

Symbolic Systems Technology

Using formal systems and reasoning tools to

- Understand how things work; why things don't work
- Design, analyze, adapt complex systems

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Plan

- What I mean by Symbolic Systems Biology
- Pathway Logic as an example
- Challenges & Opportunities

Elements of Symbolic Systems Biology

- Modeling and analysis of biological systems
- Representation in a formal system / logic
- Executable models
- Use of formal reasoning tools to answer questions

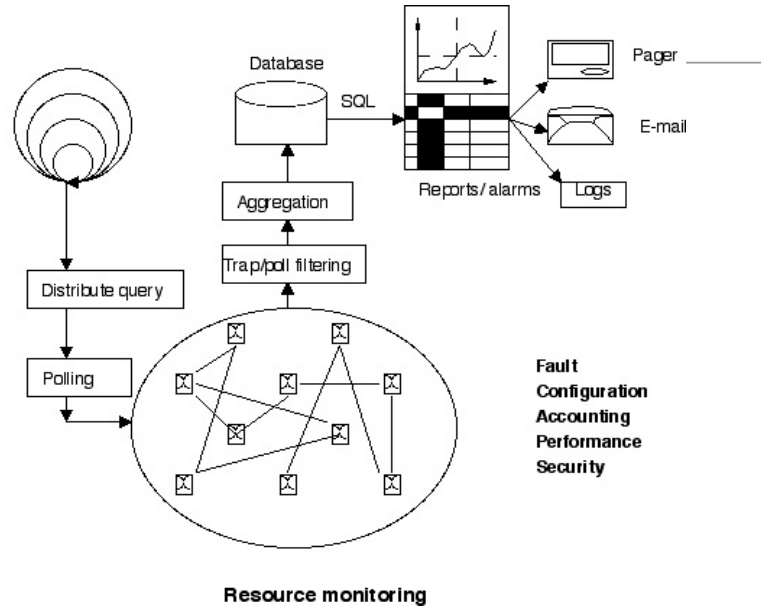
Modeling Issues

- What questions do you want the model answer?
- What can you observe/measure?
- What questions do you *really* want the model answer?
- What does that mean?
- Explain it to a computer!

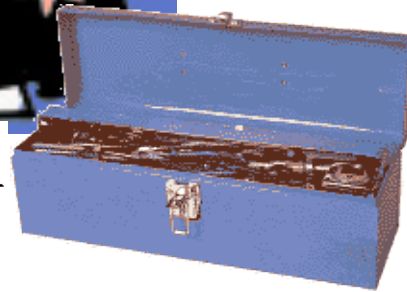
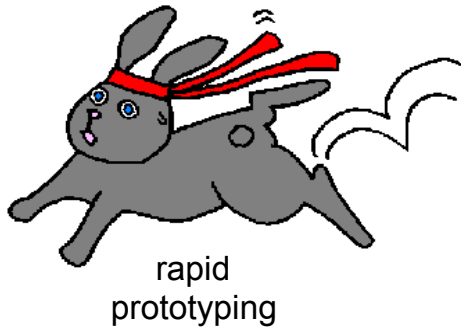
Modeling Methodology



Yearly
Monthly
Weekly
Daily
Manually

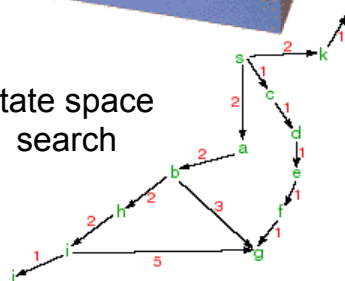


Fault
Configuration
Accounting
Performance
Security



$S \models \Phi$
model
checking

state space
search



What is a formal system?

