

# Spatio-temporal Biological Process Modelling

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# Outline

Process algebras

Bio-PEPA

Protein trafficking

Circadian clock

Other examples

Conclusion



# Process algebras

- ▶ history
  - ▶ developed to model concurrent computing (mid 1980's)
  - ▶ originally no notion of time or space, some extensions
  - ▶ Hillston developed PEPA, stochastic process algebra (1996)
  - ▶ Hillston developed ODE interpretation of PEPA (2005)



# Process algebras

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  - ▶ developed to model concurrent computing (mid 1980's)
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  - ▶ Hillston developed PEPA, stochastic process algebra (1996)
  - ▶ Hillston developed ODE interpretation of PEPA (2005)
- ▶ Bio-PEPA, a biological process algebra
  - ▶ close match between modelling artificial and natural systems
  - ▶ developed by Ciocchetta and Hillston (2009)
  - ▶ extension of PEPA, functional rates and stoichiometry



## Process algebras (cont)

- ▶ what is a process algebra?
  - ▶ compact and elegant formal language
  - ▶ behavior given by semantics defined mathematically
  - ▶ classical process algebras: labelled transition systems
  - ▶ stochastic process algebras: continuous time Markov chains



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  - ▶ classical process algebras: labelled transition systems
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- ▶ why use Bio-PEPA?
  - ▶ formalism to describe species and interactions
  - ▶ unambiguous, precise
  - ▶ different analyses available from a single description
    - deterministic simulation (population view),
    - stochastic simulation (individual view),
    - continuous time Markov chain with levels (abstract view)



## Bio-PEPA (in brief)

- ▶ species: reactions, stoichiometry, locations

$$S@L \stackrel{def}{=} (\alpha_1, \kappa_1) \text{op}_1 S@L + \dots + (\alpha_n, \kappa_n) \text{op}_n S@L$$

where  $\text{op}_i \in \{\downarrow, \uparrow, \oplus, \ominus, \odot\}$



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- ▶ other information required for modelling

$\mathcal{L}$  compartments and locations, dimensionality, sizes

$\mathcal{N}$  species quantities, minimums, maximums, step size

$\mathcal{K}$  parameter definitions

$\mathcal{F}$  functional rates for reactions, definition of  $f_\alpha$



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- ▶ definition of behavioural semantics



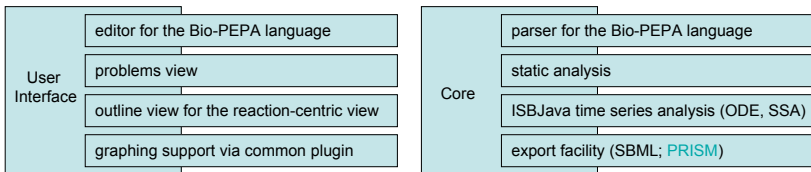
# Bio-PEPA Eclipse Plug-in

- ▶ software tool for Bio-PEPA modelling



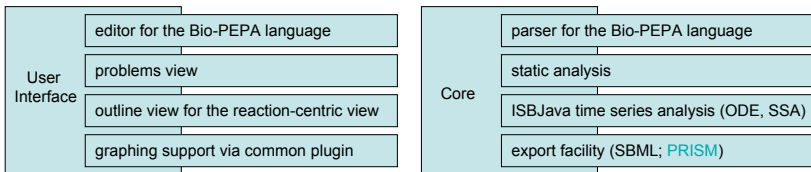
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- ▶ available for download at [www.biopepa.org](http://www.biopepa.org)
- ▶ case studies, publications, manuals

# Bio-PEPA Eclipse Plug-in (cont)

**Species**

- aM
- aX
- C
- IM
- IX

**Reactions**

- actM,  $3C + IM \rightarrow aM$
- actX,  $3aM + IX \rightarrow aX$
- createC,  $\rightarrow C$
- deactM,  $aM \rightarrow IM$
- deactX,  $aX \rightarrow IX$
- degC,  $C \rightarrow$
- degCtrgX,  $C + SaX \rightarrow$

