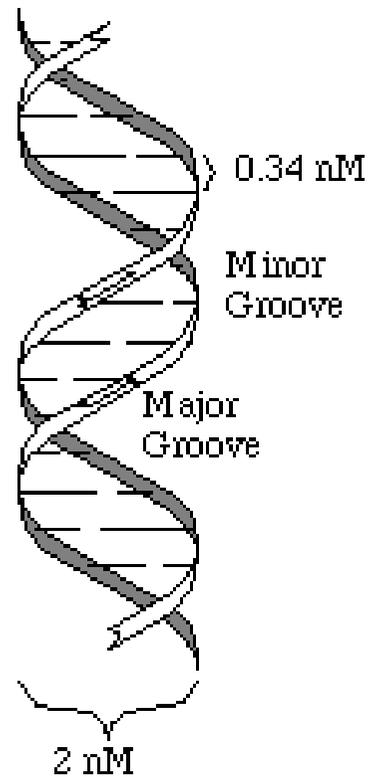
- Stephen Gilmore, Edinburgh
- Jane Hillston, Edinburgh
- Nigel Thomas, Newcastle
- Tom Thorne, Imperial College
- Helen Wilson, University College London



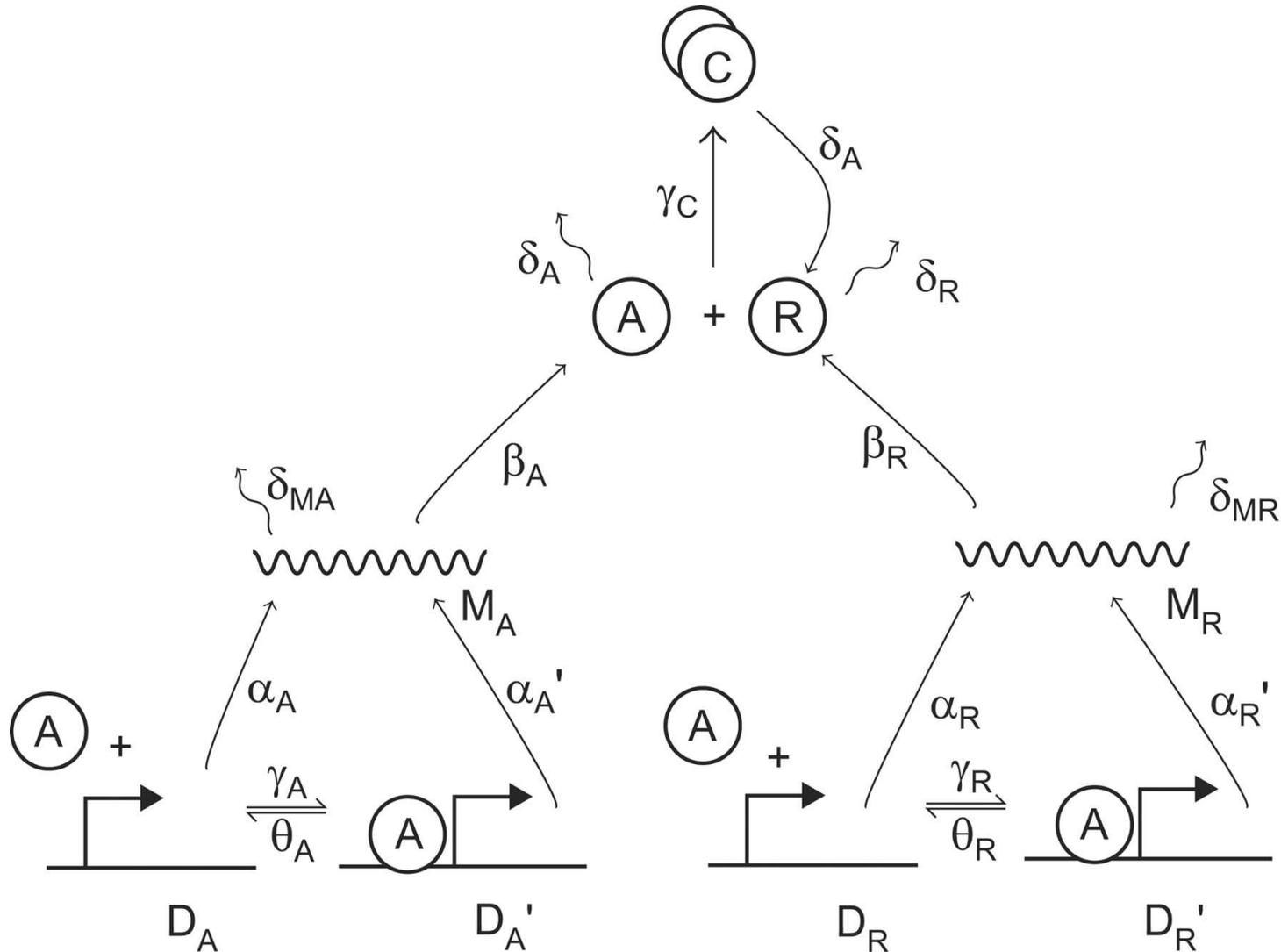


Something about genes...

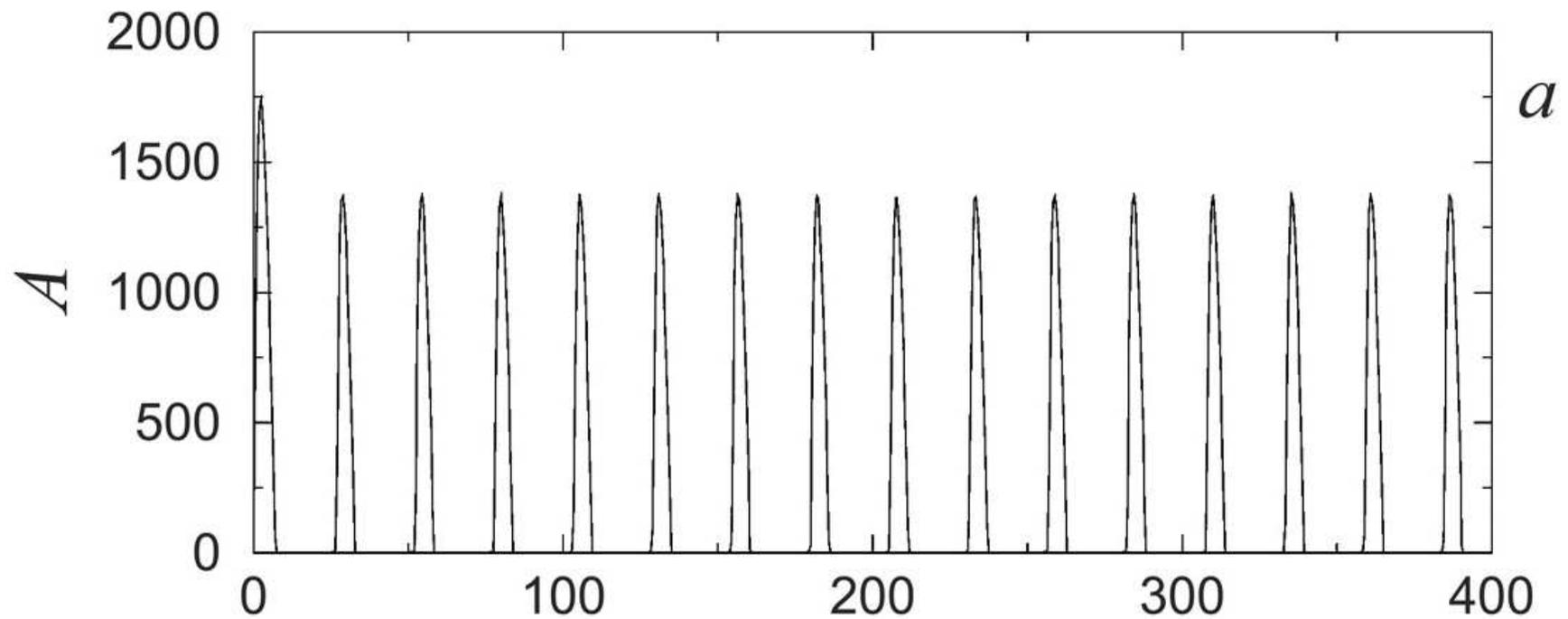
DNA → RNA → Protein



Biological Circadian Clock Model



Vilar oscillations of A



Stochastic Process Algebra: PEPA

PEPA syntax:

$$P ::= (a, \lambda).P \mid P + P \mid P \underset{L}{\bowtie} P \mid P/L \mid A$$

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Stochastic Process Algebra: PEPA

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- ➔ Competitive choice: $P_1 + P_2$

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- Constant label: A

PEPA: Example

$$\text{Sys} \stackrel{\text{def}}{=} (AA \bowtie_{\{\text{run}\}} A1) \bowtie_{\{\text{alert}\}} (BB \bowtie_{\{\text{run}\}} B1)$$

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$$\text{A1} \stackrel{\text{def}}{=} (\text{start}, r_1).\text{A2} + (\text{pause}, r_2).\text{A3}$$

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Stochastic π -calculus: subset

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$$P ::= a_\lambda.P \mid P + P \mid P \mid P \mid A$$

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Stochastic π -calculus: subset

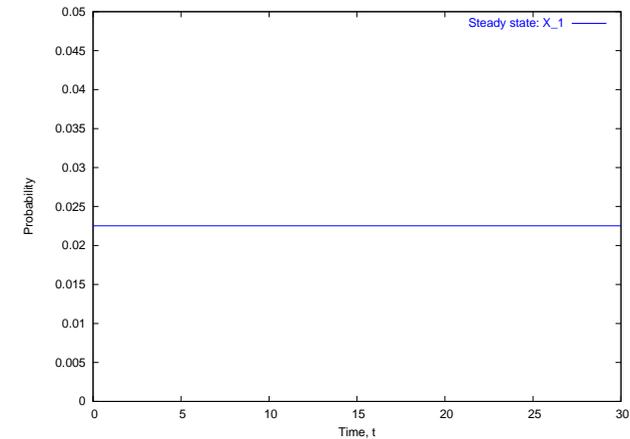
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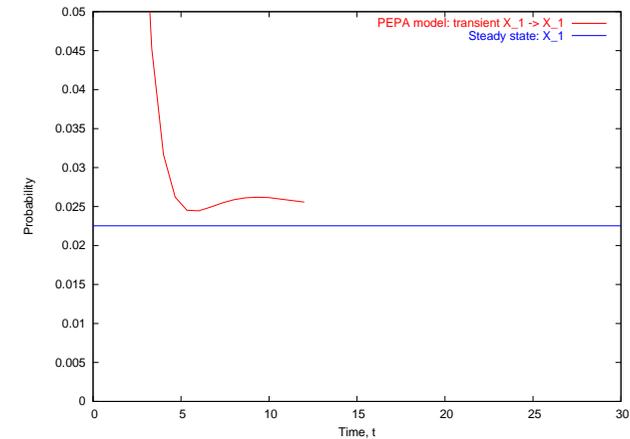
Types of Analysis

Steady-state and transient analysis in PEPA:

$$\begin{aligned} A1 &\stackrel{\text{def}}{=} (\text{start}, r_1).A2 + (\text{pause}, r_2).A3 \\ A2 &\stackrel{\text{def}}{=} (\text{run}, r_3).A1 + (\text{fail}, r_4).A3 \\ A3 &\stackrel{\text{def}}{=} (\text{recover}, r_1).A1 \\ AA &\stackrel{\text{def}}{=} (\text{run}, \top).(\text{alert}, r_5).AA \\ \text{Sys} &\stackrel{\text{def}}{=} AA \bowtie_{\{run\}} A1 \end{aligned}$$


Types of Analysis

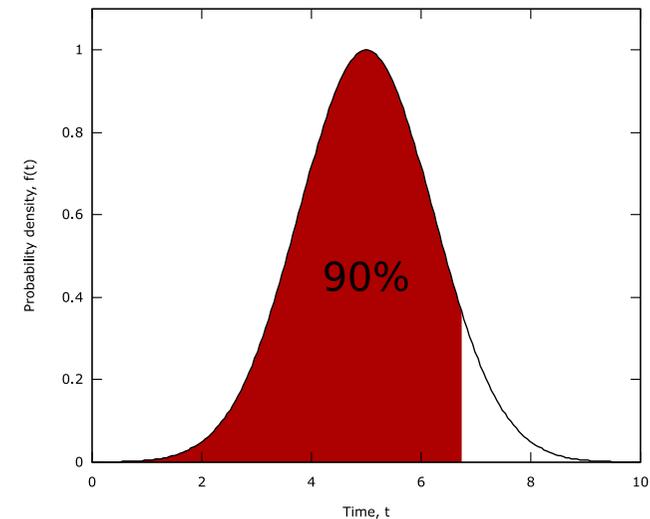
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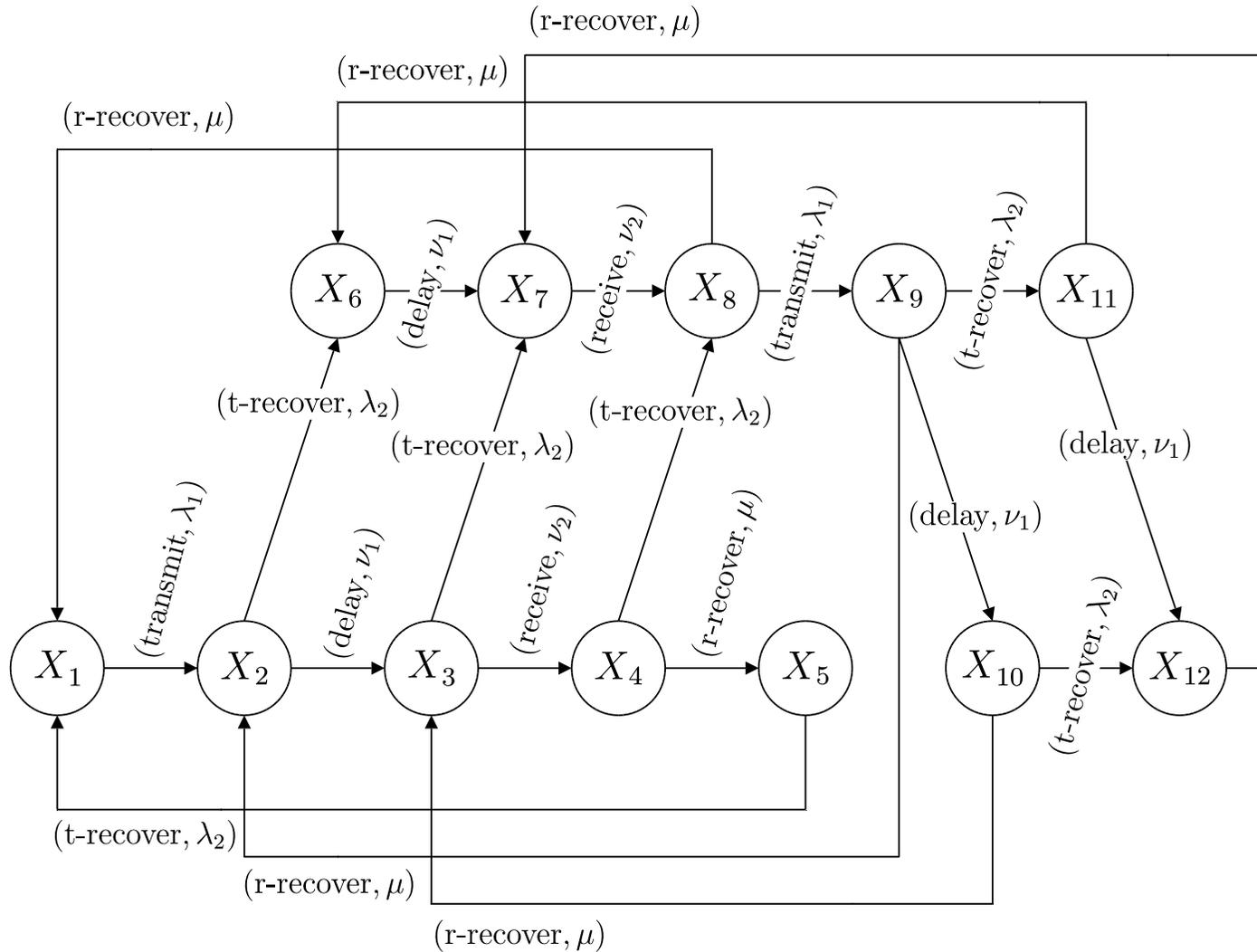
Passage-time Quantiles

Extract a passage-time density from a PEPA model:

$A1 \stackrel{\text{def}}{=} (\text{start}, r_1).A2 + (\text{pause}, r_2).A3$
 $A2 \stackrel{\text{def}}{=} (\text{run}, r_3).A1 + (\text{fail}, r_4).A3$
 $A3 \stackrel{\text{def}}{=} (\text{recover}, r_1).A1$
 $AA \stackrel{\text{def}}{=} (\text{run}, \top).(\text{alert}, r_5).AA$
 $\text{Sys} \stackrel{\text{def}}{=} AA \bowtie_{\{run\}} A1$



Need for explicit global state space



Can we approximate the state space?

Can we approximate the state space?

- ➔ In PEPA, start with a system description:

$$(A \parallel \dots \parallel A) \underset{L}{\bowtie} (B \underset{M}{\bowtie} \dots \underset{M}{\bowtie} B)$$

Can we approximate the state space?

- In PEPA, start with a system description:

$$(A \parallel \dots \parallel A) \underset{L}{\bowtie} (B \underset{M}{\bowtie} \dots \underset{M}{\bowtie} B)$$

- What if we just count the number of components in state A and B (and derivatives):

$$(N_A(t), N_{A'}(t), \dots)_{\emptyset} \underset{L}{\bowtie} (N_B(t), N_{B'}(t), \dots)_M$$

Continuous state space approximation

- For a simple system: $(X \parallel \dots \parallel X)$

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- For a simple system: $(X \parallel \cdots \parallel X)$
- Let $N_X(t)$ be a continuous variable – represents the number of components in state X at time t
- Write down a set of **coupled ordinary differential equations** to represent the rate of change in number of X in the system at time t :
 - For $X \xrightarrow{(a,\lambda)} X'$ in $(X \parallel \cdots \parallel X)$:

$$\frac{dN_X(t)}{dt} = -\lambda N_X(t)$$

Models based on...

