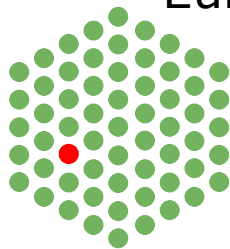


CellNOpt: modelling prior knowledge networks trained to experimental data

Julio Saez-Rodriguez

European Bioinformatics Institute



EMBL-EBI

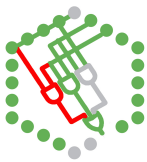


Hinxton (Cambridge) UK

www.ebi.ac.uk/saezrodriguez



Logic modelling to link protein signalling networks with functional analysis of signal transduction



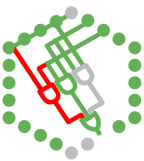
- **CellNOpt**: a flexible pipeline to model protein signalling networks
- (1) Converts protein signalling network into logic model
 - (Unless known) create all possible logic gates (AND/OR) compatible with the network
- (2) Find the combination of logic gates (i.e. the model) that best describes the experimental data

$$\theta = \theta_f + \alpha \cdot \theta_s$$

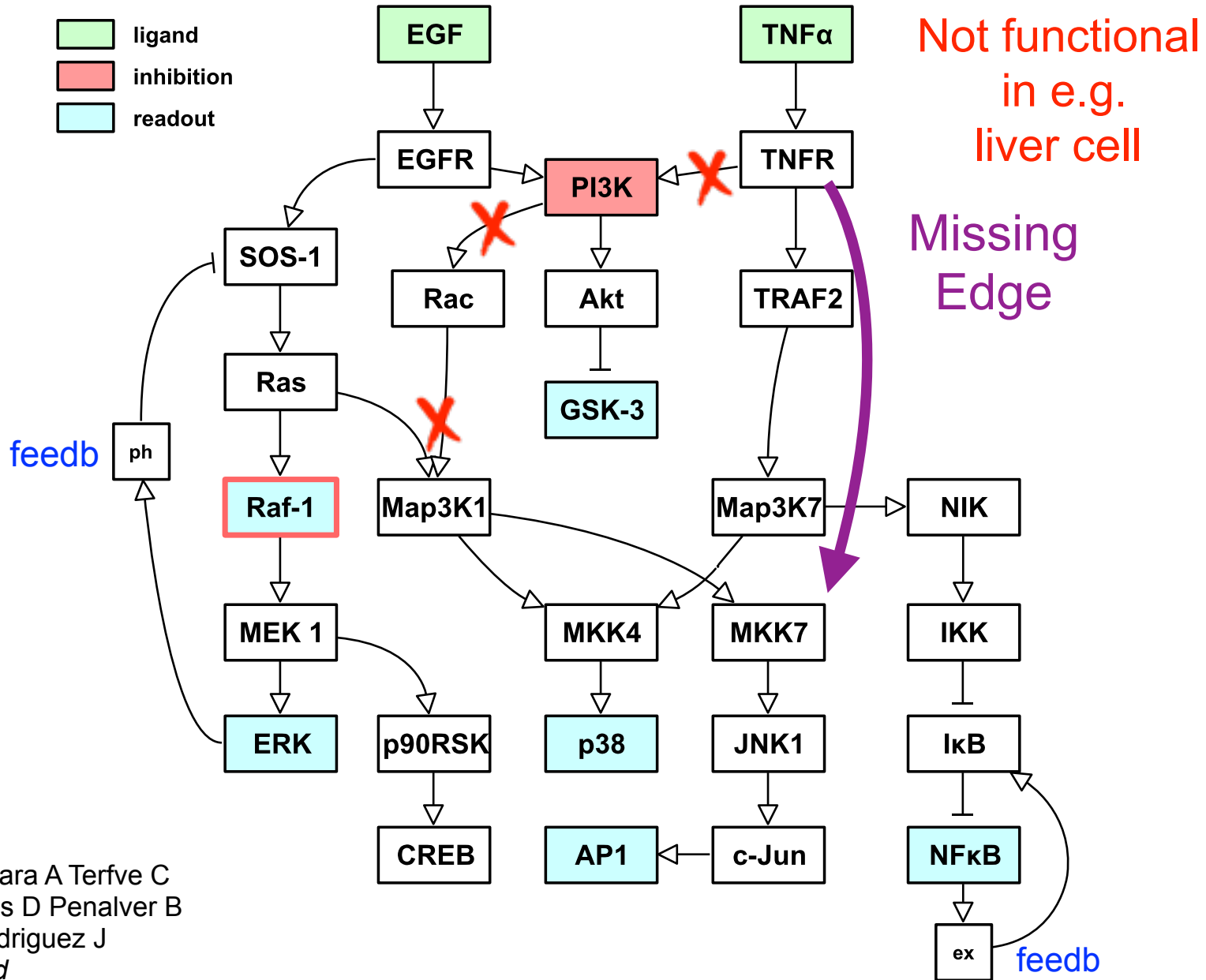
Bioconductor & Matlab,
available at www.ebi.ac.uk/saezrodriguez/software.html

Morris MK, Melas I, Saez-Rodriguez J, *Methods Mol. Biol, in press*

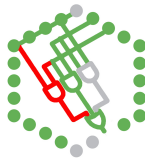
Saez-Rodriguez J, Alexopoulos LG, Epperlein J, Samaga R, Lauffenburger DA, Klamt S, Sorger PK *Mol Sys Bio* 5:331,2009



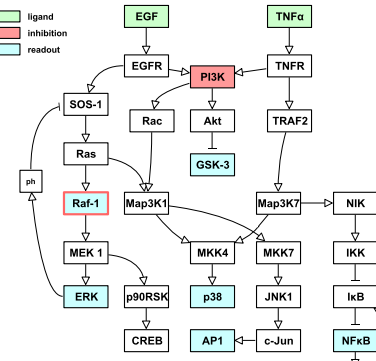
A Toy model



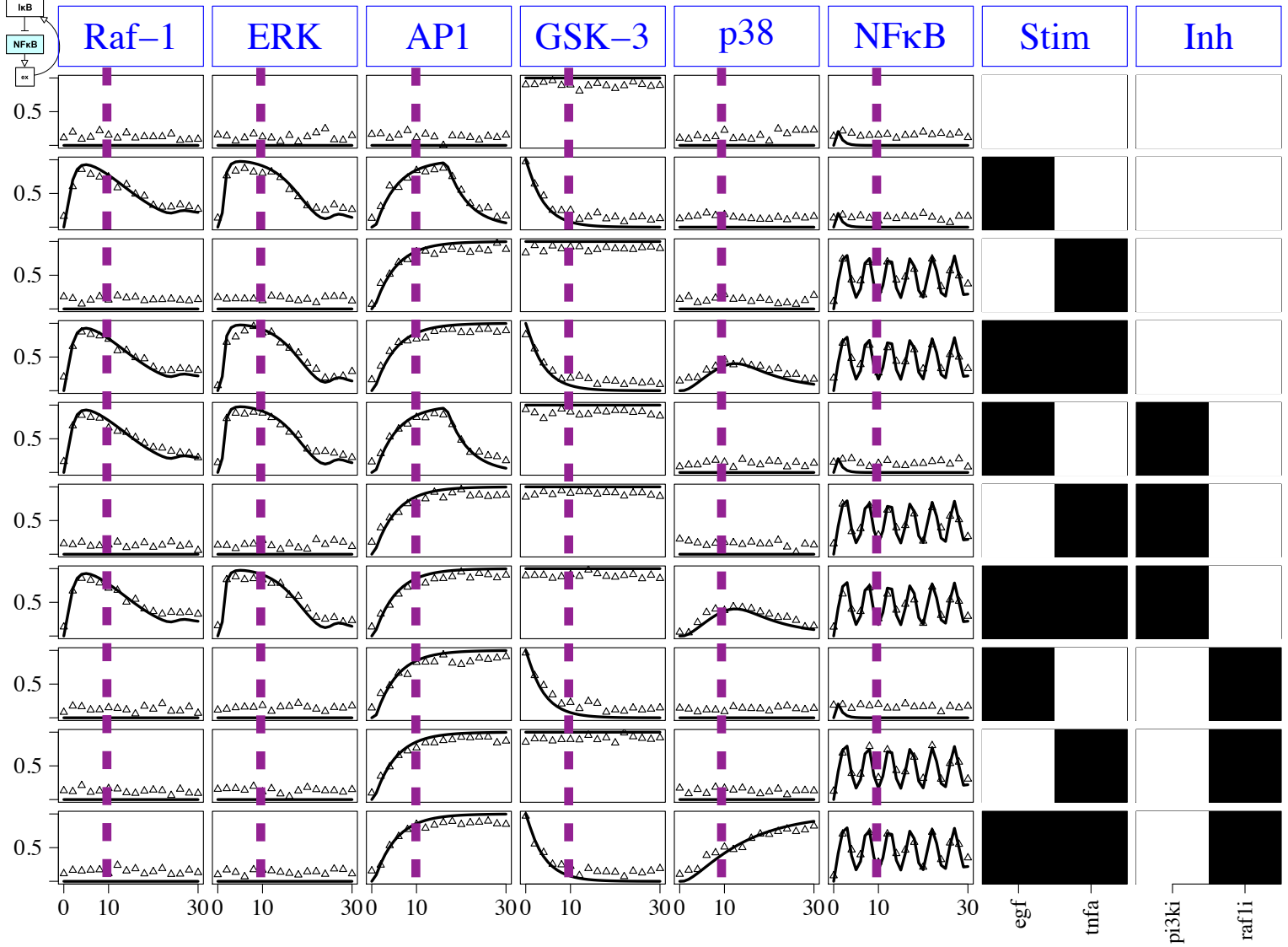
MacNamara A Terfve C
 Henriques D Penalver B
 Saez-Rodriguez J
submitted