- Language: to describe things and properties
- Semantics: thing satisfies property
- Reasoning principles: proving/disproving properties of things
- [Reflection: to model and reason about models and reasoning]

Executable formal models

- Something to play with -- model train, architectural model ...
- Computer representation of
 - System state: collections of entities
 - each with name/id, location, knowledge, resources..
 - System behavior: transition rules, response to stimuli
- Execution: application of rules, possibly concurrent
 - watch it run
 - observe effects of perturbations
- Executions as objects that we can reason about
- Properties of states (P,Q) and executions (ϕ)
 - P until Q, eventually P,
 - this event depends on that event

Symbolic analysis -- answering questions

- Forward collection -- upper bound on possible states
- Backward collection -- initial states leading to states of interest
- Search -- for states of interest
- Model checking -- do all executions satisfy ϕ , find counter example
- Constraint solving -- steady state analysis

Model Transformations: new views, faster analysis

- Mapping of formal systems
 - access to tools (RWL to Petri Nets)
 - alternative semantics (qualitative, kinetic, probabilistic/stochastic)
 - richer property specification (RWL to HOL)
- Abstracting
 - quantities (points to regions)
 - qualities (phos(Y 123) vs phosY vs phos vs act/inact)
 - entities (protein vs family or homology class)
- Canonical form -- to combine/compare models

Pathway Logic (PL) <http://pl.csl.sri.com>

- Essence
- Examples
 - Response to Stimuli
 - Bacterial Protease Network
 - TB metabolic network
 - Sleep

In a nutshell

- Biological processes represented in rewriting logic to capture some detail, mapped to Petri nets for scalable model checking
- Queryable formal knowledge base of experimental findings (Datum KB)
 - subject, assay, treatment, times, cells, result, variants, source
- Algebraic signature ~ controlled vocabulary linked to standard sources (Uniprot ...).
- Terms represent reference entity with modifications, activity state, location
- Global model: network of executable rules (RKB) inferred from Datum KB
- Local Model ~ initial state (experimental setup) + relevant rules from RKB
- Pathways (sets of biomolecules that function together) and regulation effects discovered by asking questions (answered by formal reasoning tools)

Answering questions using the PL Assistant

- Given a model (dish and rules), specify goals and avoids
 - Find the relevant subnet
 - backward collection followed by forward collection
 - Find pathway
 - assert goal not achievable and ask LoLA, pathway is counter example
 - In silico knock outs
- Comparing networks
- Following connections
- Find all rule minimal pathways (separate tool, to be integrated)
 - cluster
 - ask for essential rules/occurrences, uses

Datum query

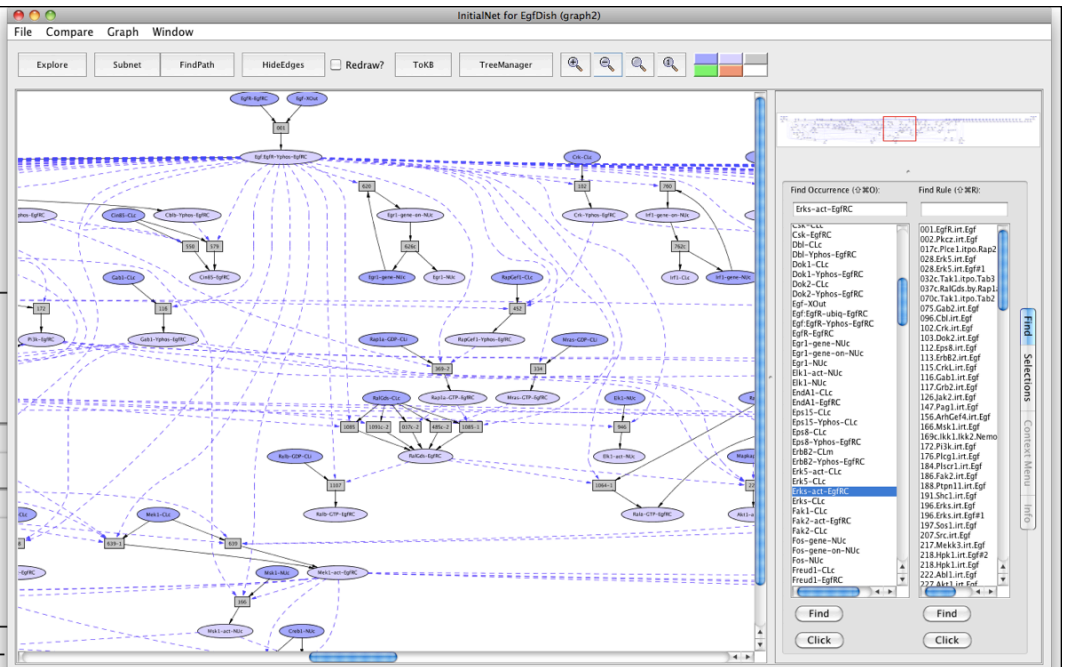
Signaling response to Egf (AMK)

