



# Cell Collective tutorial

Tomas Helikar

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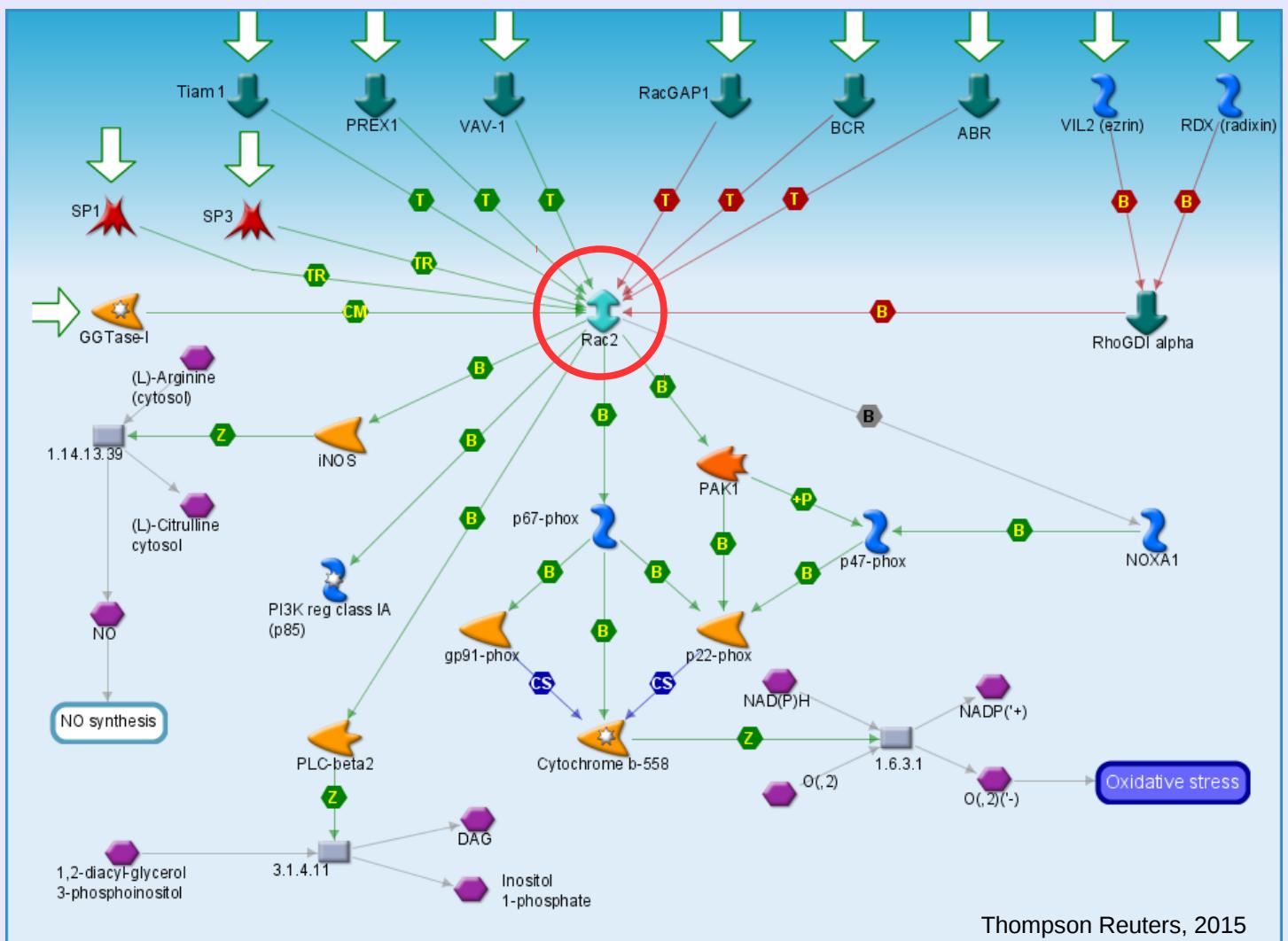


# Computational Modeling Challenges

- Combinatorial explosion of the number of states with the number of components ( $2^n$  states for  $n$  network components)
- Scalability of creating large-scale and accurate models
- Model transparency (can I believe the model?)
- Model (re-)usability and sharing



# Challenge: Complexity



Thompson Reuters, 2015



# Mathematical description of the regulatory mechanism of Rac

$$\begin{aligned} & (RasGRF \wedge \neg(RhoGDI \wedge \neg PAK) \wedge \neg(p190RhoGAP \wedge Rac) \wedge \neg(RalBP1 \wedge Rac) \\ & \wedge ECM \wedge Integrins) \vee (Tiam \wedge \neg(RhoGDI \wedge \neg PAK) \wedge \neg(p190RhoGAP \wedge Rac) \\ & \wedge \neg(RalBP1 \wedge Rac) \wedge (ECM \wedge Integrins)) \vee (Pix_{Cool} \wedge \neg(RhoGDI \wedge \neg PAK) \\ & \wedge ((PAK \wedge G\beta\gamma \wedge ((\neg Cdc42 \wedge \neg Rac) \wedge (Integrins \wedge ECM))) \vee (\neg G\beta\gamma \wedge (Cdc42 \\ & \wedge (Integrins \wedge ECM) \wedge \neg Rac)) \vee (\neg PAK \wedge (\neg RhoGDI \wedge (\neg DOCK180 \wedge \neg(RhoGDI \wedge \neg PAK) \\ & \wedge \neg(p190RhoGAP \wedge Rac) \wedge \neg(RalBP1 \wedge Rac) \wedge \neg RasGRF \wedge \neg(RhoGDI \wedge \neg PAK) \\ & \wedge \neg(p190RhoGAP \wedge Rac) \wedge \neg(RalBP1 \wedge Rac) \wedge \neg Tiam \wedge \neg(RhoGDI \wedge \neg PAK) \\ & \wedge \neg(p190RhoGAP \wedge Rac) \wedge \neg(RalBP1 \wedge Rac)) \wedge (Integrins \wedge ECM) \wedge Cdc42 \wedge \neg Rac))) \\ & \vee (DOCK180 \wedge \neg(RhoGDI \wedge \neg PAK) \wedge \neg(p190RhoGAP \wedge Rac) \wedge \neg(RalBP1 \wedge Rac) \\ & \wedge (ECM \wedge Integrins)) \end{aligned} \tag{1}$$

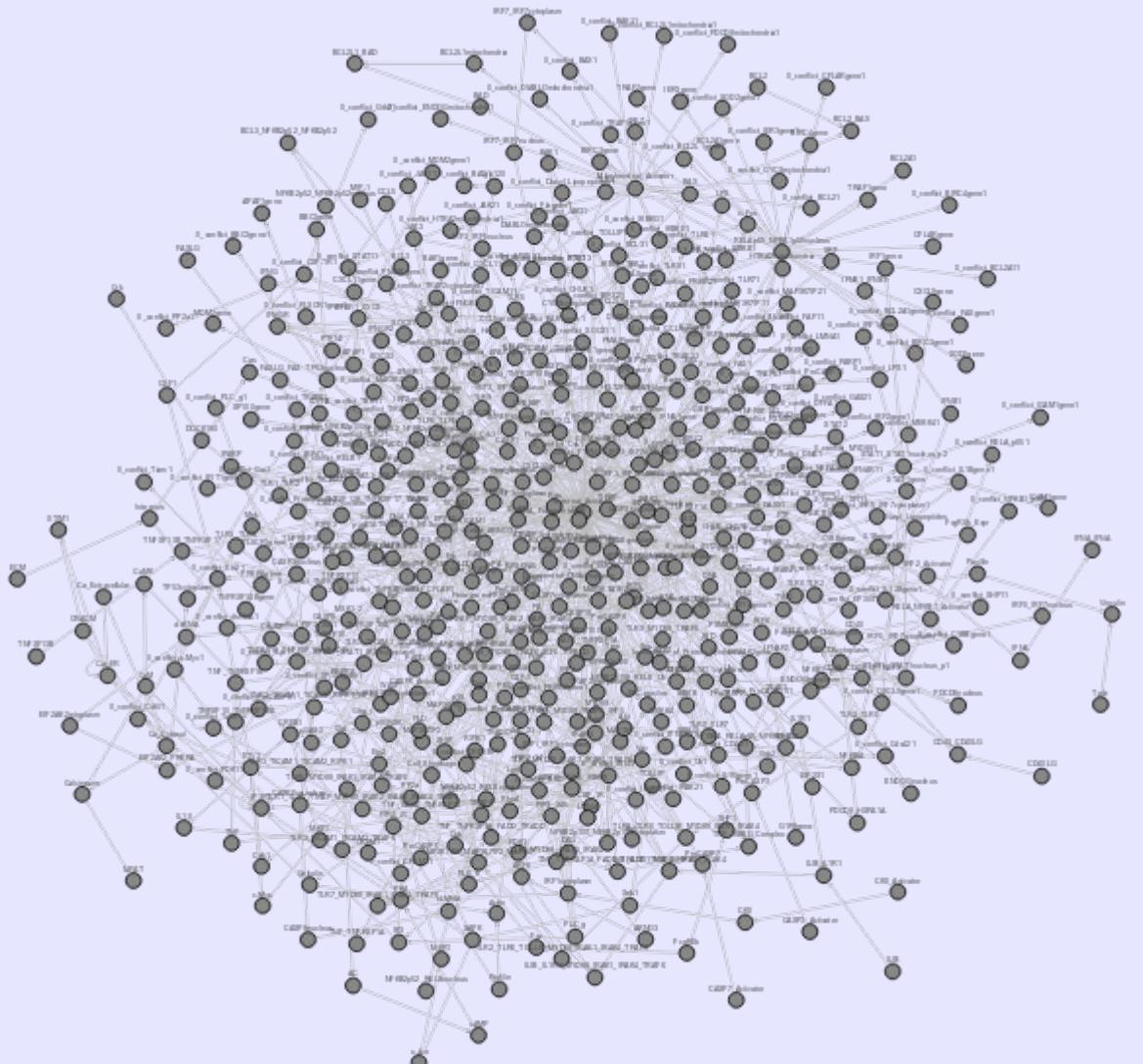
(Helikar et. al. 2013. PLoS One 8(4):e61757)



# Challenge: Size



# Macrophage Signaling and Gene Regulation



- 1,600+ components  
(proteins/protein complexes, genes, etc.)
  - HIV replication cycle
  - CCR5 (gp120, MIP-1)
  - CSF1
  - Integrin
  - IFNGR
  - Fcgr (FcgrIIb)
  - Toll-like Receptor
  - Interferon (alpha, beta, gamma)
  - NF- $\kappa$ B
  - Apoptosis (FAS, TNF)

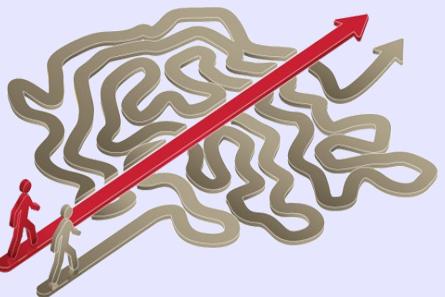


# Cell Collective Overview

**Cell Collective:** <https://www.cellcollective.org>

## Accessibility

... to non-modelers



## Collaboration

## Scalability

... bigger and more accurate  
models

## Transparency

... can I believe the models??

