

APPLICATIONS OF REWRITING LOGIC  
IN BIOLOGY  
IV  
USING THE PATHWAY LOGIC ASSISTANT

**Carolyn Talcott**  
**SRI International**  
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The background consists of three horizontal bands. The top and bottom bands are a light, pale blue, while the middle band is a slightly darker, medium blue. The text is centered within the middle band.

THE SMALL KB LIVE



# A MODEL OF EGF STIMULATION



# THE CANONICAL EGF-ERK PATHWAY

Egf → EGF → Grb2 → Sos1 → a Ras family member  
→ Raf1 → MEK1/2 → ERK1/2

- Egf binds to the EGF receptor (Egfr) and stimulates its protein tyrosine kinase activity to cause autophosphorylation.
- A complex containing the adaptor protein Grb2 and the guanine nucleotide exchange factor Sos1 docks (binds) to the autophosphorylated (activated) Egfr.
- The Sos1-containing Egfr complex activates a Ras family GTPase,
- The activated Ras protein activates Raf1, a member of the RAF serine/threonine protein kinase family.
- Raf1 then activates the dual-specificity protein kinases Mek1 and/or Mek2 (MEK1/2), which activate Erk1 and/or Erk2 (ERK1/2).



# A MODEL OF ASSEMBLED FROM THE PL KNOWLEDGE BASE

- The model is based on experimental results curated from the literature.
- It includes all events known to happen in response to Egf stimulation within ~ 15 minutes
- It shows that the series of events between activation of EgfR by Egf and activation of Erk2 may not be as simple as those described in the canonical pathway



# DATA COLLECTION

174 papers were searched for appropriate experiments and the results were listed as 1373 evidence items. Below is an example of an item used as evidence for rule E19 which requires the presence of tyrosine phosphorylated Gab1 for the activation of Erk2 in response to Egf.

## An Evidence Item

Source PMID: 11323411  
Type: data  
Figure : 2

Subject Pathway Logic name: Erk2  
Expressed: yes  
Identification method: expression tag antibody

State Change Type: kinase activity  
Direction: increase  
Assay: IP Kinase assay, MBP as substrate

Cause Stimulus: Egf  
Time: 5 minutes  
Concentration: 0.25 ng/ml

Requirement Pathway Logic name: Gab1  
Method: Y627F dominant-negative  
coexpression  
Method: Y659F dominant-negative  
coexpression

Environment Cells: COS-7  
State: serum starved for 20 hr

```
rl[E19.Erks.irt.Egf]:
  {CLm | clm ([EgfR - act] : Egf) }
  {CLi | cli [Mlk3 - act] [mek:MekS - act]
        [Gab1 - Yphos][Src - act]
        [Ptk2b - act] [IqGap1 - reloc] }
  {CLc | clc Erk1 Erk2 }
=>
  {CLm | clm ([EgfR - act] : Egf) }
  {CLi | cli [Mlk3 - act] [mek:MekS - act]
        [Gab1 - Yphos] [Src - act]
        [Ptk2b - act][IqGap1 - reloc]
        [Erk1 - act] [Erk2 - act] }
  {CLc | clc } .
```



