

# A Web Platform for Verification of Biological Network Models in the Age of Collaborative-Competition

**The sbv Improver project team** (in alphabetical order): Sam Ansari<sup>1</sup>, Di Fabio Anselmo<sup>2</sup>, Jean Binder<sup>1</sup>, Stephanie Boue<sup>1</sup>, William Hayes<sup>4</sup>, Julia Hoeng<sup>1</sup>, Anita Iskandar<sup>1</sup>, Robin Kleiman<sup>3</sup>, Raquel Norel<sup>4</sup>, Bruce O'Neel<sup>1</sup>, Manuel C. Peitsch<sup>1</sup>, Carine Poussin<sup>1</sup>, Dexter Pratt<sup>3</sup>, Kahn Rhrissorrakrai<sup>4</sup>, Walter K. Schlage<sup>1</sup>, Gustavo Stolovitzky<sup>4</sup> and Marja Talikka<sup>1</sup>

<sup>1</sup>Phillip Morris Products SA, Research and Development, Neuchâtel, Switzerland. <sup>2</sup>Applied Dynamic Solutions, LLC., NJ, USA. <sup>3</sup>Selventa, Cambridge, MA, USA. <sup>4</sup>IBM Computational Biology Center, Yorktown Heights, NY, USA. <sup>5</sup>University of California San Diego, School of Medicine, Departments of Medicine and Bioengineering, La Jolla, CA, USA.

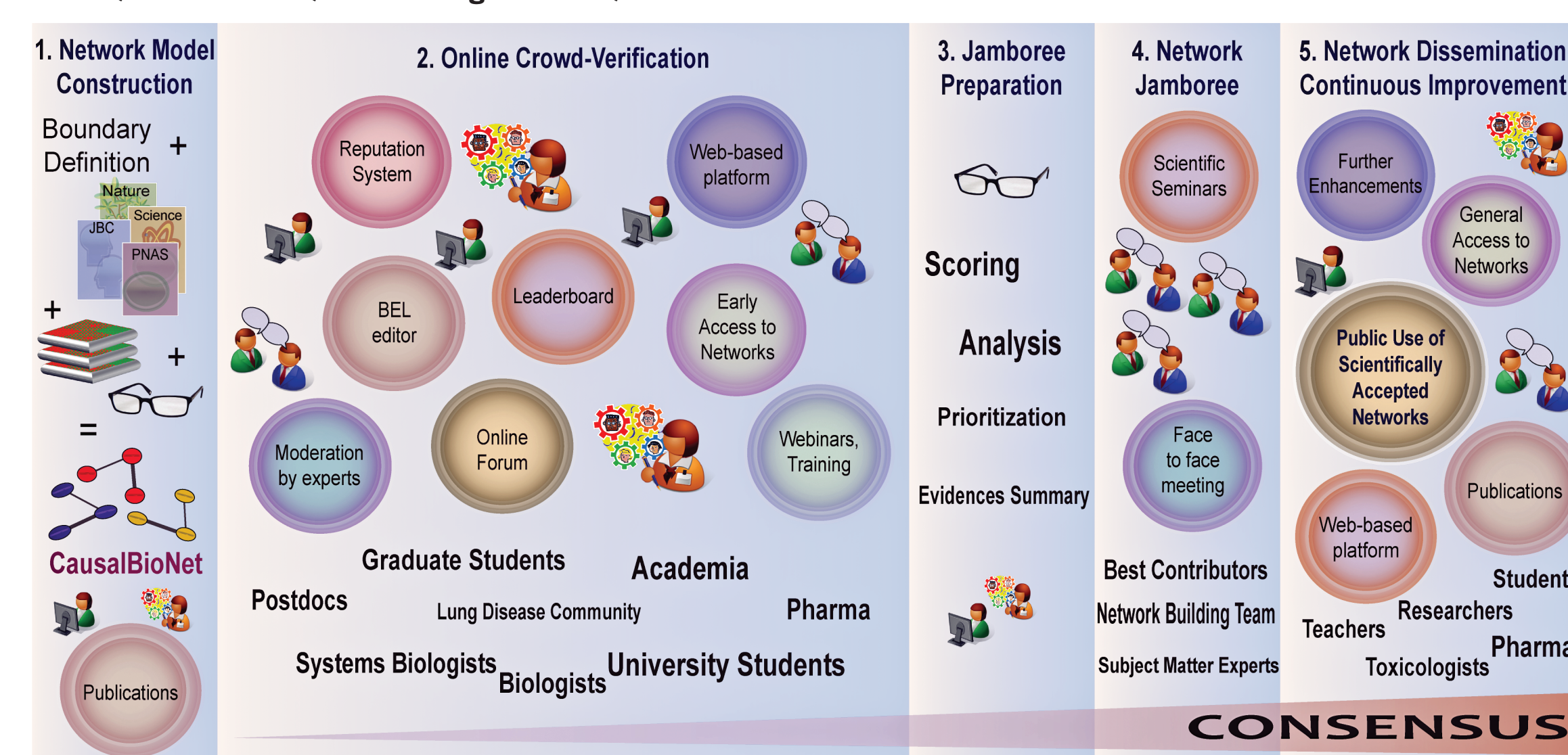
sbv IMPROVER (systems biology verification - Industrial Methodology for PROcess VERification in Research) is a challenge-based program with a specific focus on the verification of industrial research processes related to systems biology.

