Process Algebras for Quantitative Analysis

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Outline

Introduction

Compositionality: Interaction and Independence

Applications and Acceptance

Conclusions

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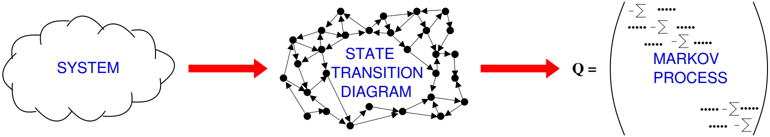
- We have sought to investigate and exploit the interplay between the process algebra and the continuous time Markov chain (CTMC).

Performance Modelling using CTMC



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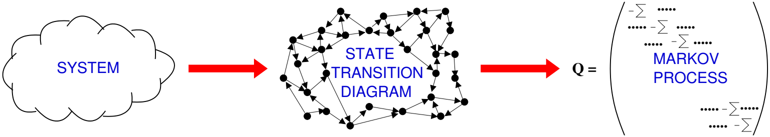

A stochastic process $X(t)$ is a Markov process iff for all $t_0 < t_1 < \dots < t_n < t_{n+1}$, the joint probability distribution of $(X(t_0), X(t_1), \dots, X(t_n), X(t_{n+1}))$ is such that

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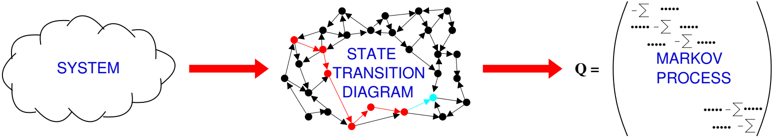

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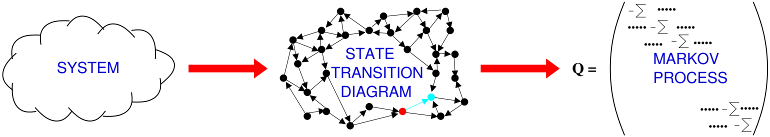

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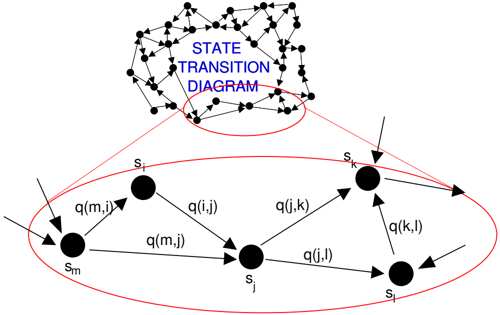

A negative exponentially distributed duration is associated with each transition.

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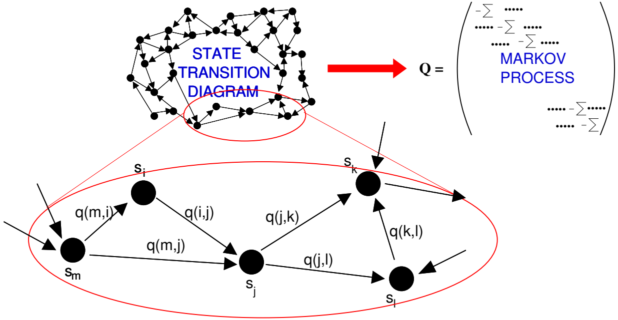

these parameters form the entries of the infinitesimal generator matrix Q

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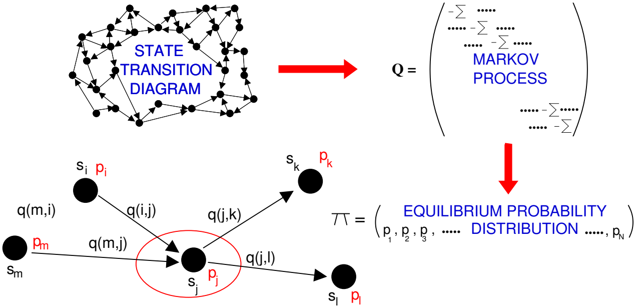

In steady state the probability flux out of a state is balanced by the flux in.

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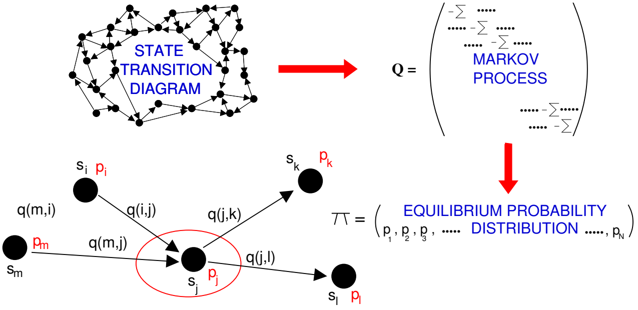

"Global balance equations" captured by $\pi Q = 0$ solved by linear algebra

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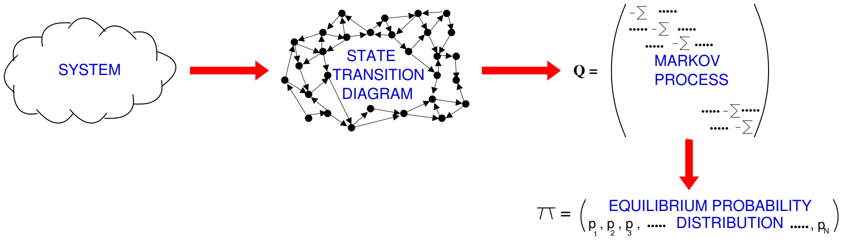