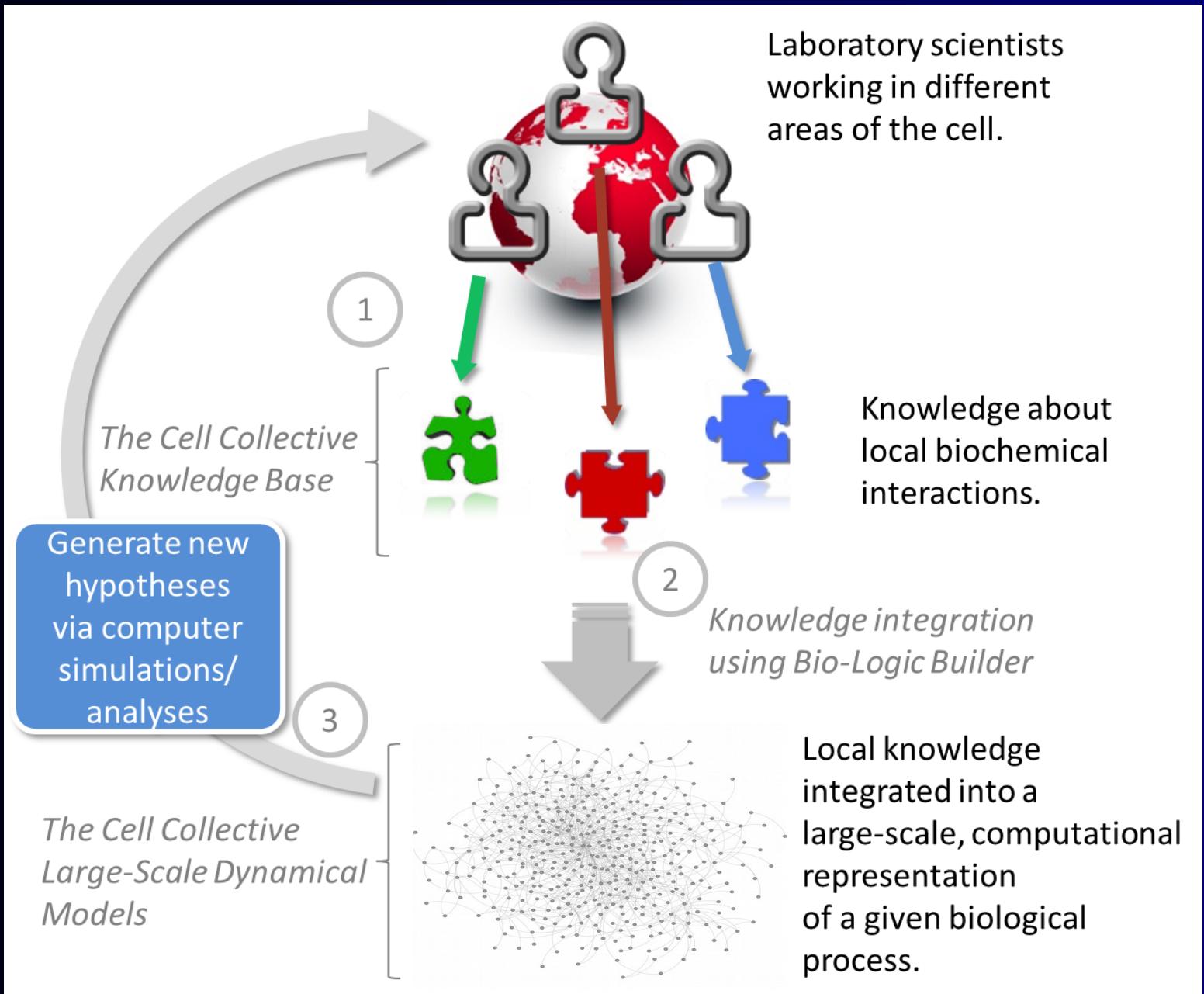


## Re-usability & Reproducibility

(Helikar et. al. 2012. BMC Systems Biology. 6:96; Helikar et. al. 2013. Clin Pharm & Ther.)

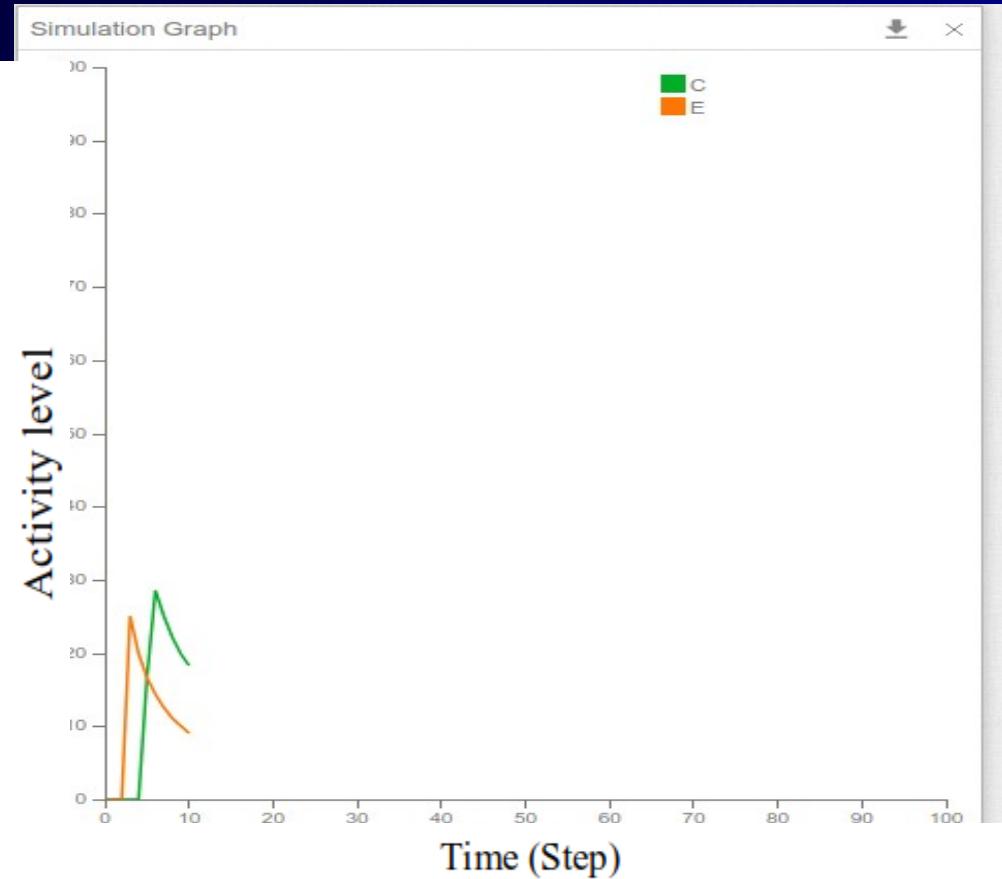
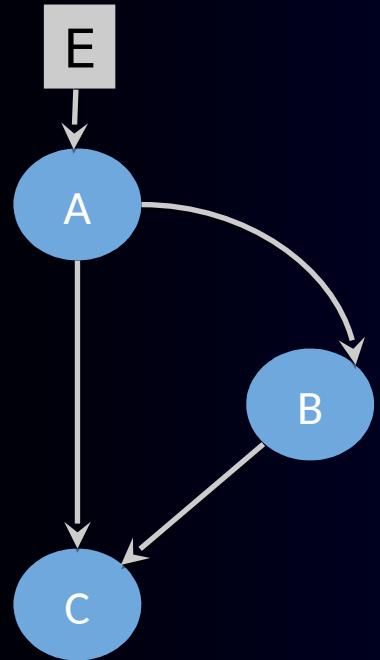


# Cell Collective Overview





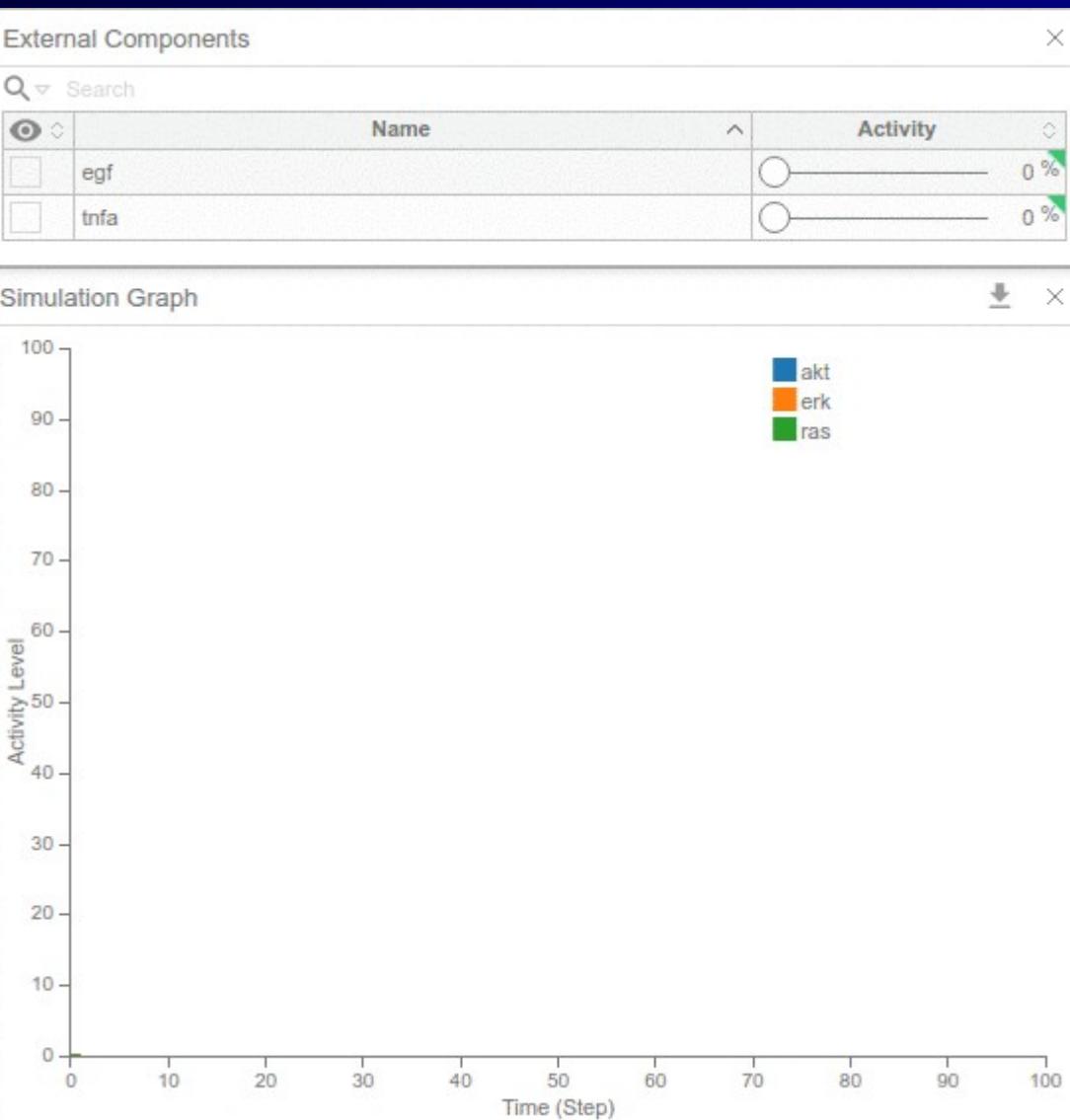
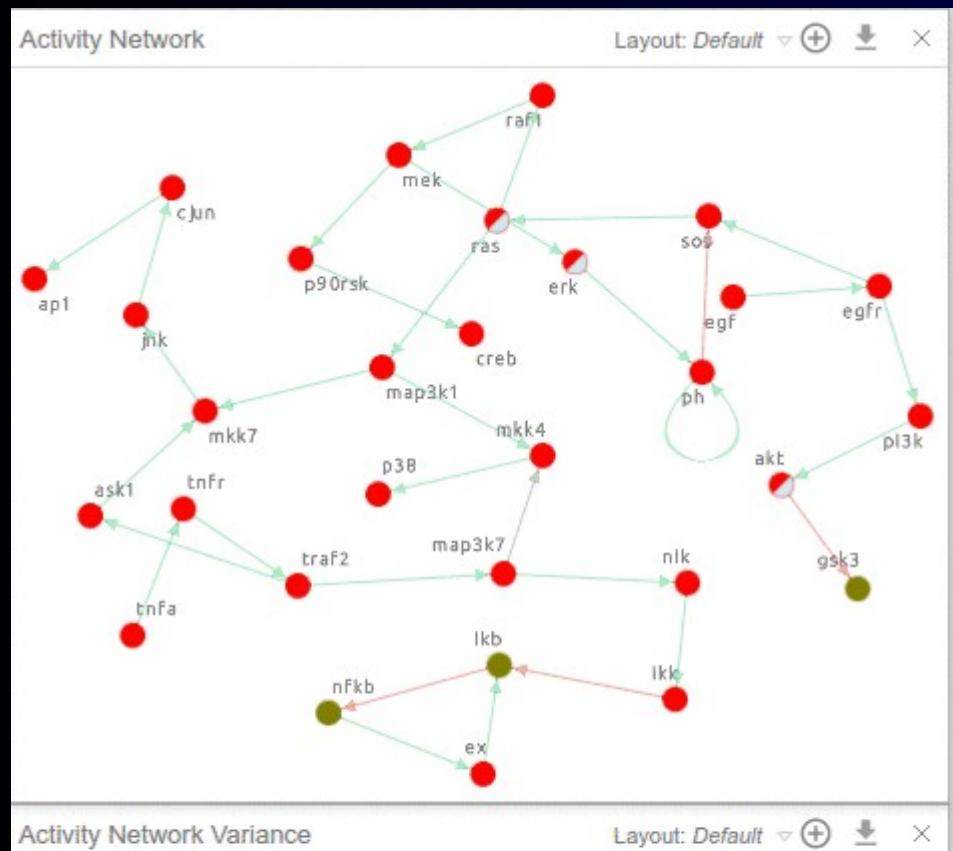
# Logical Model