**source actions**

- createC,  $\rightarrow C$

**sink actions**

- degC,  $C \rightarrow$
- degCtrgX,  $C + SaX \rightarrow$

**cell-cycleBIOMD04.biopepa - results**

Graph showing the time evolution of species counts (Y-axis, 0 to 75000) over time (X-axis, 0 to 110). The species are aM (red), aX (blue), and C (green). The graph shows oscillatory behavior, with aM and aX peaking around 70000 and C peaking around 50000.

```

AV = floor(Cell * A);
//AV = 1;

//V1 = VM1 + C / (C + (Kc * AV));
//V3 = VM3 + aM / AV;

// Initial values

C_init = floor(0.01 * AV); // Cyclin
aM_init = floor(0.01 * AV); // CDC-2 Kinase (active)
aX_init = floor(0.01 * AV); // Cyclin Protease (active)
IM_init = floor(0.99 * AV); // CDC-2 Kinase (inactive)
IX_init = floor(0.99 * AV); // Cyclin Protease (inactive)

// Unscaled since not clear how to modify rates
// Functional rates

kineticLawOf createC : cell * vi * AV;
kineticLawOf degC : cell * kd * C;
kineticLawOf degCtrgX : cell * vd * C * aX / (C + (Kd * AV));
kineticLawOf actM : cell * (VM1 * AV) + IM * C
kineticLawOf deactM : cell / ((C + (Kc * AV)) * (IM + (KI * AV)));
kineticLawOf actX : cell * (VM3 * AV) * aM / (aM + (K2 * AV));
kineticLawOf deactX : cell * (V4 * AV) * aX / (aX + (K4 * AV));

// Species
C = createC >> degC << degCtrgX << actM (.);
aM = actM >> deactM << actX (.);
aX = actX >> deactX << degCtrgX (.);
IM = actM << deactM >>;
IX = actX << deactX >>;

// System
C [C_init]
<+> aM [aM_init]
<+> aX [aX_init]
<+> IM [IM_init]
<+> IX [IX_init]
  
```

# Protein trafficking in the cell

- ▶ research from the Frame laboratory at Cancer Research UK



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There is more inactive Src in endosomes closer to the nucleus than those further away. Furthermore, almost all Src at the membrane is active. Hence, there is a gradient of inactive Src to active Src. (Sandilands *et al*, 2004)



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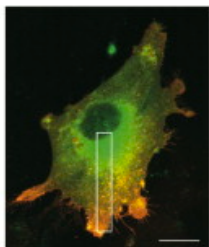
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The persistence of active Src at the membrane is inversely related to the quantity of FGF added. (Sandilands *et al*, 2007)

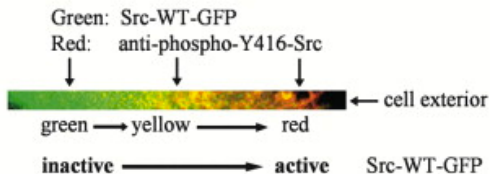


## Src: gradient from inactive to active

A

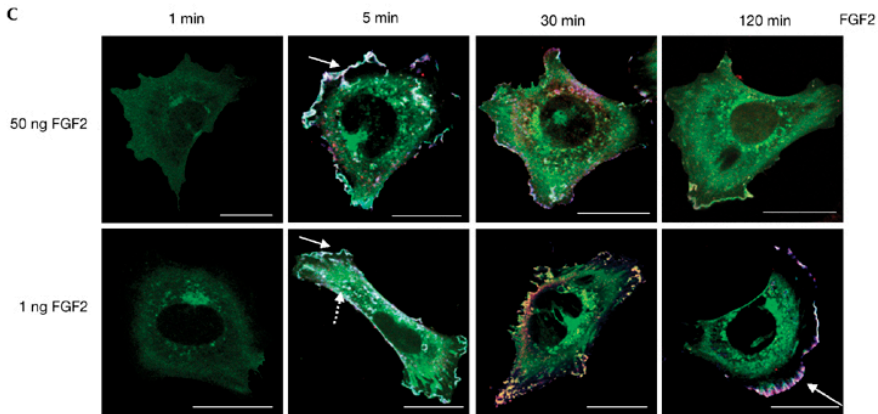


+ LPA  
Swiss 3T3 cells



(Sandilands *et al*, Dev. Cell 7, 2004)