Predicates

subject entity matches

assay type is a

[Add a predicate](#) [Remove all predicates](#)



50 of 407 Results

Export all results to [txt](#) or [csv](#)

Page 1 of 9 [Next](#)

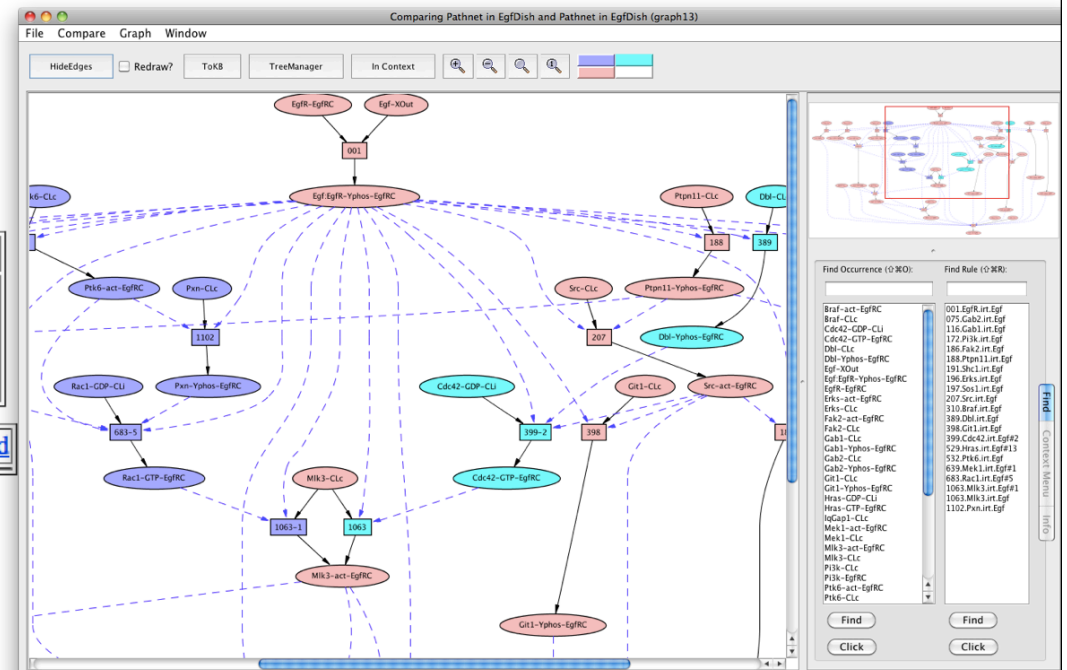
[Expand All](#) | [Collapse All](#)

Erks[Ab]IP IVKA(MBP)[32P-ATP] is increased irt Lps (times) [Expand](#)