- Mechanistic
- Qualitative logic, i.e., “Proteins A or B activate protein C” ( $A \vee B \rightarrow C$ )
- (Kinetic) parameter independent
- Efficient simulations

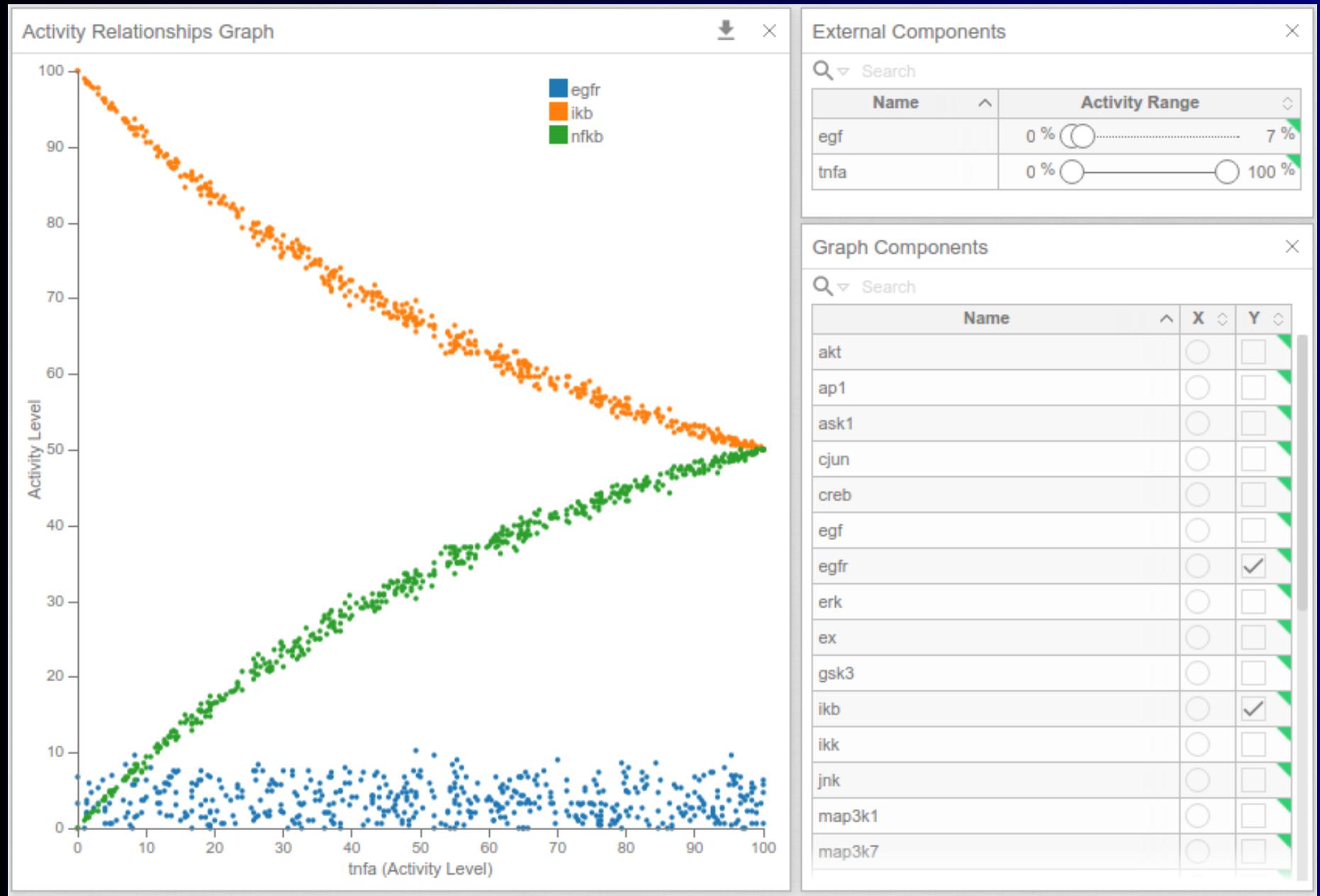


# Cell Collective Real-Time Simulations



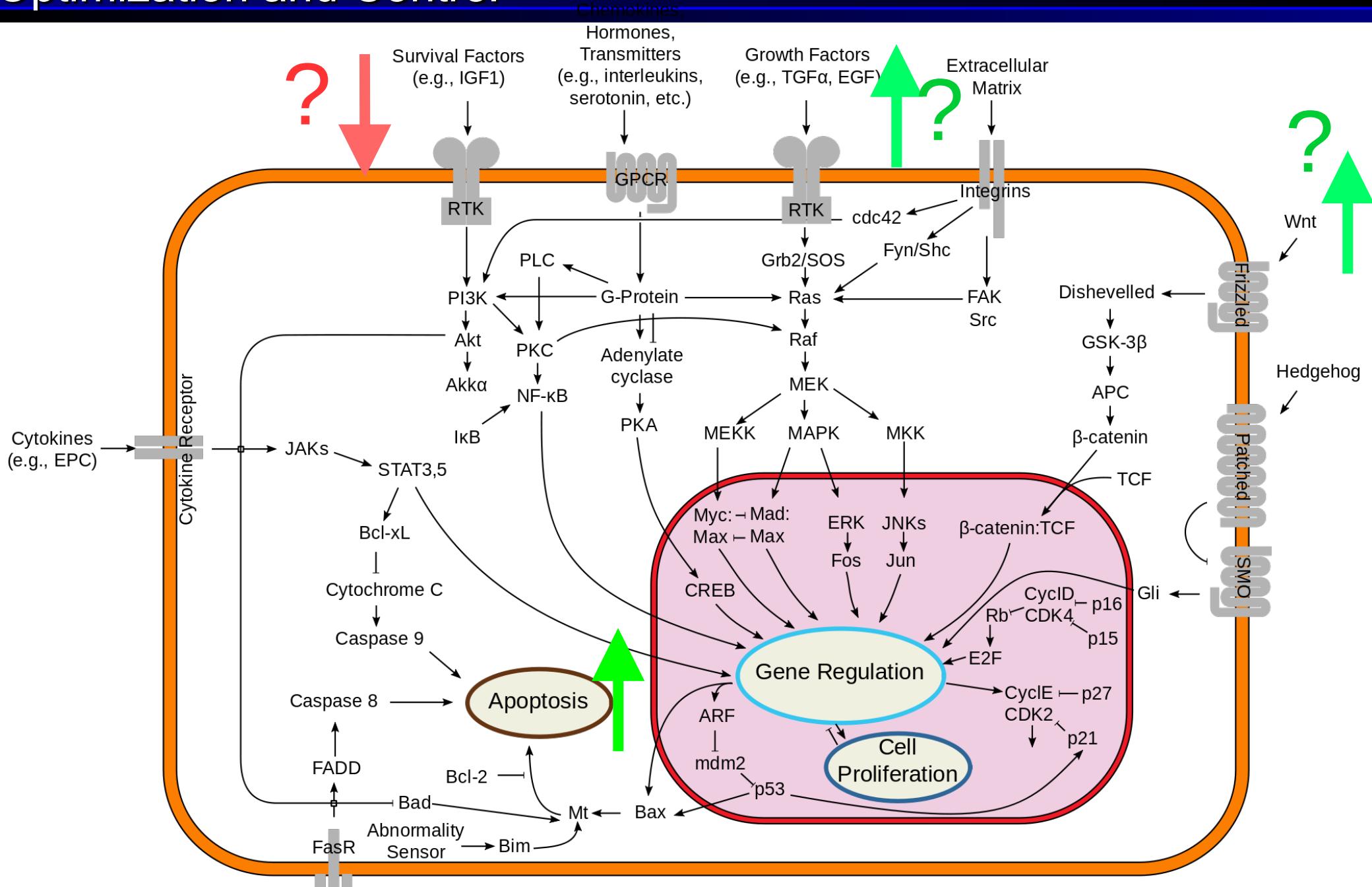


# Input-Output Analysis (titration curves)





# Optimization and Control





# Cell Collective: Models annotation and transparency

**cellcollective**

IGV mutations in chronic lymphocytic leukemia.

- Knowledge Base
- Simulation
- Analysis
- Model
- Description

**Components**

Name
ADM
AEBP1
AFF1
AICDA
AKAP12
AKT3
ALOX5
ANXA2
APLP2
APOBEC3G
APP
BLNK
BMI1
CASP3
CAV1
CCL5
CCND2
CD27
CD63
CD69
CD70

**Knowledge Base ADM**

**Description**

- Adrenomedullin
- Gene ID: 133
- ADM and PAMP act as hypotensive and vasodilator agents. Both mediate the loss of plasma volume in the brain and pituitary gland and inhibit aldosterone secretion. (Álvarez-Silva MC, 2015)
- Gene: ADM
- UniProt ID: P35318

**Regulatory Mechanism Summary**

HSP90AA1 or TNF in conjunction with HSP90AA1 activates ADM. (Hofbauer KH, 2002) (Masoud GN, 2015)

**Upstream Regulators**

**HSP90AA1**  
HSP90AA1 indirectly upregulates ADM expression. (Masoud GN, 2015)

**TNF**  
Cells treated with TNF showed upregulation of ADM mRNA. (Hofbauer KH, 2002)

**References**

1. Hofbauer KH, Schoof E, Kurtz A, and Sandner P. Inflammatory cytokines stimulate adrenomedullin expression through nitric oxide-dependent and -independent pathways. *Hypertension* 2002 Jan;39;(1) 161-7. pmid:11799096
2. Masoud GN and Li W. HIF-1α pathway: role, regulation and intervention for cancer therapy. *Acta Pharm Sin B* 2015 Sep;5;(5) 378-89. pmid:26579469
3. Álvarez-Silva MC, Yepes S, Torres MM, and Barrios AF. Proteins interaction network and modeling

**Reference Graph**

Layout: Default



# Cell Collective: Collaboration and Model Repository

SBML Qual Paper Final Model demo

Knowledge Base   Simulation   Analysis   Model   Description

Share with Collaborators   +   -   X

Search

Email: audrey.crowther@huskers.unl.edu

PUBLISH   Model cannot be published.

