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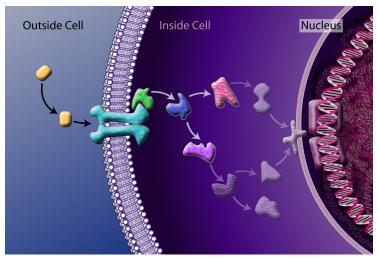
Setting parameters for biological models with ANIMO

Stefano Schivo, Jetse Scholma, Marcel Karperien, Janine N. Post, Jaco van de Pol, Rom Langerak University of Twente, Enschede, The Netherlands SynCoP 2014



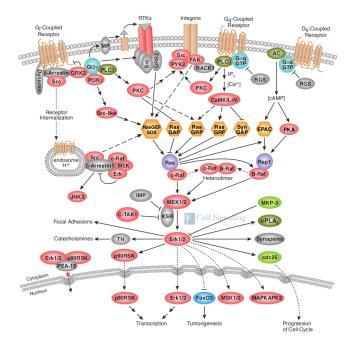


Signalling Pathways

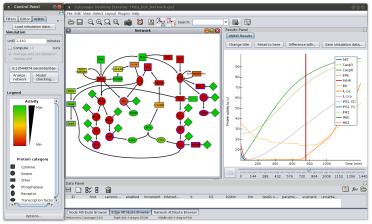


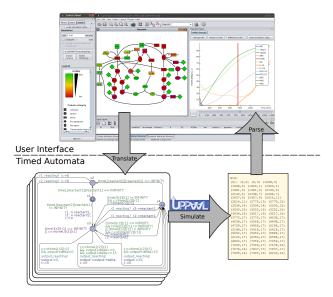
Credit: National Science Foundation

G-Protein Coupled Receptor Signaling to MAPK/ERK



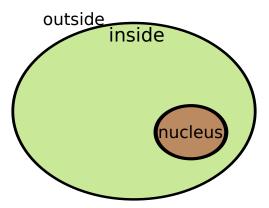
Interaction based

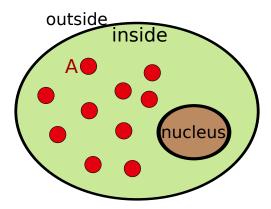


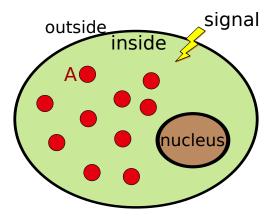


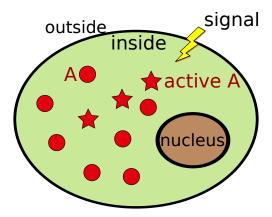
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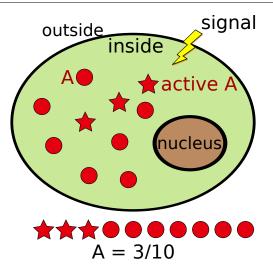
- Interaction based
- Discrete concentration/activity levels

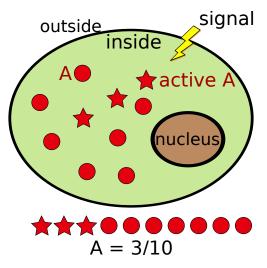












Let the user choose granularity: 2 - 100 discrete levels

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- Precise reactions \Rightarrow abstract *interactions*

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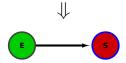
 $E + S + ATP \rightleftharpoons ES + ATP \rightarrow ES^{P} + ADP \rightleftharpoons E + S^{P} + ADP$

(with $S + S^P$ = constant and ATP + ADP = constant)

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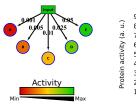
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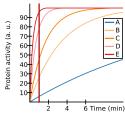
(with $S + S^P$ = constant and ATP + ADP = constant)



- Interaction based
- Discrete concentration/activity levels
- Precise reactions \Rightarrow abstract *interactions*
- Simplified scenarios for rate computation