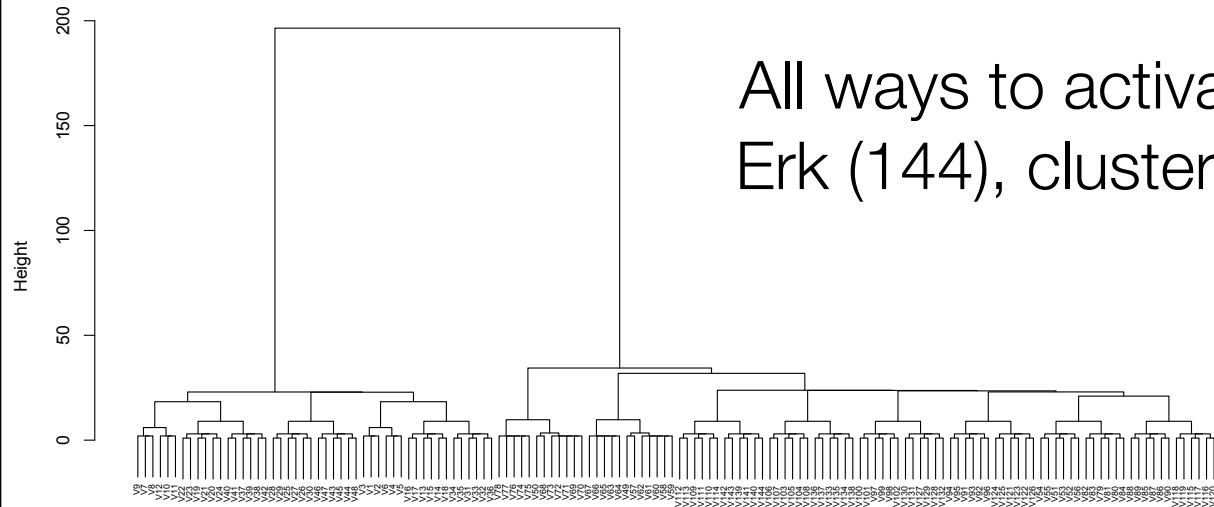
- cells: mPECs in BMS
- times: 0 7+ 15+ 30 60 90 min
- partially reqs: Irak1 [KO]
- source: [10754329-Fig-3c](#)

Erks[Ab]IP IVKA(Elk1)[32P-ATP] is increased irt Lps (30 min) [Expand](#)