J. Vilar, H.Y. Kueh, N. Barkai and S. Leibler.
“Mechanisms of noise-resistance in genetic oscillators“,
PNAS, vol. 90, pp. 5988–5992. April, 2002.

Stochastic π -Calculus model

$$D_A \stackrel{\text{def}}{=} \text{bind}_{A\gamma_A}.AD_A + \tau_{\alpha_A}.(D_A \mid M_A)$$

$$AD_A \stackrel{\text{def}}{=} \tau_{\theta_A}.(D_A \mid A) + \tau_{\alpha_{A'}}.(AD_A \mid M_A)$$

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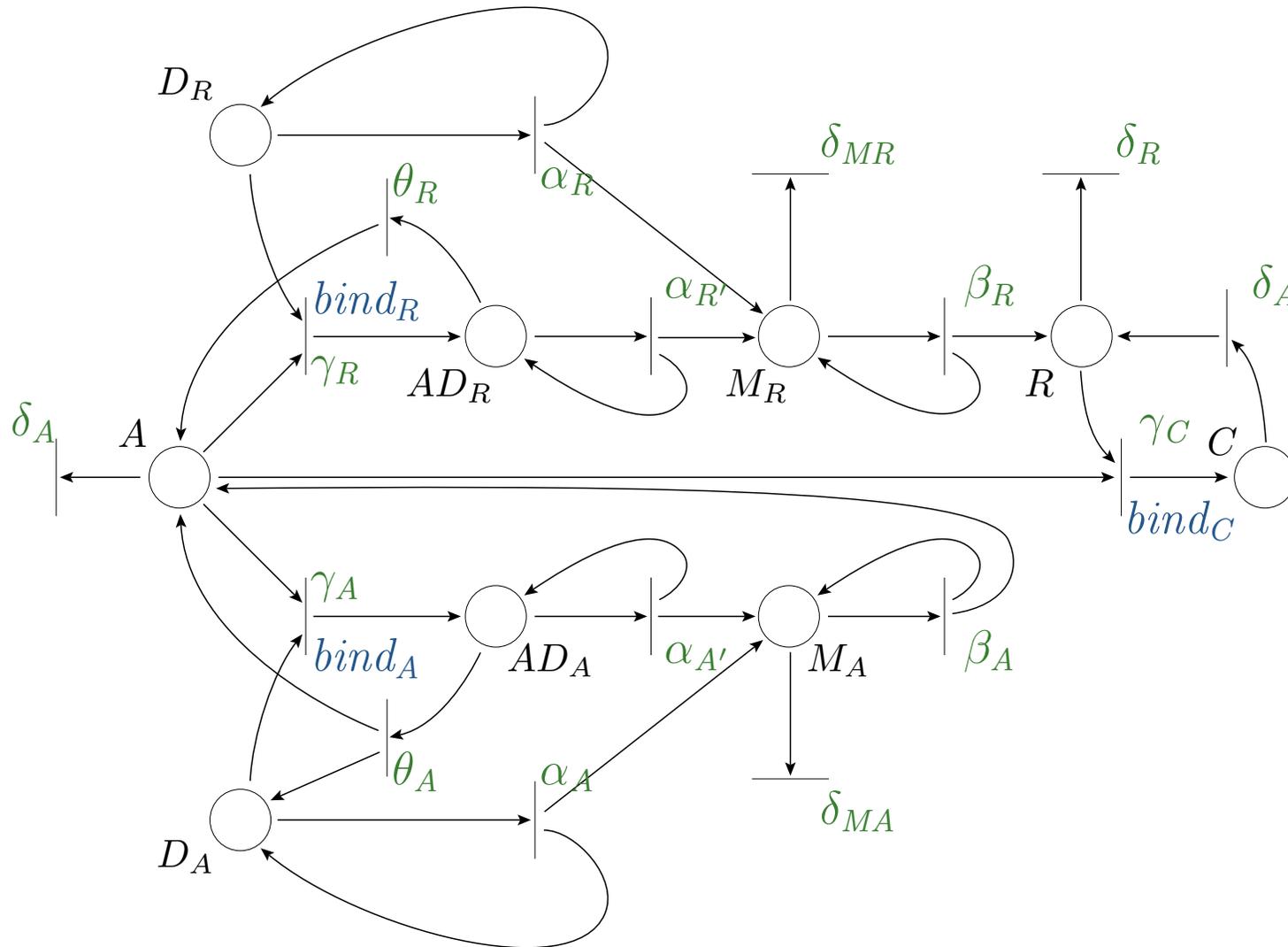
$$M_R \stackrel{\text{def}}{=} \tau_{\delta_{MR}}.\emptyset + \tau_{\beta_R}.(M_R \mid R)$$

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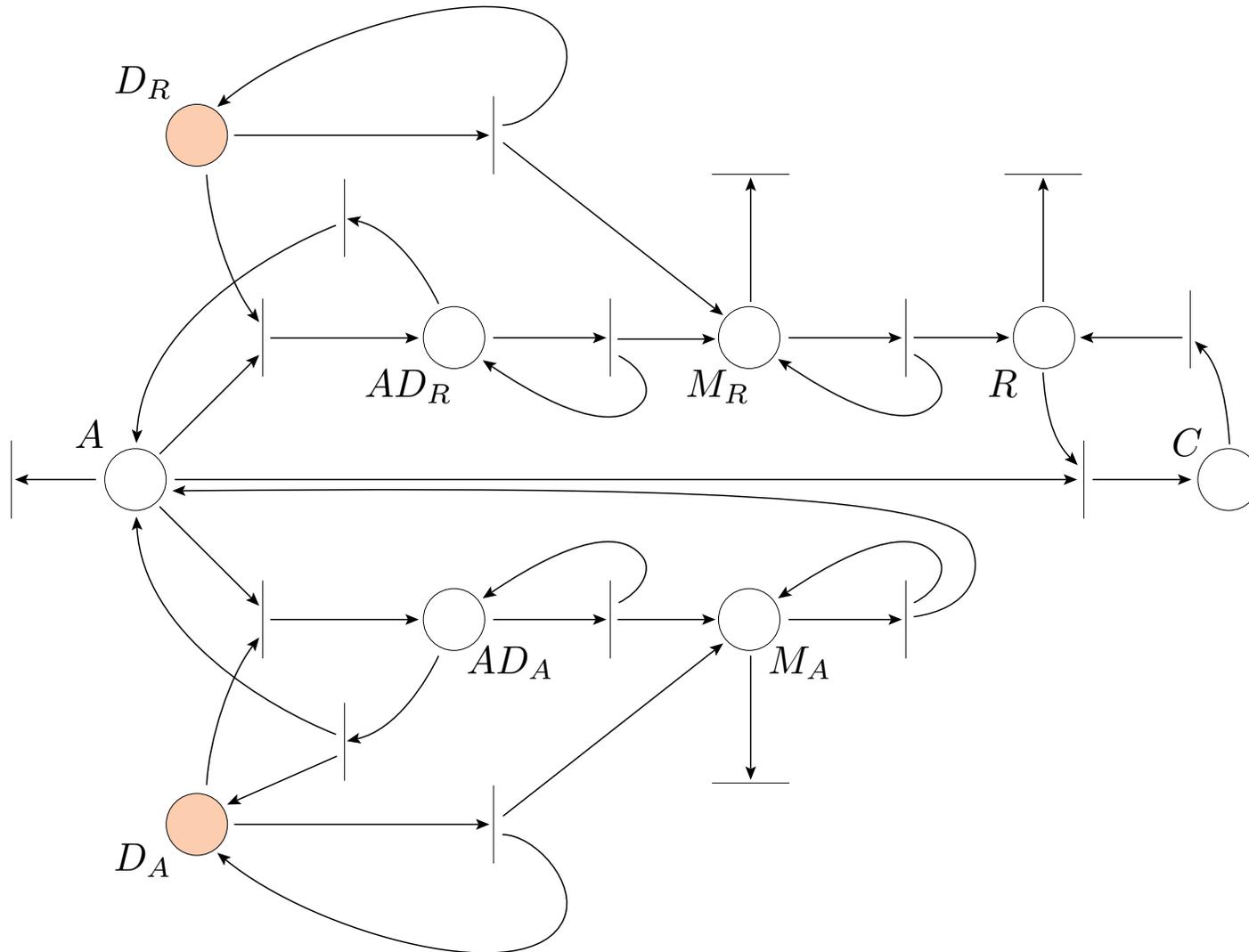
$$R \stackrel{\text{def}}{=} \text{bind}_{C\gamma_C}.C + \tau_{\delta_R}.$$

$$C \stackrel{\text{def}}{=} \tau_{\delta_A}.R$$

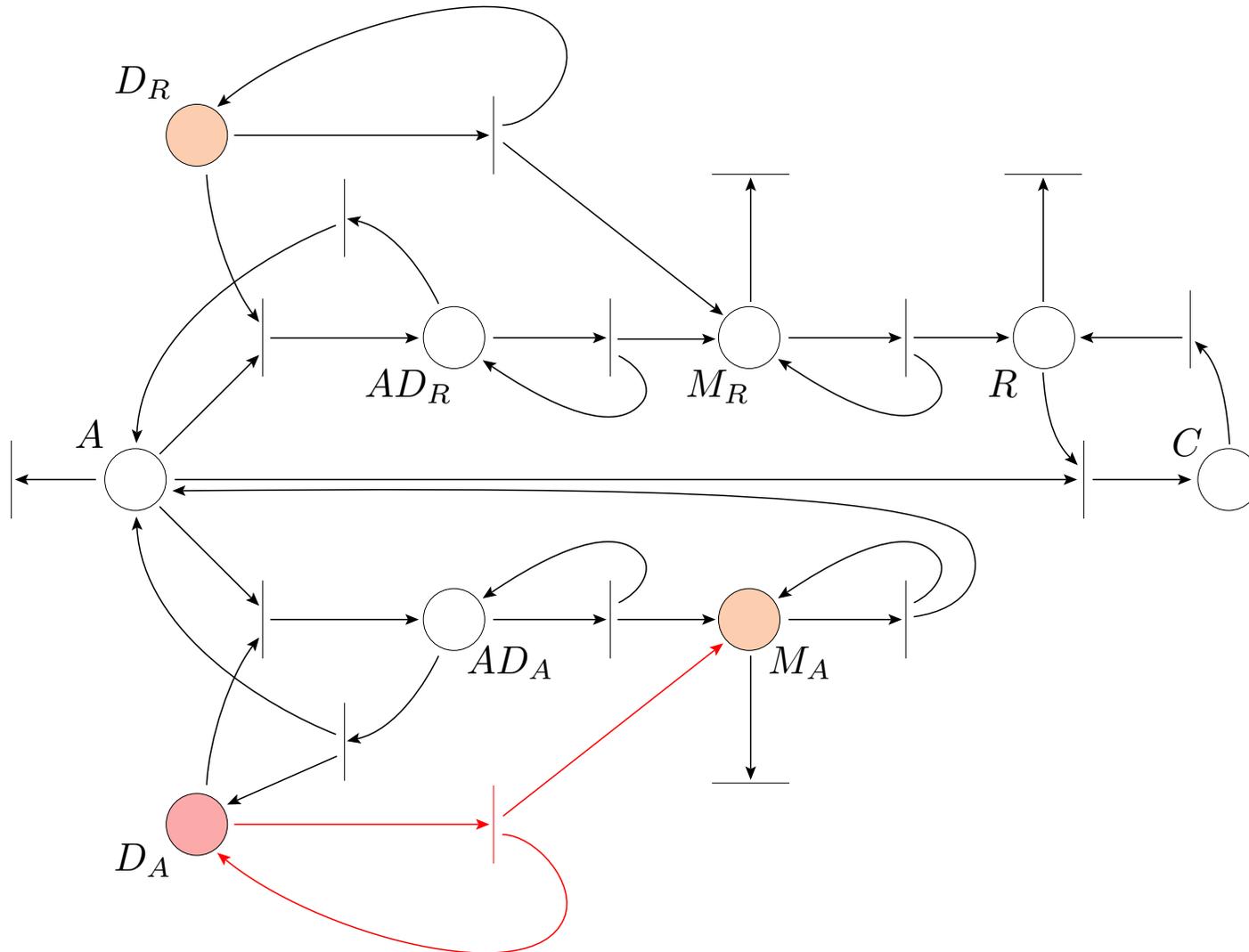
Circadian clock: as a Petri net!