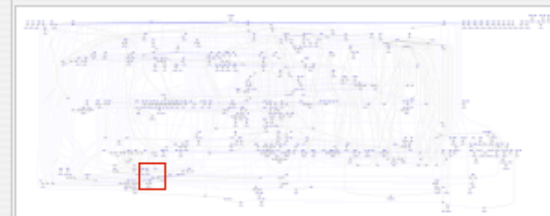
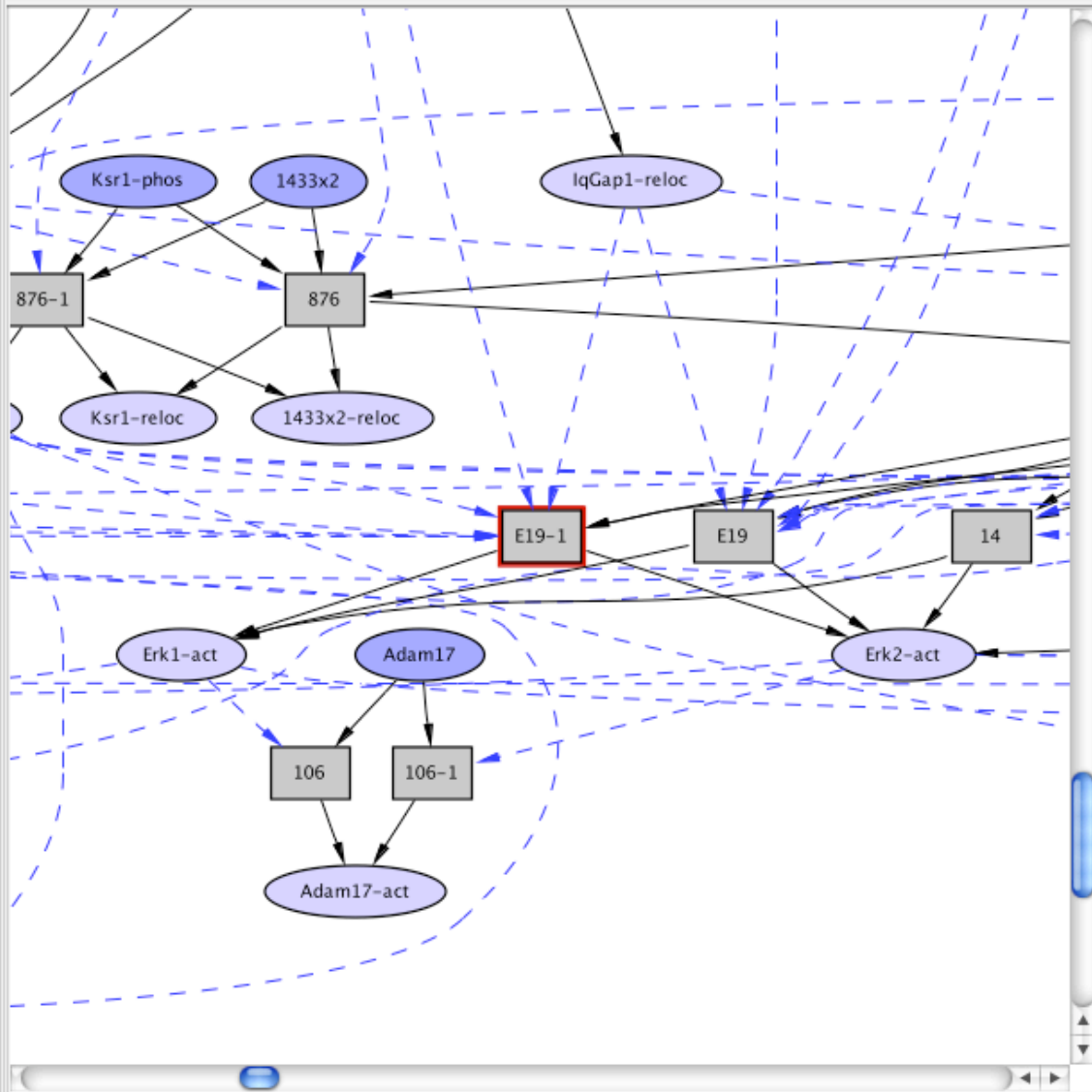
# GENERATING THE MODEL

- Step 1: Generate a knowledge base from the curated rules and components. (It contains 1953 occurrences and 3440 transitions.)
- Step 2: Define the initial state (dish). It contains Egf in the supernatant, EgfR in the membrane and other proteins known to be expressed in epithelial-like cells.

```
PD (Egf [Cell | {CLo | ...} {CLm | EgfR ...}  
      {CLi | ...} {CLc | ...} ...])
```

- Step 3: Generate the network relevant to this dish. (It contains 468 occurrences and 374 transitions. Complex!)

InitExplore(Occs) InitExplore(Rules) Subnet FindPath Compare ToKB



Find Occurrence (⇧⌘O): Find Rule (⇧⌘R):

- |                   |                    |
|-------------------|--------------------|
| Erk1-act-CLi      | E19.Erks.irt.Egf#1 |
| Eif4e:mRNA-CLc    | E08.Creb1.irt.Egf  |
| Eif4ebp1-CLc      | E09.Crk.irt.Egf    |
| Eif4ebp1-phos-CLc | E10.Crkl.irt.Egf   |
| Eif4g1-CLc        | E11.Csk.irt.Egf    |
| Eif4g1-phos-CLc   | E12.Ctnnb1.irt.E   |
| Elmo1-CLc         | E13.Ctnnd1.irt.E   |
| Elmo1-reloc-CLi   | E14.Dok1.irt.Egf   |
| Eps15-CLc         | E15.Dok2.irt.Egf   |
| Eps15-Yphos-CLi   | E16.Ywhaz.irt.E    |
| Eps8-CLc          | E17.Eps15.irt.Eg   |
| Eps8-Yphos-CLi    | E18.ErbB2.irt.Eg   |
| ErbB2-CLm         | E19.Erks.irt.Egf   |
| ErbB2-act-CLm     | E19.Erks.irt.Egf#4 |
| Erk1-CLc          | E20.Fer.irt.Egf    |
| Erk1-act-CLi      | E21.Gab1.irt.Egf   |
| Erk2-CLc          | E22.Grb2.irt.Egf   |
| Erk2-act-CLi      | E23.Hgs.irt.Egf    |
| Fer-CLi           | E24.Hpk1.irt.Egf   |
| Fer-Yphos-CLi     | E25.Hras.irt.Egf   |
| Fnbp1l-CLc        | E25.Hras.irt.Egf#1 |
| Frap1-CLc         | E26.Inpp1.irt.Eg   |
| Frap1-act-CLc     | E27.Irk1.irt.Egf   |