Publishing requirements

✗ *Model has to have been included in at least one peer-reviewed publication.*  
There are no publications associated with this model (You can add publications under the Description page).

✗ *Each model component should be annotated in the knowledge base in an effort to make models more reproducible, transparent and accessible to the community.*  
Components without knowledge base information:

akt ap1 ask1 cjun creb egf egfr erk ex gsk3 ikb ikk jnk map3k1 map3k7 mek  
mkk4 mkk7 nfkb nik p38 p90rsk ph pi3k raf1 ras sos tnfa tnfr traf2

✓ *User profile of the model owner has to be filled.*

Experiments Publishing

Search

Name: TNFalpha titration

Shareable Links   +   -   X

Search

Link: https://cellcollective.org/#a2b73520-ffc4



# Cell Collective: Collaboration and Model Repository

Published Models (76) My Models (45) Shared with Me (133)



## RECENTLY PUBLISHED

### Mammalian Cell Cycle

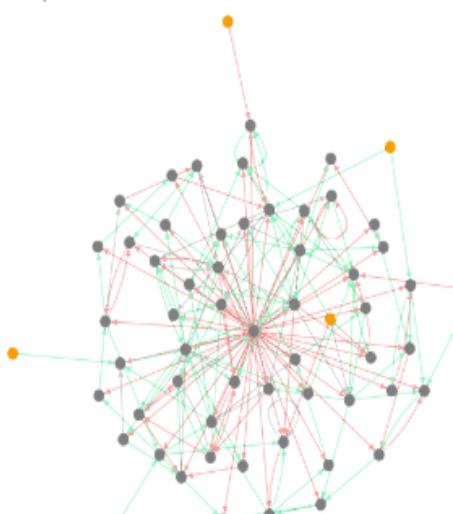
version 1.0  
Components: 20  
Interactions: 51



Author: O Sahin et. al.  
Score: 51.1  
Created: 10/19/2011  
Cited: 124  
Updated: 6/7/2018

### T-LGL Survival Network 2011

version 1.0  
Components: 60  
Interactions: 195



Author: A Sadatpour et. al.  
Score: 30.0  
Created: 6/2/2014  
Cited: 56  
Updated: 6/5/2018

### Aurora Kinase A in Neuroblastoma

version 1.0  
Components: 23  
Interactions: 43



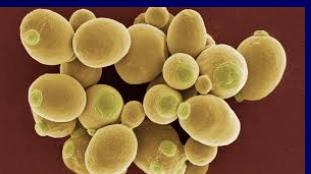
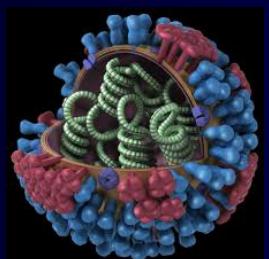
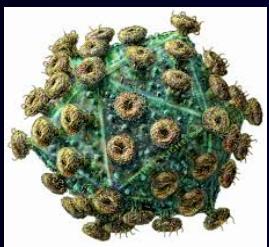
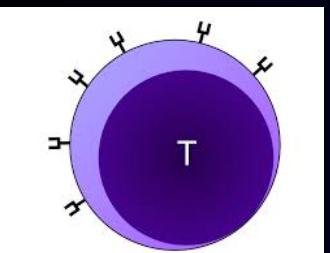
Author: M Dahlhaus et. al.  
Score: 25.0  
Created: 4/20/2017  
Cited: 0  
Updated: 4/23/2018

### Yeast Apoptosis

version 1.0  
Components: 73  
Interactions: 114



Author: L Kazemzadeh et. al.  
Score: 48.0  
Created: 6/4/2013  
Cited: 10  
Updated: 4/18/2018





## Example Case Studies



# Applications and Case Studies

Hamid Band, M.D., Ph.D.  
Mayumi Naramura, M.D.

Howard Fox, M.D., Ph.D.  
Pawel Ciborowski, Ph.D.  
Christine Cutucache, Ph.D.

(Helikar T, et.al. 2012.  
PLoS One, 8(4):e61757)

Christine Cutucache, Ph.D

Caveolin1  
In  
T Cells

(Conroy et. al. 2014.  
Frontiers Immunology,  
*Under Review*)

Robb Todd, Ph.D

Yeast Cell  
Cycle

(Madrahimov et. al. 2012.  
*Bull Math Biol*,  
75(6):988-1011)

Immune  
System

Cell Collective

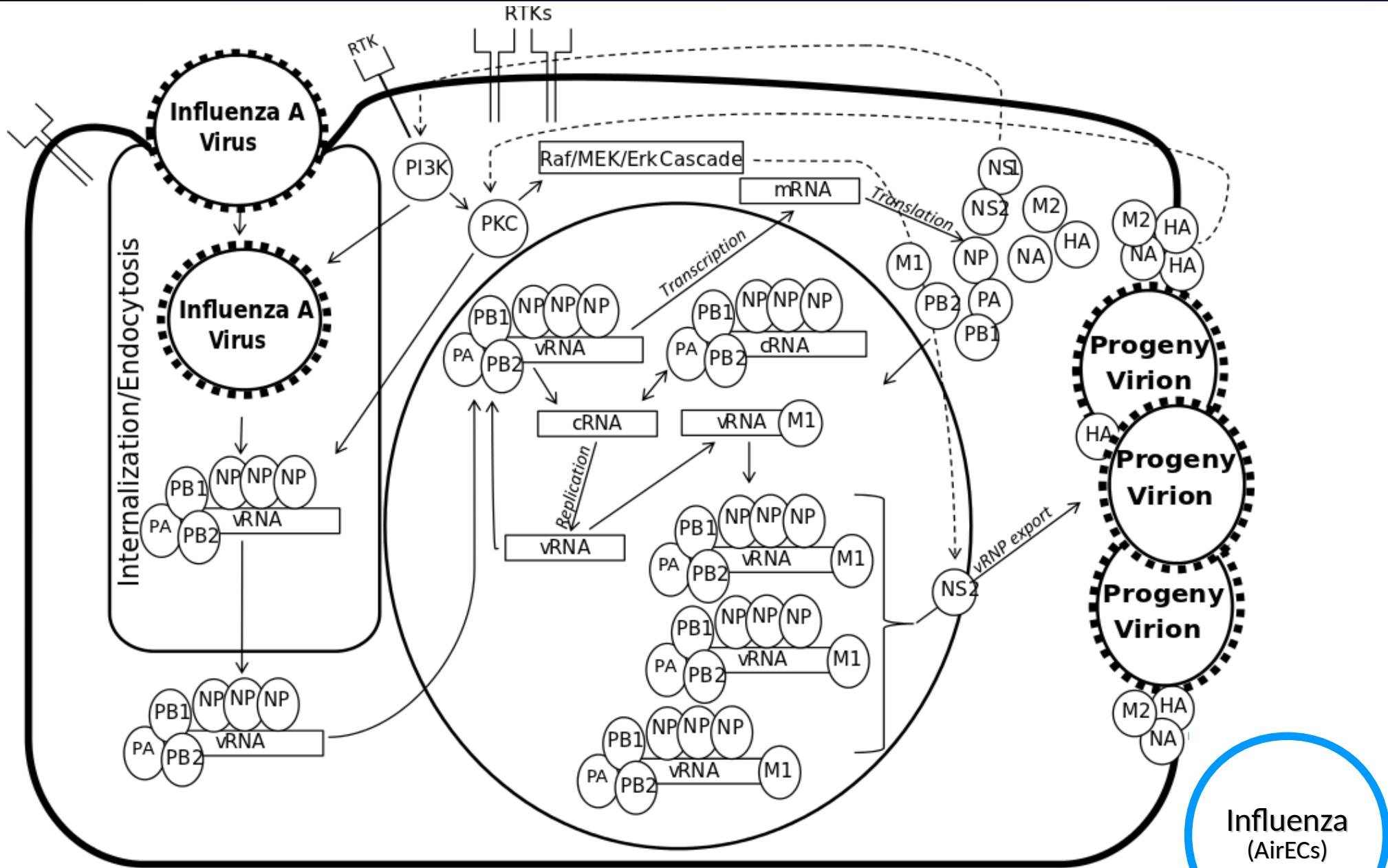
Influenza  
(AirECs)

(Todd R & Helikar T. 2012.  
PLoS One, 7(10):e45780)

Breast  
Cancer  
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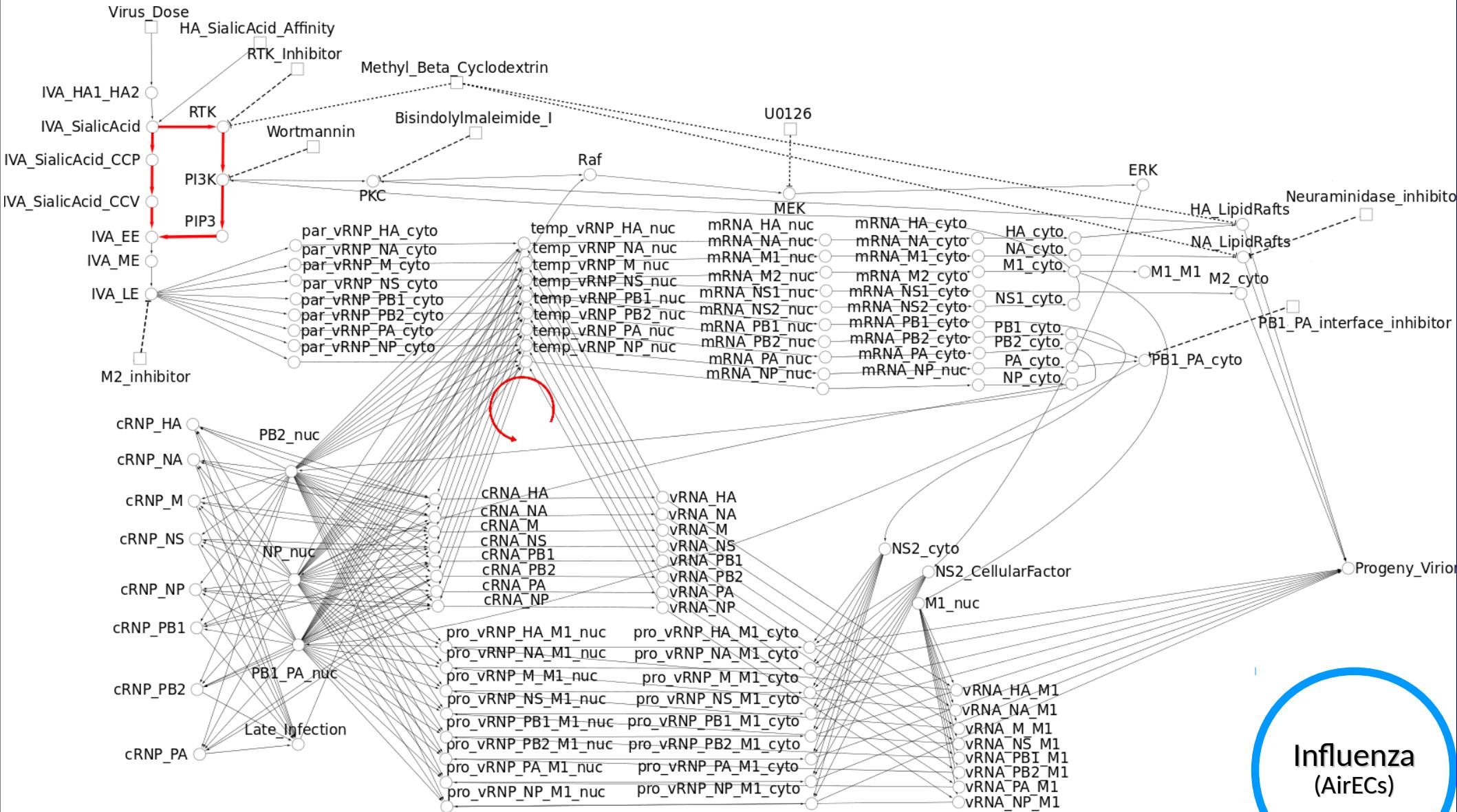