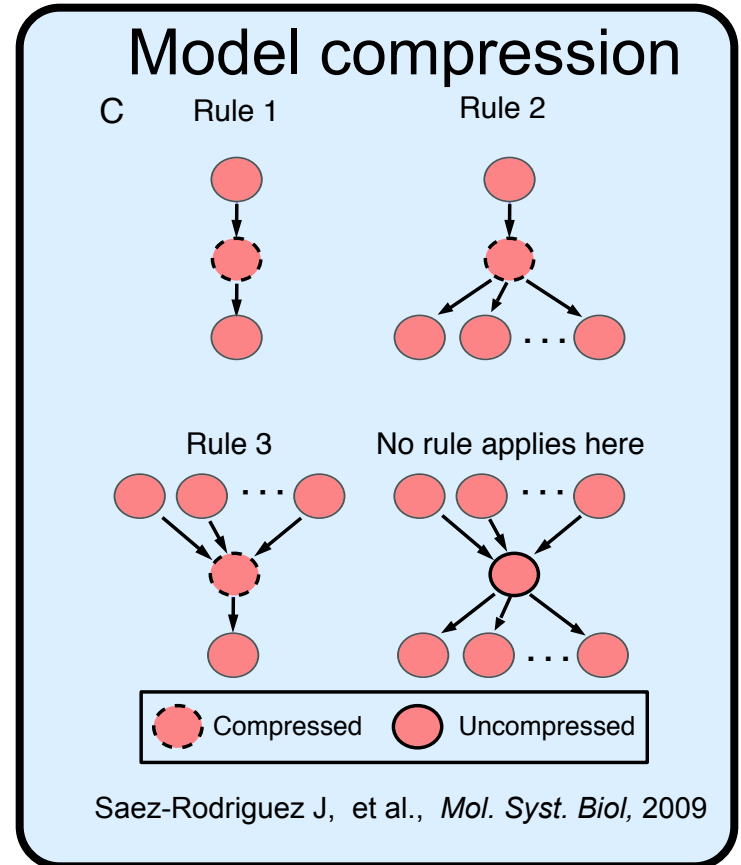
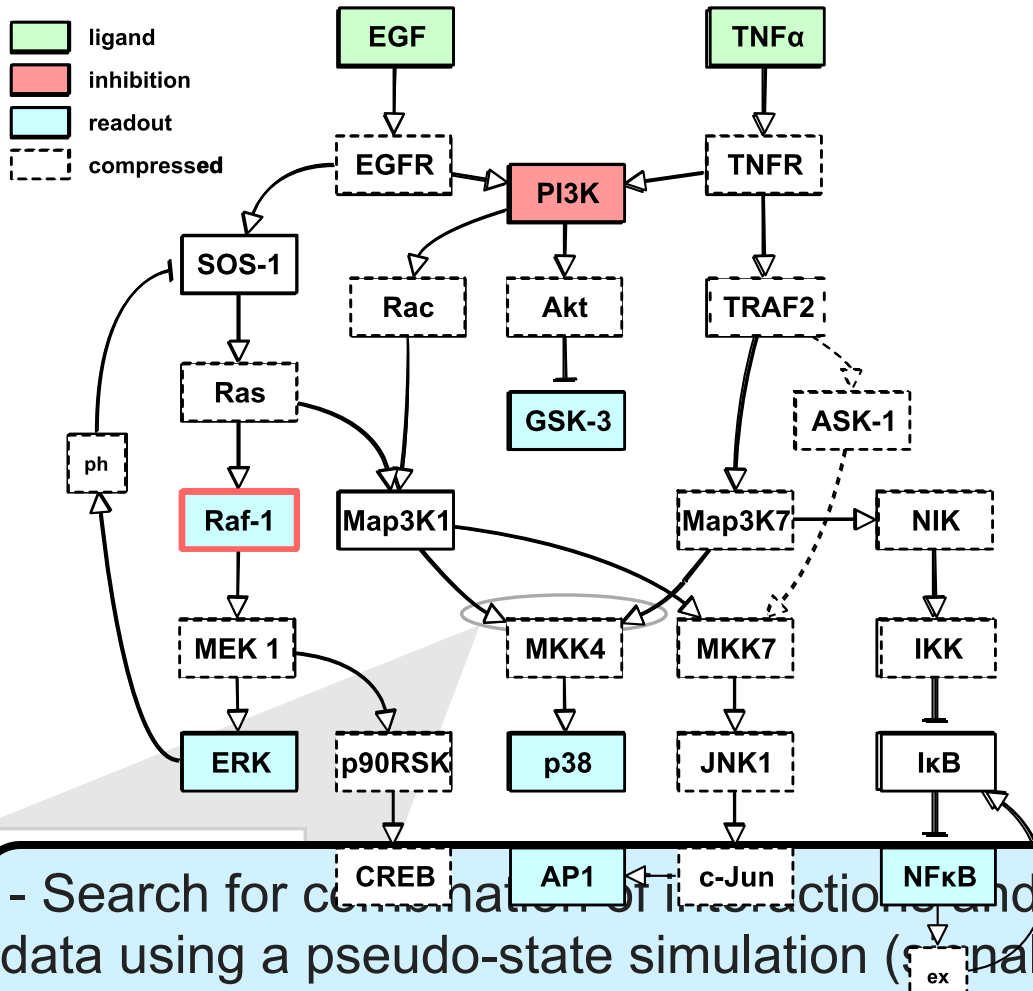
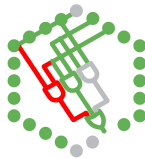
The 'real' data



How to pick right time to measure?