Find Selections Context Menu Info

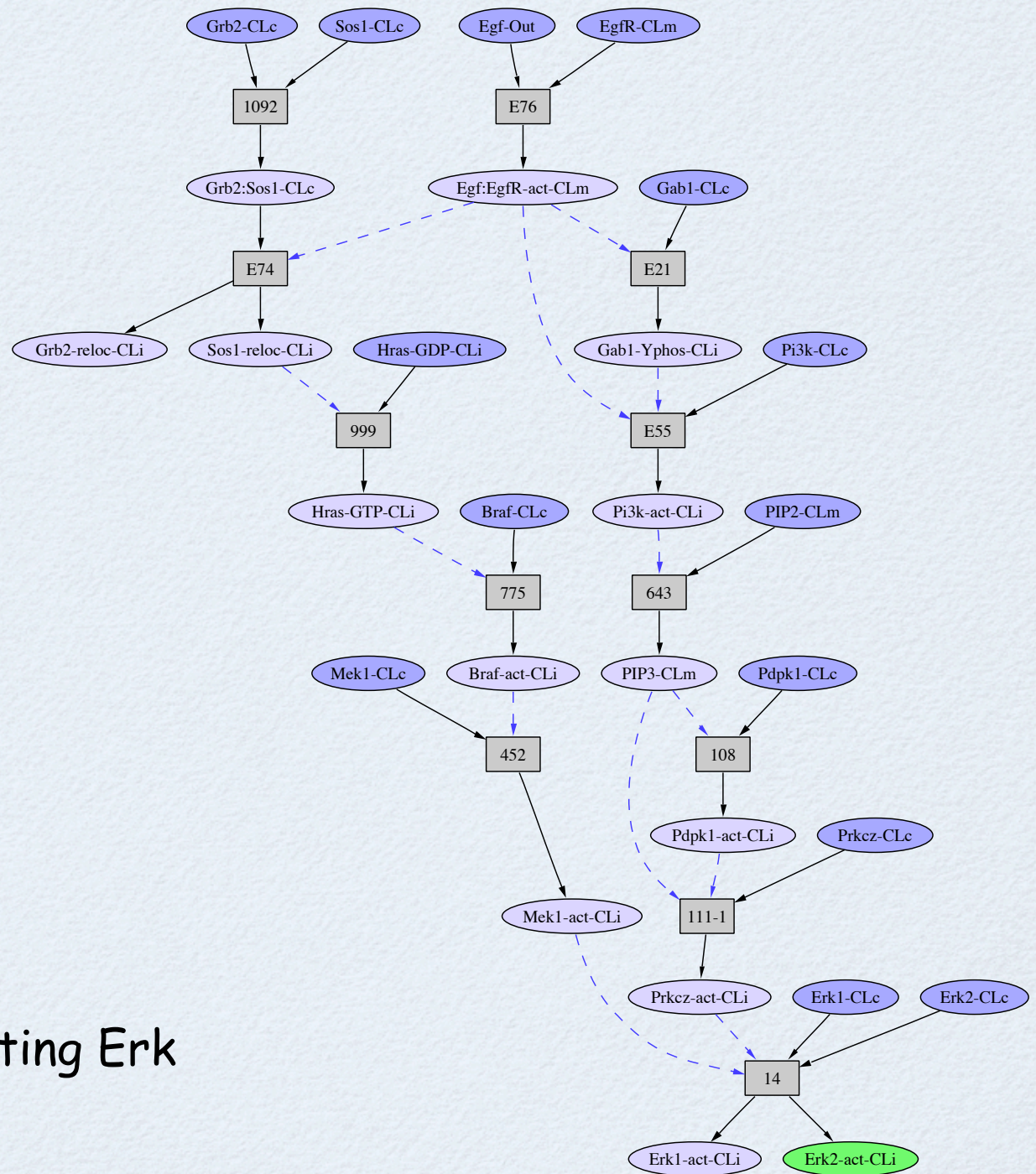
Find Click Find Click



# ACTIVATION OF ERKS

- Step 4: Select Erk2-act-CLi as a goal
  - Find a path in the dishnet
  - Hide a suspicious rule (452) and find another path
  - Generate the relevant subnet and find a path here
  - Compare the different paths