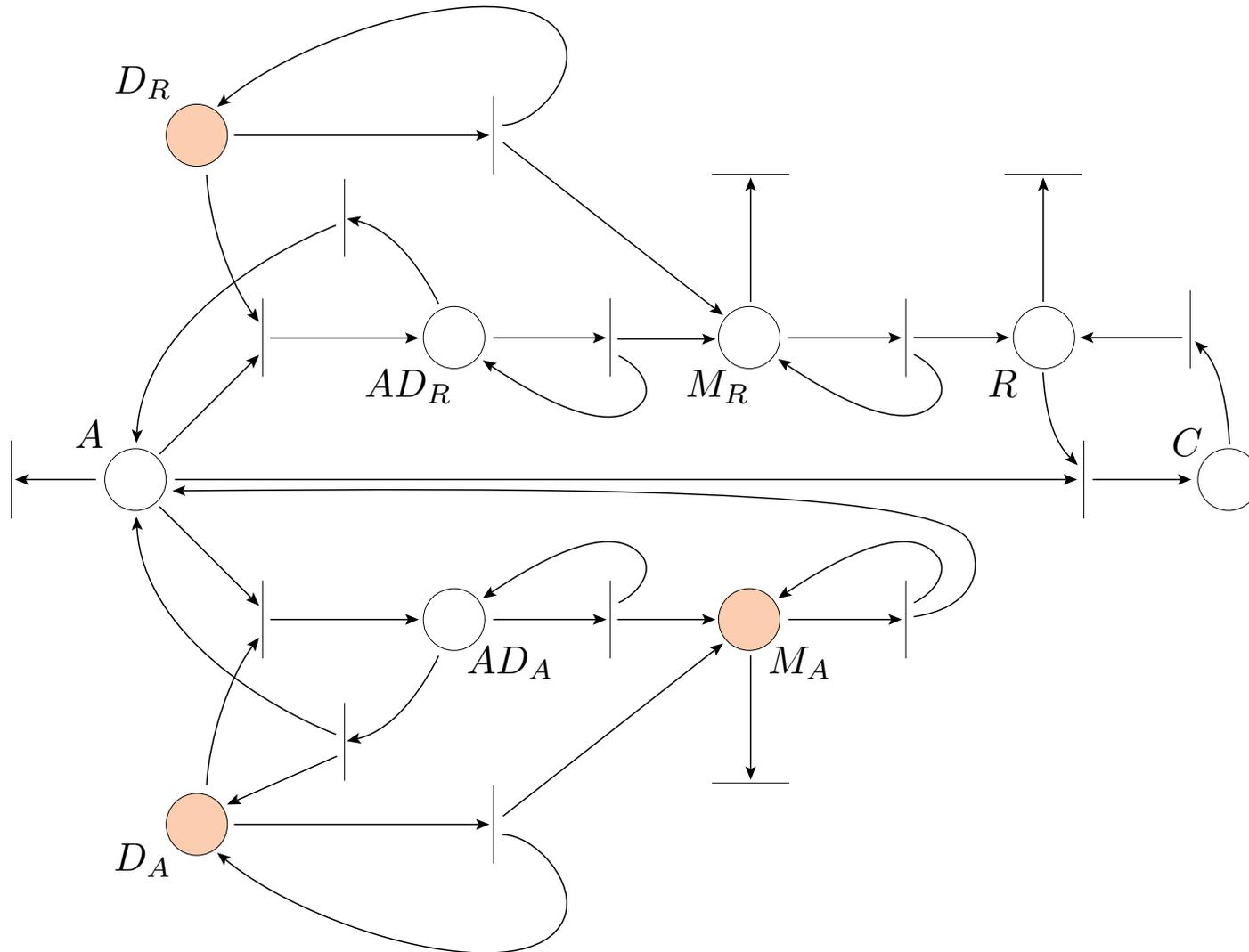
Circadian clock: an explanation



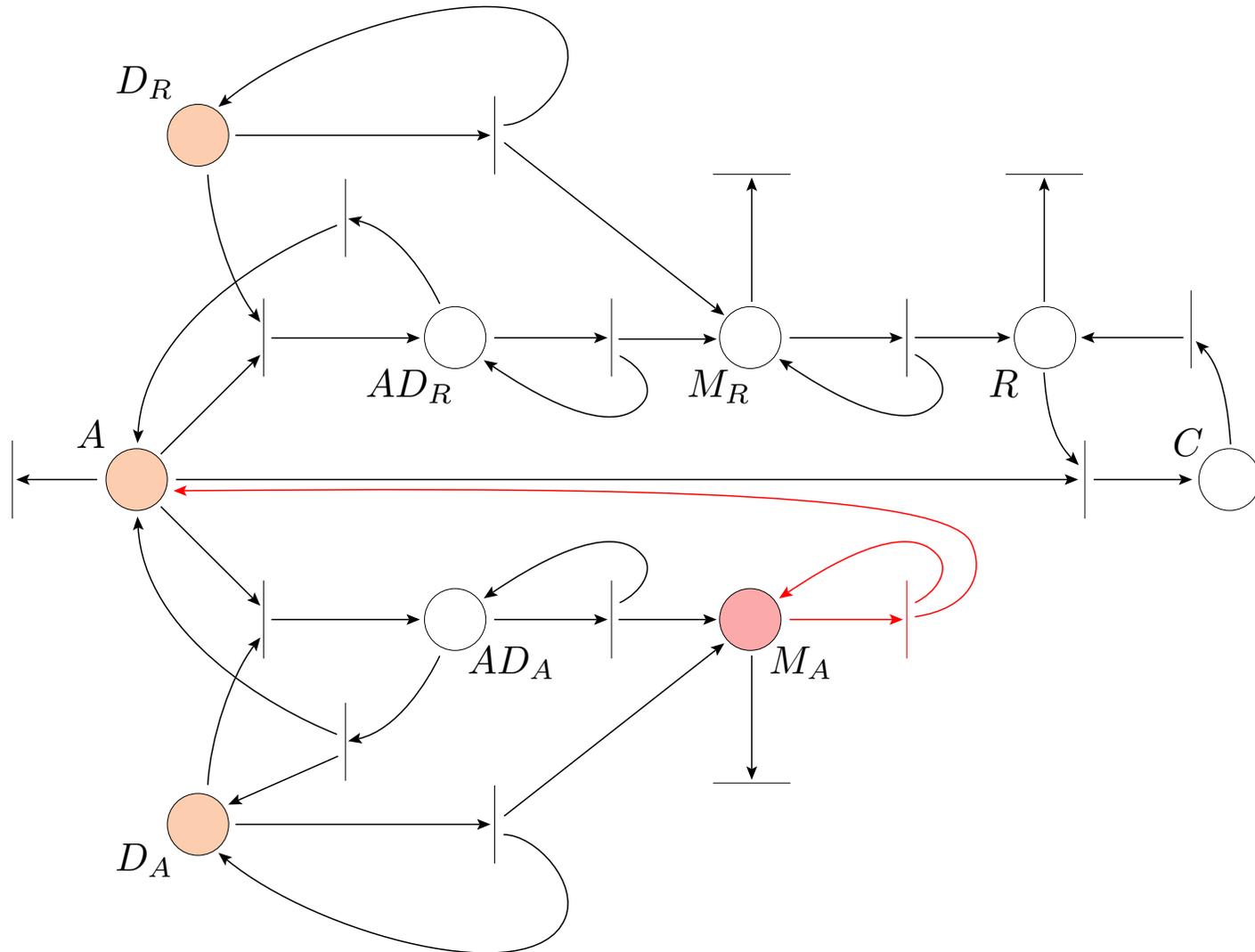
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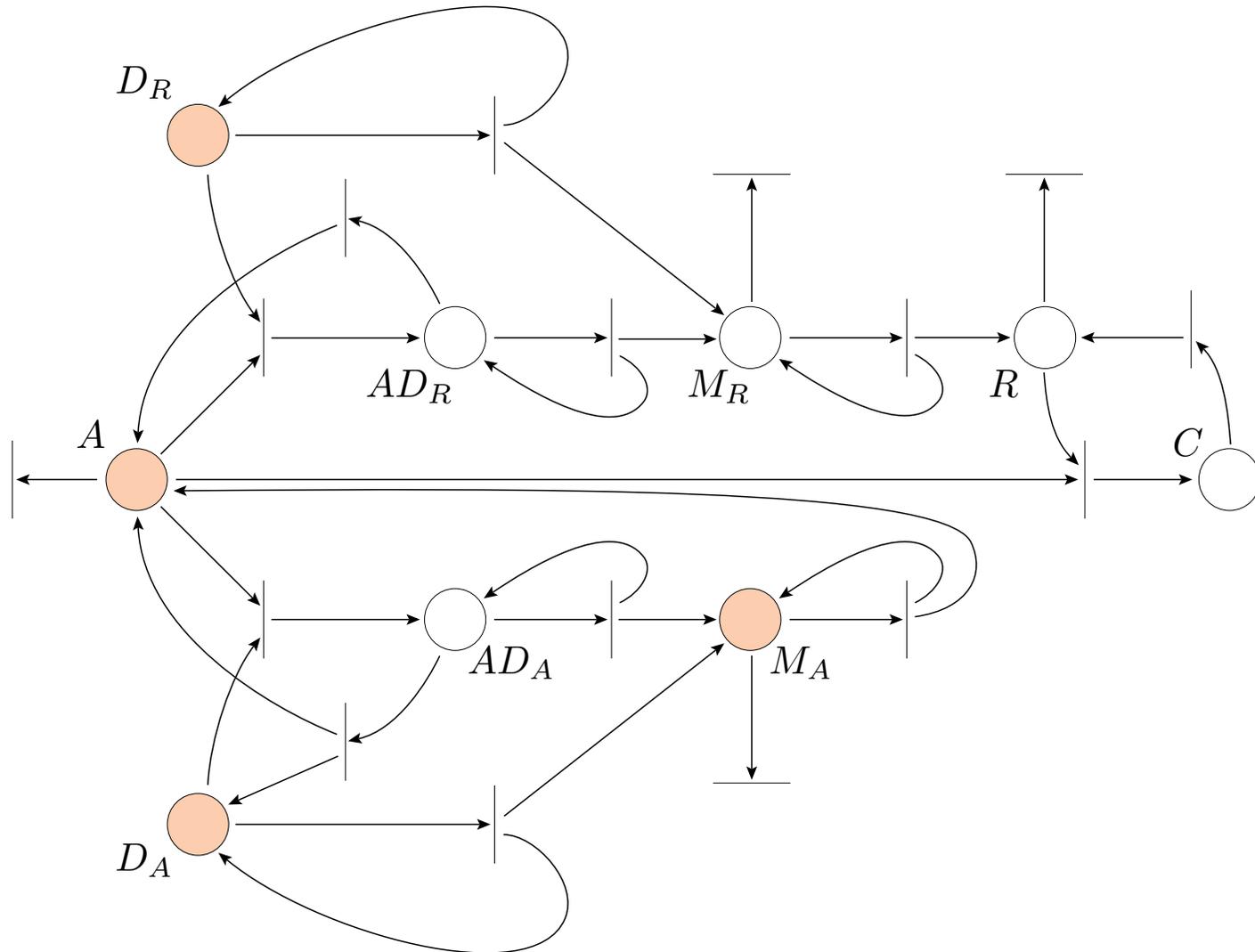
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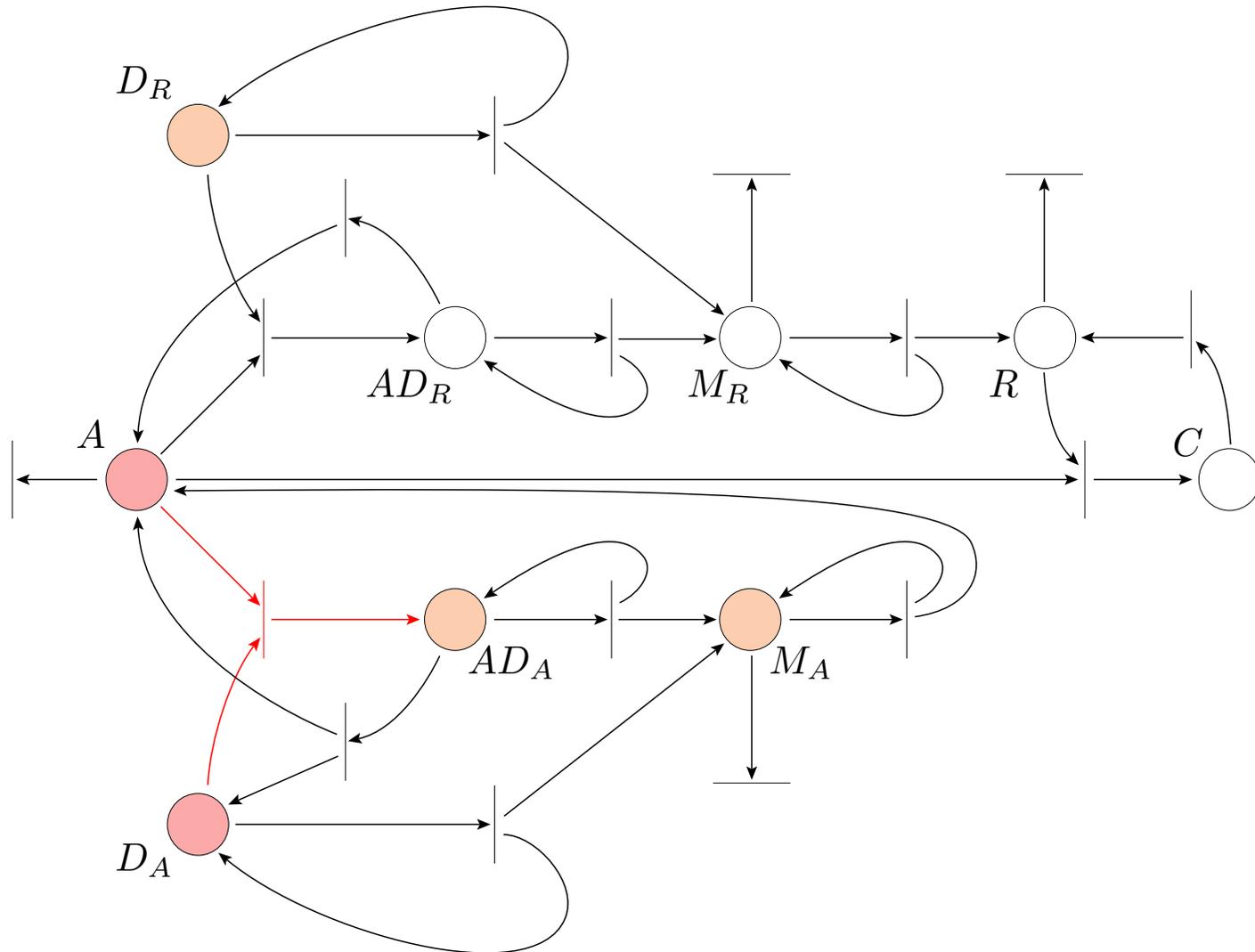
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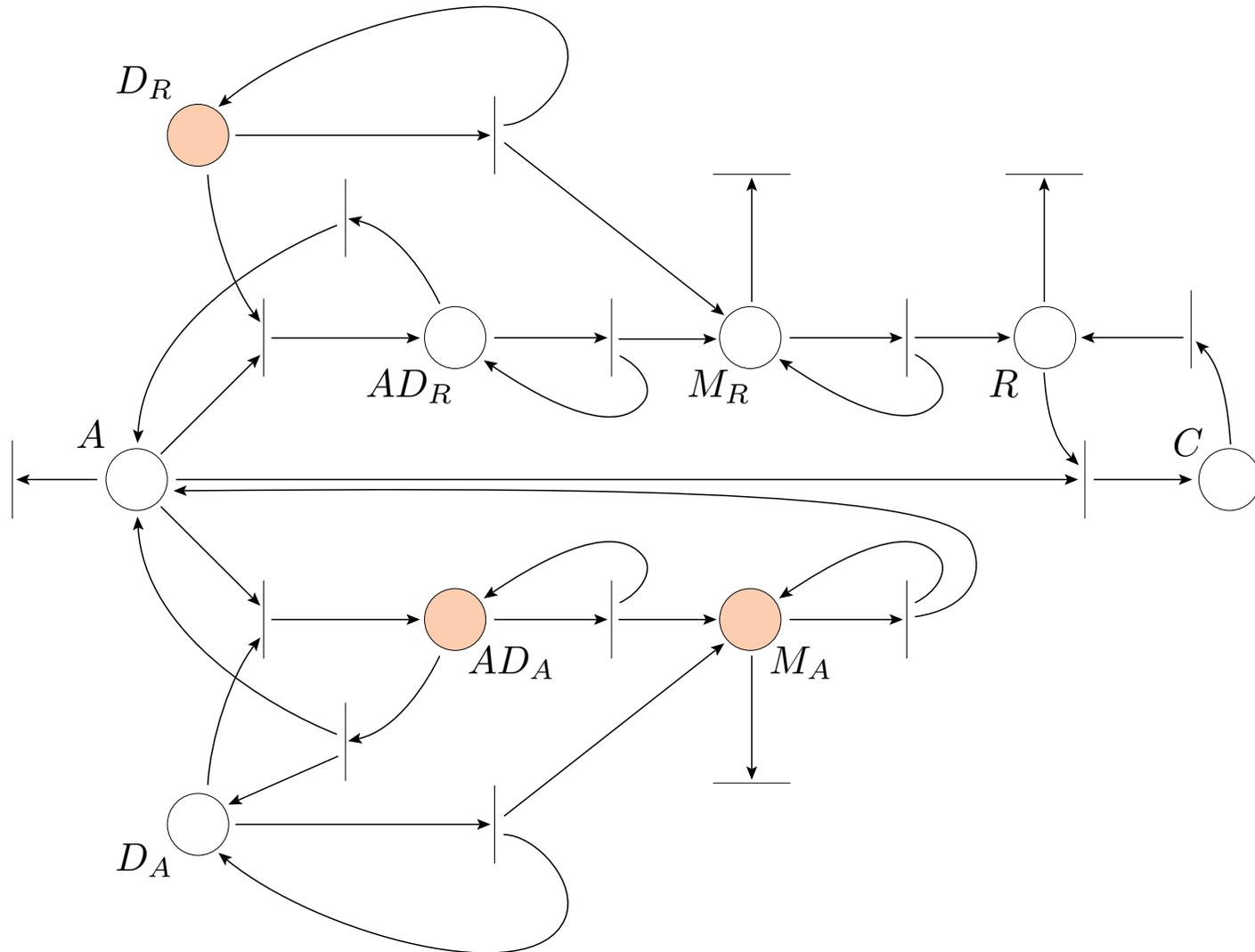
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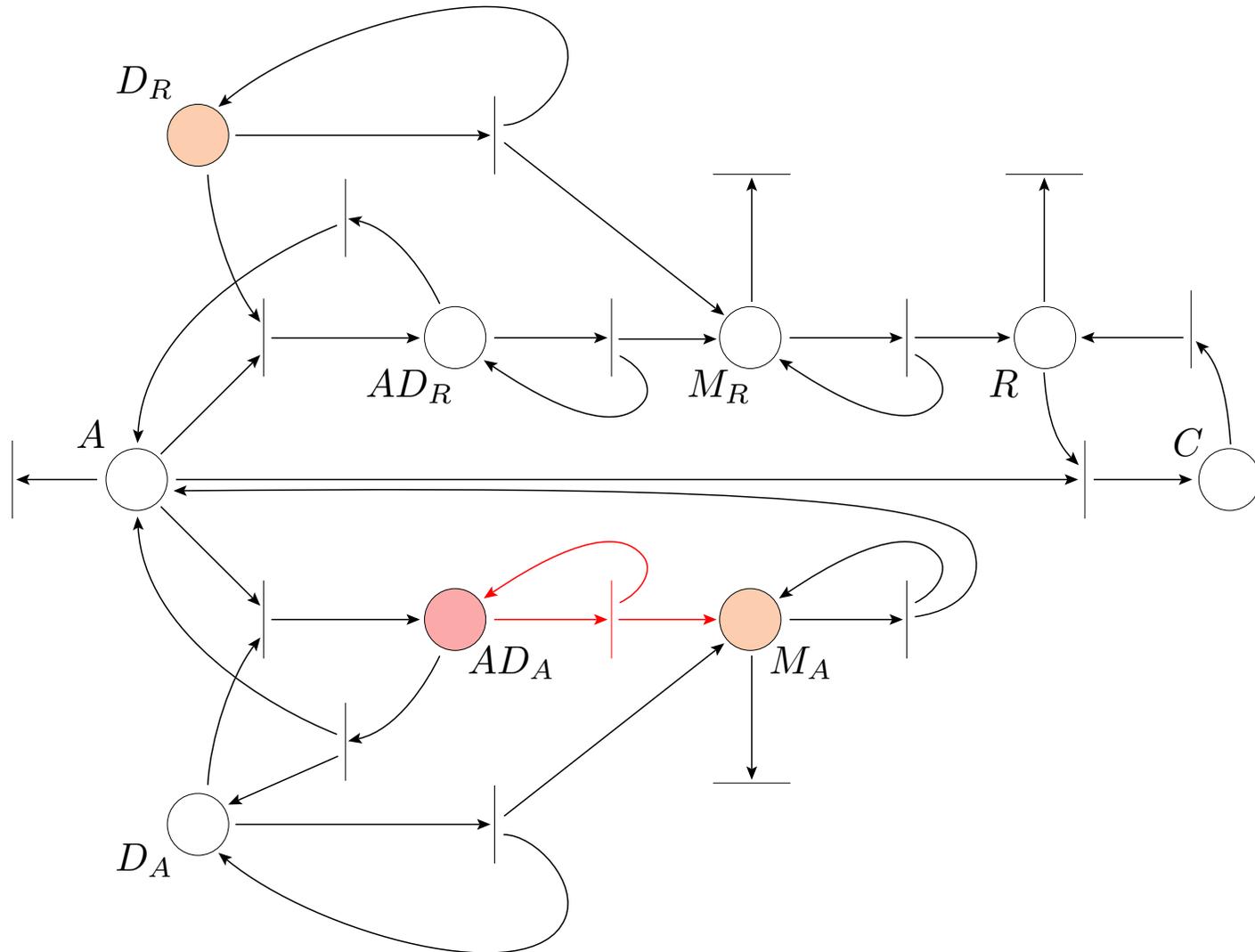
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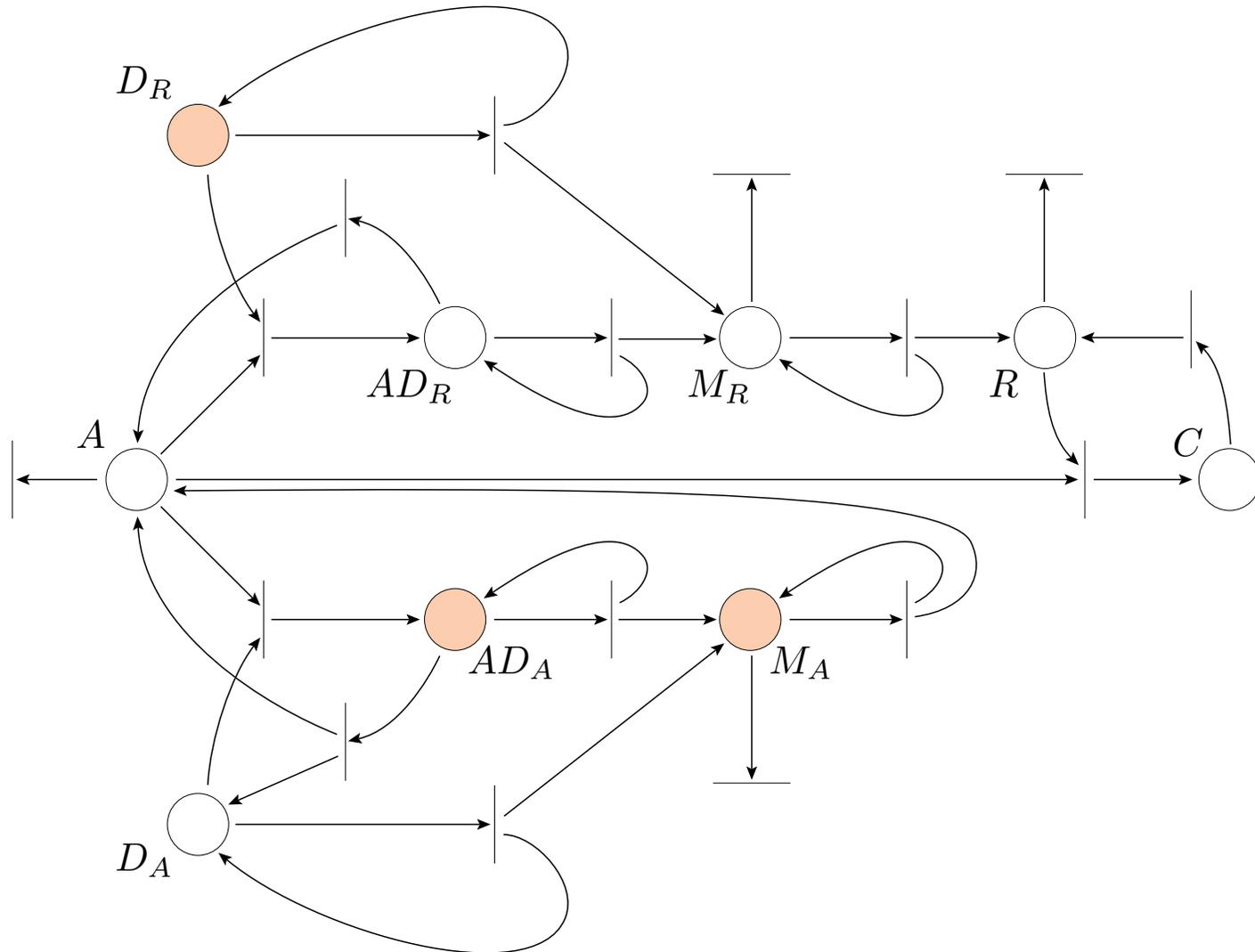
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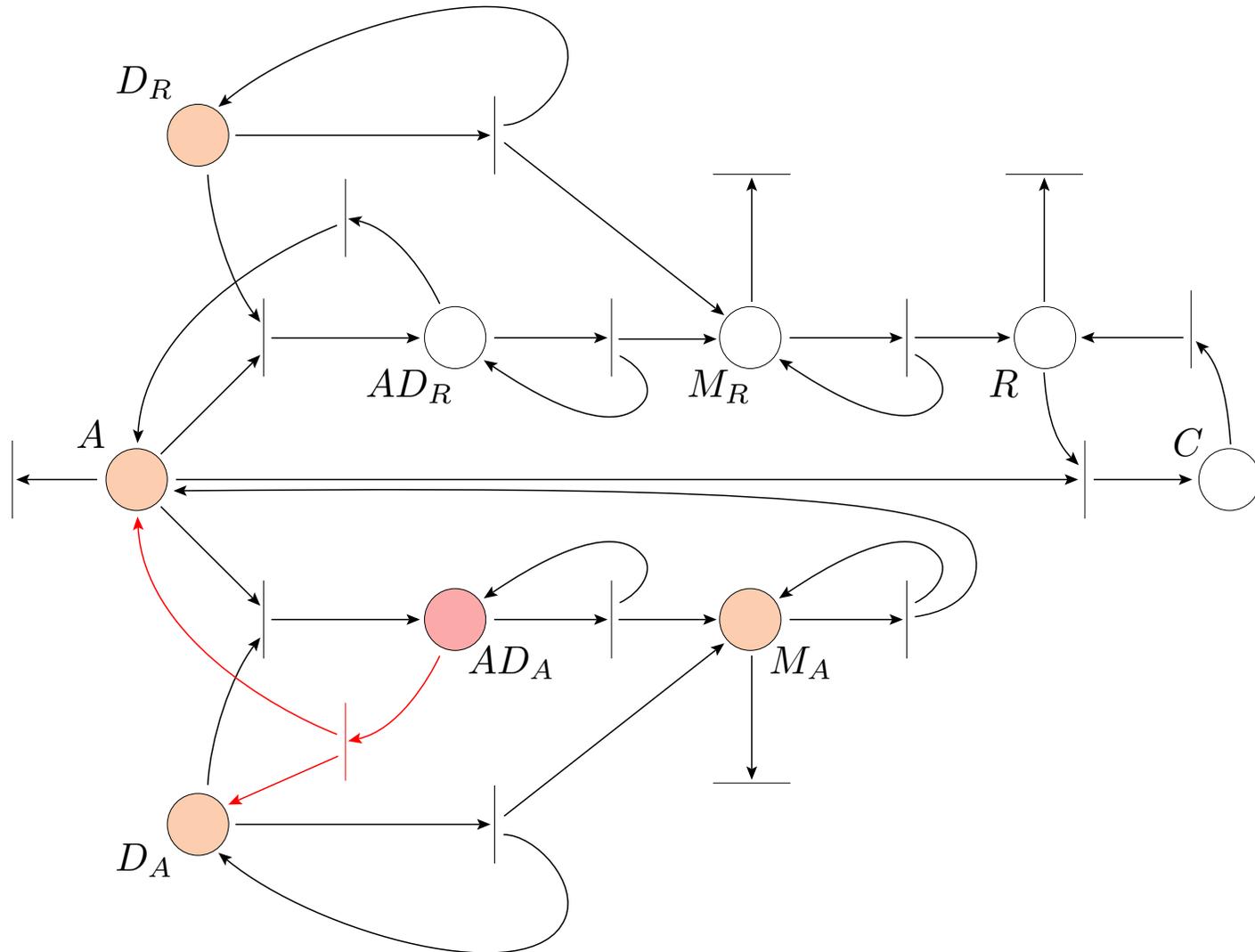
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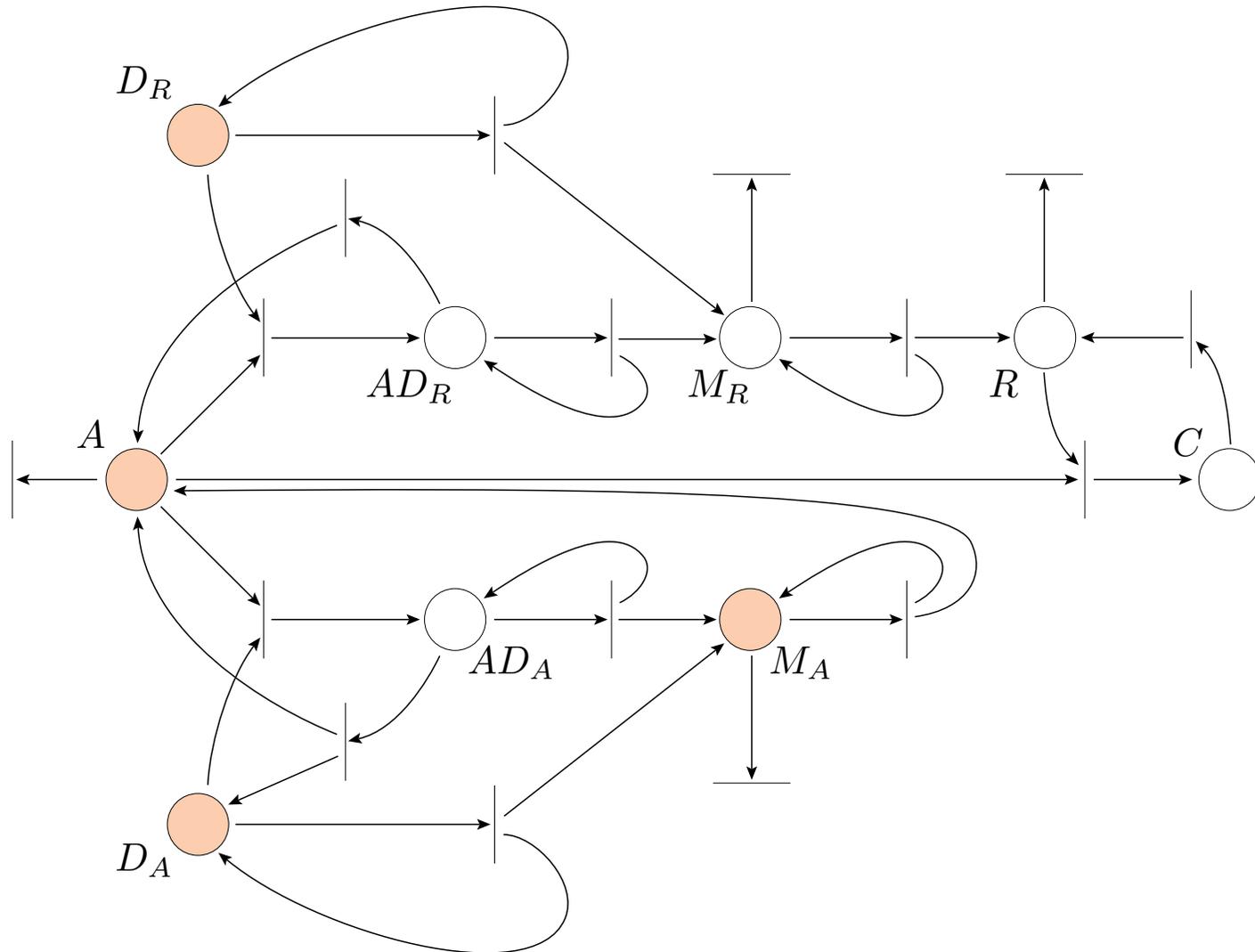