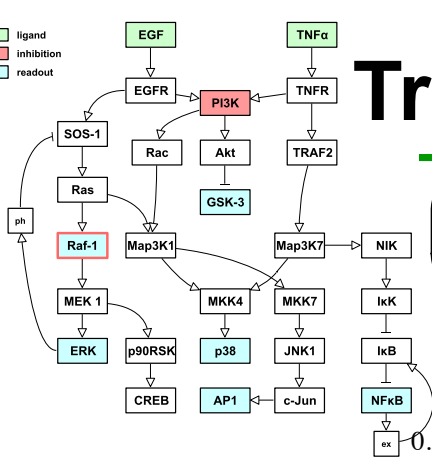


Model preprocessing: compression and expansion of gates

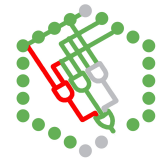


- Search for combinations of interactions and gates that best describe the data using a pseudo-state simulation (signal propagation);
- Search is an optimization problem that can be solved
 - (1) Enumeration
 - (2) Heuristic (e.g. genetic algorithm)
 - (3) Integer Linear Programming (Mitsos et al. Plos Comp Bio 2009)

█ ligand
█ inhibition
█ readout

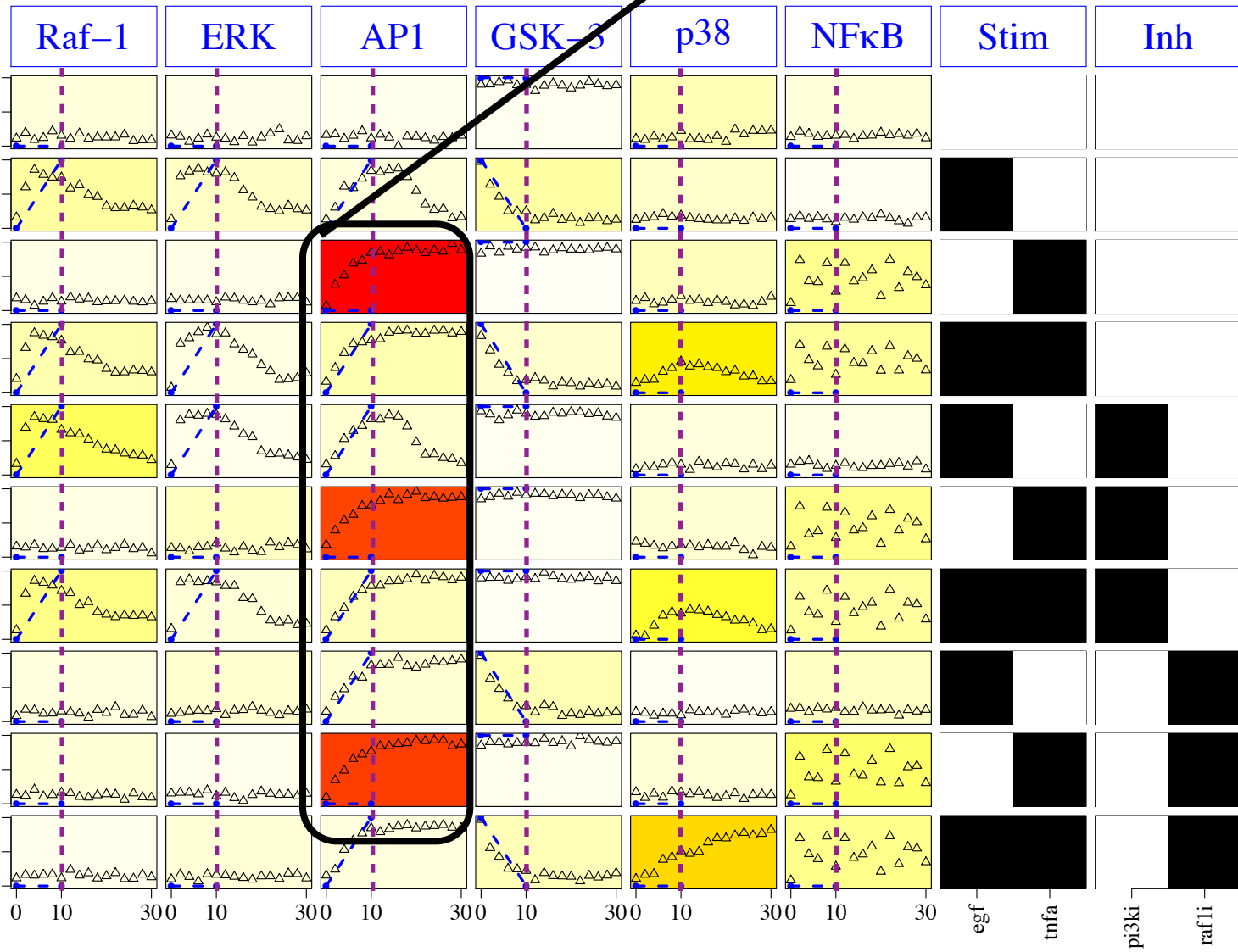


Training to data recovers structure



Identifies active/non-active links (except feedbacks)

Can not explain data due to missing links



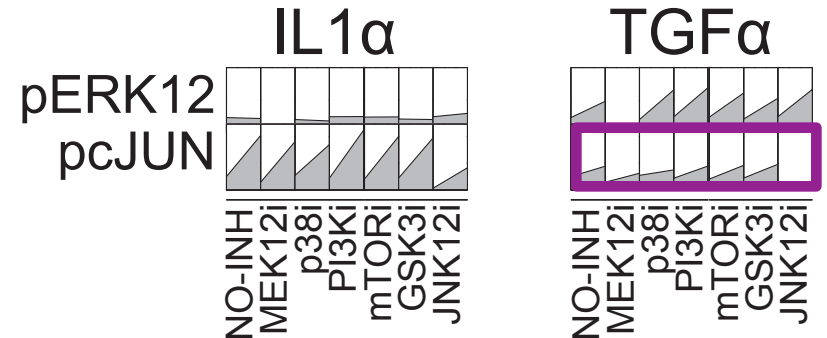
MacNamara A Terfve C
 Henriques D Penalver B
 Saez-Rodriguez J
submitted



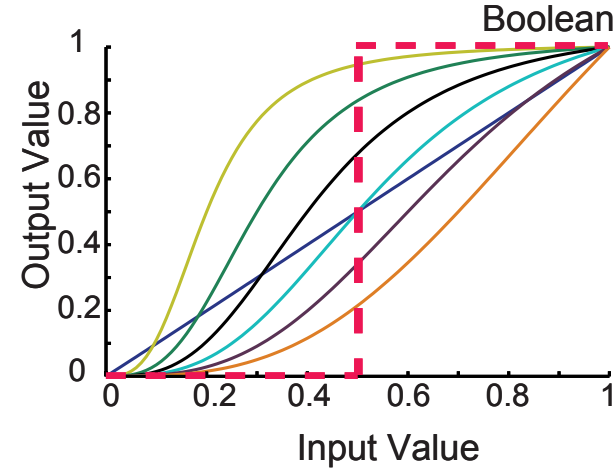
Constrained Fuzzy Logic can handle quantitative differences



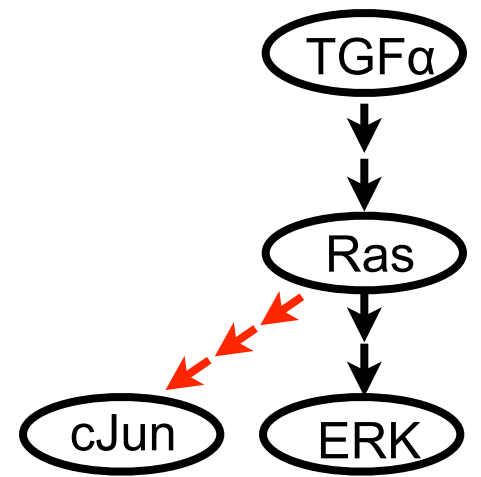
- Boolean modeling can **not** describe **quantitative** aspects (e.g. intermediate activation)



- Fuzzy logic can model quantitative signaling data (Aldridge et al. *Plos Comp. Bio.* 2009)