One pathway activating Erk





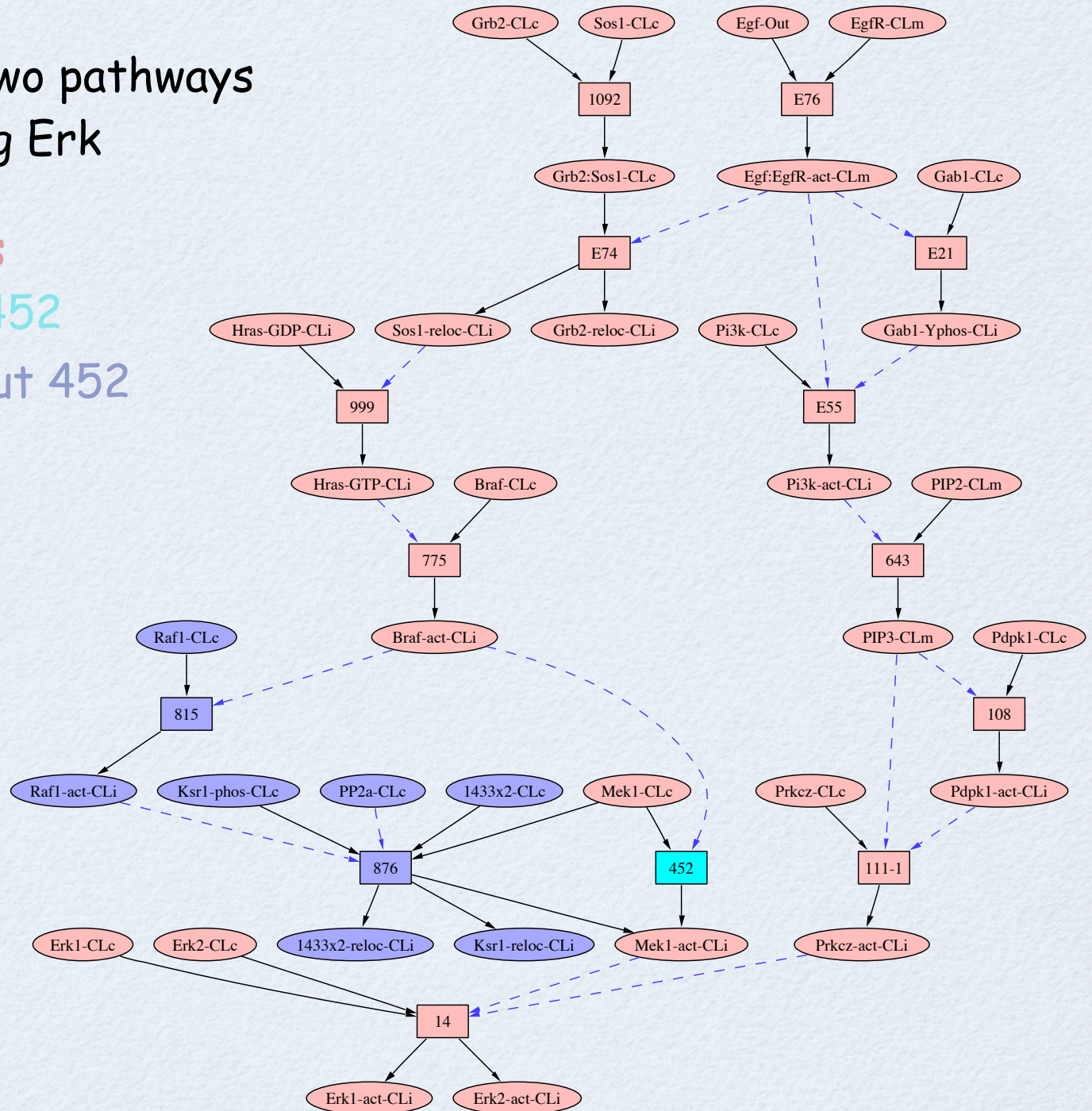


# Comparing the two pathways activating Erk

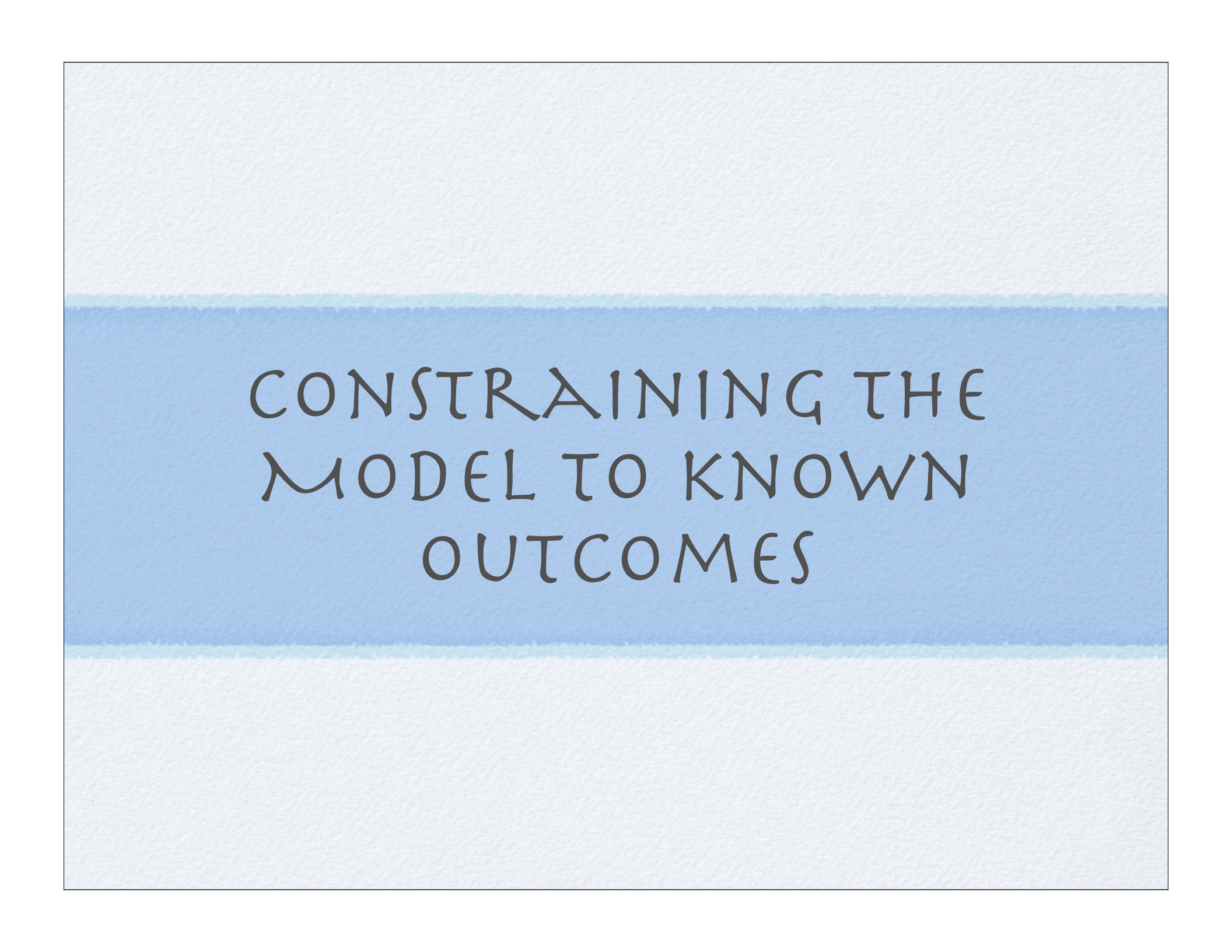
Both pathways

Pathway with 452

Pathway without 452







CONSTRAINING THE  
MODEL TO KNOWN  
OUTCOMES



# THE CONSTRAINTS

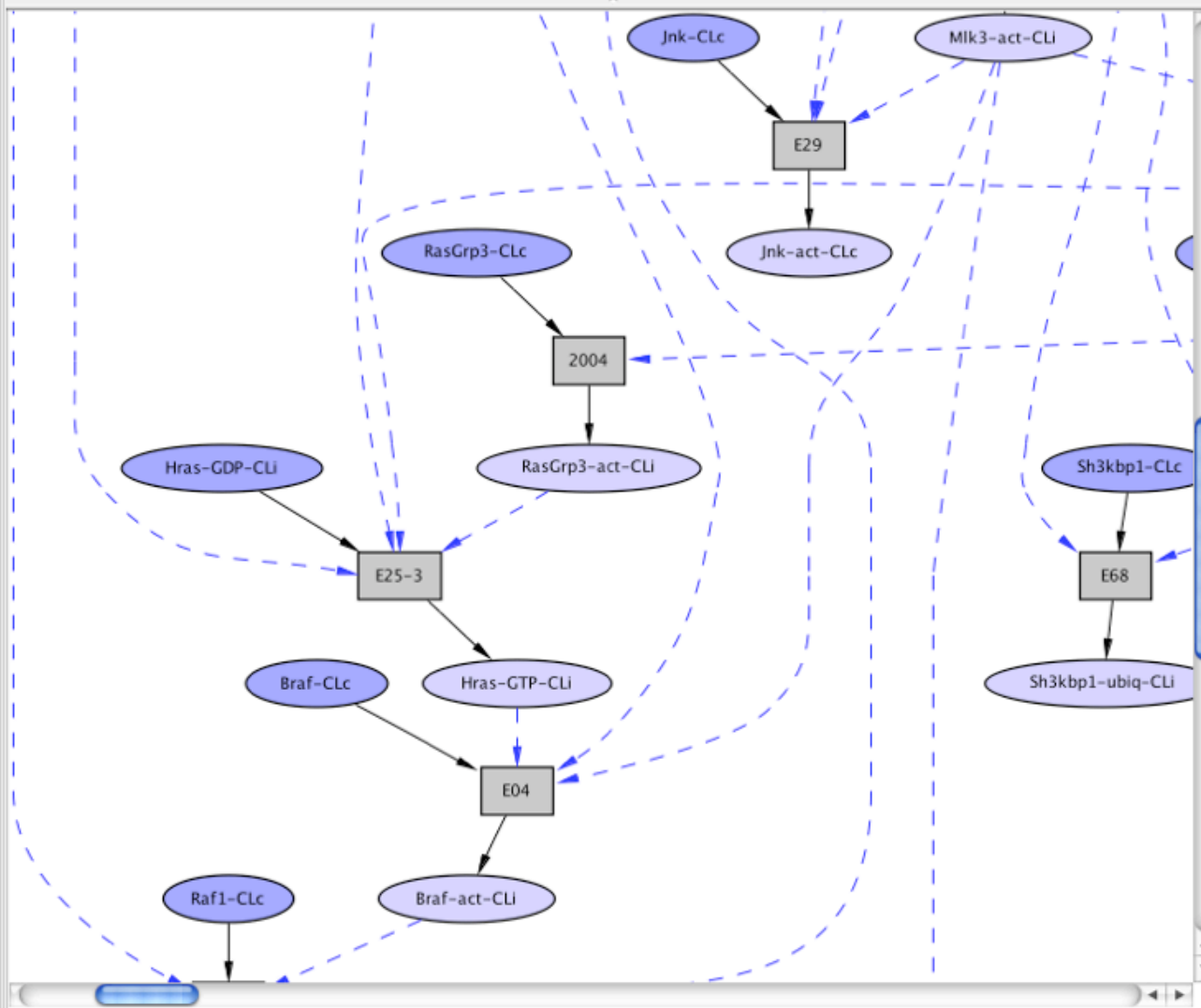
- The model is constrained by giving precedence to events specifically found in response to Egf.
- The full model contains two types of rules: Common Rules formalizing local reactions, independent of the larger context, and Egf Rules formalizing requirements specific to Egf signaling that must be satisfied before they can fire.
- The Egf Rules are given precedence by hiding corresponding Common Rules.
- A list of 85 protein state changes demonstrated experimentally to occur in response to a short stimulus with Egf was collected as part of the curation process. These states are made goals.
- Finally a path is found satisfying these constraints.



File Find Selections Compare View Window

InitExplore(Occs) InitExplore(Rules) Subnet FindPath Compare ToKB In Context

Goals: Stat5-act-CLi Pxn-Yphos-CLi Stat3-act-CLi Abl1-act-CLi Ptpn11-Yphos-CLi Ap2-reloc-CLi  
Pan1-Yphos-CLi m Shc2-reloc-CLi Dok2-Yphos-CLi Pik3c2h-reloc-CLi Msk1-act-CLi Mek1-act-CLi