# Influenza Infection Dynamics



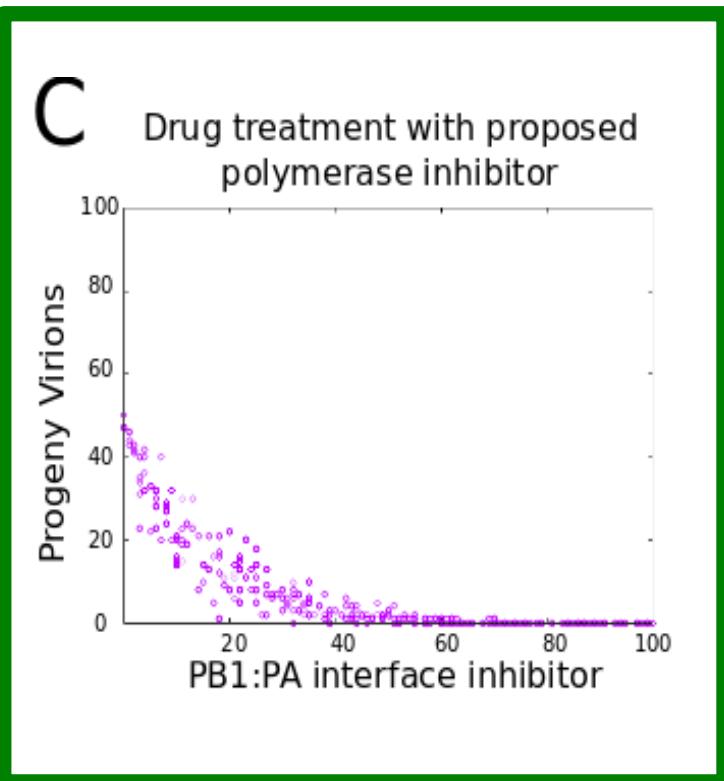
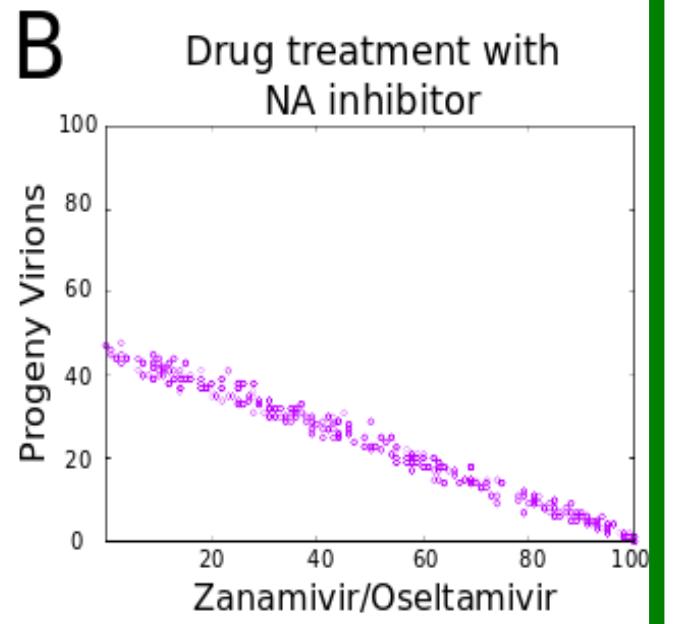
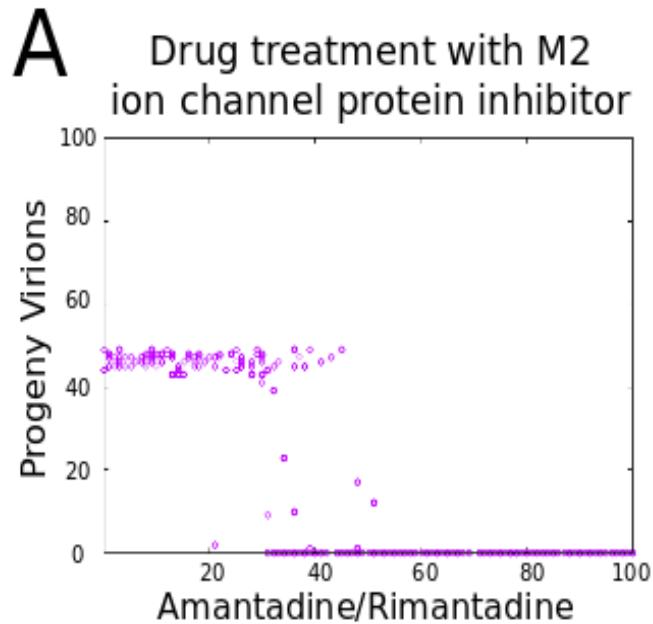


# Influenza Infection Dynamics





# Influenza Infection Dynamics



Progeny virion exit

Virus entry

Viral replication

Influenza  
(AirECs)



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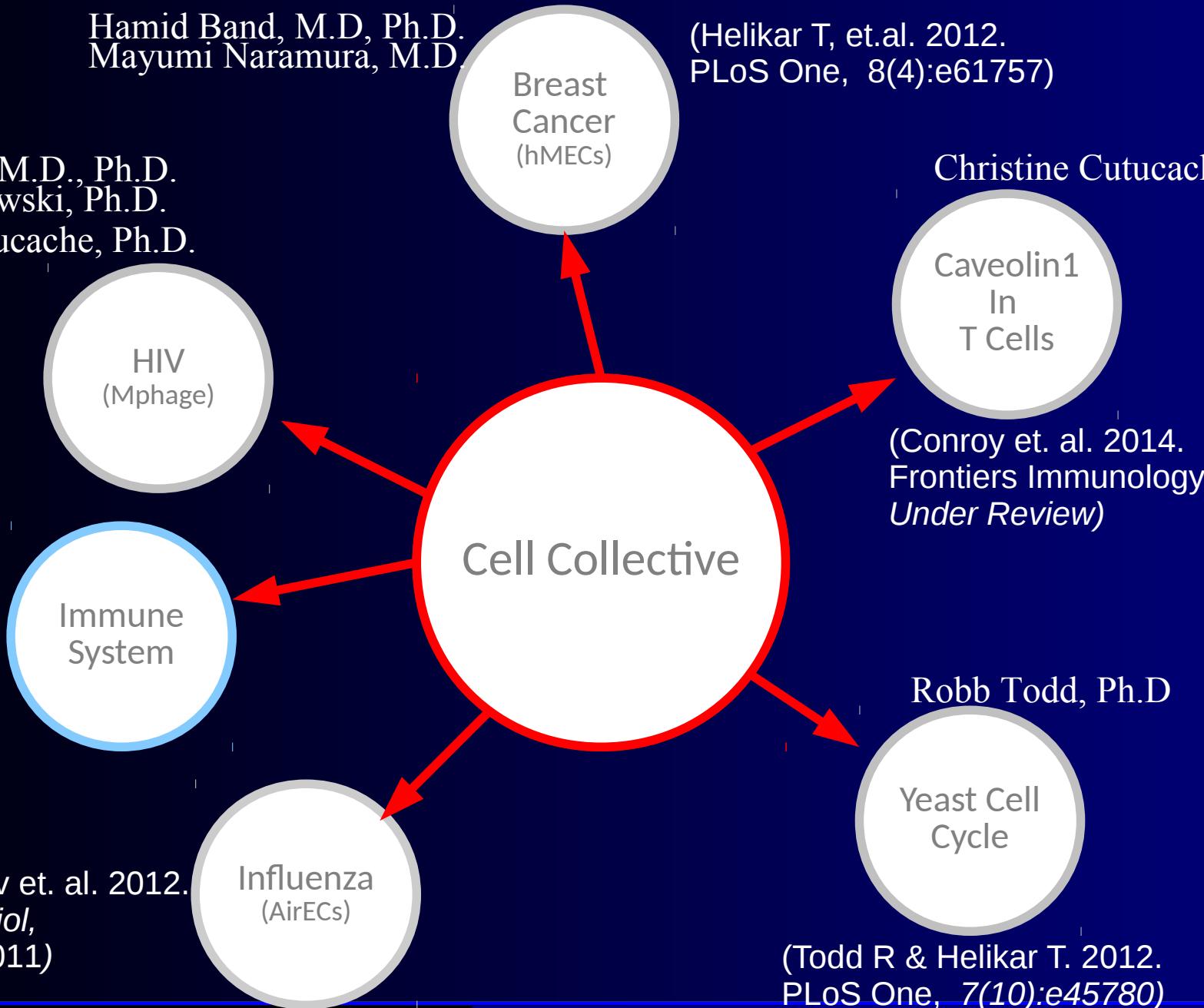
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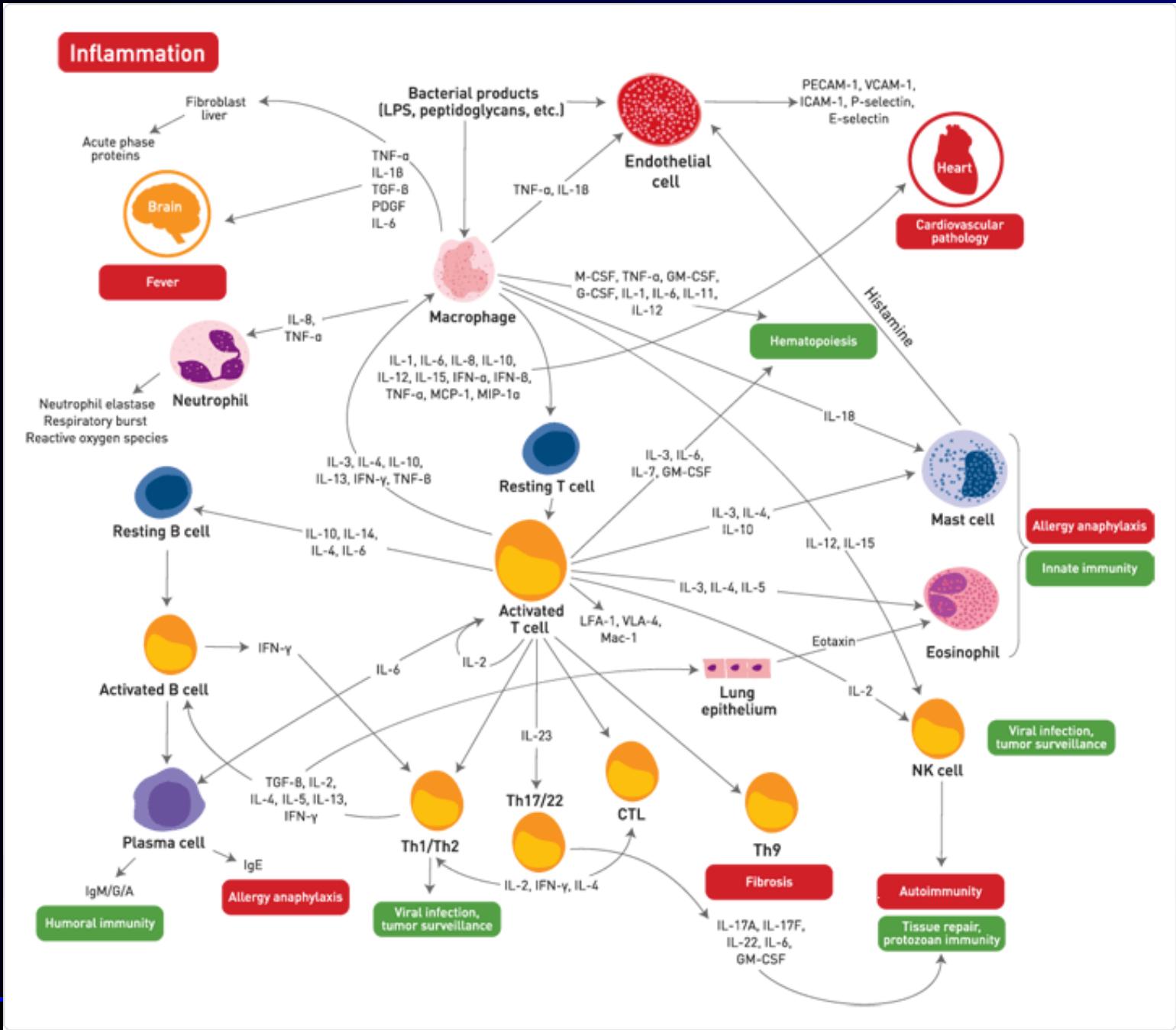
Yeast Cell  
Cycle