Two ways to activate Erk



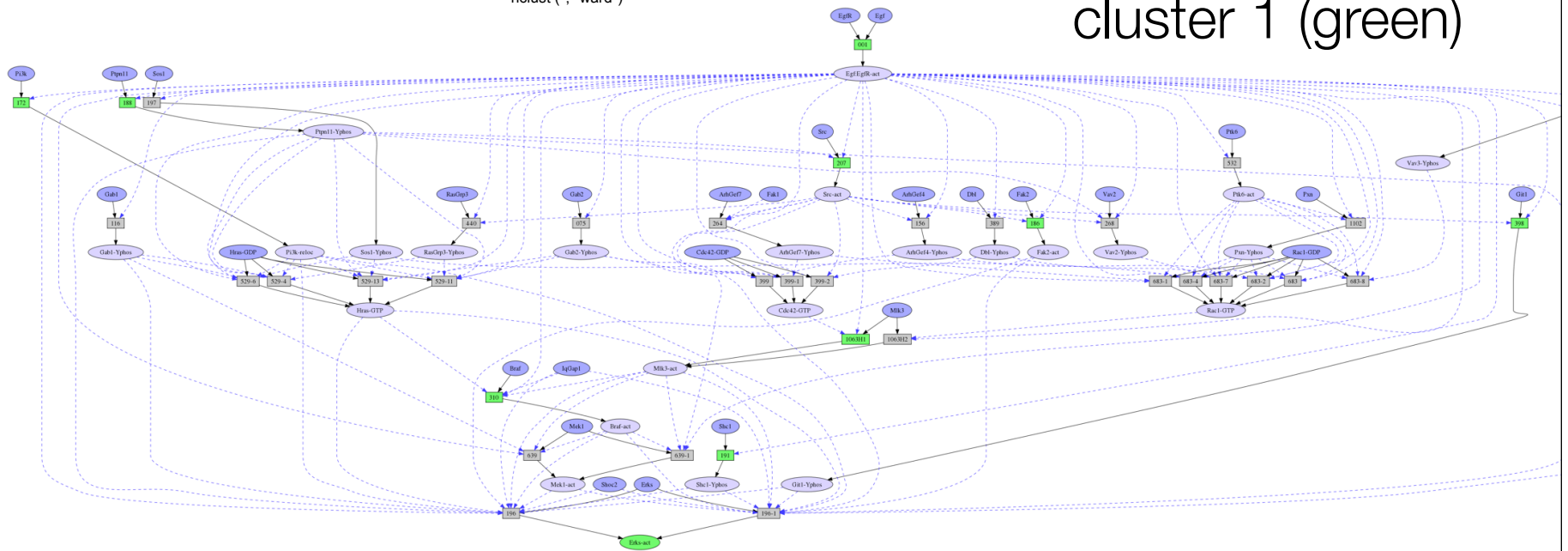
Cluster Dendrogram



All ways to activate
Erk (144), clustered

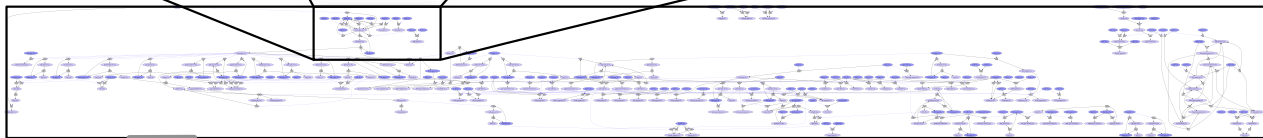
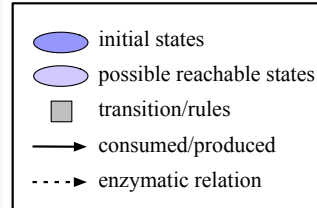
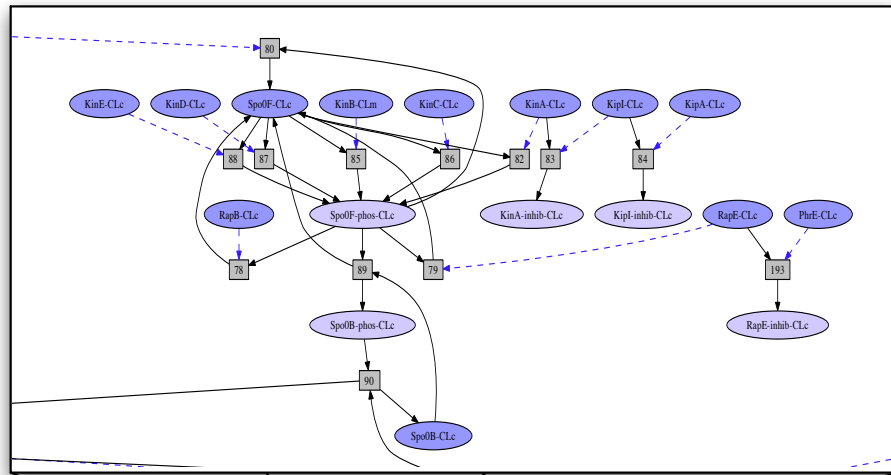
dataDist
hclust (*, "ward")

Essential rules
cluster 1 (green)