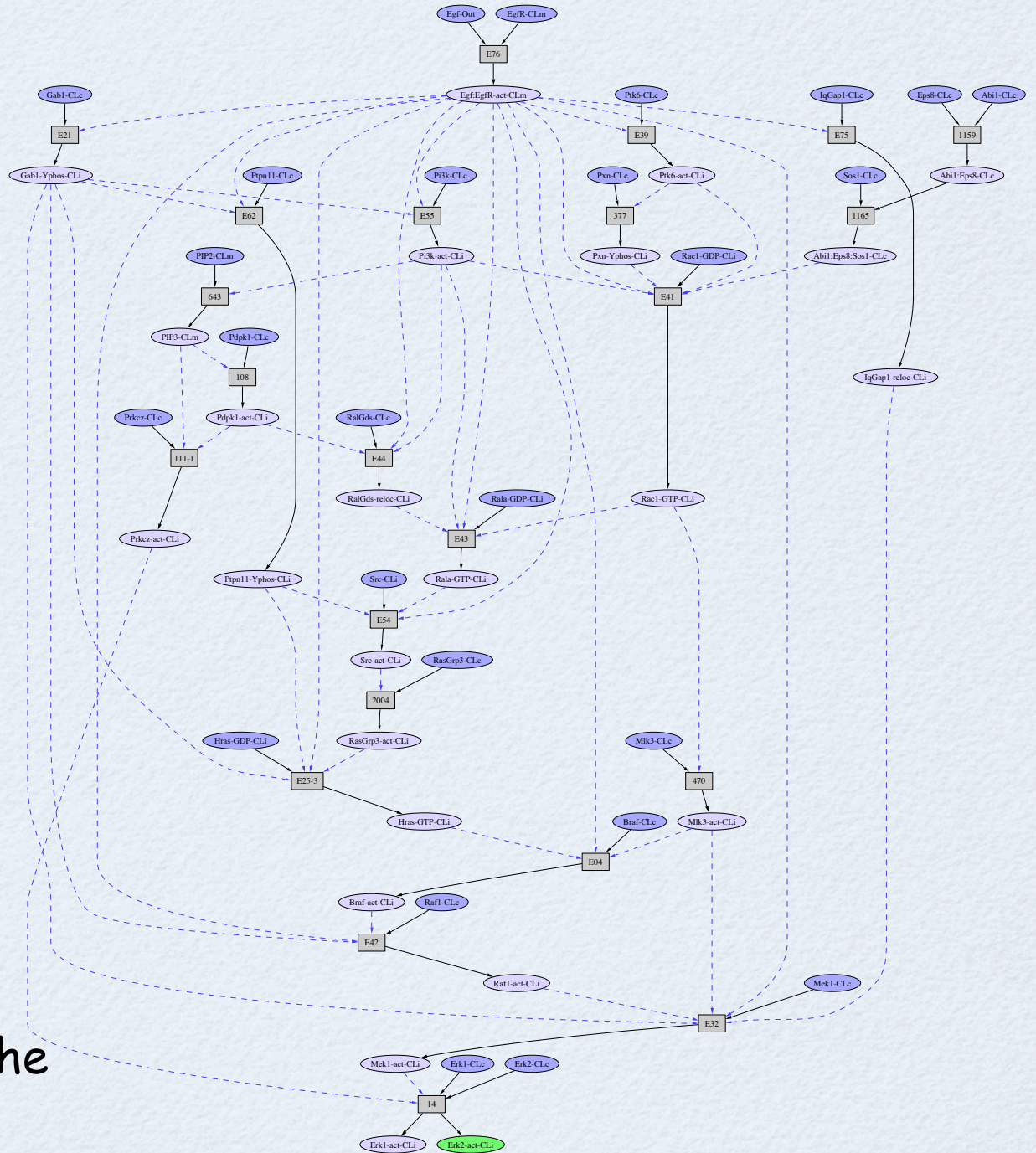
Find Occurrence (⇧O): Find Rule (⇧R):

- |                        |                  |
|------------------------|------------------|
| Erk2-act-CLi           |                  |
| Eps8-CLc               | 108.Pdpk1.by.PIF |
| ErbB2-act-CLm          | 1093.Ppp1ca.Sho  |
| ErbB2-CLm              | 1094.Ppp1ca.by.f |
| Erk1-act-CLi           | 111.aPrkc.on#1   |
| Erk1-CLc               | 1123.Mapkap2.    |
| Erk2-act-CLi           | 1129.Mapkap1.R   |
| Erk2-CLc               | 1159.Abi1.Eps8   |
| Fer-CLi                | 1165.Sos1.Abi1.E |
| Fer-Yphos-CLi          | 14.Erk5.by.Meks. |
| Frap1-CLc              | 149.Gsk3.xby.Rsl |
| Frap1:Lst8-CLc         | 171.RapGef1.by.f |
| Frap1:Lst8:Mapkap1:Ric | 2004.RasGrp3.by  |
| Gab1-CLc               | 218.Rap1a.by.Ra  |
| Gab1-Yphos-CLi         | 364.Cofilin.phos |
| Grb2-CLc               | 377.Pxn.phos     |
| Grb2-reloc-CLi         | 470.MIK3.by.Rac  |
| Gsk3-CLc               | 472.Frap1.Lst8.c |
| Gsk3-Sphos-CLc         | 473.Map3k1.by.F  |
| Hgs-CLi                | 643.PIP3.from.PI |
| Hgs-Yphos-CLi          | 675.Limk1.by.Pal |
| Hpk1-act-CLi           | 736.RasGrf1.on   |
| Hpk1-CLc               | 739.Mcf2.on      |