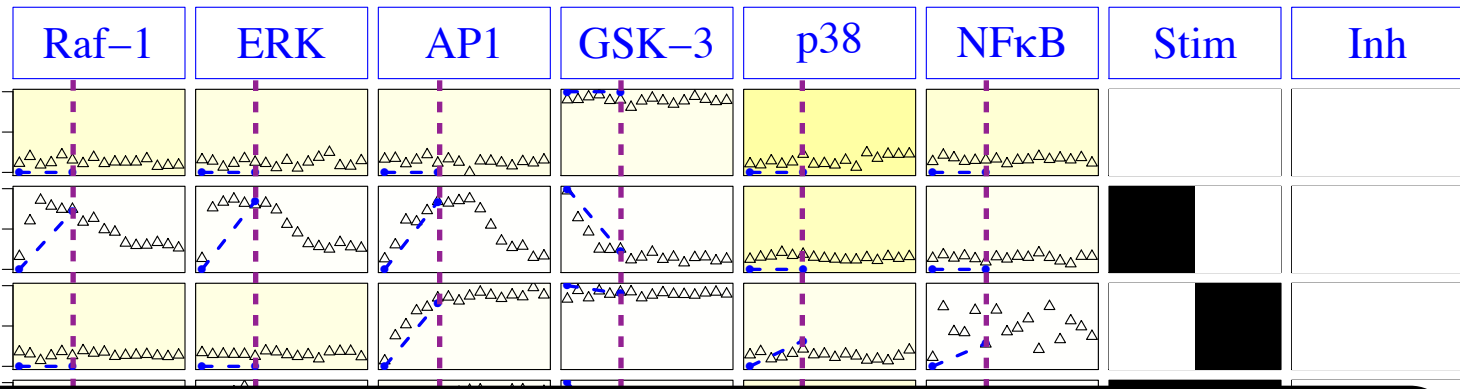
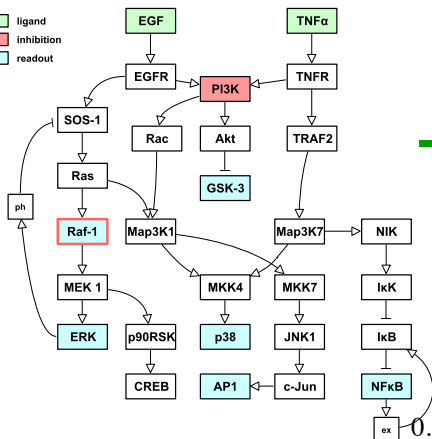
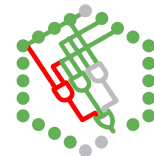


- Development of **Constrained Fuzzy Logic** & implementation within *CellNOpt*



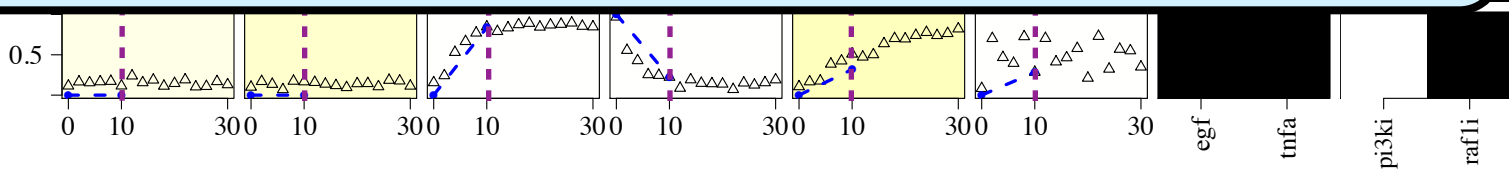
ligand
inhibition
readout

fit of fuzzy toy model

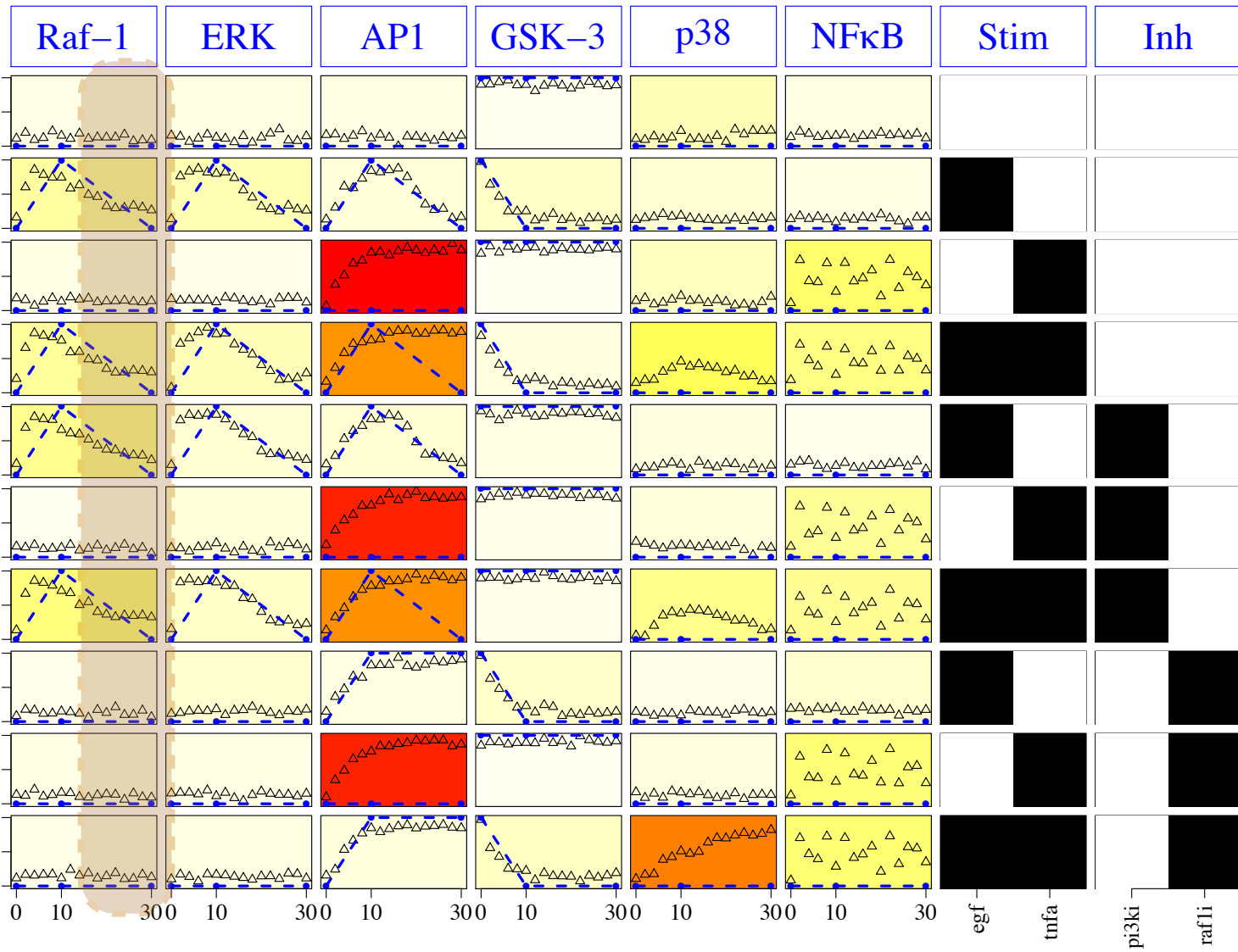
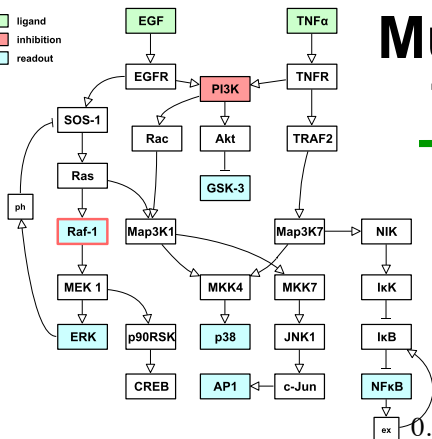
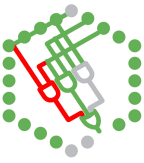


How can we model feedback effects?