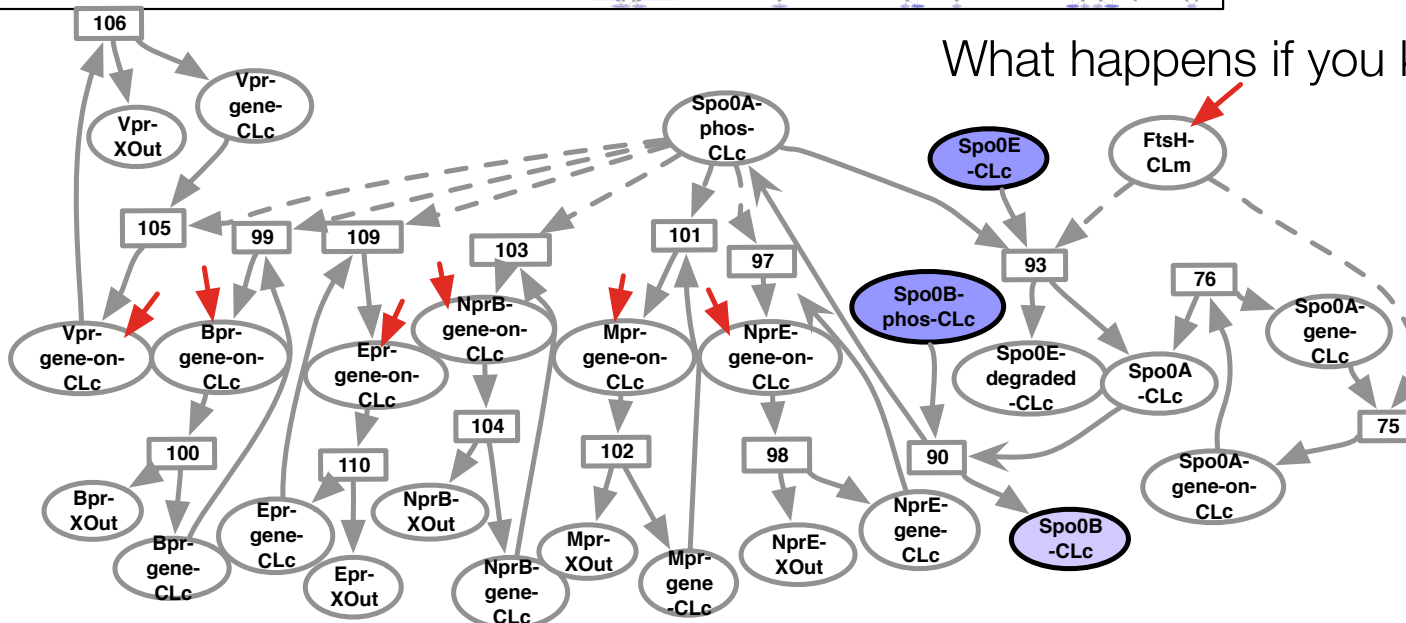


Protease interaction network (Gram Positive Bacteria) (Anupama)