(Todd R & Helikar T. 2012.  
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# Immune system dynamics



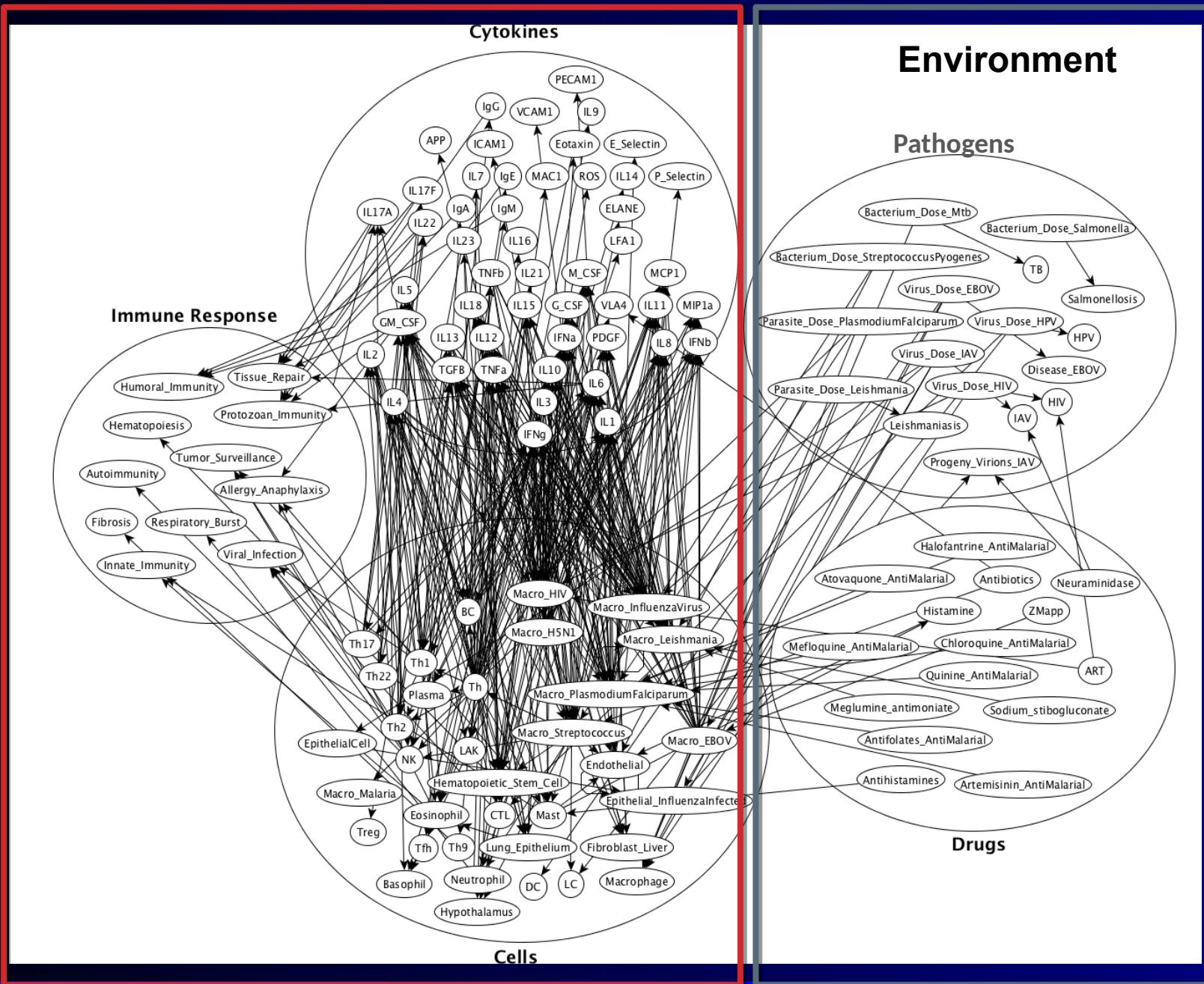


# Comprehensive Computational Model of the Immune System

- \* 164 Components
- \* 9 Pathogens:

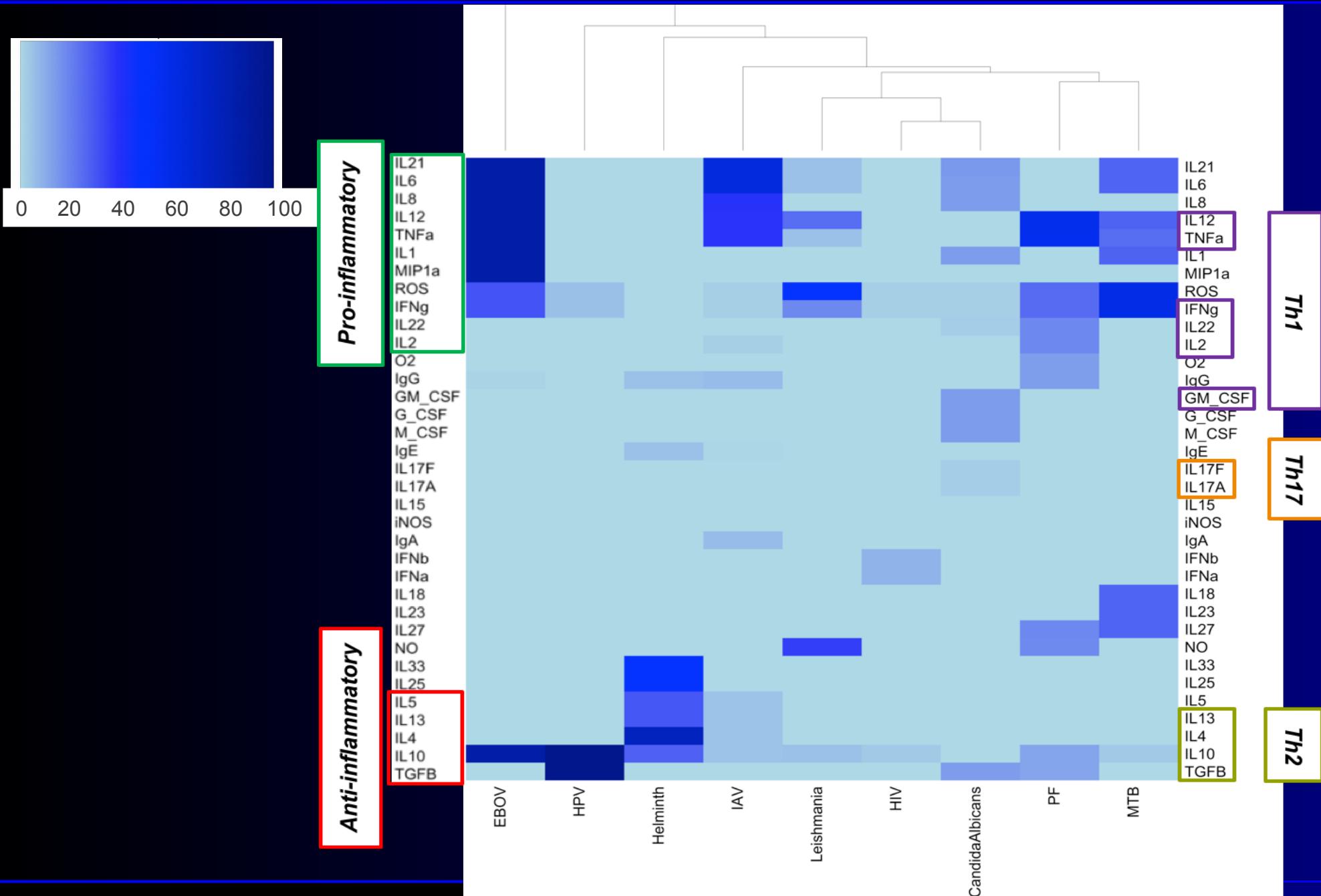
*Mtb*  
*Helminth*  
*Influenza*  
*Ebola*  
*HIV*  
*HPV*  
*Leishmania*  
*Candida Albicans*  
*Plasmodium Falc*

- \* 35 Cytokines
- \* 26 Cell types
- \* 506 interactions
- \* 224 papers





## Model Simulations





## Comprehensive Computational Model of the Immune System - validation

Infectious Agent	Cell Target	Immune Response	Reference
<i>HIV</i>	DCs, Macrophages, CD4 T	Th1, Th2, CD8+	<i>Banks et al. 2008</i>
<i>HPV</i>	Keratinocytes	Th1, CD8+	<i>Scott et al. 2001</i>
<i>Ebola</i>	Dendritic Cells, Macrophages, Monocytes	Th1, Th2, CD8+, IgG	<i>Le Roy et al. 2001</i>
<i>Influenza A virus</i>	Epithelial, Dendritic	Th1, Th2, CD8+, IgA, IgG, IgM	<i>Ada et al. 1986</i>
<i>Mycobacterium tuberculosis</i>	Macrophages, Neutrophils	Th1, CD8+	<i>O'Garra et al. 2013</i>
<i>Helminth</i>	Endothelial, Epithelial, Macrophages, NKT	Th2, IgE, IgG	<i>Gause et al. 2003</i>
<i>Plasmodium</i>	Erythrocytes	Th1, IgE, IgG	<i>Malaguarnera et al. 2002</i>
<i>Leishmania</i>	DCs, Mac, Monocytes, Neutrophil, NK	Th1, IgE	<i>Awasthi et al. 2004</i>



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Caveolin1  
In  
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(Conroy et. al. 2014.  
Frontiers Immunology,