MacNamara A Terfve C
Henriques D Penalver B
Saez-Rodriguez J
submitted

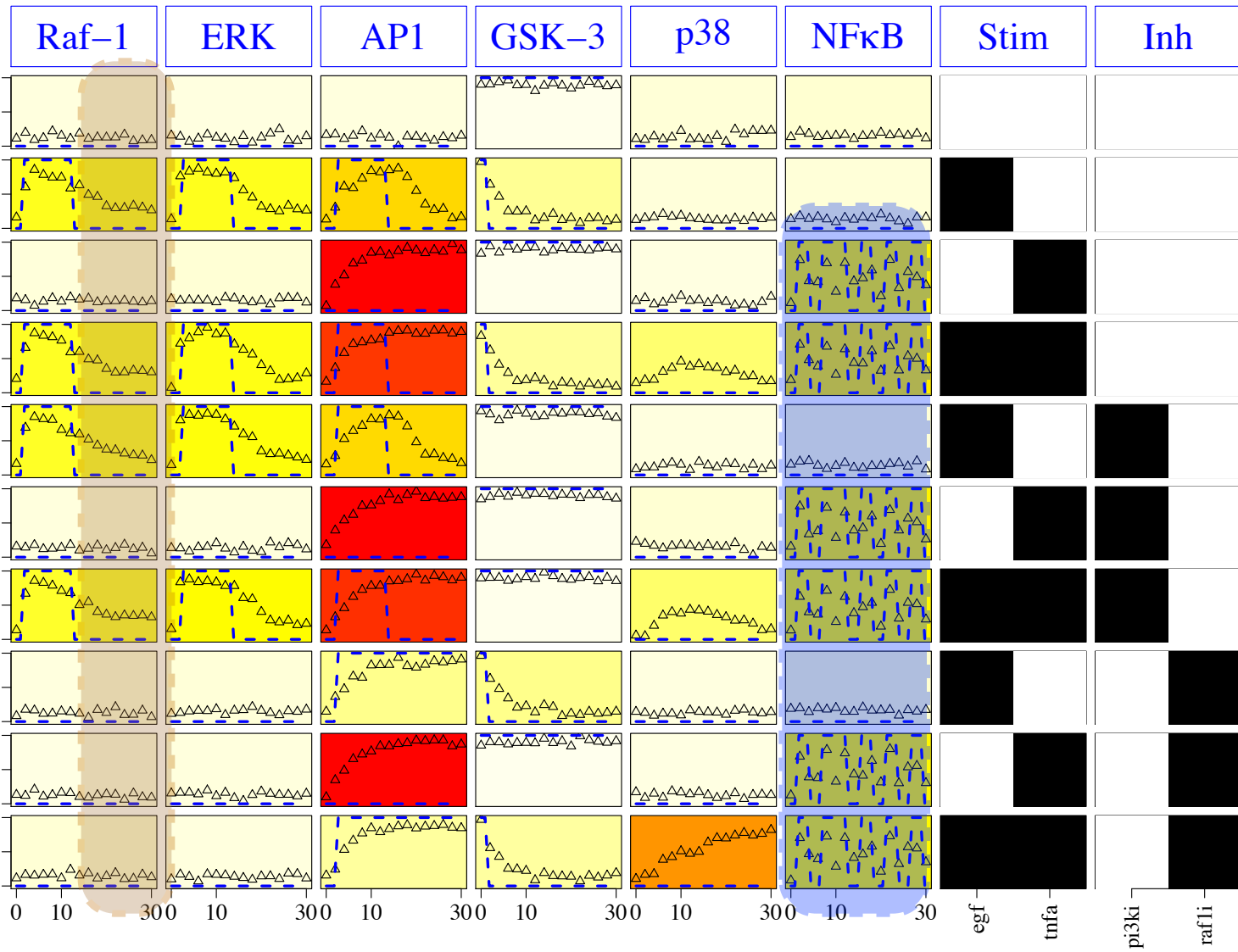
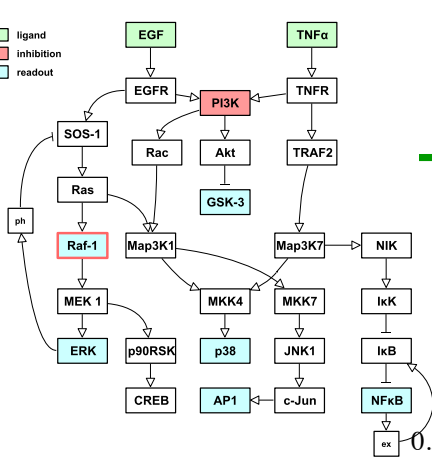
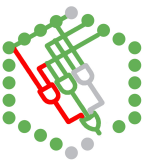


Multiple pseudo-steady-state simulations capture feedback effects that lead to transient signals



MacNamara A Terfve C
 Henriques D Penalver B
 Saez-Rodriguez J
 submitted

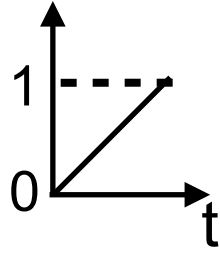
Synchronous simulation captures oscillatory behaviour



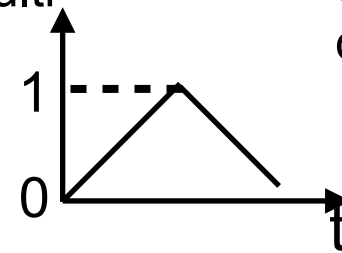
MacNamara A Terfve C
 Henriques D Penalver B
 Saez-Rodriguez J
submitted

From Boolean to continuous and dynamic models within *CellNOpt*

Boolean (binary)
logic steady state

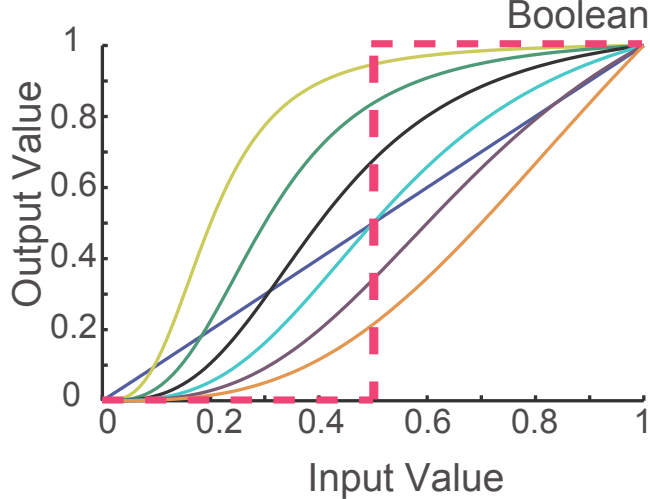


Boolean multi
time-scale



sync.
dynamics

Fuzzy logic (quantitative)



Morris et al., PloS Comp Bio 2011



Logic-based ODEs



- Convert Boolean update function B_i into a *continuous homologue* \bar{B}_i using multivariate polynomial interpolation (Odefy: Wittman et al)
 - **Accuracy** (same behavior as B_i for 0/1
→ same monotony & steady state behavior)
 - Good **analytical** properties (smoothness)
 - **Minimal and unique**

- Make non linear replacing variable with Hill function
- Transform into differential equation

$$f(\bar{x}_i) = \frac{\bar{x}_i^n}{(\bar{x}_i^n + k^n)}$$

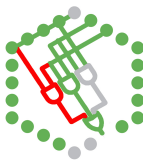
$$\bar{x}_i(t + 1) = \bar{B}_i(\bar{x}_{i1}(t), \bar{x}_{i2}(t), \dots, \bar{x}_{iN_i}(t))$$

$$\dot{\bar{x}}_i = \frac{1}{\tau_i} \cdot (\bar{B}_i(\bar{x}_{i1}, \bar{x}_{i2}, \dots, \bar{x}_{iN}) - \bar{x}_i)$$