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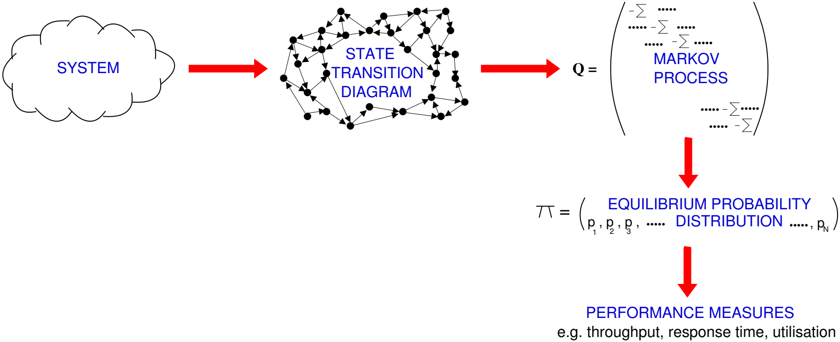

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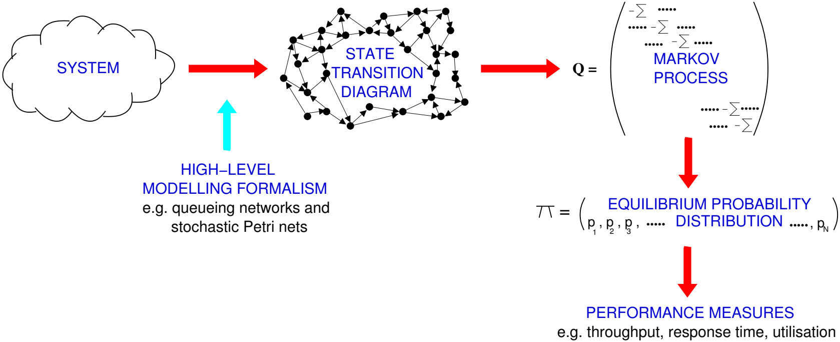

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action type or name

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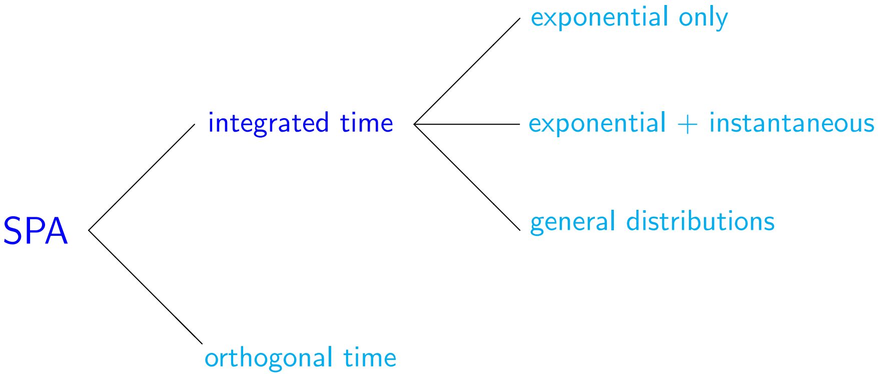

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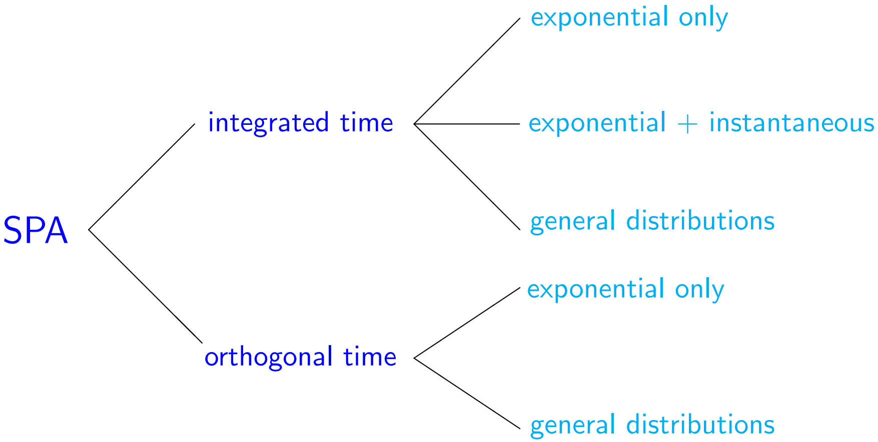

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      PEPA, Stochastic π-calculus
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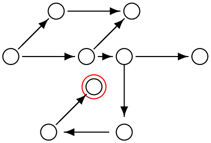

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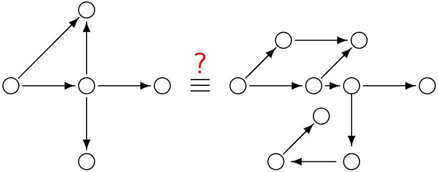

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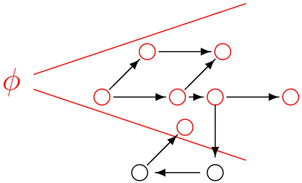

Integrated analysis

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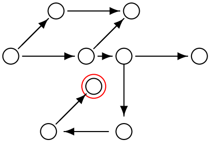
Reachability analysis

How long will it take for the system to arrive in a particular state?



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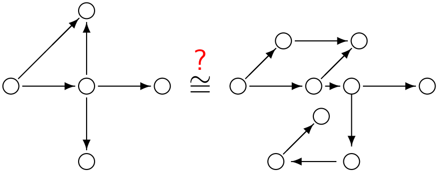
Specification matching

With what probability does system behaviour match its specification?



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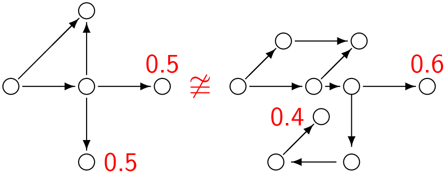
Does the "*frequency profile*" of the system match that of the specification?