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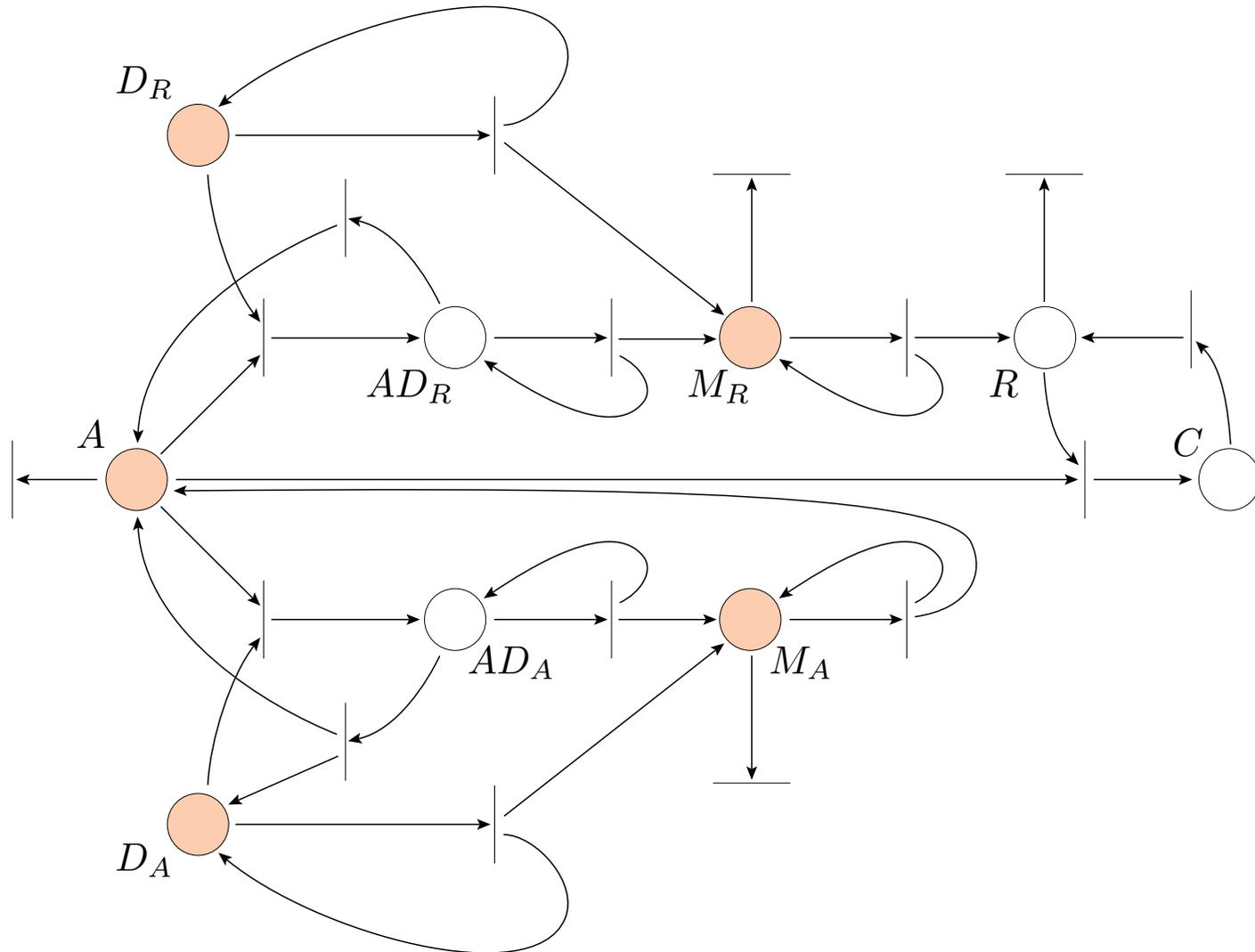
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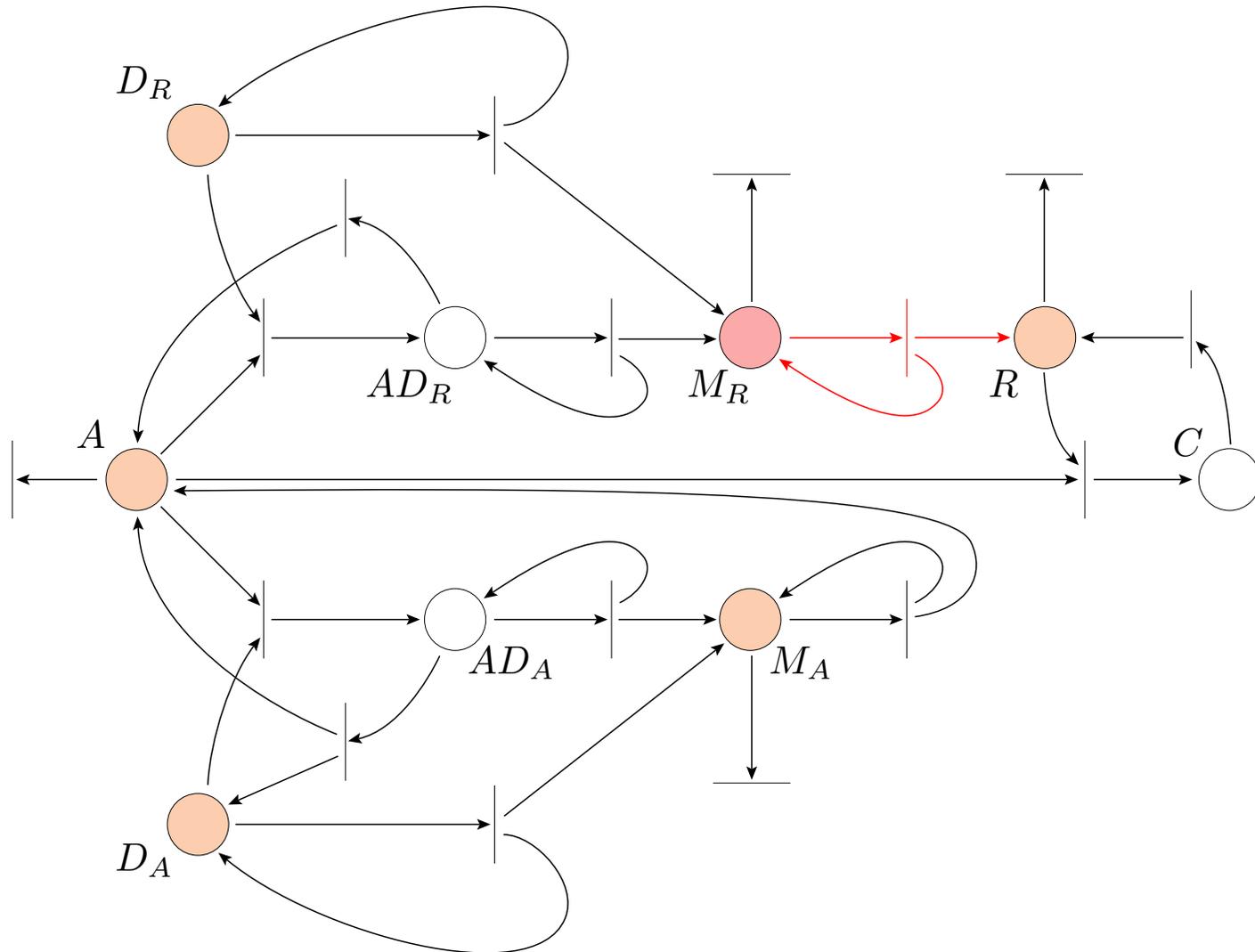
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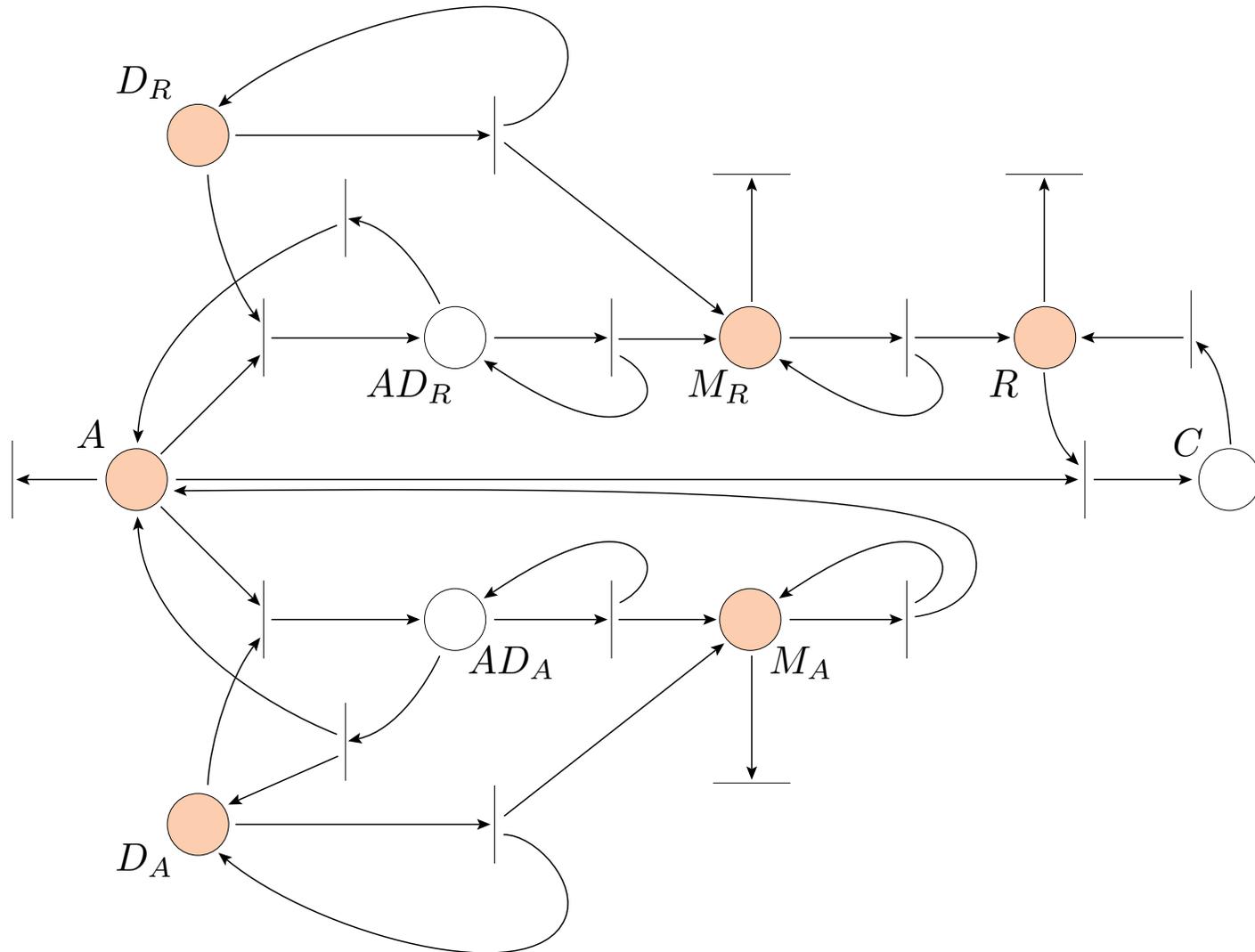
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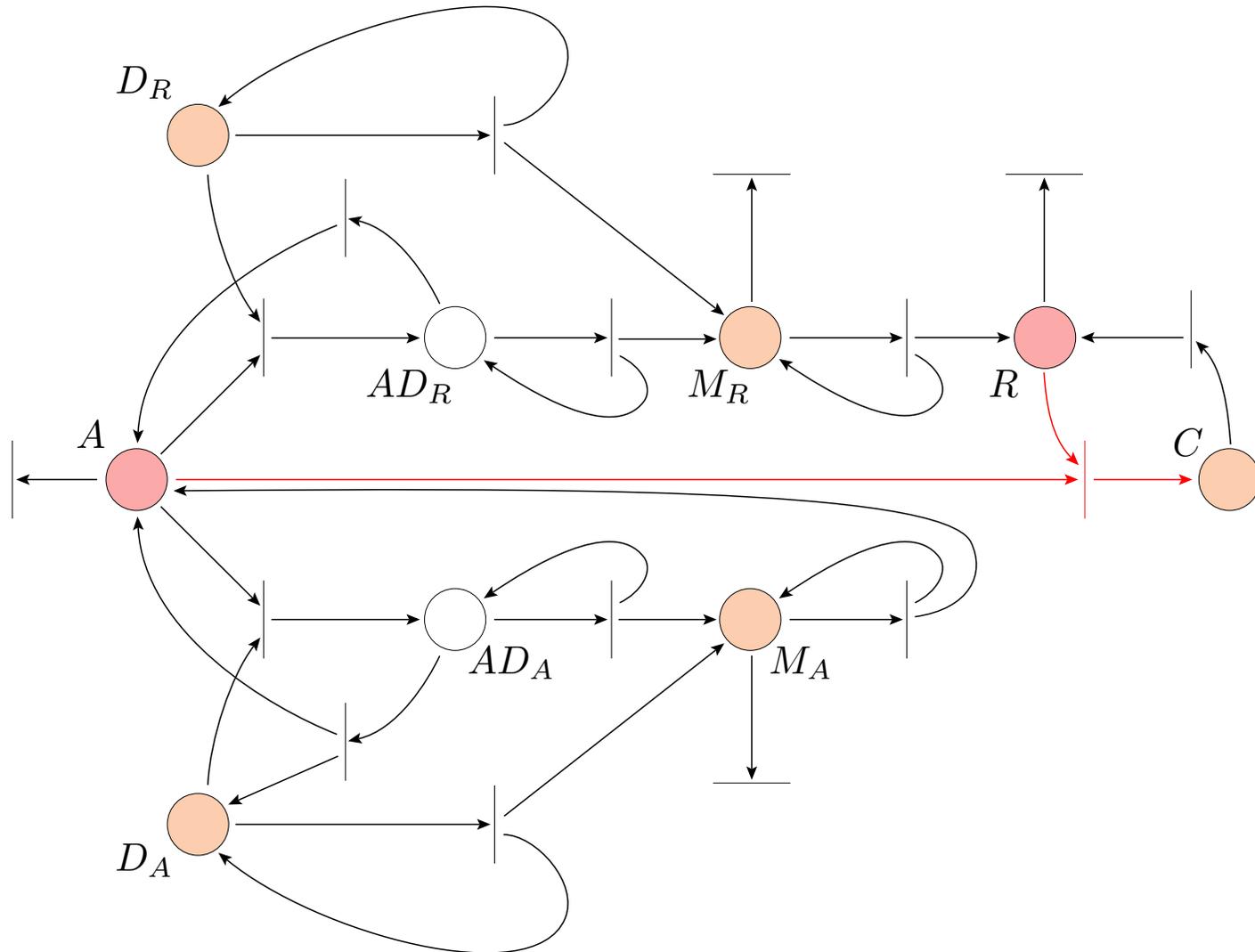
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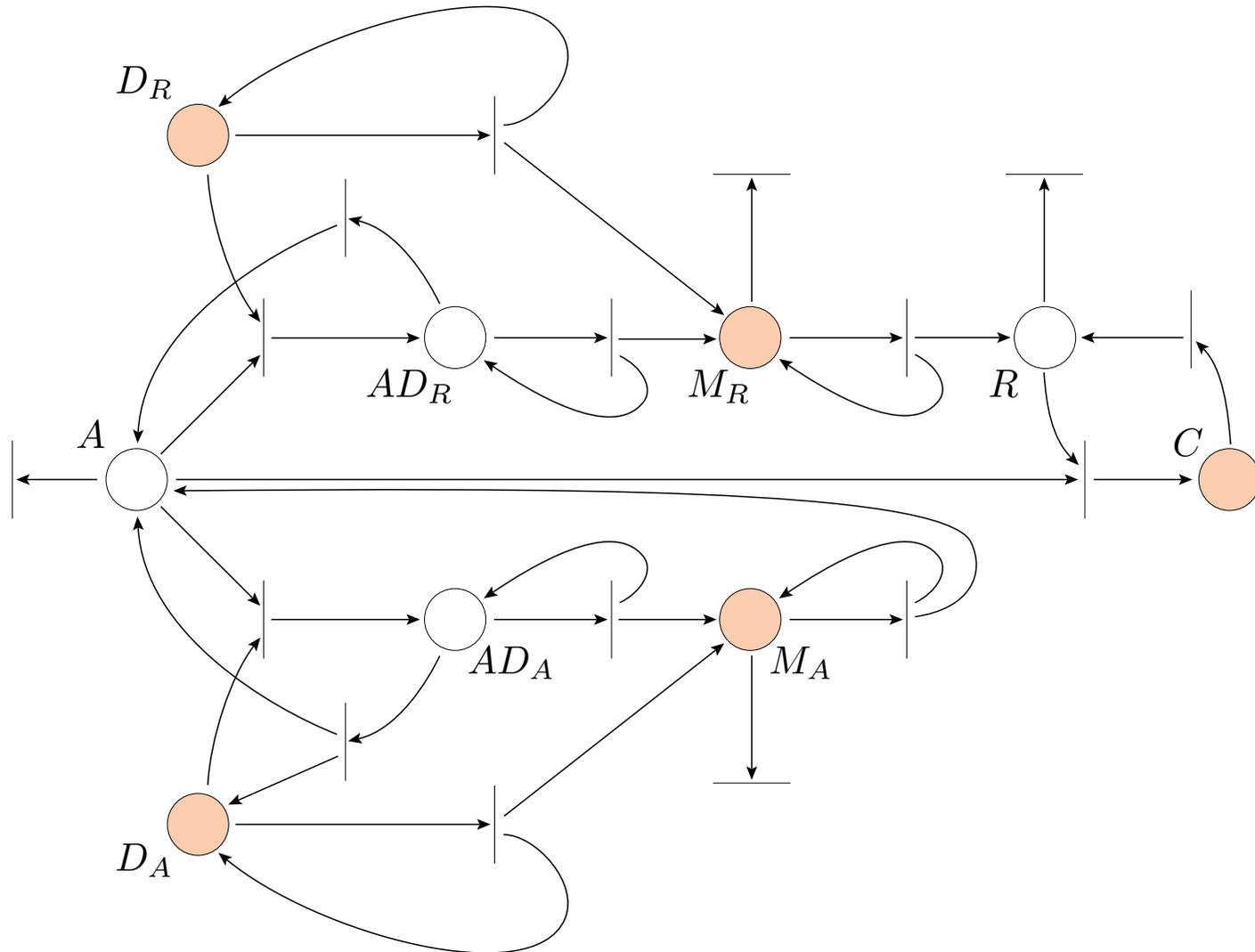
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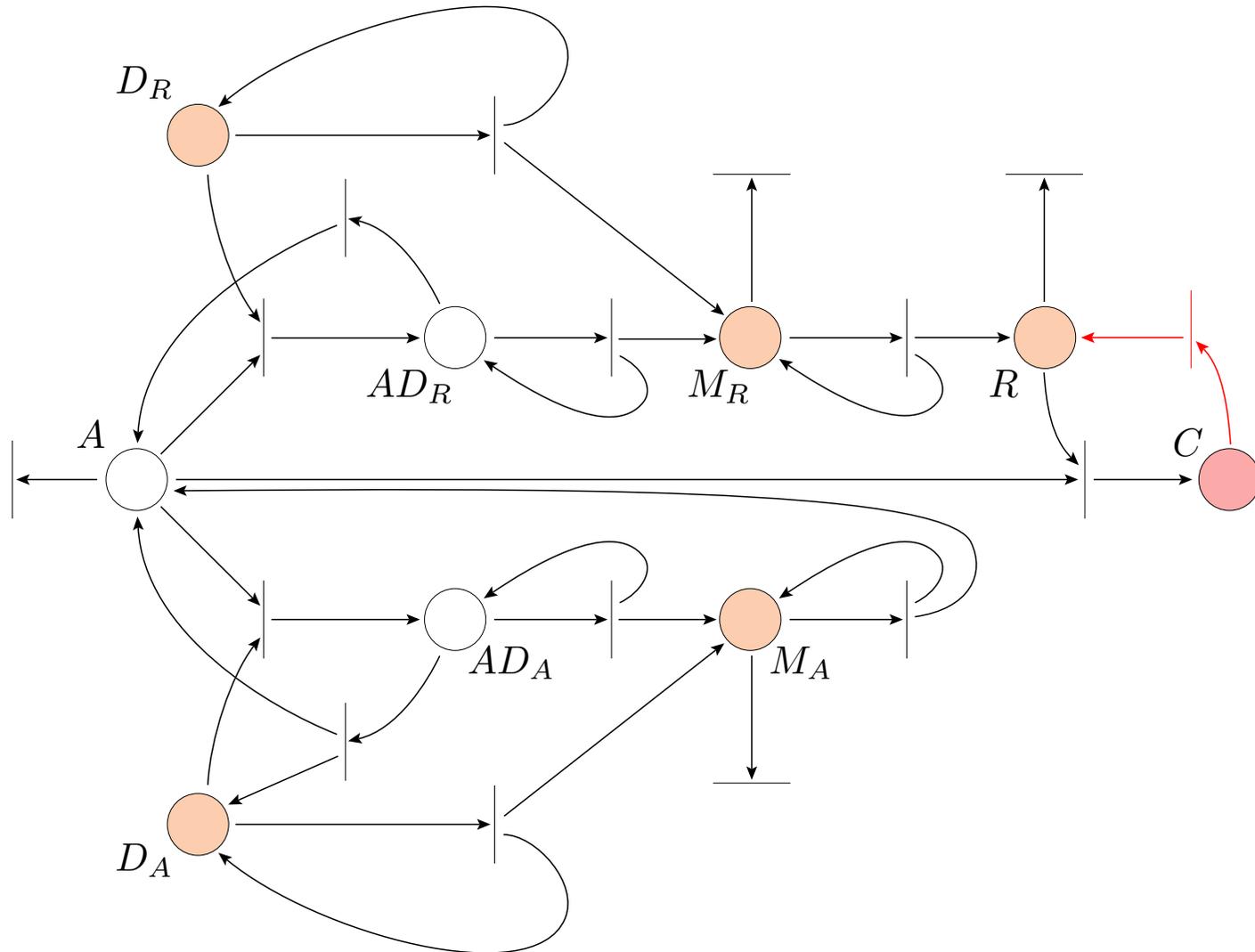
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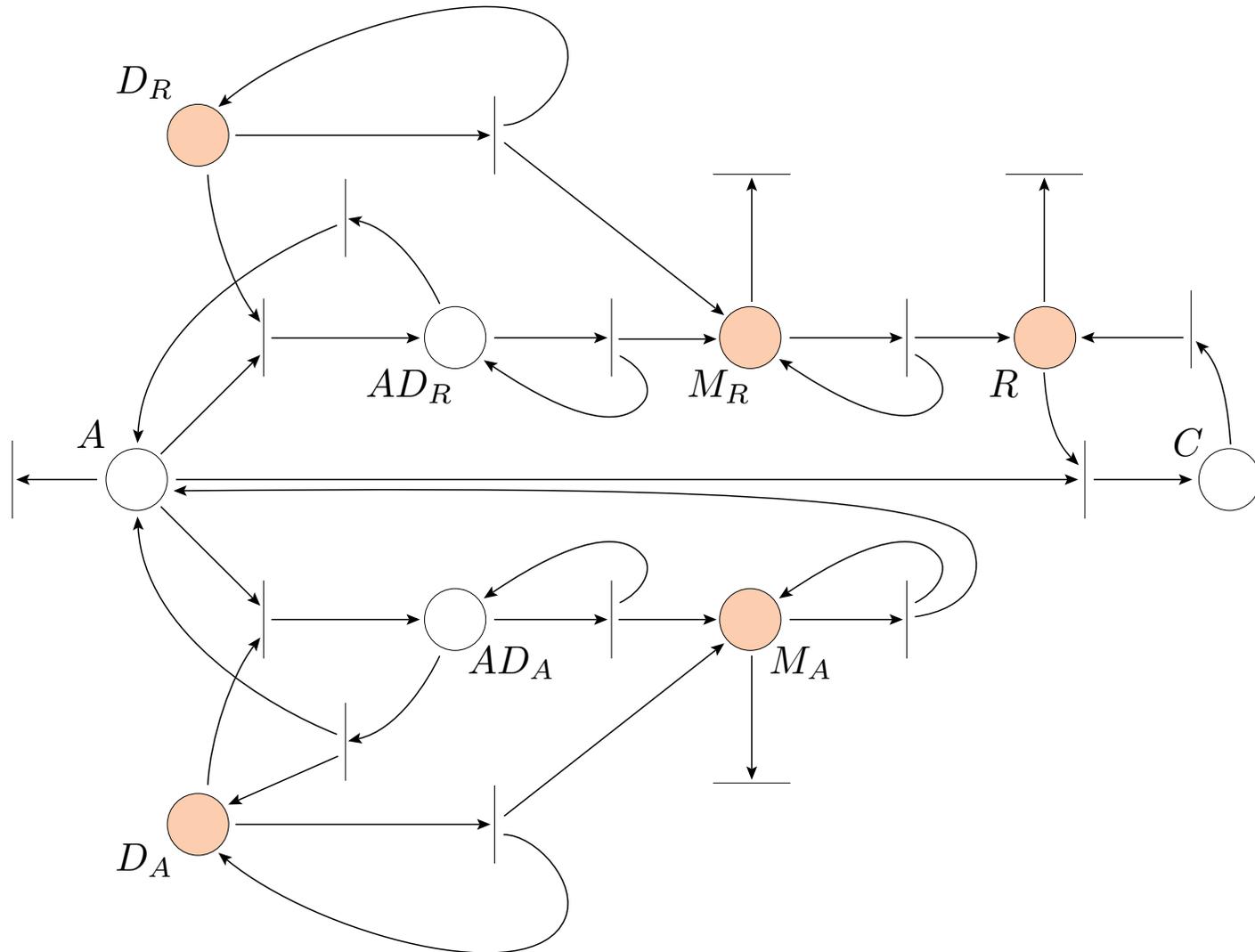
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Modelling Styles