- E.g. a AND b inactivate C

$$\frac{d}{dt}c = \frac{1}{\tau} \left(\frac{a^{n_a} * (1 + k_a^{n_a}) * (1 - b^{n_b}) * (1 + k_b^{n_b})}{(a^{n_a} + k_a^{n_a}) * (b^{n_b} + k_b^{n_b})} + \frac{(1 - a^{n_a}) * (1 + k_a^{n_a}) * b^{n_b} * (1 + k_b^{n_b})}{(a^{n_a} + k_a^{n_a}) * (b^{n_b} + k_b^{n_b})} + \frac{a^{n_a} * (1 + k_a^{n_a}) * b^{n_b} * (1 + k_b^{n_b})}{(a^{n_a} + k_a^{n_a}) * (b^{n_b} + k_b^{n_b})} - c \right)$$

ODEs can be automatically generated from Boolean model (Odefy)



$d/dt(tnfa) = 0*(1 - tnfa_inh)$ %Note that this implies a continuous stimulus

$d/dt(tgfa) = 0*$

$d/dt(raf) = ((egfr_inh)$

$d/dt(pi3k) = ((egfr_tauinv)*$
 $(1 - pi3k_inh)$

$d/dt(ikb) = ((tnfa$
 $(pi3k^{ikb_n_pi3k}$
 $+ ikb_k_tnfa^{ikb_n_pi3k}$
 $(1 + ikb_k_pi3k^{ikb_n_pi3k}$
 $* pi3k^{ikb_n_pi3k}$

$d/dt(gsk3) = ((gsk3_tauinv)*$

$d/dt(erk12) = ((ikb^{erk12_n_ikb}$
 $(raf^{erk12_n_ikb}$
 $+ erk12_k_ikb^{erk12_n_ikb}$
 $(1 + erk12_k_raf^{erk12_n_ikb}$
 $* erk12^{erk12_n_ikb}$

Problem: even if structure is known need Identify parameters, difficult optimisation problem (collab with J. Banga group)

$$\frac{d}{dt} c = \frac{1}{\tau} \left(\frac{a^{n_a} * (1 + k_a^{n_a}) * (1 - k_b^{n_b}) * (1 + k_b^{n_b})}{(a^{n_a} + k_a^{n_a}) * (b^{n_b} + k_b^{n_b})} + \frac{(1 - a^{n_a}) * (1 + k_a^{n_a}) * b^{n_b} * (1 + k_b^{n_b})}{(a^{n_a} + k_a^{n_a}) * (b^{n_b} + k_b^{n_b})} + \frac{a^{n_a} * (1 + k_a^{n_a}) * b^{n_b} * (1 + k_b^{n_b})}{(a^{n_a} + k_a^{n_a}) * (b^{n_b} + k_b^{n_b})} - c \right)$$

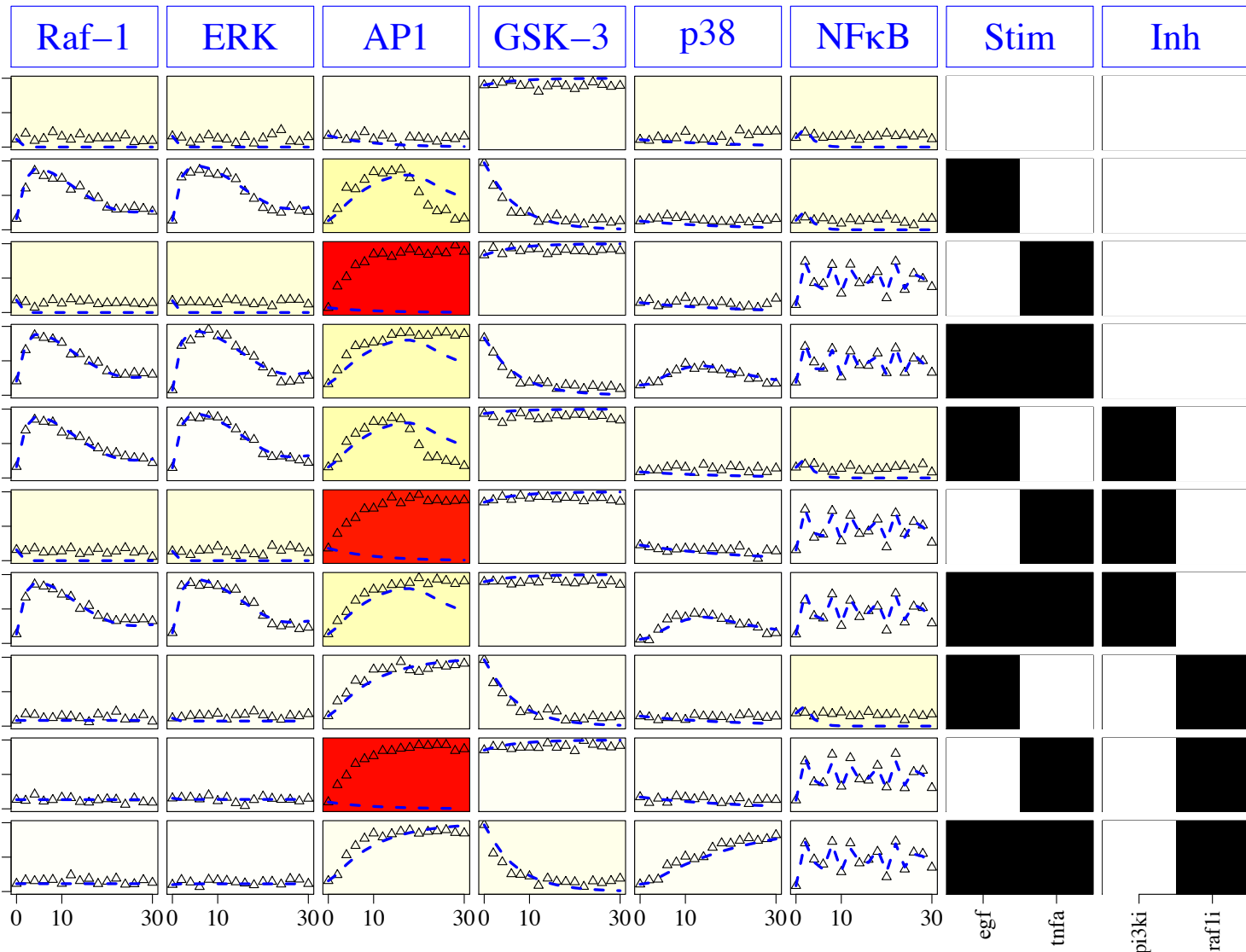
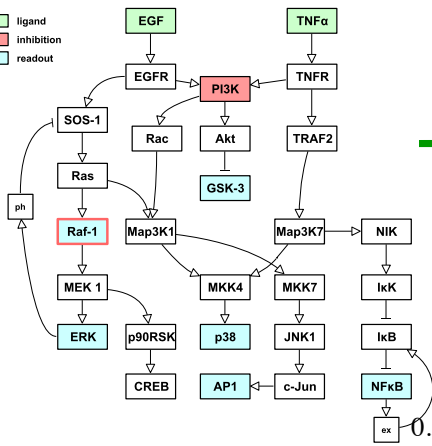
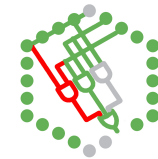
$d/dt(egfr) = ((tgfa^{egfr_n_tgfa} / (tgfa^{egfr_n_tgfa} + egfr_k_tgfa^{egfr_n_tgfa}) * (1 + egfr_k_tgfa^{egfr_n_tgfa}) - egfr) * egfr_tauinv) * (1 - egfr_inh)$

$d/dt(casp8) = ((tnfa^{casp8_n_tnfa} / (tnfa^{casp8_n_tnfa} + casp8_k_tnfa^{casp8_n_tnfa}) * (1 + casp8_k_tnfa^{casp8_n_tnfa}) - casp8) * casp8_tauinv) * (1 - casp8_inh)$