## Src: persistence of response to FGF



(Sandilands *et al*, EMBO Reports 8, 2007)

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- ▶ work in progress: Bio-PEPA, HYPE





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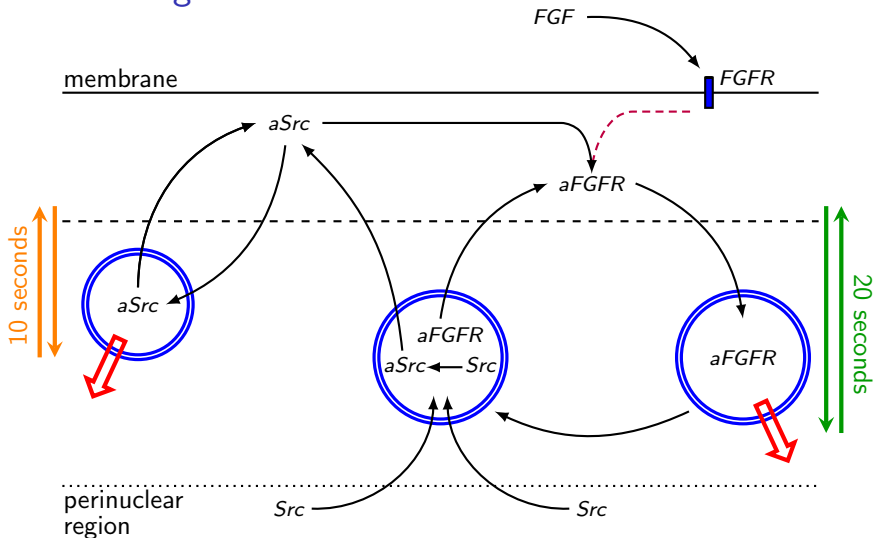


# Modelling

- ▶ work in progress: Bio-PEPA, HYPE
- ▶ identification of recycling loops: number and type
- ▶ assume one long and one short
- ▶ data is very limited
- ▶ qualitative
  - ▶ gradient of inactive versus active, activation within endosomes
  - ▶ endosome movement is directional along microfilaments/microtubules
- ▶ quantitative
  - ▶ estimates of endosome speeds and length of recycling loops
  - ▶ timing from FGF stimulation experiment



# Src trafficking



## Simplified Bio-PEPA model

- ▶ active Src at membrane

```
aSrc@mb = (bind,1) << aSrc@mb + (out_sh,150) << aSrc@mb +  
          (in_sh,75) >> aSrc@mb + (in_long,100) >> aSrc@mb;
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- ▶ endosome in short recycling loop

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Endo_short@cyto = (out_sh,1) >> Endo_short@cyto +
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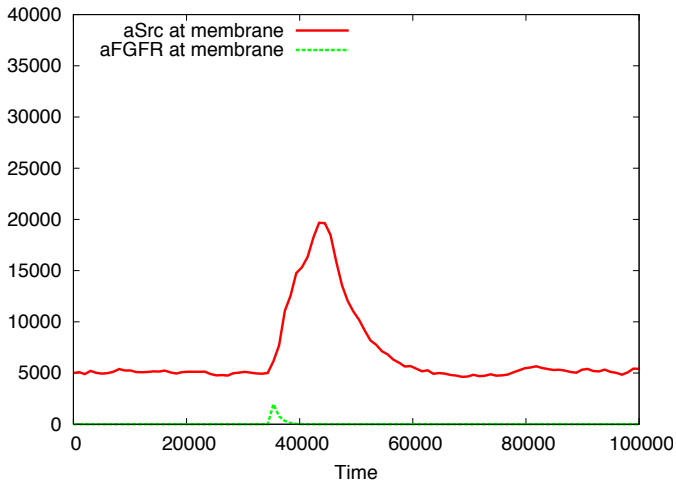
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```

- ▶ reactions