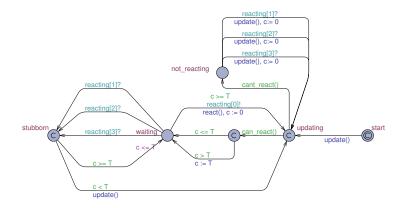




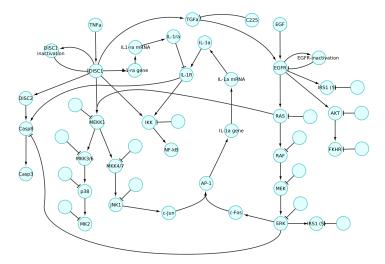


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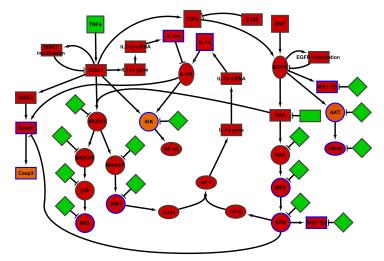
Timed Automata model



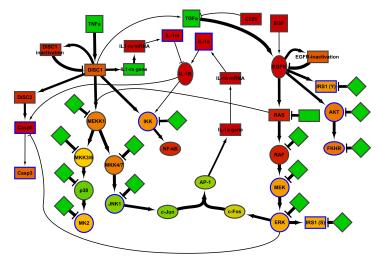
Start from static network topology



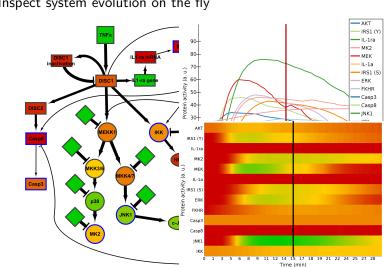
Add kinetics and choose initial activities



Inspect system evolution on the fly



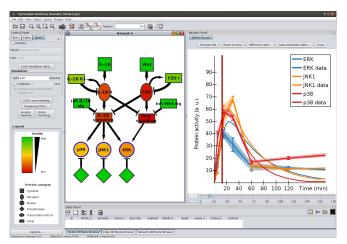
Inspect system evolution on the fly AKT IRS1 (Y) IL-1ra 90-MK2 80-- MEK IL-1a 70-Protein activity (a. u.) 6 0 0 0 0 0 0 - IRS1 (S) -ra ge - ERK FKHR Casp3 Casp8 JNK1 IKK MEKK 20 IKK 10-10 12 14 16 18 20 22 24 Time (min 8 IKK3/ Casp3 MEK p38 JNK1 -Fo MK2 ERK RS1 (S)



Inspect system evolution on the fly

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Experimental data as reference



Use data and model to improve knowledge, generate hypotheses.

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All good and nice, but...

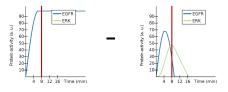
How to find the parameters?

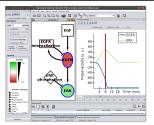
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All good and nice, but...

How to find the parameters?

- Insert parameters manually
- Compare model versions subtracting their activity graphs



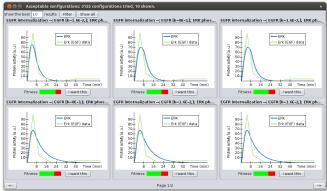


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All good and nice, but...

How to find the parameters?

- Insert parameters manually
- Compare model versions subtracting their activity graphs
- Perform automatic parameter scans



ANIMO live demo



 ► Cytoscape → static representation, Timed Automata → dynamic behaviour

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 - repeat until satisfied

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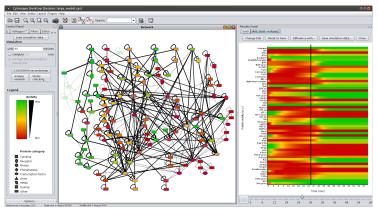
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- ANIMO allows biologists to draw network "sketches"
- Parameter choice:
 - manual settings, choice of qualitative parameters
 - comparison of different model versions
 - parameter sweeps

Deal with parameter sensitivity and model robustness

Deal with parameter sensitivity and model *robustness* Typically, biological networks are robust: smaller parameter variations do not change the behavior of the network

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ANIMO - Analysis of Networks with Interactive MOdeling

- Deal with parameter sensitivity and model *robustness* Typically, biological networks are robust: smaller parameter variations do not change the behavior of the network
- ► Get a model by feeding data: Automata Learning
- ► Use *in-silico experiments* to infer biological hypotheses which can be verified through in-vitro experiments
- Abstraction techniques to deal with large models

Thank you

Analysis of Networks with Interactive MOdelling

http://fmt.cs.utwente.nl/tools/animo