[Front Physiol. 2018; 9: 878.](#)

Published online 2018 Aug 2. doi: [10.3389/fphys.2018.00878](https://doi.org/10.3389/fphys.2018.00878)

PMCID: PMC6083813

PMID: [30116195](#)

## A Mechanistic Computational Model Reveals That Plasticity of CD4<sup>+</sup> T Cell Differentiation Is a Function of Cytokine Composition and Dosage

[Bhanwar Lal Puniya](#),<sup>1</sup> [Robert G. Todd](#),<sup>2,\*</sup> [Akram Mohammed](#),<sup>1</sup> [Deborah M. Brown](#),<sup>3,4</sup> [Matteo Barberis](#),<sup>5,6,\*</sup> and [Tomáš Helikar](#)<sup>1,\*</sup>

(Madrahimov et. al. 2012.  
*Bull Math Biol*,  
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Caveolin1  
In  
T Cells

## ORIGINAL RESEARCH ARTICLE

Front. Bioeng. Biotechnol., 11 February 2016 | <http://dx.doi.org/10.3389/fbioe.2016.00010>



4.  
ogy,

## Systems Perturbation Analysis of a Large-Scale Signal Transduction Model Reveals Potentially Influential Candidates for Cancer Therapeutics

(Madrahimov et. al. 2012.  
*Bull Math Biol*,  
75(6):988-1011)

Influenza  
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(Todd R & Helikar T. 2012.  
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Caveolin1  
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Cancer  
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## ORIGINAL RESEARCH ARTICLE

Front. Immunol., 05 December 2014 | <http://dx.doi.org/10.3389/fimmu.2014.00599>

# Design, assessment, and *in vivo* evaluation of a computational model illustrating the role of CAV1 in CD4<sup>+</sup> T-lymphocytes

Brittany D. Conroy<sup>1†</sup>, Tyler A. Herek<sup>1†</sup>, Timothy D. Shew<sup>1†</sup>, Matthew Latner<sup>1</sup>,  
Joshua J. Larson<sup>1</sup>, Laura Allen<sup>1</sup>, Paul H. Davis<sup>1</sup>, Tomáš Helikar<sup>2</sup> and Christine E.  
Cutucache<sup>1\*</sup>

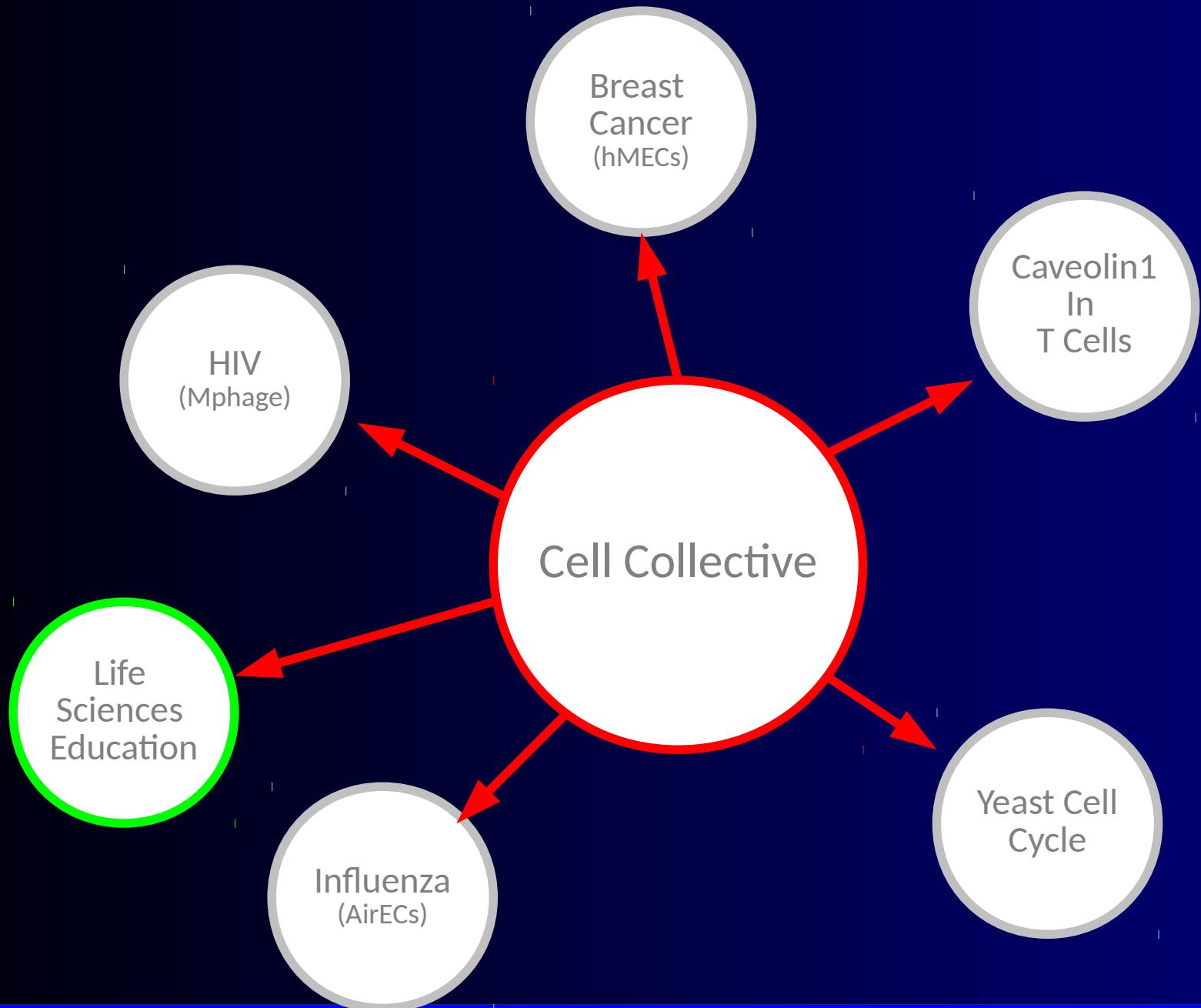
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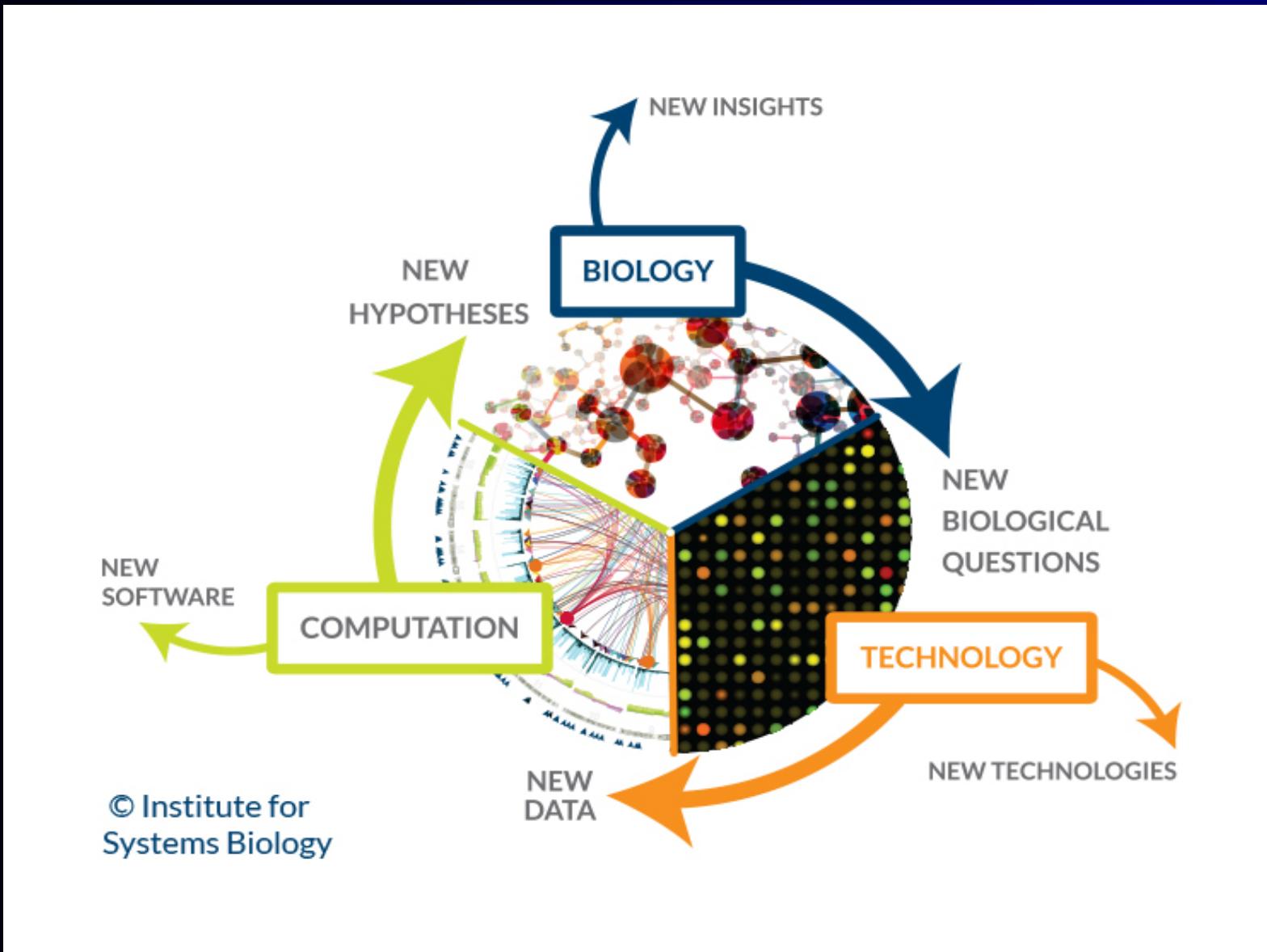
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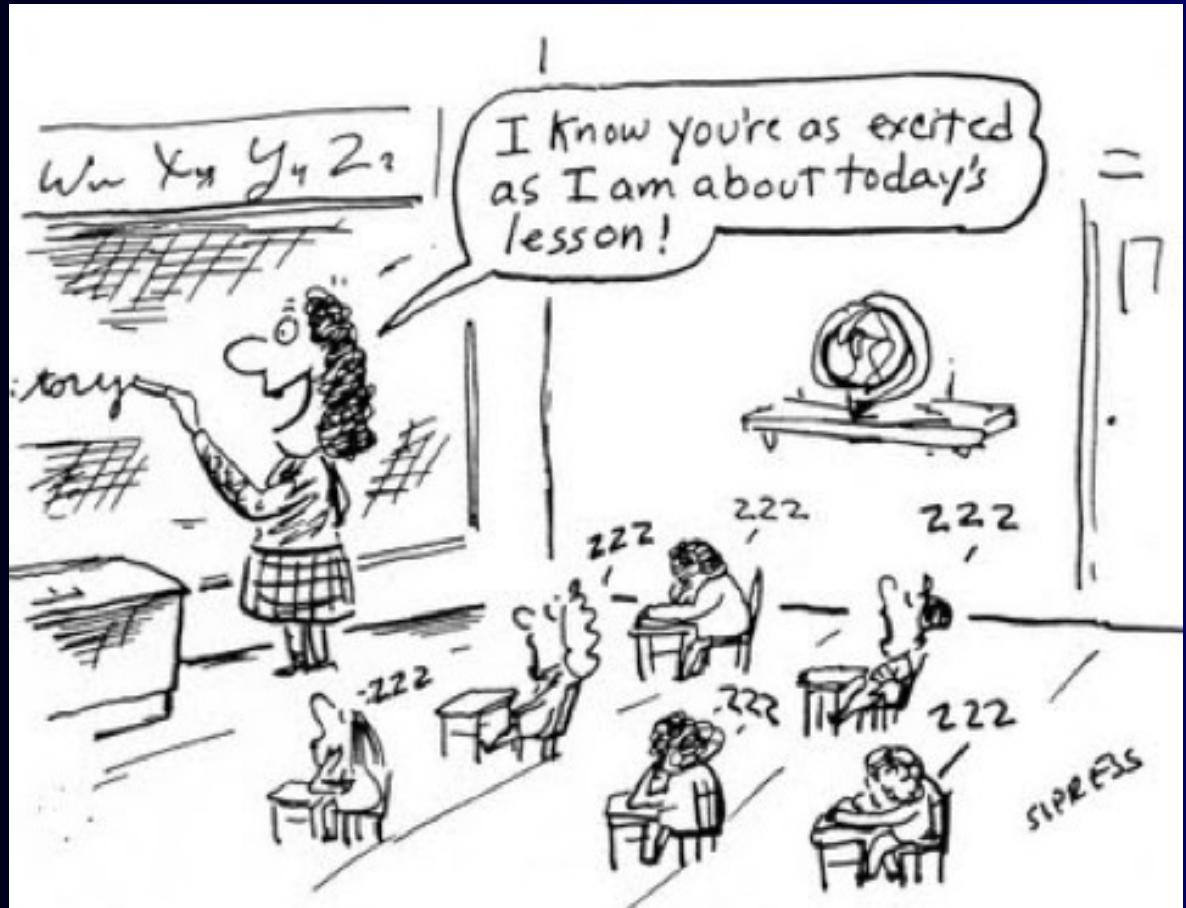
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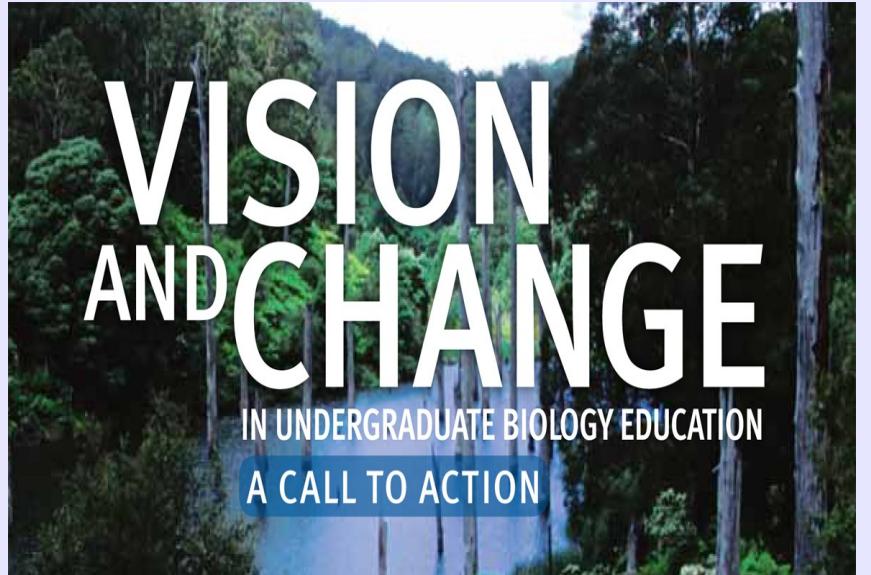