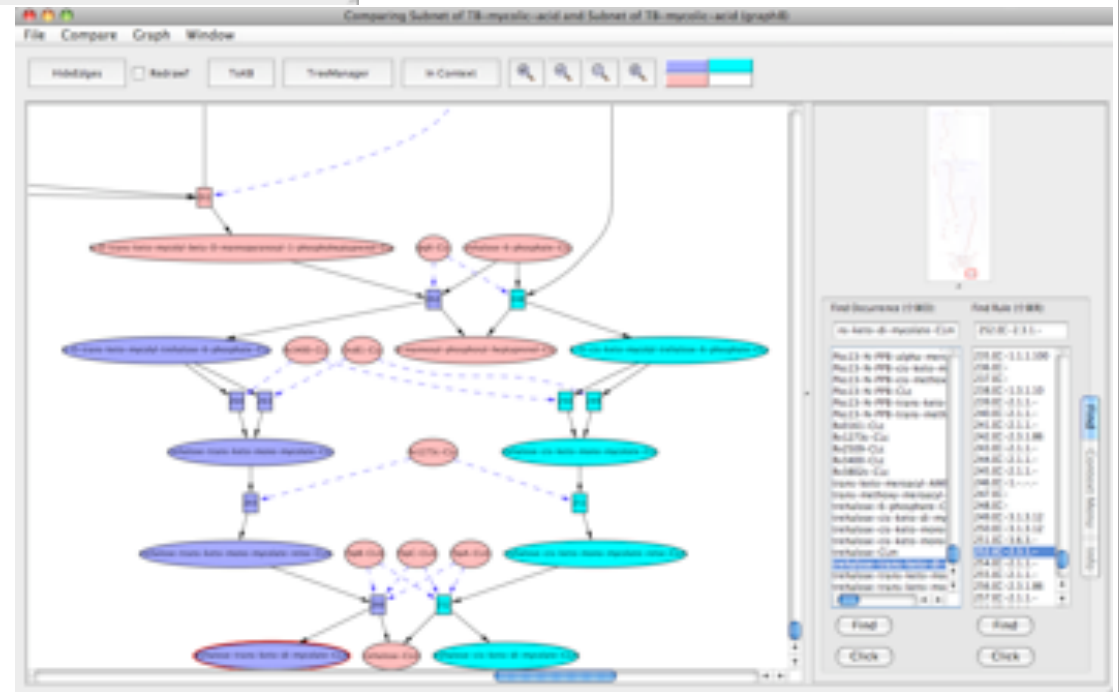
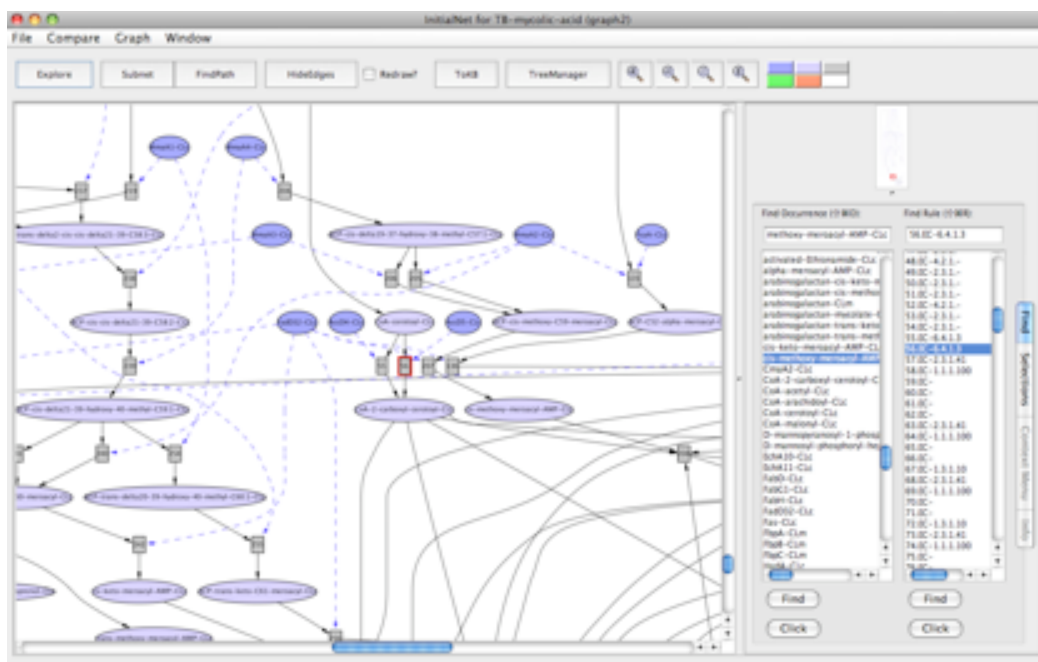
What regulates a protease, what does it regulate



What happens if you knockout FtsH?