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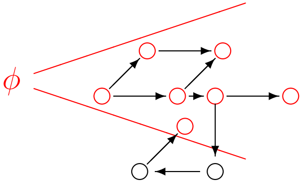
Model checking

Does a given property ϕ hold within the system with a given probability?



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For a given starting state
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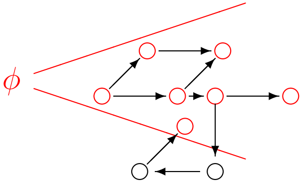

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- From the process algebra side the Markov chain had a profound influence on the design of the language and in particular on the interactions between components.
- From the Markov chain perspective the process algebra structure has been exploited to find aspects of independence even between interacting components.

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The memoryless property of the negative exponential distribution means that residual times do not need to be recorded.

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We retain the expansion law of classical process algebra:

$$
\begin{aligned}
&(\alpha, r).Stop \parallel (\beta, s).Stop = \\
&\qquad (\alpha, r).(\beta, s).(Stop \parallel Stop) + (\beta, s).(\alpha, r).(Stop \parallel Stop)
\end{aligned}
$$

only if the negative exponential distribution is assumed.

Timed synchronisation

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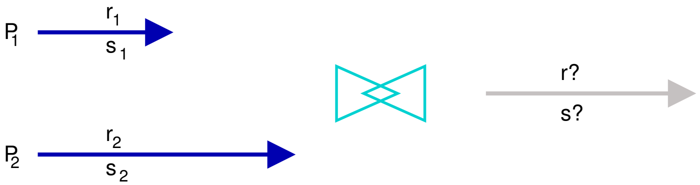

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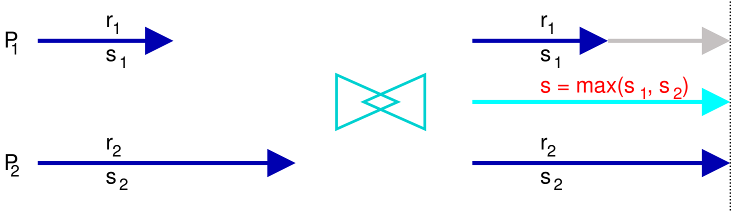

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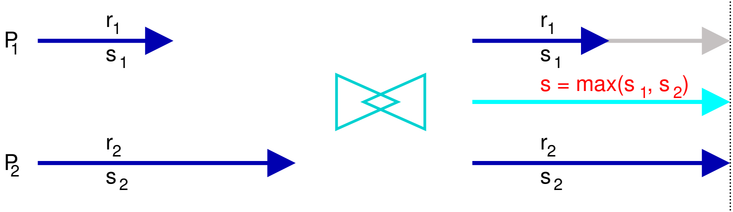

s is no longer exponentially distributed

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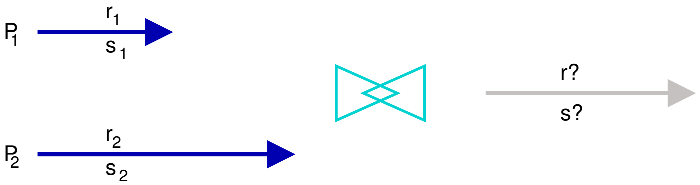

algebraic considerations limit choices

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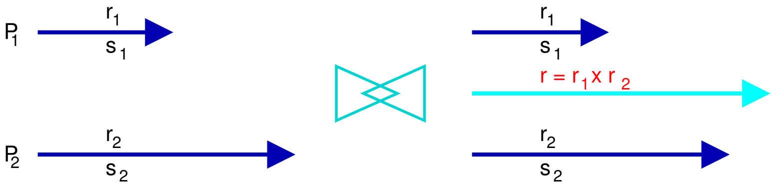

TIPP: new rate is product of individual rates

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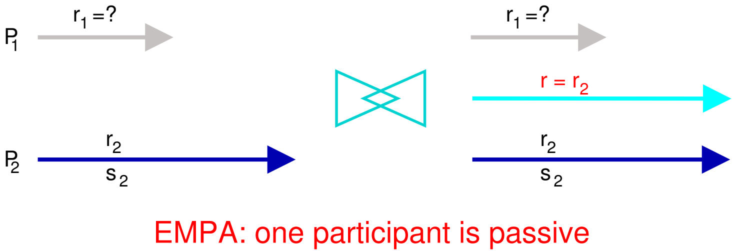

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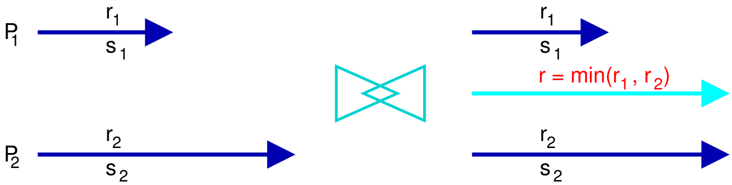

bounded capacity: new rate is the minimum of the rates

Cooperation in PEPA

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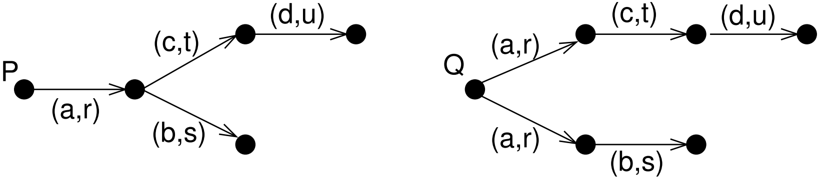
- Synchronisation, or cooperation cannot make a component exceed its bounded capacity.
- Thus the apparent rate of a cooperation is the minimum of the apparent rates of the co-operands.