```
out_sh:    150 aSrc    ->    Endo_short
in_sh:    Endo_short  ->    75 aSrc
```



## Two loop trafficking model – results



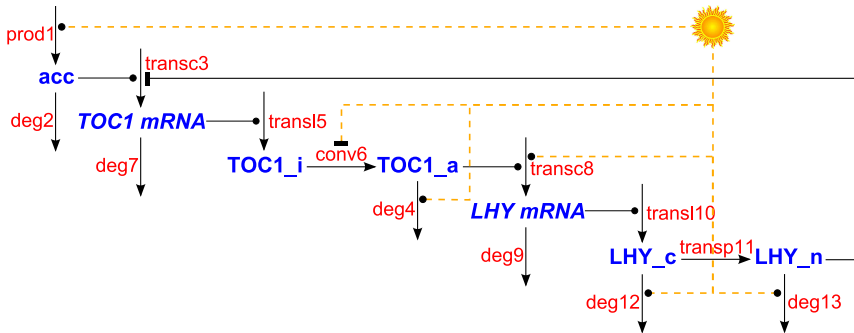
# Circadian clock

- ▶ *Ostreococcus tauri*, tiny green alga



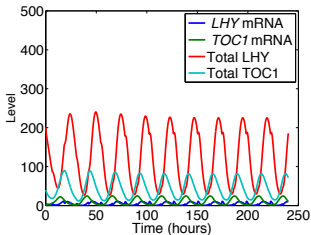
# Circadian clock

- ▶ *Ostreococcus tauri*, tiny green alga
- ▶ two genes involved in circadian rhythm

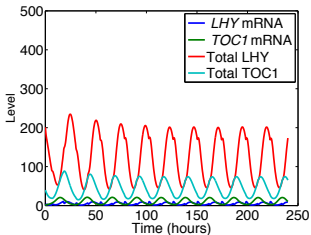


(Akman *et al*, FBTC 10, EPTCS 19, 2010)

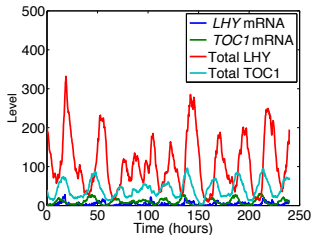
# Circadian clock in Bio-PEPA: alternating light dark



(d) LD 12:12 – ODE



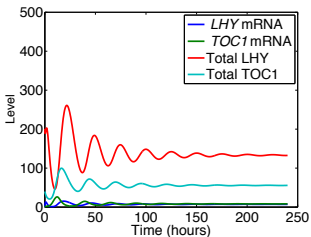
(e) LD 12:12 – average 10000 SSA runs



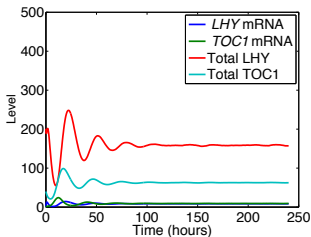
(f) LD 12:12 – single SSA run

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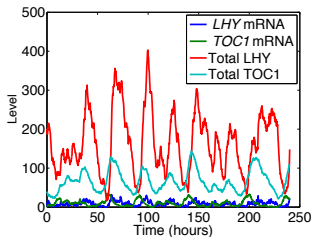
# Circadian clock in Bio-PEPA: light only



(d) LL – ODE



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## Other Bio-PEPA case studies

- ▶ Goldbeter's model of oscillation of cyclin in the cell cycle
- ▶ Edelstein's model for the acetylcholine receptor
- ▶ gp130/JAK/STAT pathway
- ▶ circadian clock in Neurospora
- ▶ various models from BioModels Database



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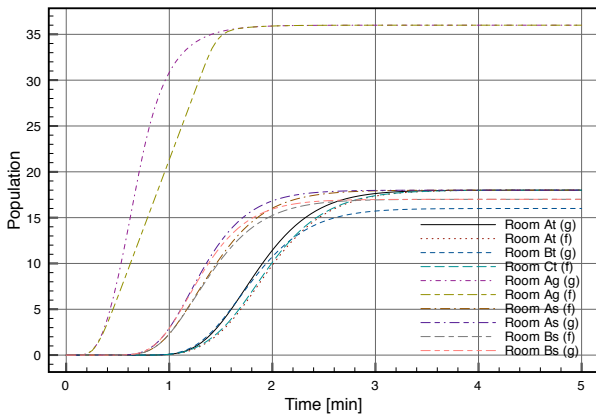


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- ▶ see [www.biopepa.org](http://www.biopepa.org) for more details



# Emergency egress modelling in Bio-PEPA



(Massink *et al*, SEFM 2010)



# Conclusion

- ▶ Bio-PEPA
  - ▶ biological process algebra
  - ▶ formal and unambiguous description of a system
  - ▶ behaviour derived mathematically
  - ▶ various analyses can be applied to a model
  - ▶ abstraction is a key principle



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  - ▶ formal and unambiguous description of a system
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  - ▶ various analyses can be applied to a model
  - ▶ abstraction is a key principle
- ▶ how can Bio-PEPA contribute towards atlases?



# Thank you



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- ▶ initial parameters for species representing basal behaviour
  - ▶ no decision species, no added FGF, no active FGFR
  - ▶ long recycling loop inactive so no species from it
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- ▶ input and output stoichiometry for each loop
  - ▶ short loop: input and output the same
  - ▶ long loop: output much larger than input
- ▶ creation rate of active Src during basal behaviour
- ▶ binding rate for active Src and active FGFR
- ▶ time to pick up inactive Src in perinuclear region