Note the different modelling styles
in the use of *stochastic* π and
PEPA

Modelling with π -Calculus



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$$D_R \stackrel{\text{def}}{=} \text{bind}_{R\gamma_R}.AD_R + \tau_{\alpha_R}.(D_R \mid M_R)$$

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$$R \stackrel{\text{def}}{=} \text{bind}_{C\gamma_C}.C + \tau_{\delta_R}.\emptyset$$

$$AD_R \stackrel{\text{def}}{=} \tau_{\theta_R}.(D_R \mid A) + \tau_{\alpha_{R'}}.(AD_R \mid M_R)$$

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PEPA model: Circadian Clock

$$D_A \stackrel{\text{def}}{=} (bind_{AD_A}, \gamma_A).AD_A + (mk_{MA}, \alpha_A).D_A$$

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$$A' \stackrel{\text{def}}{=} (mk_A, \top).A$$

$$A \stackrel{\text{def}}{=} (bind_{AD_A}, \gamma_A).AD_A + (bind_{AD_R}, \gamma_R).AD_R \\ + (bind_{AR}, \gamma_C).A_C + (decay_A, \delta_A).A'$$

PEPA model: Circadian Clock

$$D_A \stackrel{\text{def}}{=} (bind_{AD_A}, \gamma_A).AD_A + (mk_{MA}, \alpha_A).D_A$$

$$AD_A \stackrel{\text{def}}{=} (unbind_{AD_A}, \theta_A).D_A + (mk_{MA}, \alpha_{A'}).AD_A$$

$$M'_A \stackrel{\text{def}}{=} (mk_{MA}, \top).M_A$$

$$M_A \stackrel{\text{def}}{=} (decay_{M_A}, \delta_{M_A}).M'_A + (mk_A, \beta_A).M_A$$

$$A' \stackrel{\text{def}}{=} (mk_A, \top).A$$

$$A \stackrel{\text{def}}{=} (bind_{AD_A}, \gamma_A).AD_A + (bind_{AD_R}, \gamma_R).AD_R \\ + (bind_{AR}, \gamma_C).AC + (decay_A, \delta_A).A'$$

$$AD_A \stackrel{\text{def}}{=} (unbind_{AD_A}, \top).A$$

...