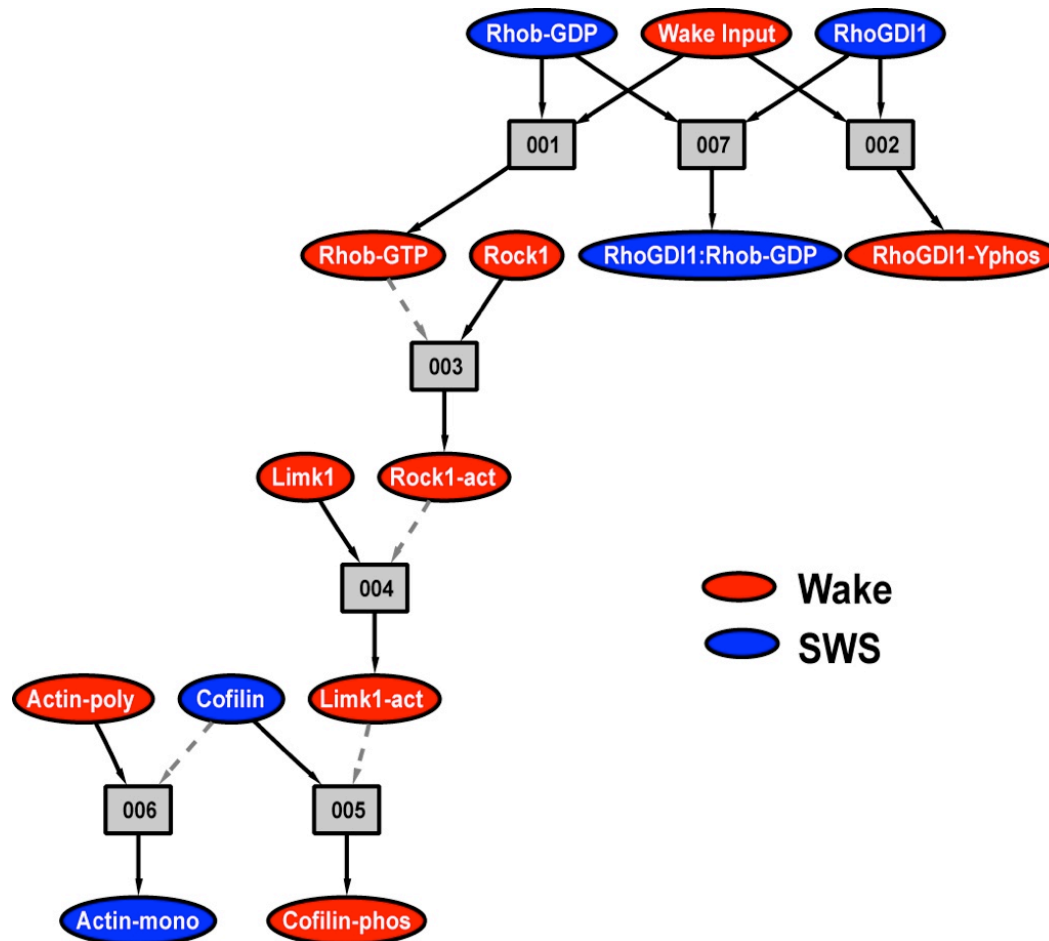


TB-mycolic-acid synthesis (Malabika)



Multiple synthesis routes

A Hypothetical Model Pathway Relating State and Synaptic Plasticity



Wake state:

unknown signal(s)

=> phosphorylation of Rock1

=> activation of Limk1

=> phosphorylation of cofilin

=> increase in polymerized actin

(Phosphorylated cofilin is unable to depolymerize actin)

SWS:

RhoGDI1 binds Rhob-GDP

(is not phosphorylated)

=> Rock1, Limk1, and cofilin would not be phosphorylated and

=> actin depolymerization

=> decrease in synaptic weight

Challenges and Opportunities

We need good models not just good analysis tools

- Alternative computational methods to check a prediction (example: proximity)
- Type checking: using basic biological knowledge
 - P has TS phosphorylation sites, Q is a tyrosine kinase
 - A rule that says Q phosphorylates P is either wrong or missing intermediate steps
- Better ways to capture experimental data.
 - Semantic data mining
 - Symbolic supplementary data
- Inferring rules from experimental data.
 - Needs representation of relevant biological knowledge
 - What do experiments tell you?
 - Roles -- adaptor, scaffold, transformer

Model Integration

- Aggregation -- different representation of the same process
 - PID EgfR signalling + Reactome EgfR signalling
- Complementation -- different parts of a response
- Making a model executable
 - Reactome pathways are disconnected -- missing rules, multiple levels of detail -- when are two entities the same?
- Multiple computational models
 - multi scale
 - qualitative + quantitative

Managing Complexity

- Query of complex models may give complex answers (all paths)
 - How to visualize, make sense of the results
- Scaling
 - Divide and conquer
 - Property preserving abstractions
 - zooming in and out

Synergy

- Finding a shared representation of relevant biological knowledge
- Combining results from multiple analyses
 - how can our different tools work together?
- Biologist friendly scripting

The end! (The beginning?)