Equivalence Relations

In process algebra equivalence relations are defined based on the notion of observability:



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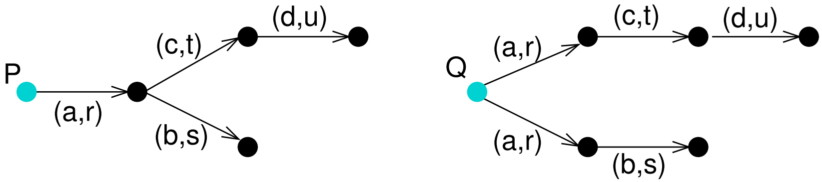

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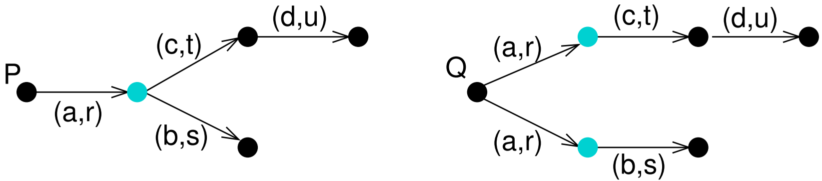

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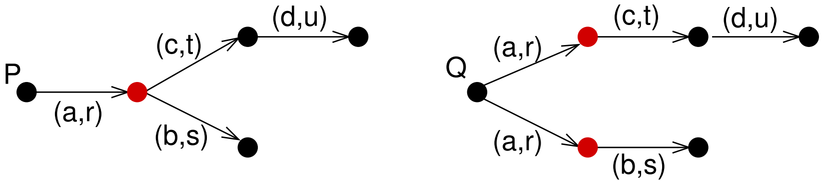

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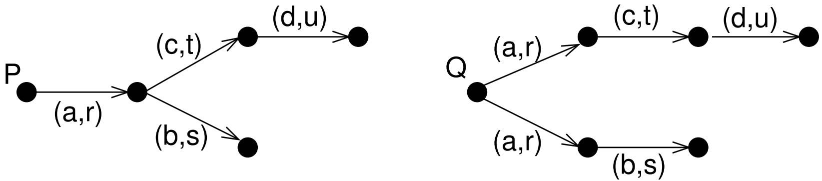

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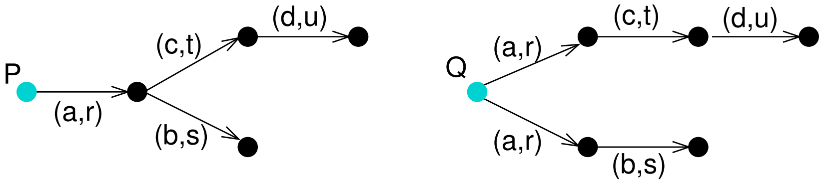

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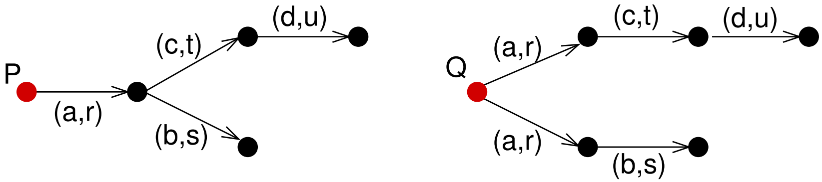

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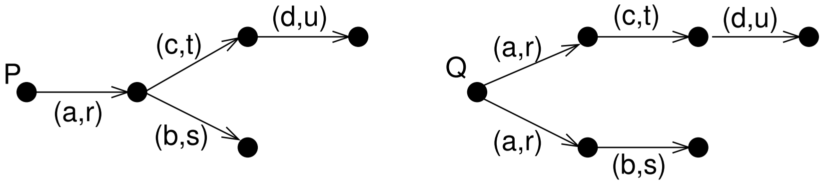

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The resulting equivalence relation is a bisimulation in the style of Larsen and Skou, and coincides with the Markov process notion of lumpability.

Aggregation and lumpability

Model aggregation: use a state-state equivalence to establish a partition of the state space of a model, and replace each set of states by one macro-state, i.e. take a different stochastic representation of the same model.

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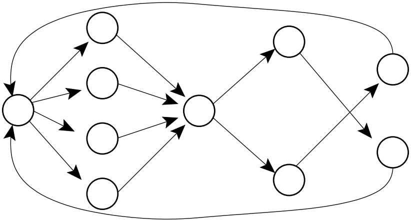

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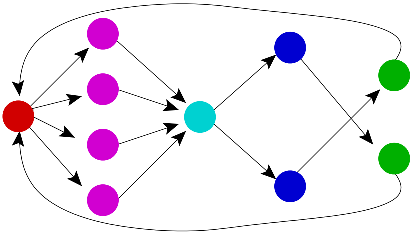

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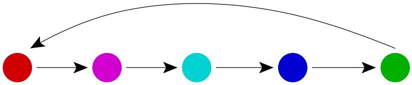

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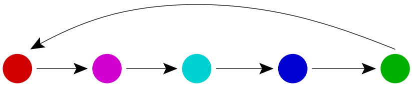
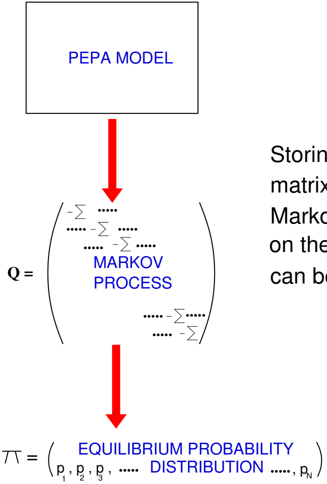


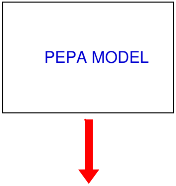
A lumpable partition is the only partition of a Markov process which preserves the Markov property.