PEPA Combination

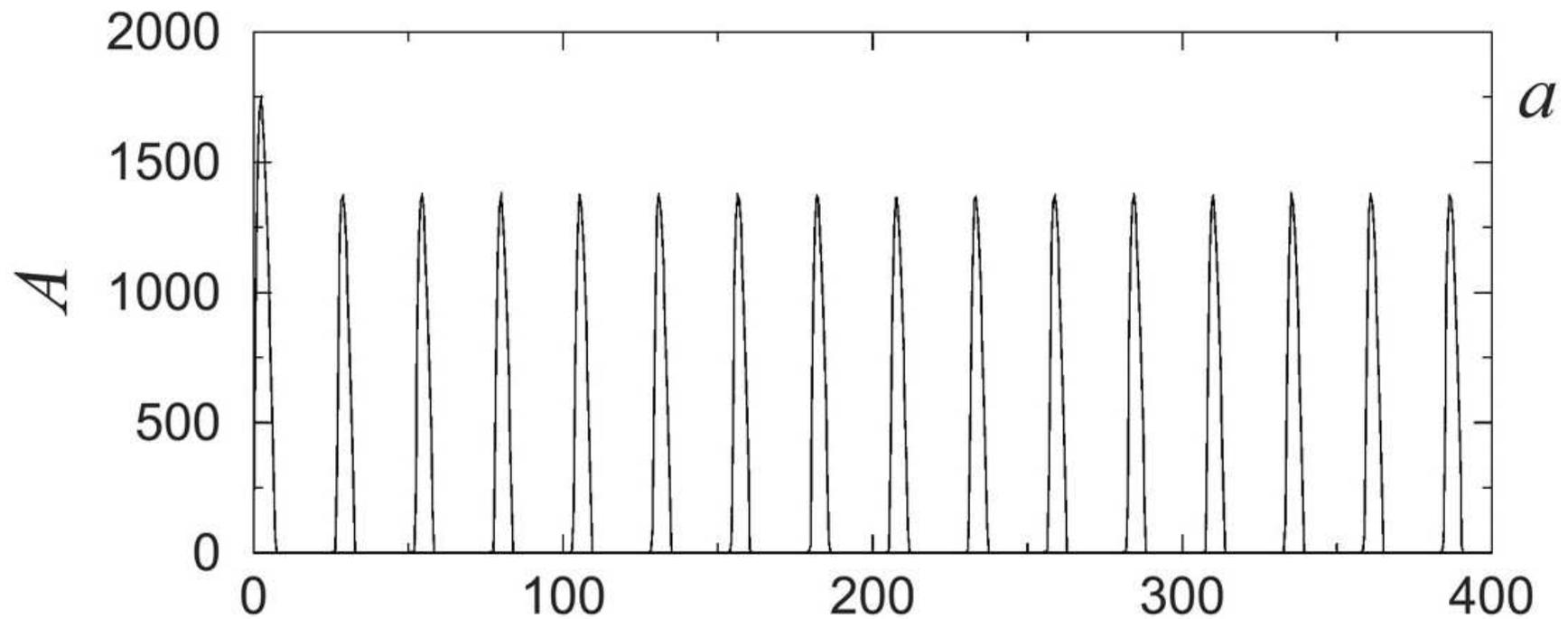
Part of PEPA system combination looks like:

$$((D_A \bowtie_L M'_A[500]) \bowtie_M A'[2500]) \bowtie_N \dots$$

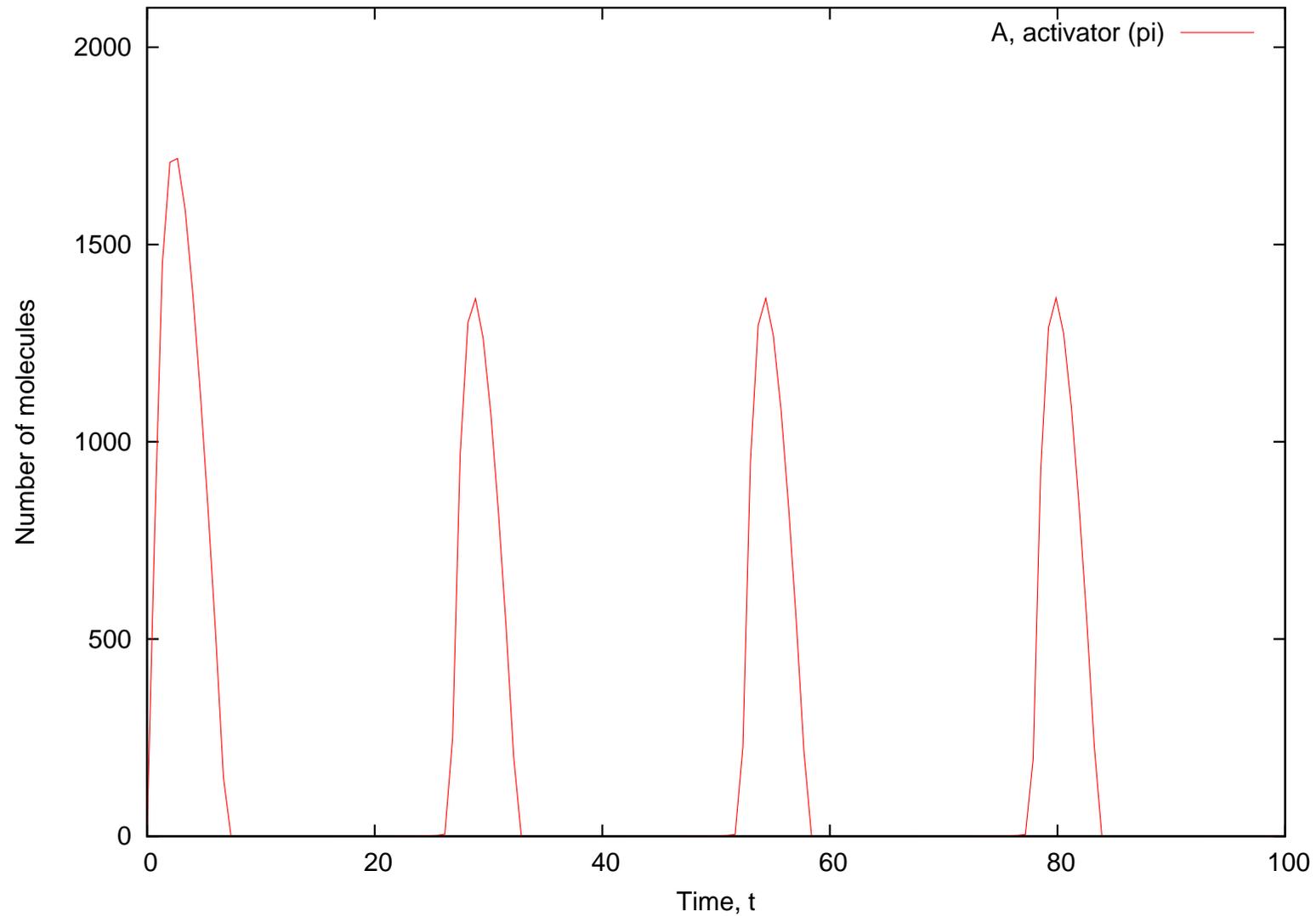
where:

- ➔ $L = \{mk_{MA}\}$
- ➔ $M = \{mk_A, bind_{AD_A}\}$

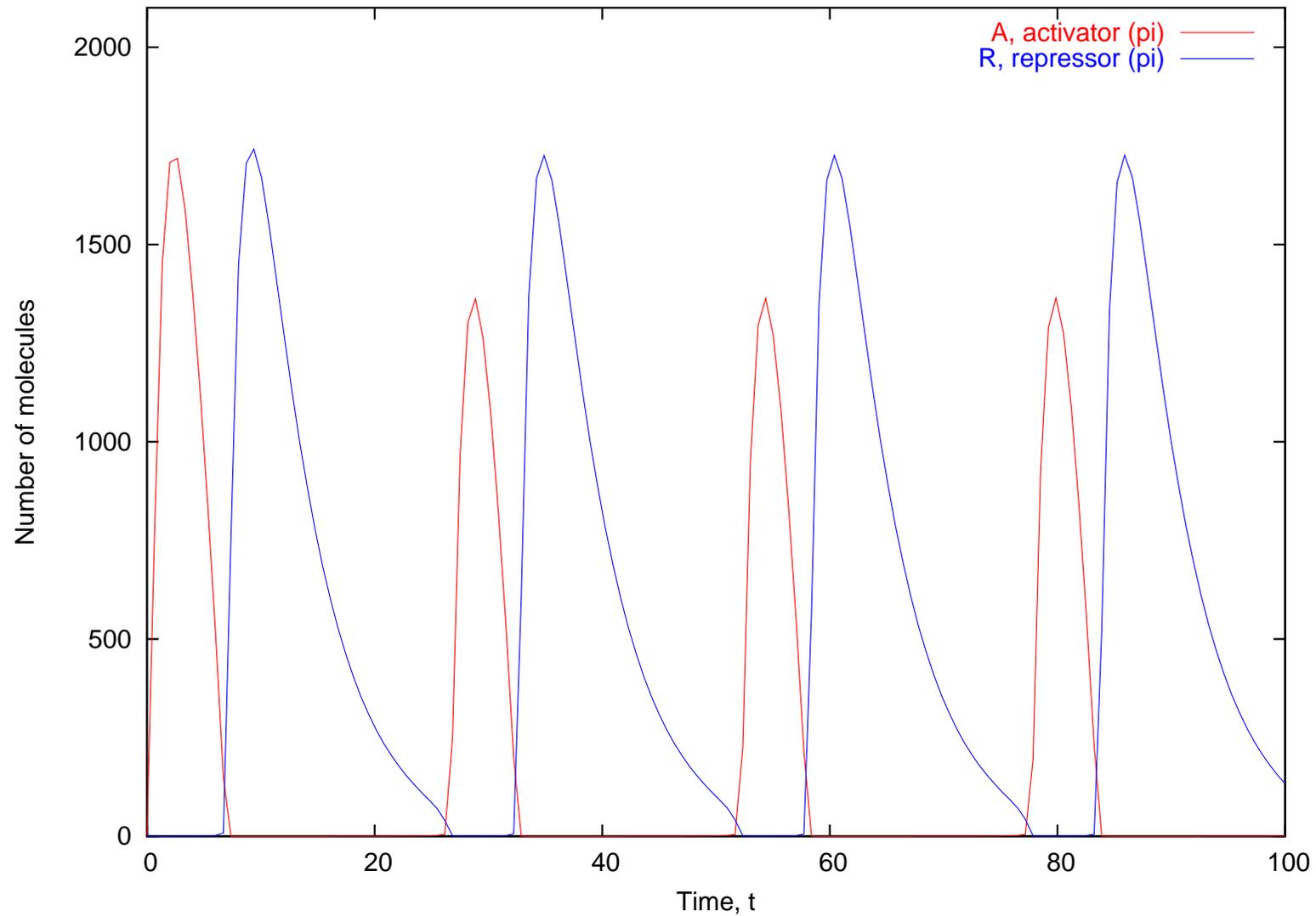
Vilar oscillations of A : reminder



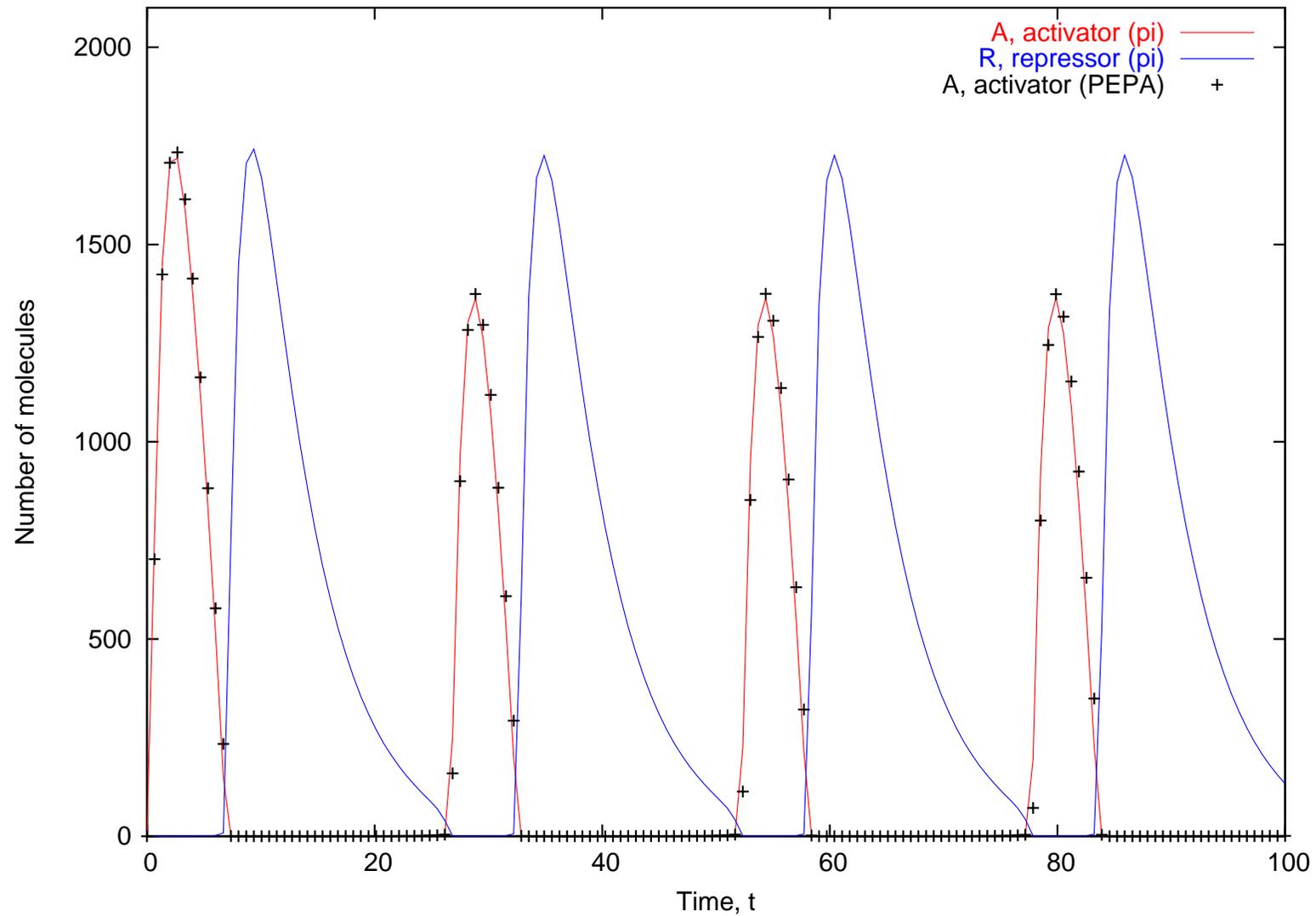
Stochastic π model results



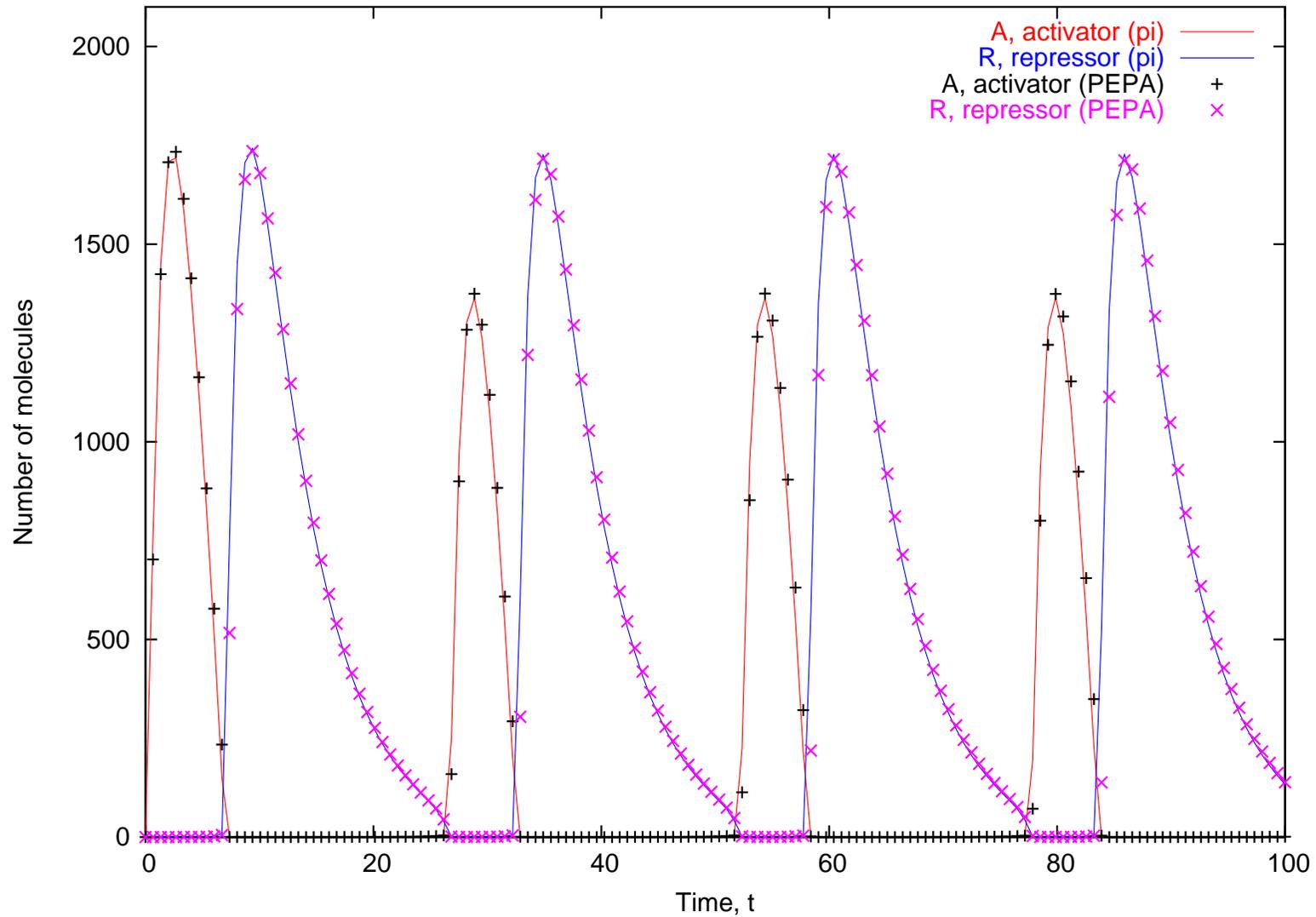
Results: π v PEPA



Results: π v PEPA



Results: π v PEPA



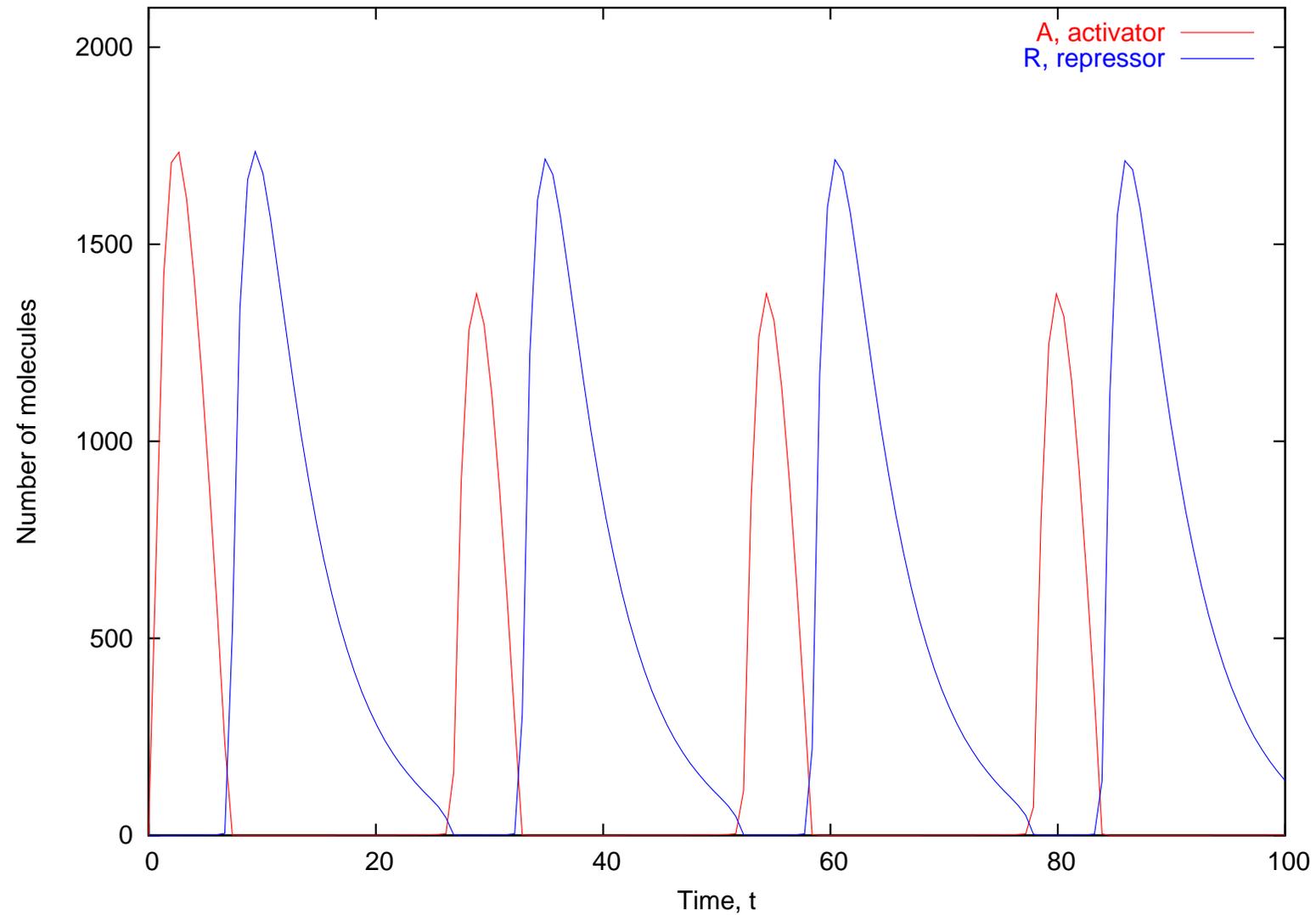
Resource restriction

PEPA model explicitly represents the available resources:

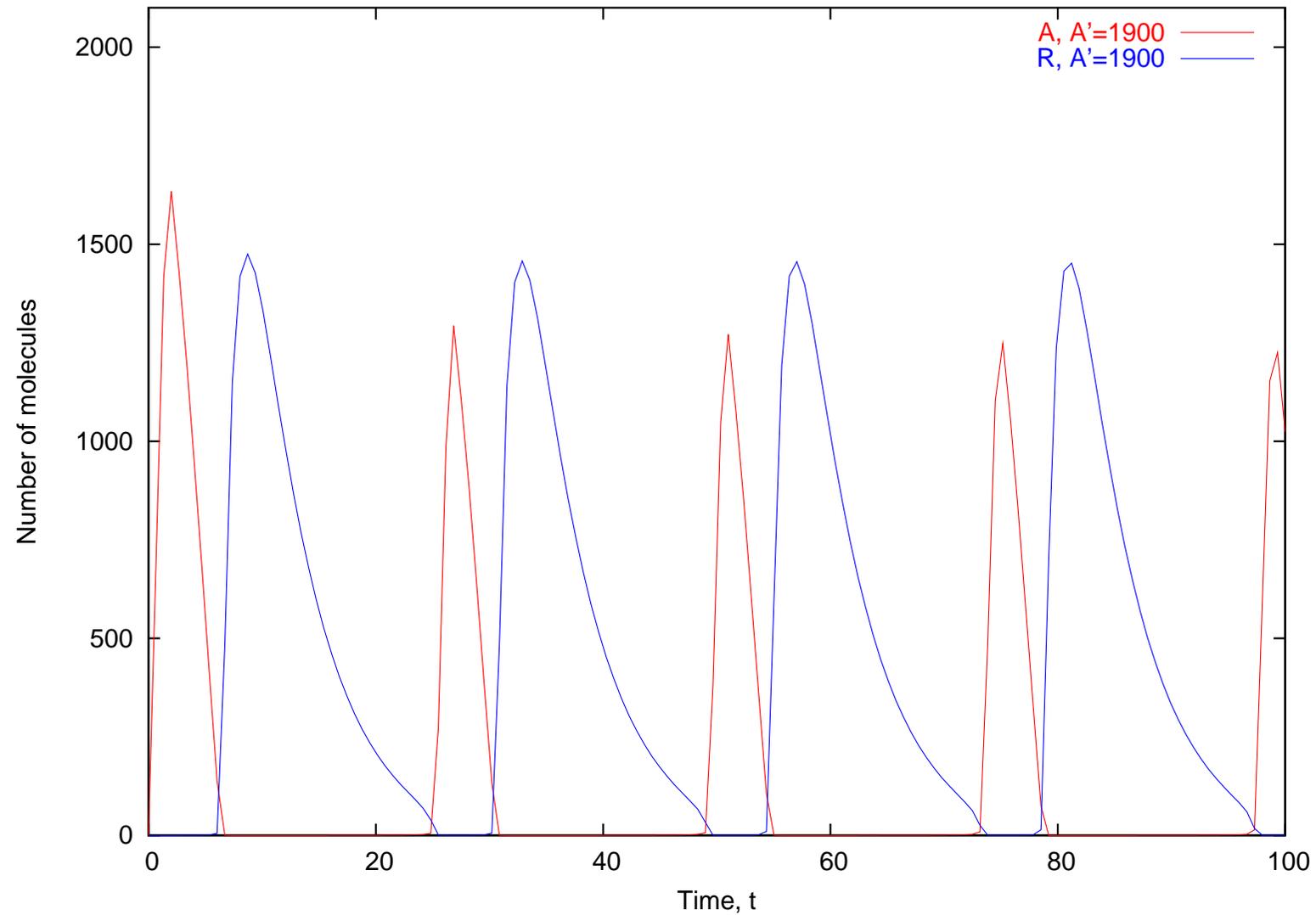
$$((D_A \underset{L}{\bowtie} M'_A[500]) \underset{M}{\bowtie} A'[2500]) \underset{N}{\bowtie} \dots$$

...so what happens if we limit the number of molecules in the system

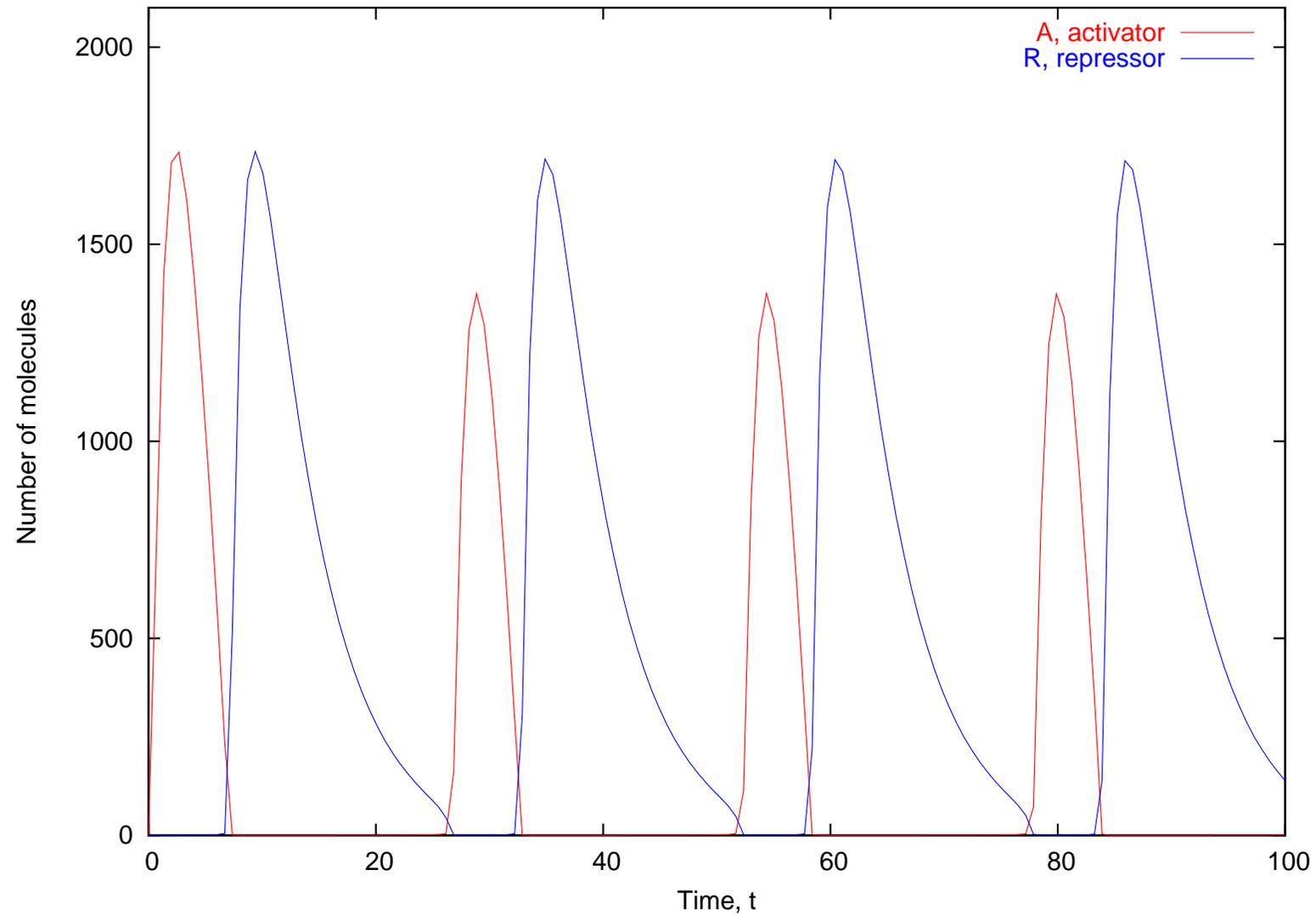
Limiting protein A: PEPA



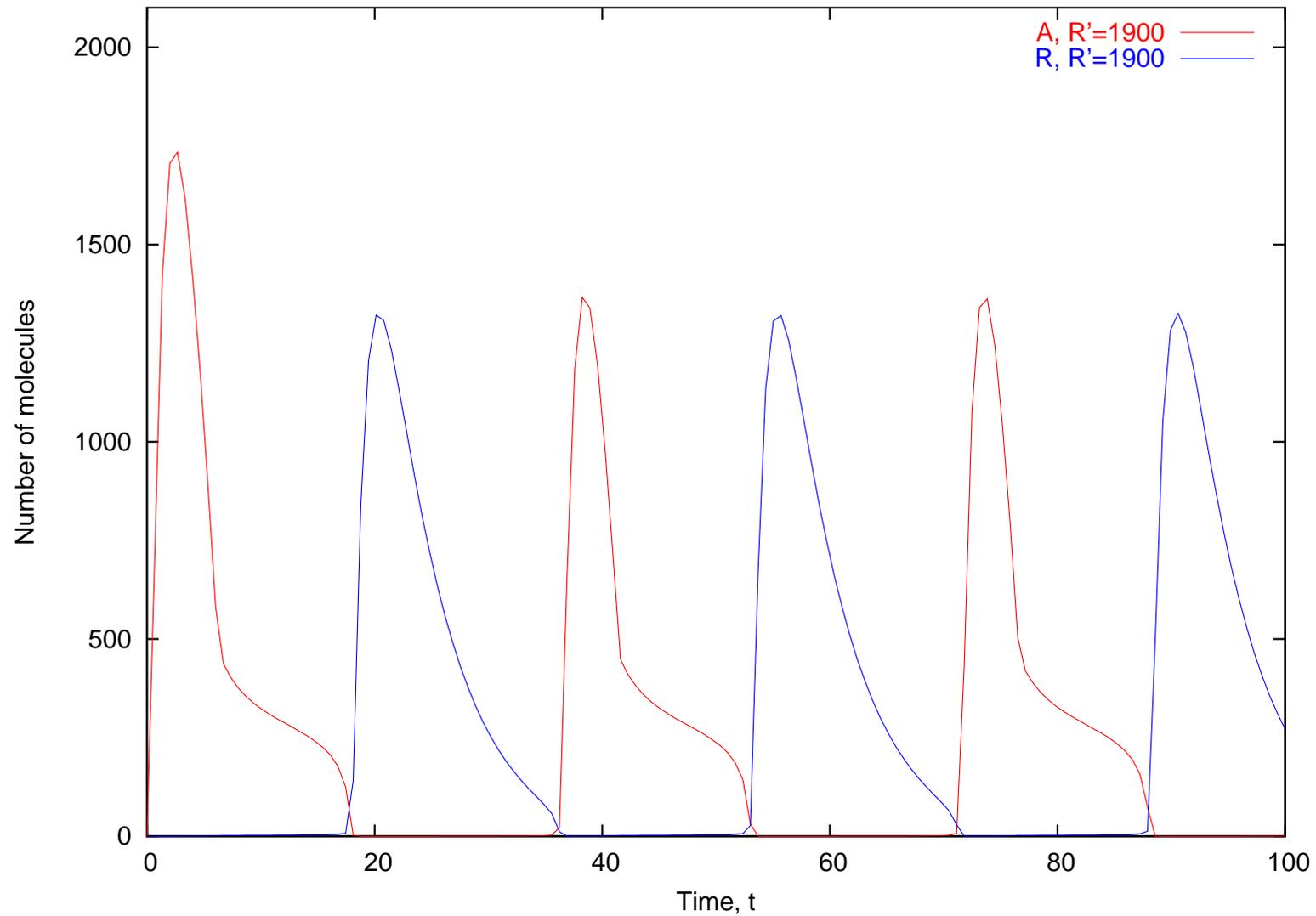
Limiting protein A: PEPA



Limiting protein R: PEPA



Limiting protein R: PEPA



Why am I late?