The first challenge (Diagnostic Signature) was designed to determine to what extent transcriptomic data can be used for phenotype prediction and to identify best-performing computational methods.

The second challenge (Species Translation) was designed to address the extent to which biological effects of stimulus-induced perturbations in rats translate to those in humans.

In the current challenge (Network Verification) we provide the community with network models of molecular events contributing to the Chronic Obstructive Pulmonary Disease (COPD). These models of key biological processes include access to underlying scientific literature citations that have been expertly curated to provide mechanistic substantiation for each molecular relationship represented. The scientific community will be encouraged in the review of the relationships between molecular entities and to make improvements on the represented biology covering fundamental processes involved in respiratory disease. Web-based graphical interfaces are used to visualize the biological relationships. Crowdsourcing principles enable participants to annotate these relationships based on literature evidences. A text analytics web service can be used by participants to assist with the creation of OpenBEL compliant knowledge statements given evidence lines from references. Best performers in the crowd-verification phase will be invited to a 3-day event to resolve controversies with subject matter experts, finalizing and publishing the network models. The resulting models will represent the current status of biological knowledge within the defined boundaries. For some period following conclusion of the challenge, the published models will remain available for continuous use and expansion by the scientific community.

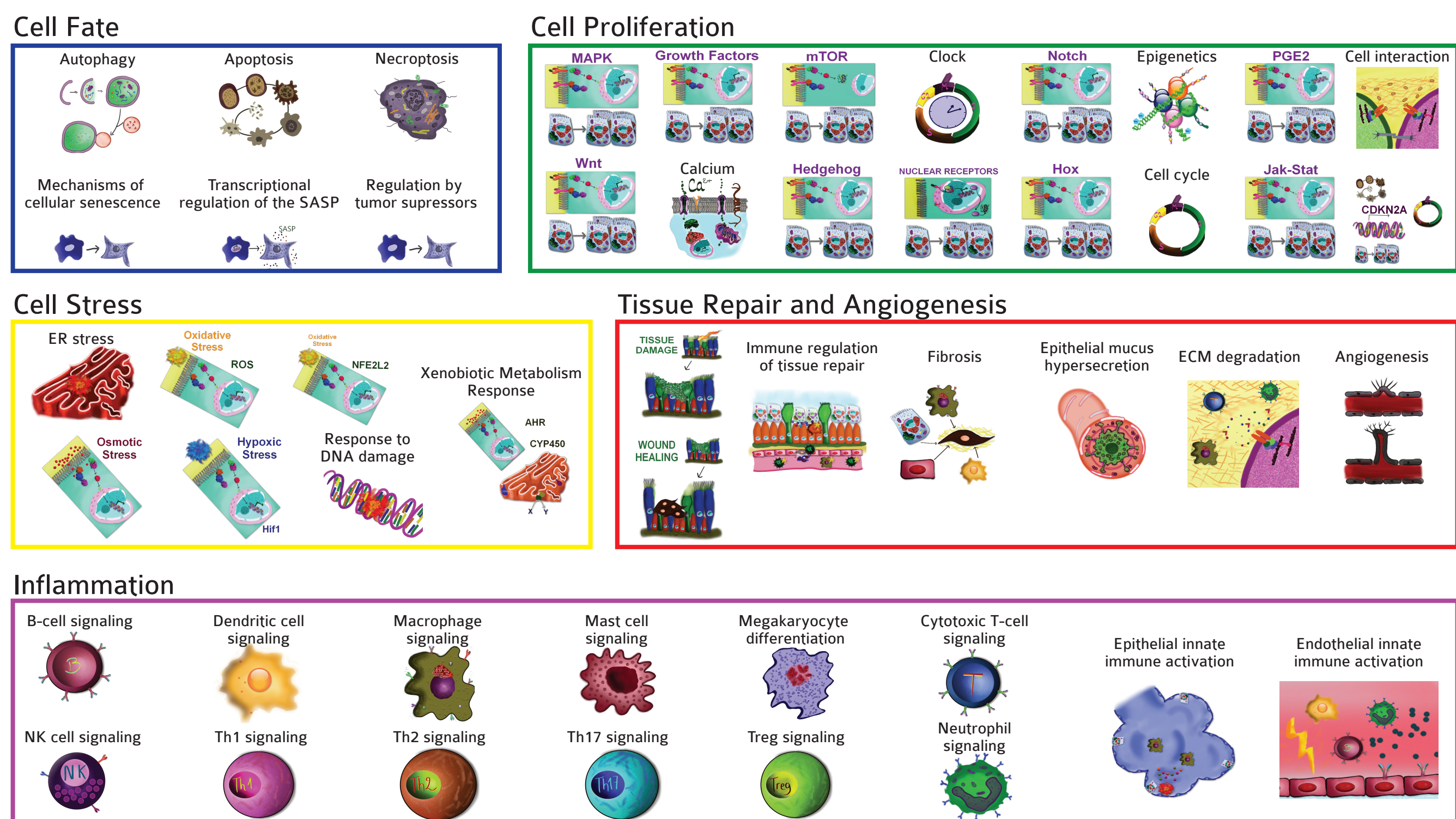
## The Network Verification Challenge in a Nutshell