Characterising efficient solution

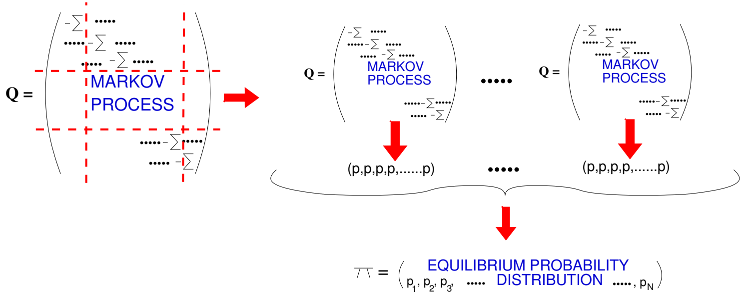


Storing and manipulating the matrix which represents the Markov process places limitations on the size of model which can be analysed.

Characterising efficient solution



Certain structures in the matrix are known to be amenable to efficient, decomposed solution.



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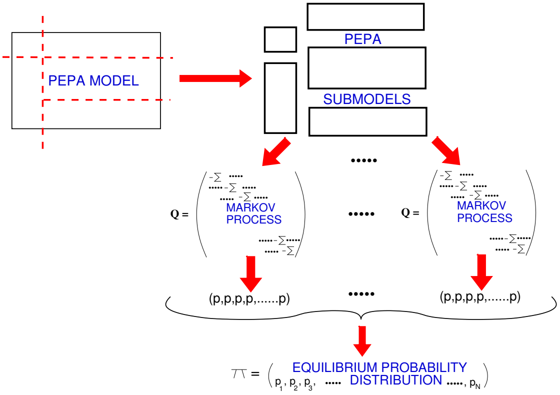
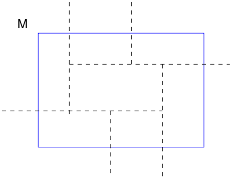
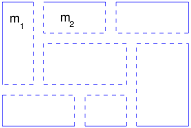


Finding the corresponding structures in the process algebra means that these techniques can be applied automatically, before the monolithic matrix is formed.

Decomposed solution: product form models



$M = (m_1, m_2, \ldots, m_n)$



p(M)

$p(M) = G \times p(m_1) \times p(m_2) \times \ldots \times p(m_n)$

Partition the model M into n statistically independent submodels $m_1, m_2, \ldots, m_n$

In isolation, find the steady state distribution p for each of the submodels m_i

Form the steady state distribution of M as the product of the solutions for each submodel m_i and a normalising constant

When do PEPA components behave as if they were statistically independent...?

Product Form PEPA Models

$$P \equiv S_1 \parallel S_2$$

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Add restricted direct interaction between components with a particular structure

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S_1, S_2 and L all restricted

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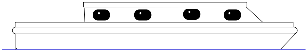
Applications and Acceptance

- Developing models of real applications has always been an integral part of the PEPA project.
- This allows us to demonstrate to ourselves and others that the theory we have developed is useful.
- It serves to promote the acceptance of both stochastic process algebra itself and performance modelling more generally.
- It is also a valuable source of inspiration for new theory and future directions.

PEPA Case Studies (1)

- Multiprocessor access-contention protocols (Gilmore, Hillston and Ribaudo, Edinburgh and Turin)
- Protocols for fault-tolerant systems (Clark, Gilmore, Hillston and Ribaudo, Edinburgh and Turin)
- Multimedia traffic characteristics (Bowman et al, Kent)
- Database systems (The STEADY group, Heriot-Watt University)
- Software Architectures (Pooley, Bradley and Thomas, Heriot-Watt and Durham)
- Switch behaviour in active networks (Hillston, Kloul and Mokhtari, Edinburgh and Versailles)

PEPA Case Studies (2)



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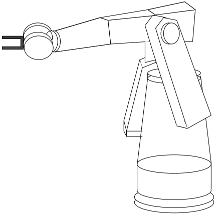

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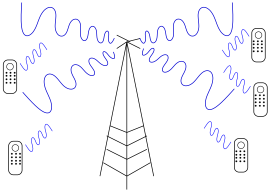

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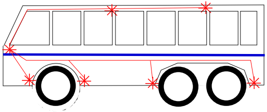
- Automotive diagnostic expert systems (Console, Picardi and Ribaudo, Turin)



Tool Support

PEPA
Workbench
(Edinburgh University)

Imperial PEPA
Compiler/Dnamaca
and Hydra
(Imperial College)

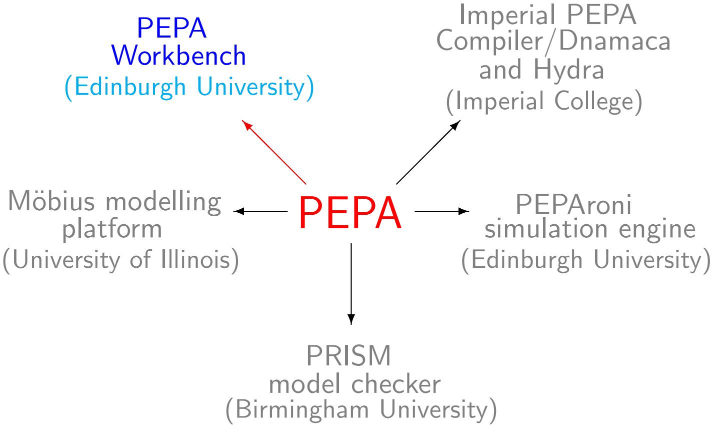
Möbius modelling
platform
(University of Illinois)