$d/dt(akt) = ((pi3k^{akt_n_pi3k} / (pi3k^{akt_n_pi3k} + akt_k_pi3k^{akt_n_pi3k}) * (1 + akt_k_pi3k^{akt_n_pi3k}) - akt) * akt_tauinv) * (1 - akt_inh)$

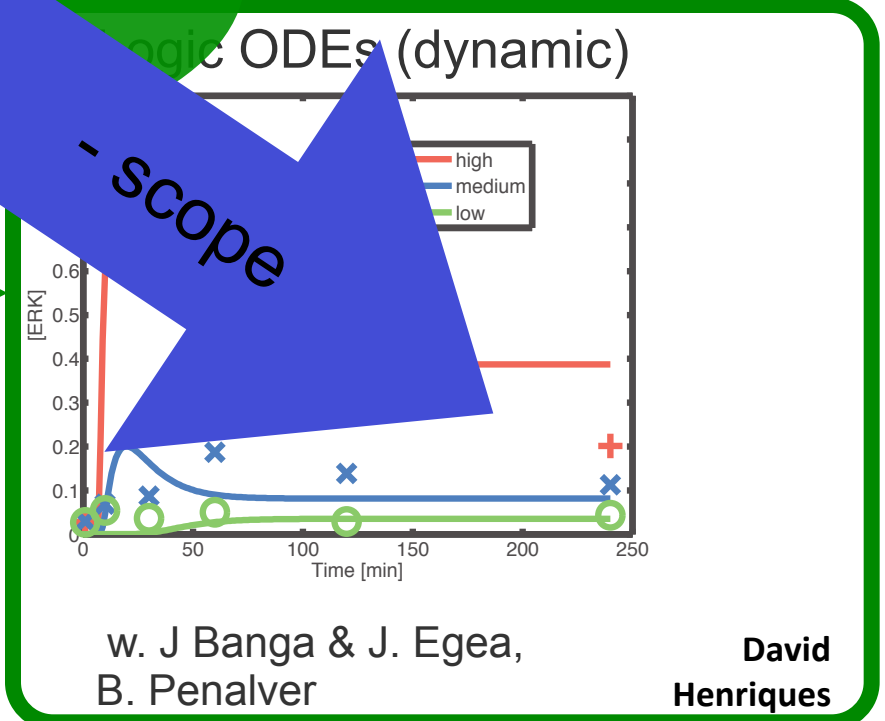
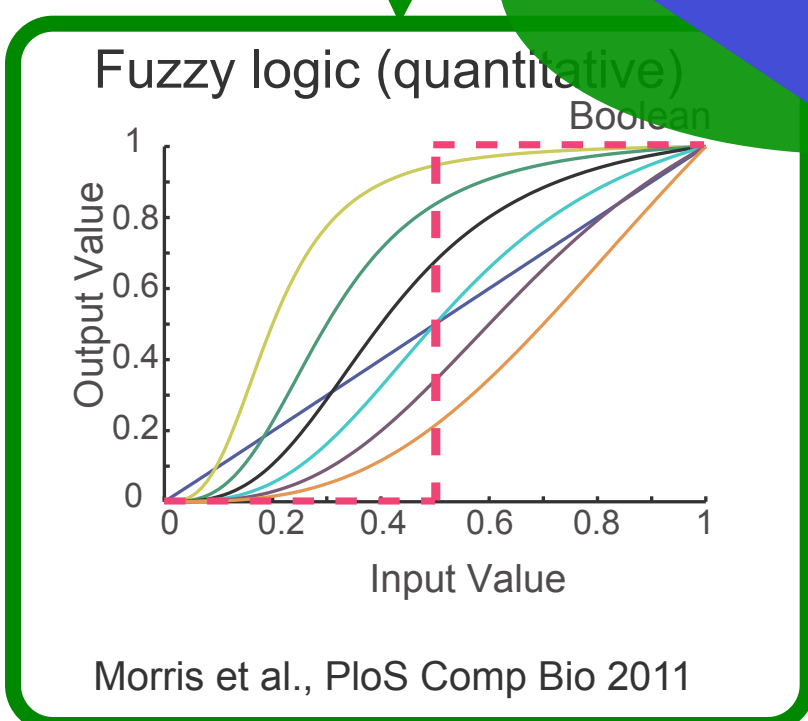
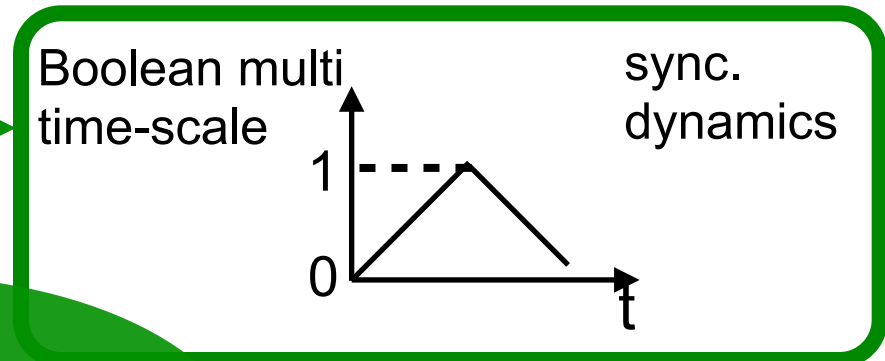
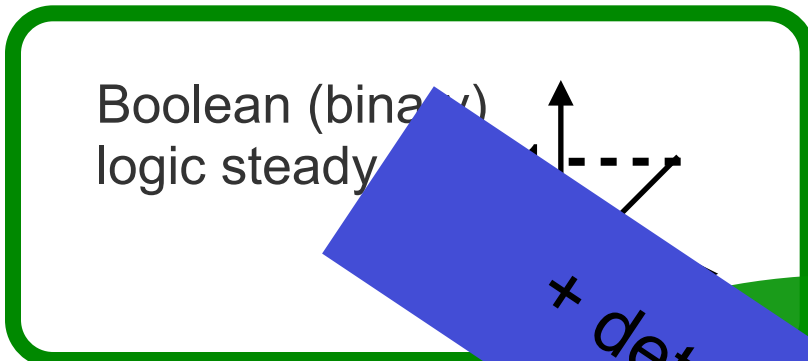
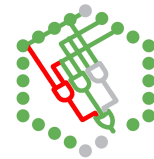
█ ligand
█ inhibition
█ readout