Find Selections Context Menu Info

Find Find Click Click





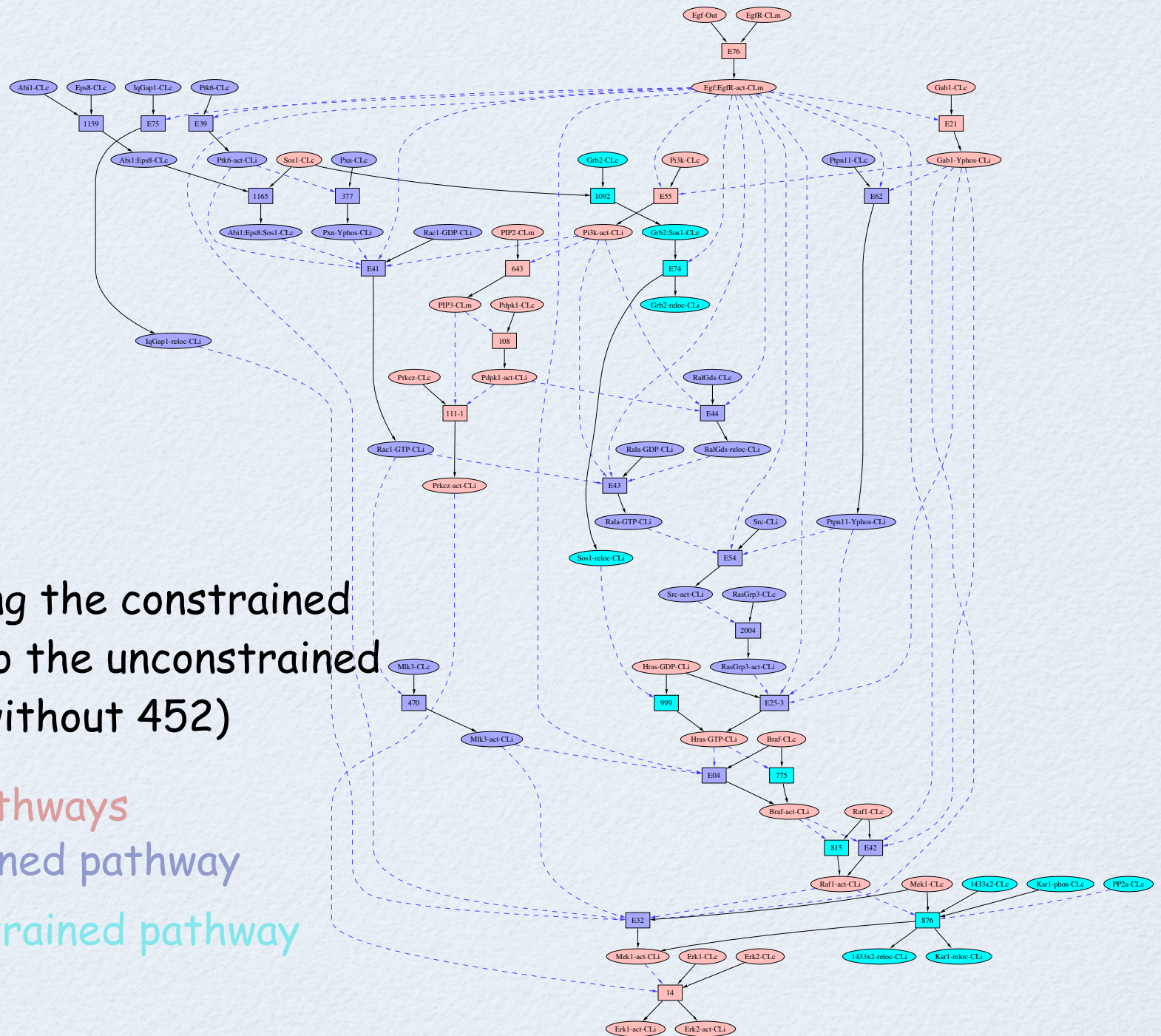
The Erk pathway in the constrained model



Comparing the constrained pathway to the unconstrained (without 452)

Both pathways  
Constrained pathway

Unconstrained pathway





# PATHWAY LOGIC TEAM

- Keith Laderoute
- Patrick Lincoln
- Carolyn Talcott
  
- Linda Briesemeister
- Steven Eker
- Merrill Knapp
- Ian Mason
- Andy Poggio
- Malabika Sarker
  
- Biology Computer Science Students