PEPA

PEPAroni
simulation engine
(Edinburgh University)

PRISM
model checker
(Birmingham University)

Tool Support



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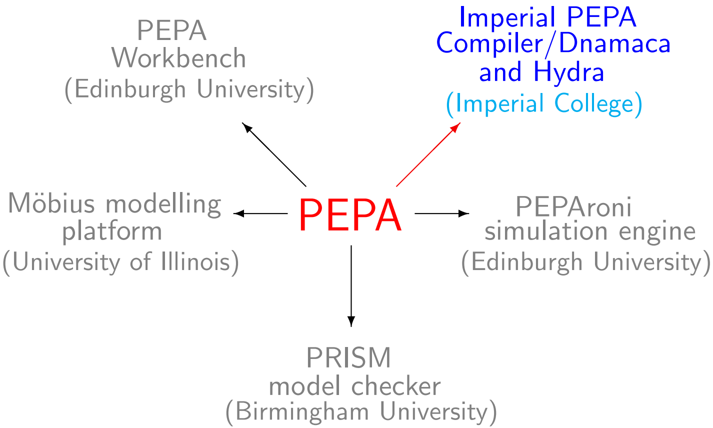

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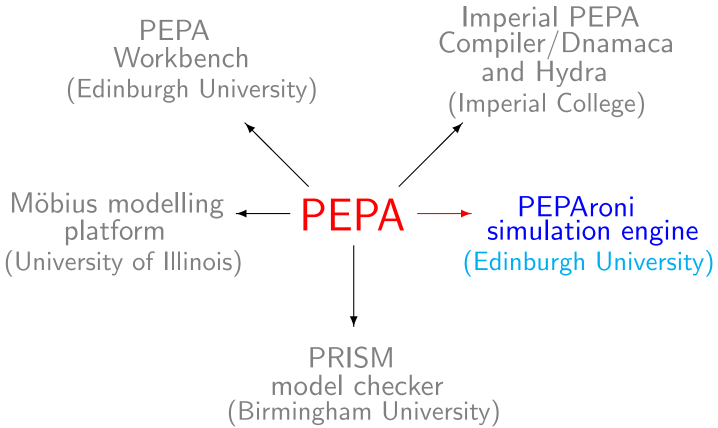

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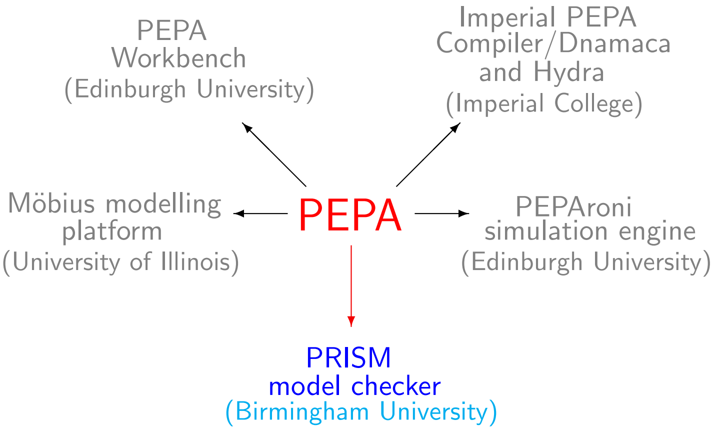

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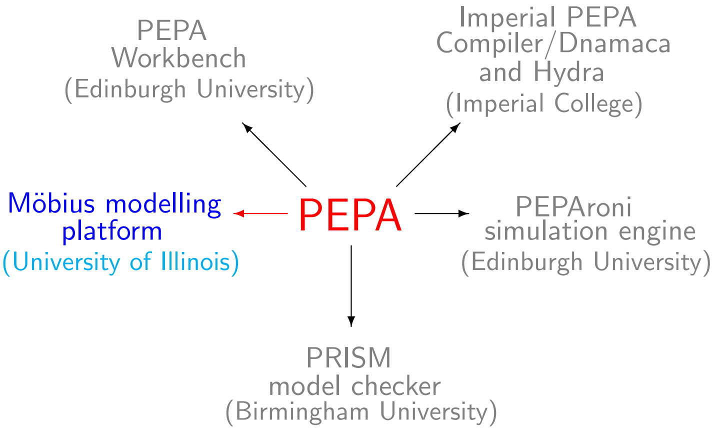

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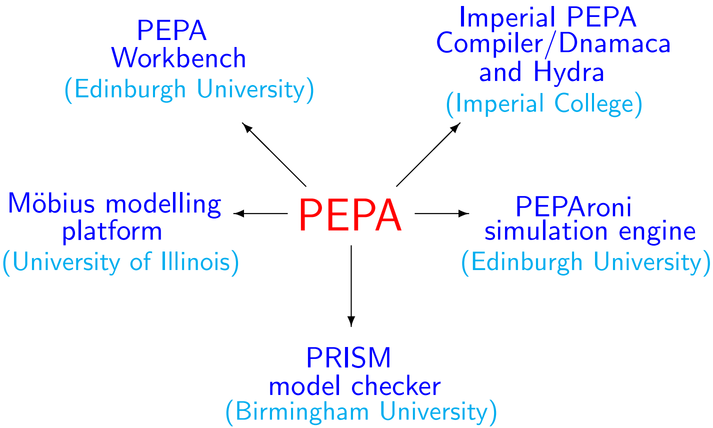

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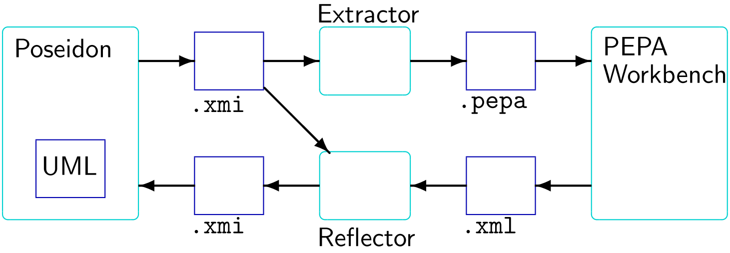
- ...UML...
- Thus recent work has explored this route.