# Computational biology in complex networks









## Core Concepts

### ■ **Systems**

- Structure and function
- Information flow, exchange, storage
- Evolution
- Pathways and transformation of energy and matter



## Core Competencies

### ■ **Modeling, simulations, computational, and systems-level approaches to discovery and analysis**

- Process of science
- Quantitative reasoning
- Interdisciplinary communication and collaboration
- Science and Society



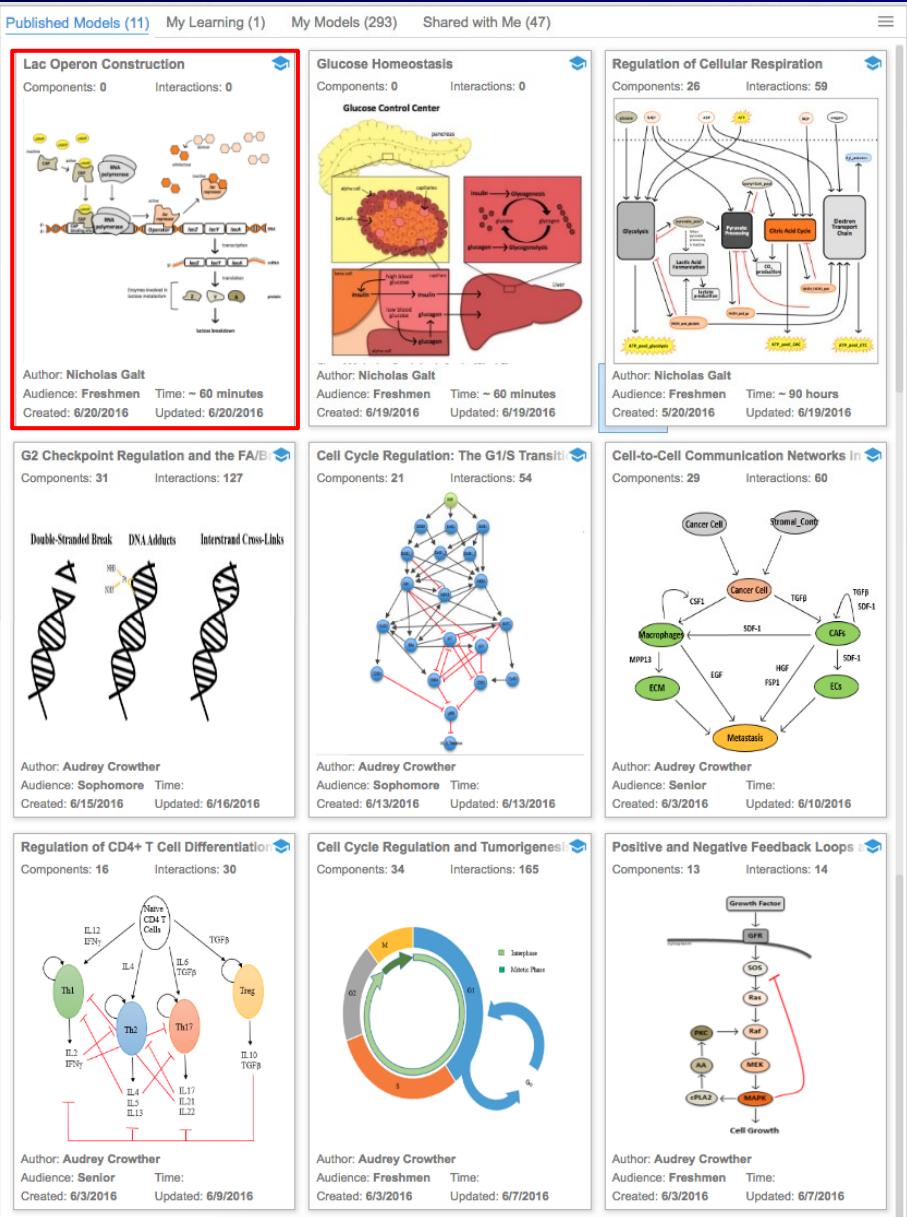
# Broad application

## Activity Types

- Concept Maps
- Simulation and investigation of pre-constructed models
- Model Construction and Simulation

## Key Design Features

- Self-contained
- Simple, turn-key implementation
- Predict/observe/explain scenarios
- Assessible
- Modular implementation
  - Laboratory activity
  - Homework
  - In-class activity





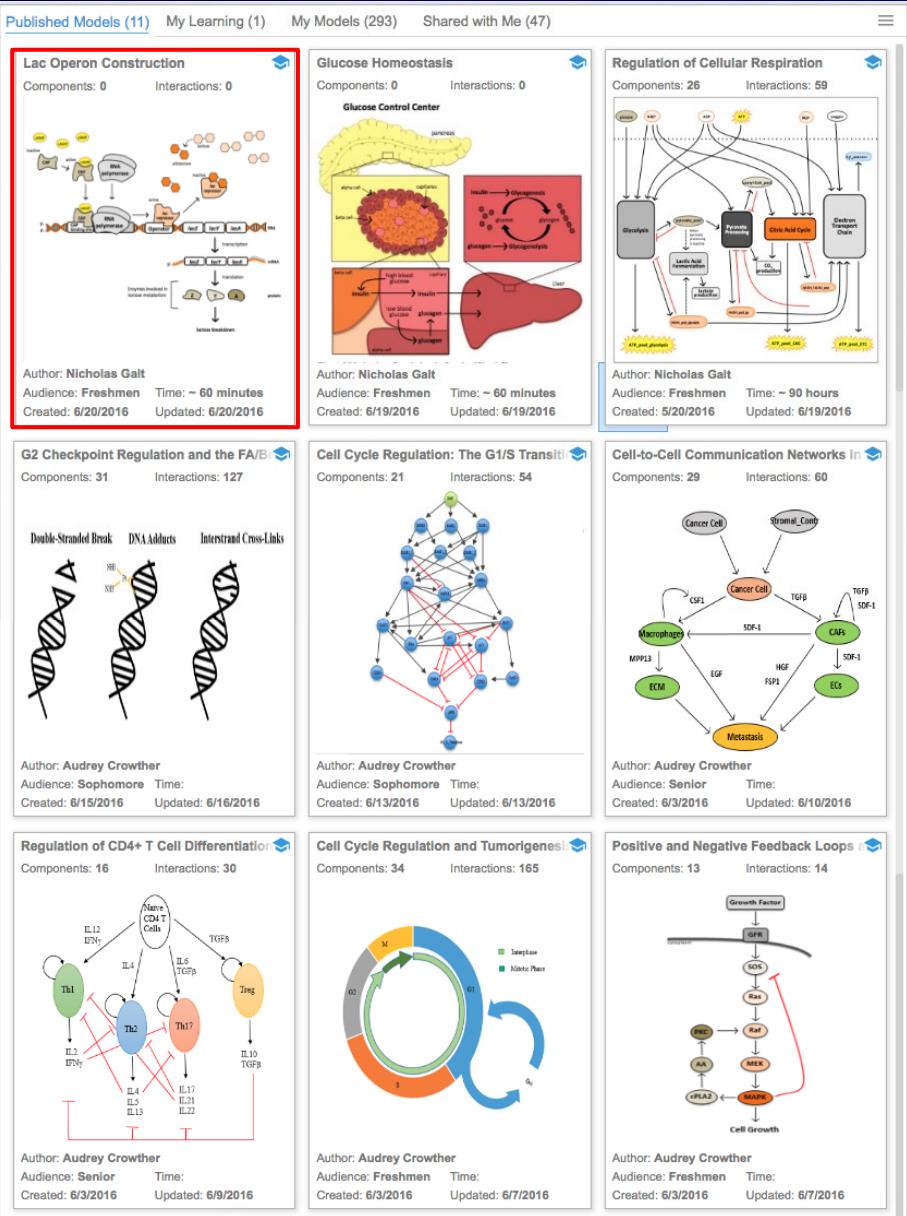
# Broad application

## Topics

- Cell respiration
- Glucose homeostasis
- Cell cycle
- Photosynthesis
- Gene regulation
- Food web dynamics

## Courses

- Biochemistry
- Intro biology courses
- Immunology
- Cancer Biology
- Many others





**Questions?**



**[Https://www.cellcollective.org](https://www.cellcollective.org)**