Fit of ODE model



MacNamara A Terfve C
 Henriques D Penalver B
 Saez-Rodriguez J
submitted

From Boolean to continuous and dynamic models within *CellNOpt*

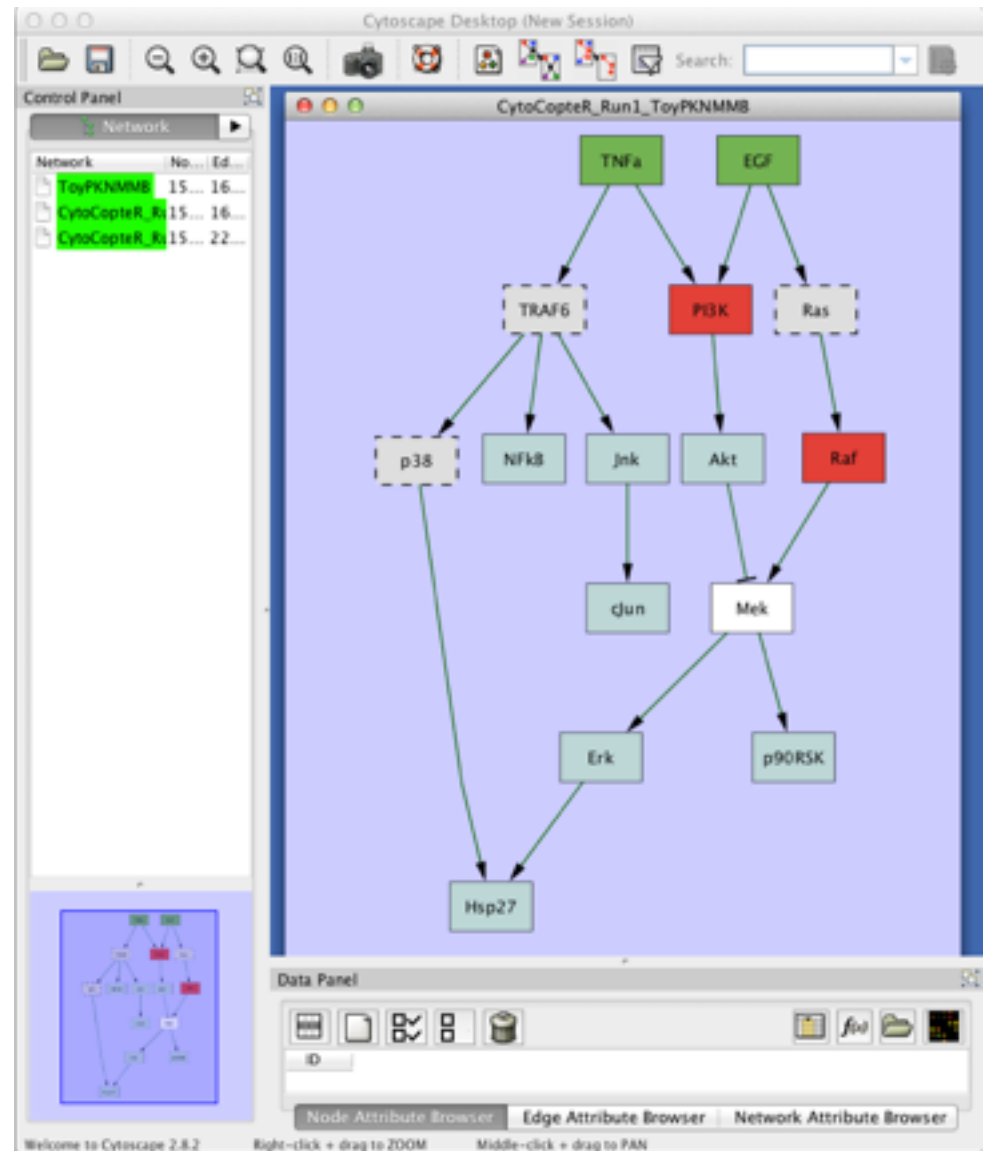
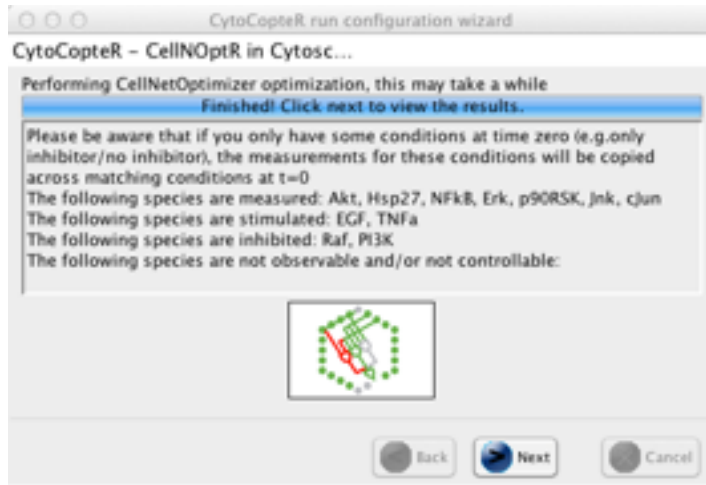
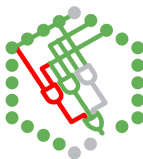


+ detail

- scope



Cytoscape plugin (Cytocopter)



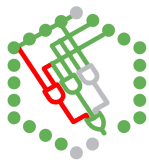
Martijn van Iersel



Emanuel Gonçalves



Explore sources of prior knowledge

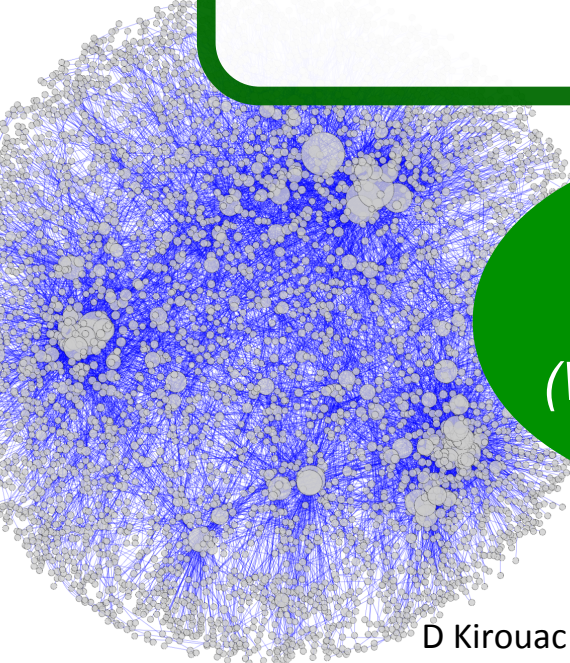
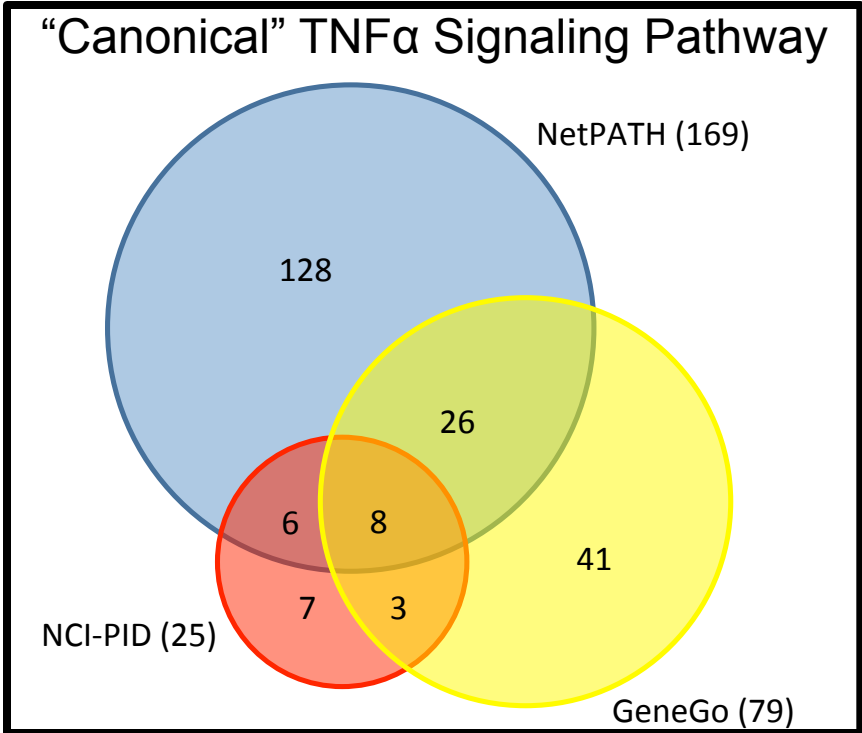


- **Databases** of curated **pathways** (Reactome, KEGG, Wikipathways, ...) incomplete, low overlap, different qualities
 - Path2Models (standardized pathway resources: w. LeNovere)
- Protein **Interaction** Networks
- Literature mining

Link CellNOpt to methods to infer new links



Federica Eduati



collaborative efforts (WikiPathways)?

D Kirouac
J Saez-Rodriguez
et al, *submitted*

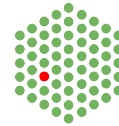
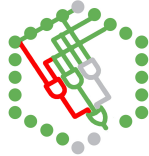


Martijn van Iersel



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www.ebi.ac.uk/saezrodriguez



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