PEPA via UML

In the European-funded DEGAS research project we have been investigating ways to make performance modelling using PEPA more accessible to software designers.



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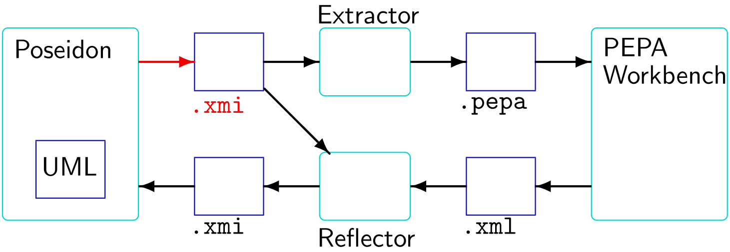

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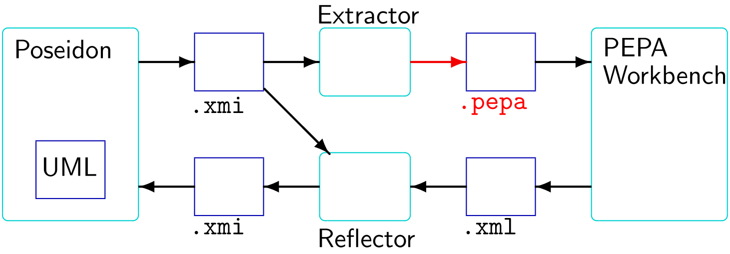

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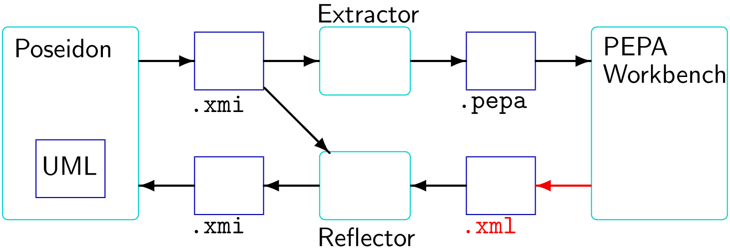

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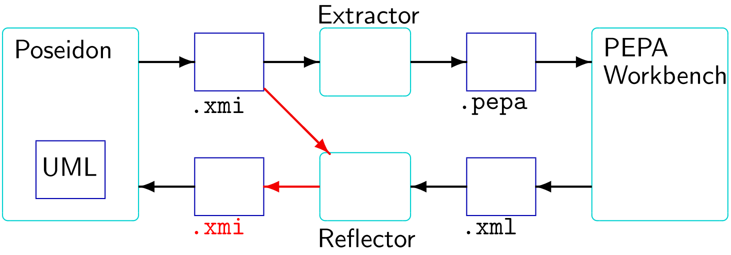

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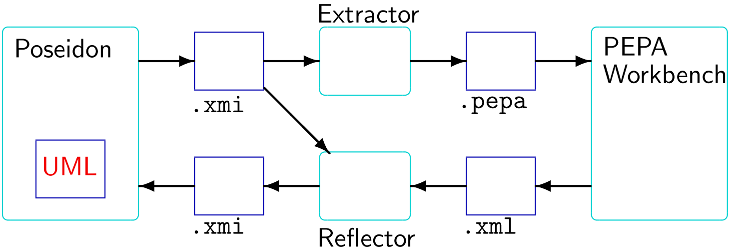

It is essential that results are reported in terms which make sense to the software designer, i.e. in terms of the original UML model.

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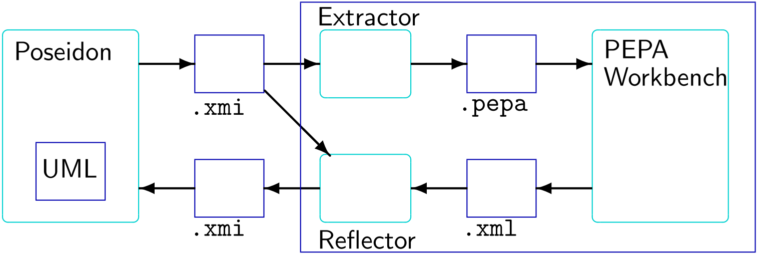

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Compositionality: In addition to the clear benefits for model construction, it has been established that compositionality can be exploited during Markovian analysis. There is more to do here e.g. with respect to model checking.

Initial Objectives

Qualitative analysis: Only fully realised with the definition of appropriate complementary logics, this objective has been perhaps the most successful.

Compositionality: In addition to the clear benefits for model construction, it has been established that compositionality can be exploited during Markovian analysis. There is more to do here e.g. with respect to model checking.

Wide acceptance: Initial hopes were perhaps naïve, but SPA is now playing a part in encouraging the wider adoption of performance analysis in software analysis.

Future Work

Many possibilities, for example:

- The state space explosion problem still remains a major challenge.
- Extending the range of applicability of the modelling language for new application areas.
- Improving the analysis capabilities of the modelling tools.

New mathematical structures

For a generation, performance modellers have seen their choices as being:

- Closed form analytical models;

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- Numerical solution of continuous time Markov chains (CTMC)

The major limitations of the CTMC approach are the state space explosion problem and the reliance on exponential distributions.