Why am I late?

Obviously not enough R
repressor!

The Nature of Synchronisation (in Nature)

- The type of synchronisation/reaction between sets of molecules determines:
 - ODE translation
 - stochastic simulation
- Synchronisation/reaction rate is affected by:
 - Location of molecules
 - Shape of molecules
 - How molecules are moving during reaction phase

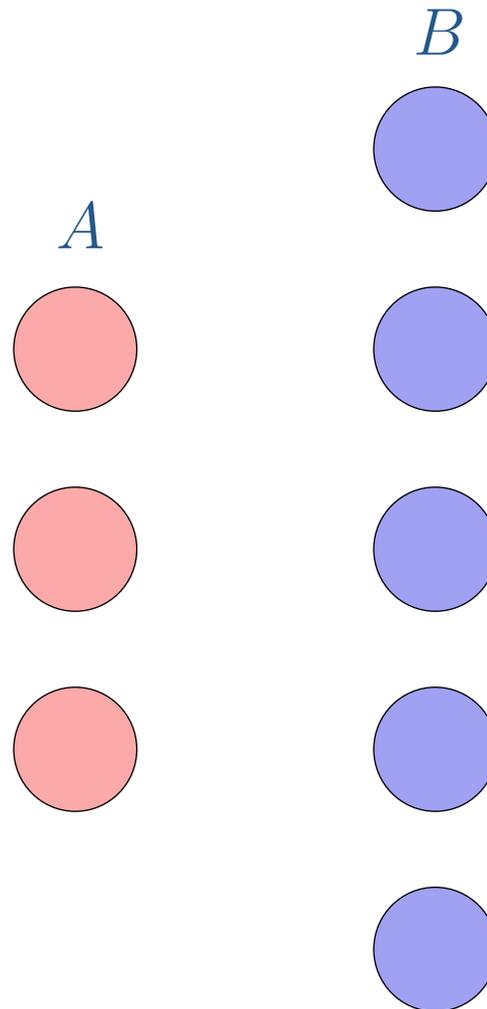
Synchronisation: Mass action

- ➔ Reaction between e.g. well-mixed fluids and gases
- ➔ Molecules diffuse (Brownian motion)
- ➔ Molecules can potentially react with any other co-reagent molecule
- ➔ Example reaction:

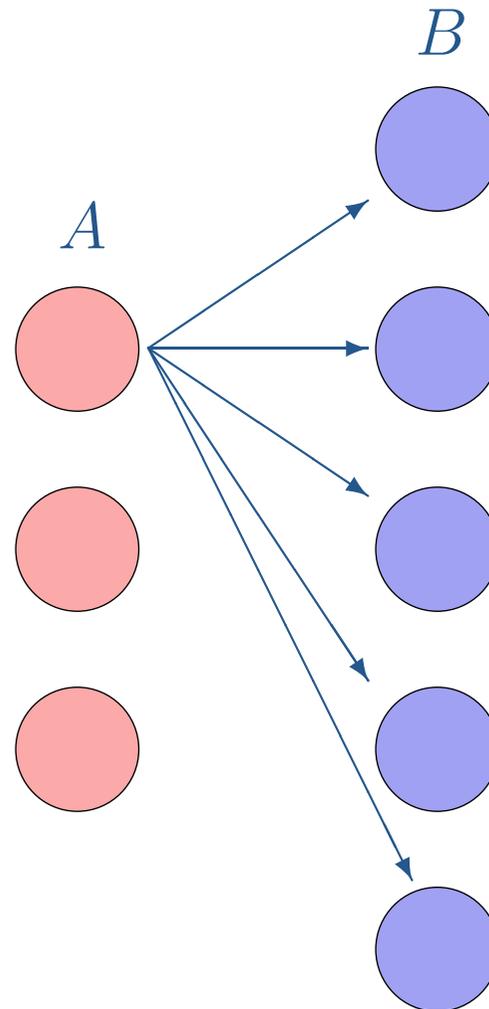


- ➔ Initially m A molecules, n B molecules

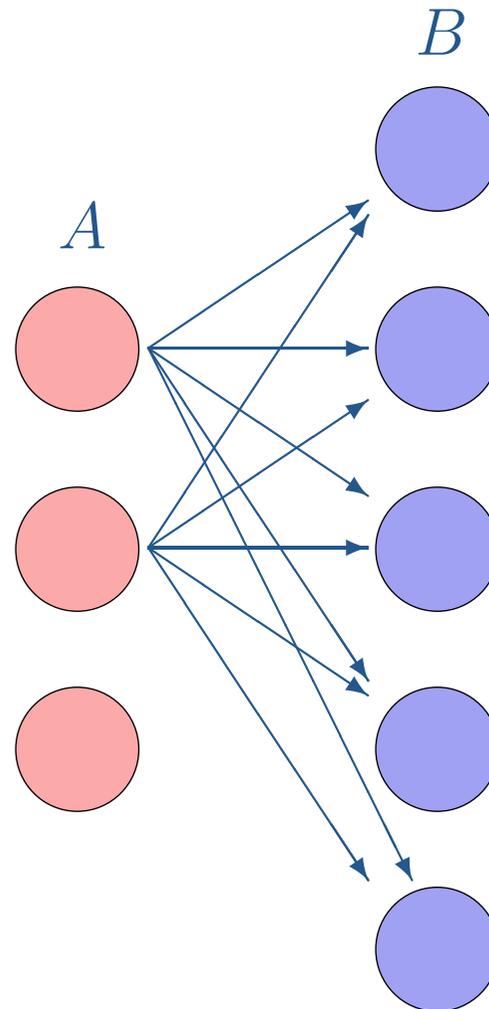
Synchronisation: Mass action



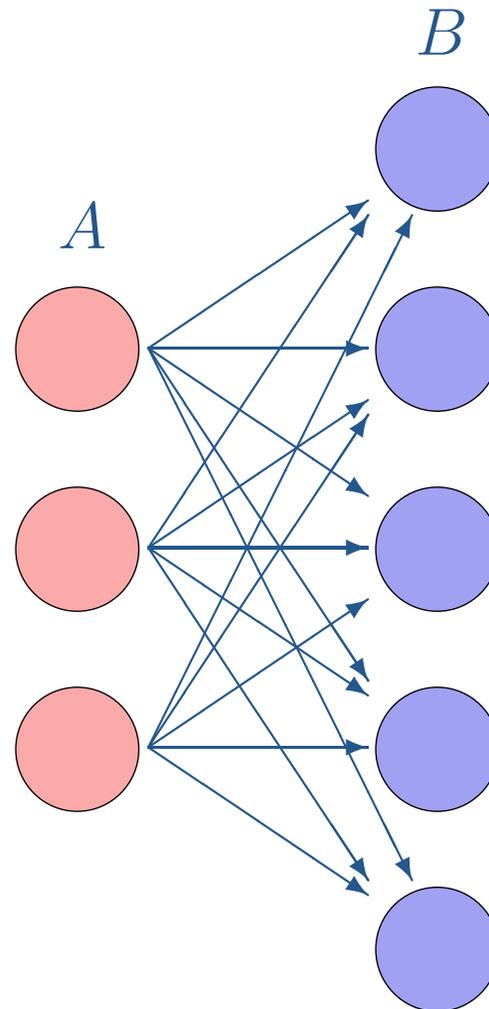
Synchronisation: Mass action



Synchronisation: Mass action

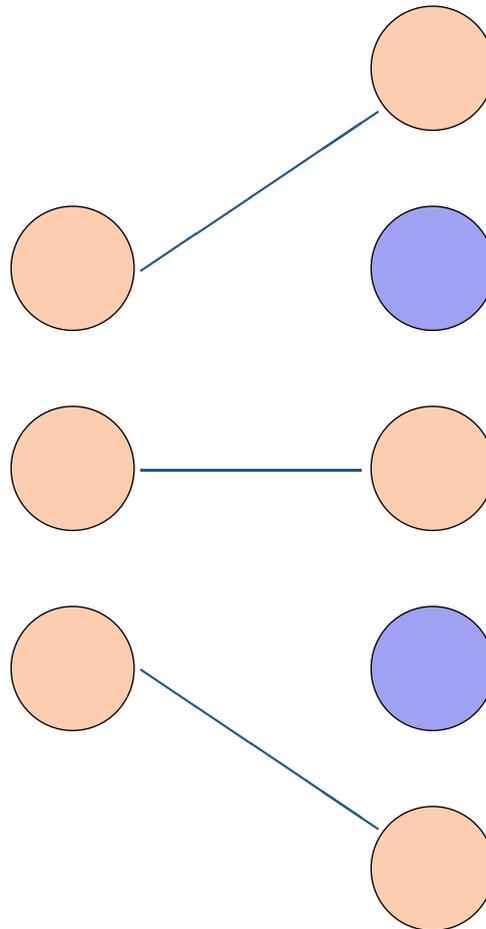


Synchronisation: Mass action



- ➔ Total number of possible interactions: mn

Synchronisation: Mass action



➔ Total number of actual AB products: $\min(m, n)$

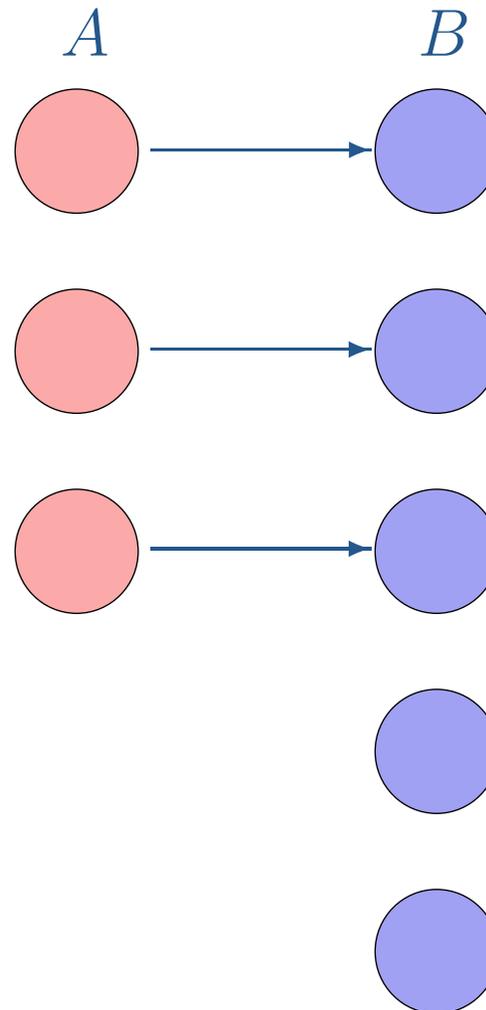
Synchronisation: Local action

- ➔ Reaction between e.g. surface of two solids, two jellies, two very viscous fluids
- ➔ No molecule diffusion
- ➔ Molecules react with closest local neighbour
- ➔ No reaction competition
- ➔ Example reaction:



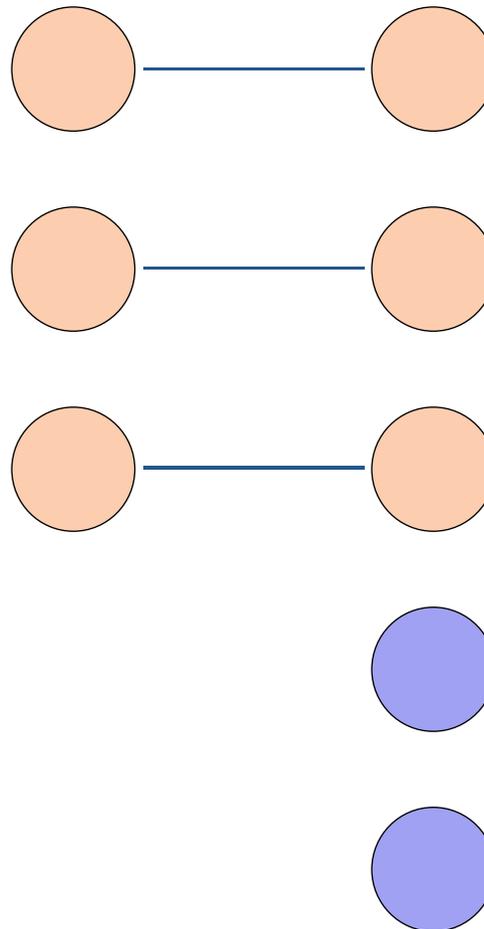
- ➔ Initially m A molecules, n B molecules

Synchronisation: Local action



➔ Total number of possible reactions: $\min(m, n)$

Synchronisation: Local action



➔ Total number of AB products: $\min(m, n)$

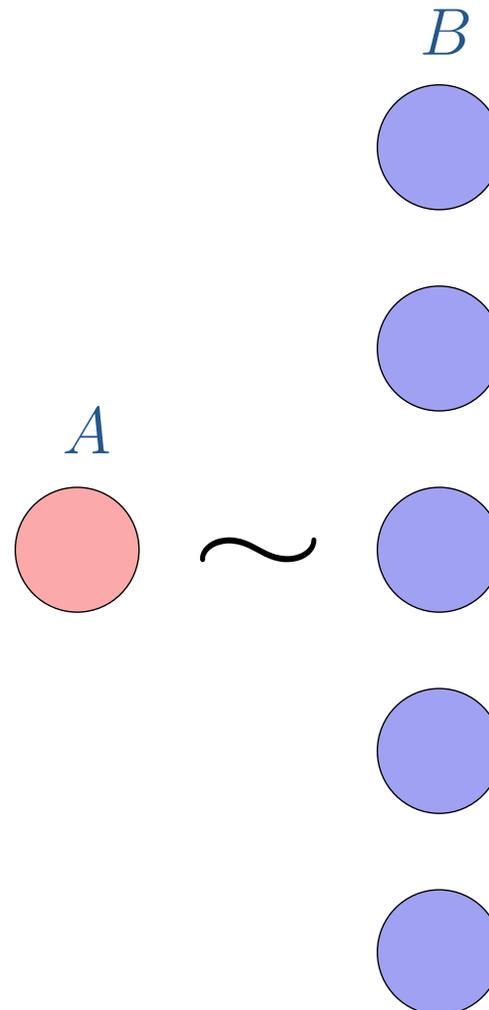
Synchronisation: Passive action

- ➔ Reaction catalysed by one or more passive molecules
- ➔ Heavily spatially dependent on catalyst shape/configuration
- ➔ Example reaction:



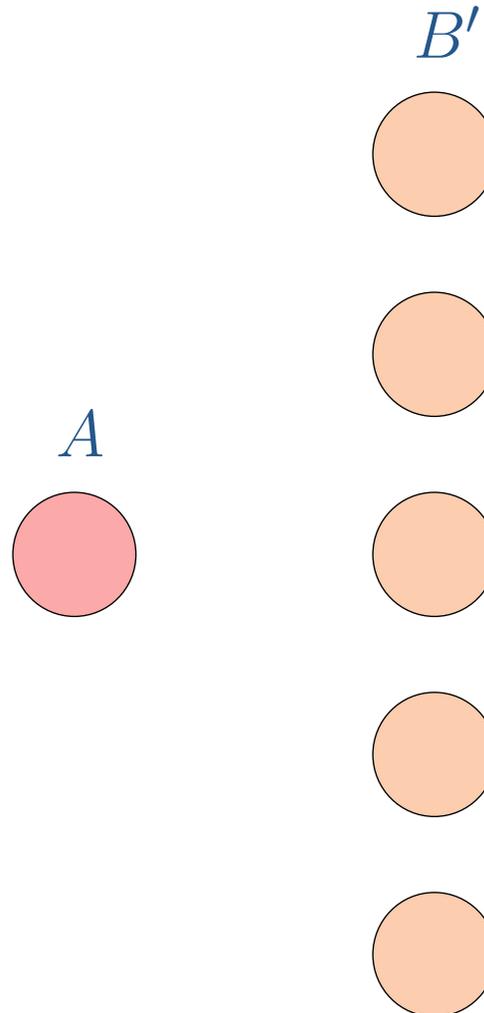
- ➔ Initially 1 A molecule, n B molecules

Synchronisation: Passive action



- ➔ Total number of possible reactions: $I(m > 0) n$

Synchronisation: Catalyst



➔ Total number of B' products: $I(m > 0) n$

Synchronisation and ODEs

- ➔ For a reaction, starting: $A + B \xrightarrow{\lambda}$
 - ➔ Mass action leads to ODEs of form:

$$\frac{d}{dt}[A] = -\lambda[A][B]$$

- ➔ Local action leads to ODEs of form:

$$\frac{d}{dt}[A] = -\lambda \min([A], [B])$$

- ➔ Passive action leads to ODEs of form:

$$\frac{d}{dt}[A] = -\lambda I([A] > 0) [B]$$

Synchronisation and SPA

- Local action maps well onto *active synchronisation* in PEPA

$$Sys \stackrel{\text{def}}{=} A[m] \boxtimes_{\{a\}} B[n]$$

$$A \stackrel{\text{def}}{=} (a, \lambda).A'$$

$$B \stackrel{\text{def}}{=} (a, \lambda).B'$$

Synchronisation and SPA

- ➔ Passive action maps well onto *passive synchronisation* in PEPA

$$Sys \stackrel{\text{def}}{=} A[m] \underset{\{a\}}{\boxtimes} B[n]$$

$$A \stackrel{\text{def}}{=} (a, \lambda).A'$$

$$B \stackrel{\text{def}}{=} (a, \top).B'$$

- ➔ Mass action, until now, has not been used in SPA world (not TIPP!)