- ▶ assume time taken in each loop fixed using calculations



## Parameters (continued)

- ▶ at least 13 unknown parameters – not so simple



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- ▶ enable short recycling loop only
- ▶ find parameters to balance short loop
  - ▶ 50% of active Src at membrane
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- ▶ 6 parameters not yet specified



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- ▶ 6 parameters not yet specified
- ▶ enable the long recycling loop
- ▶ guess some parameters
- ▶ enable the doser and see what happens



## Bio-PEPA syntax

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- ▶ sequential component, species

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- ▶ need a more constrained form



## Well-defined Bio-PEPA systems

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- ▶ well-defined Bio-PEPA model

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## Well-defined Bio-PEPA systems

- ▶ well-defined Bio-PEPA species

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- ▶ well-defined Bio-PEPA model component with levels
  - ▶ minimum and maximum concentrations/number of molecules
  - ▶ fix step size, convert to minimum and maximum levels
  - ▶ species  $S$ : 0 to  $N_S$  levels



## Example: reaction with enzyme



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- $$\blacktriangleright S(l_S) \bowtie_* E(l_E) \bowtie_* SE(l_{SE}) \bowtie_* P(l_P) \text{ where}$$

$$S \stackrel{\text{def}}{=} (\alpha, 1) \downarrow S + (\beta, 1) \uparrow S$$

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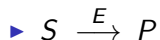


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## Example: reaction with enzyme



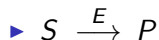
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## Example: reaction with enzyme

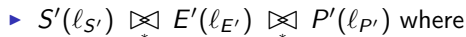
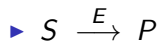


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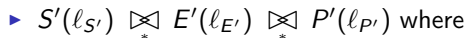
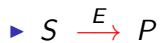


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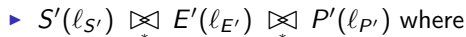
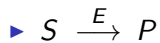


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$$((\alpha, \kappa) \uparrow S)(\ell) \xrightarrow{(\alpha, [S: \uparrow(\ell, \kappa)])}_c S(\ell + \kappa) \quad 0 \leq \ell \leq N_S - \kappa$$

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- ▶ Cooperation for  $\alpha \in L$

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- ▶ Bio-PEPA system:  $\mathcal{P} = \langle \mathcal{T}, P \rangle$