New mathematical structures: differential equations

In a PEPA model the state at any current time is the local derivative or state of each component of the model. When we have large numbers of repeated components it can make sense to represent each component type as a continuous variable, and the state of the model as a whole as the set of such variables. The evolution of each such variable can then be described by an ODE.

New mathematical structures: differential equations

The PEPA definitions of the component specify the activities which can increase or decrease the number of components exhibited in the current state. The cooperations show when the number of instances of another component will have an influence on the evolution of this component.

New mathematical structures: differential equations

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Only appropriate for some models, but results are promising in those cases.

New application domains: biochemical signalling pathways

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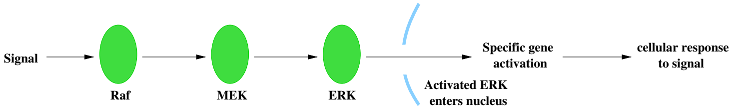
- Systems biology aims to develop a better understanding of the processes involved.
- Stochastic process algebras have found a new role in developing models for systems biology, allowing biologists to test hypotheses and prioritise experiments.

Extracellular signalling

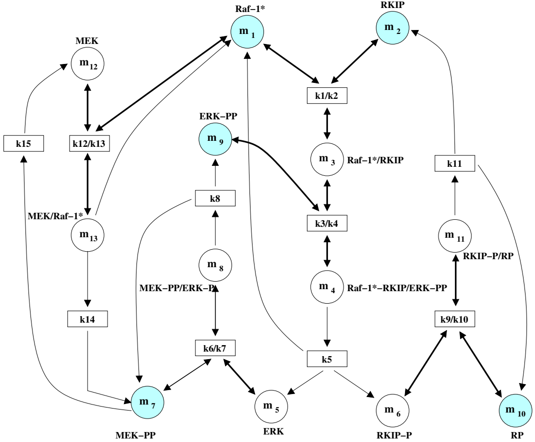
Extracellular signalling — communication between cells.

- signalling molecules released by one cell migrate to another;
- these molecules enter the cell and instigate a pathway, or series of reactions, which carries the information from the membrane to the nucleus;
- the Ras/Raf-1/MEK/ERK pathway conveys differentiation signals to the nucleus of a cell.



Special relevance to cancer research because when pathways operate abnormally cells divide uncontrollably.

The Ras/Raf-1/MEK/ERK pathway



We have constructed two, complementary, PEPA models of the pathway.

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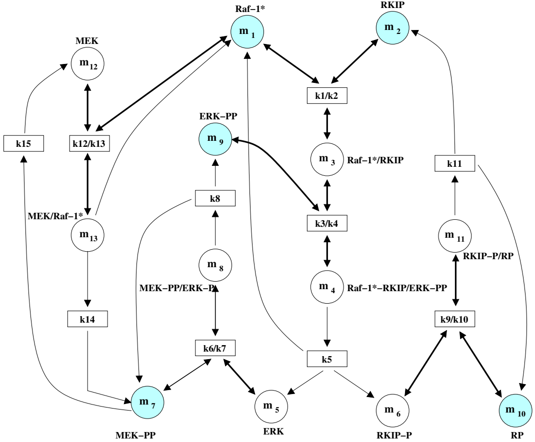

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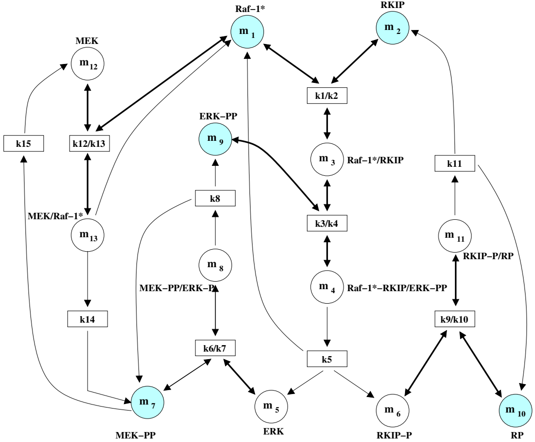

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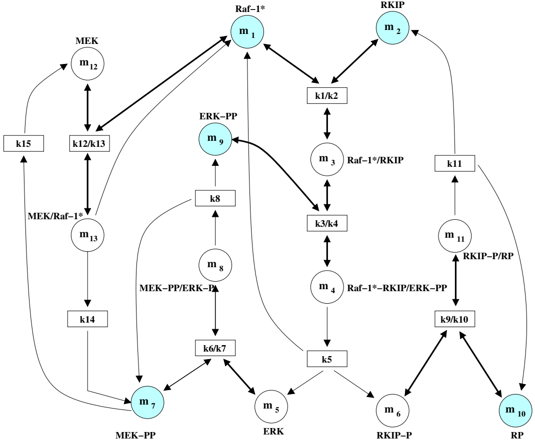

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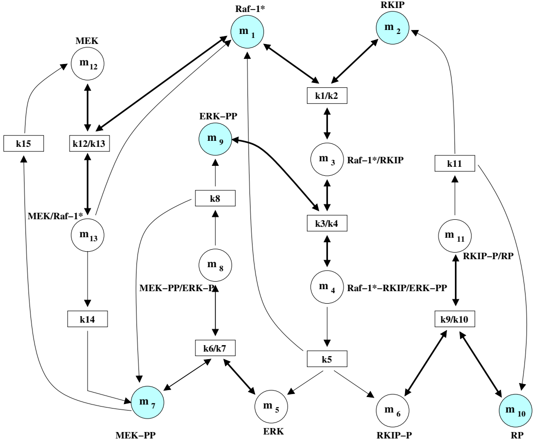

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and shown them to be equivalent.

Acknowledgements

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