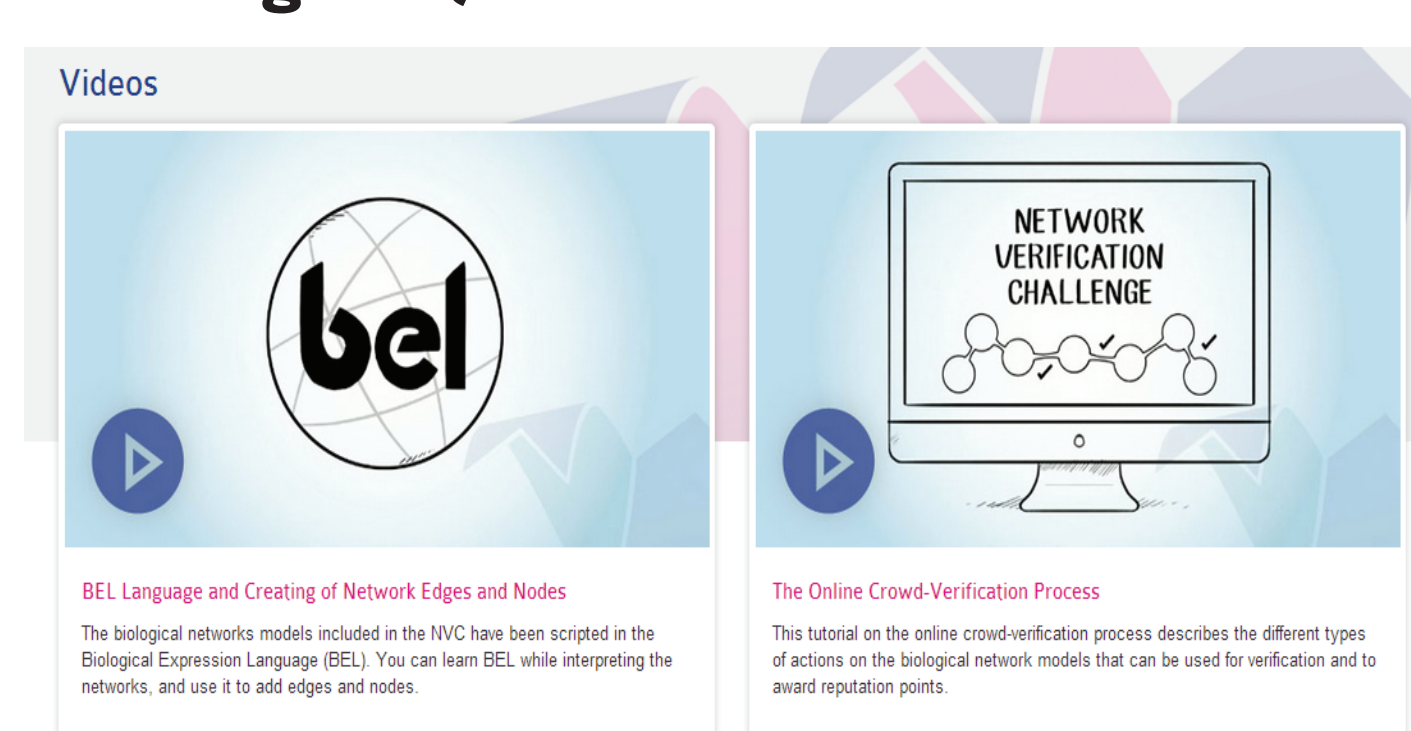
The network verification challenge consists of five phases. In the first phase, network models are constructed based on the literature and data-driven hypothesis validation. The models are imported into a Web-based platform (CausalBioNet) for the second phase (online Crowd-verification). In phase 2, experts and biology students and researchers are encouraged to access and verify/enhance the network models directly on the platform. This process is set up as a reputation-based collaborative competition, where actions on the network are given points that are recorded in a leaderboard. After this online phase is closed, in phase 3, the results and actions are analyzed, and the organizers select a number of edges that appeared to be the most controversial for discussion in a jamboree (phase 4) that will gather together scientific experts and the best contributors in the online phase. After a wrap up of the conclusions and actions on the network discussed during the jamboree, in phase 5, verified versions of the networks will be released for the scientific community at large to use.

From: The sbv Improver project team, Ansari S, Binder J, Boue S, Di Fabio A, Hayes W, Hoeng J, Iskandar A, Kleiman R, Norel R, Neel B, Peitsch MC, Poussin C, Pratt D, Rhrissorrakrai K, Schlage WK, Stolovitzky G, Talikka M. On Crowd-verification of Biological Networks. Bioinformatics and biology insights. 2013;7:307-25.

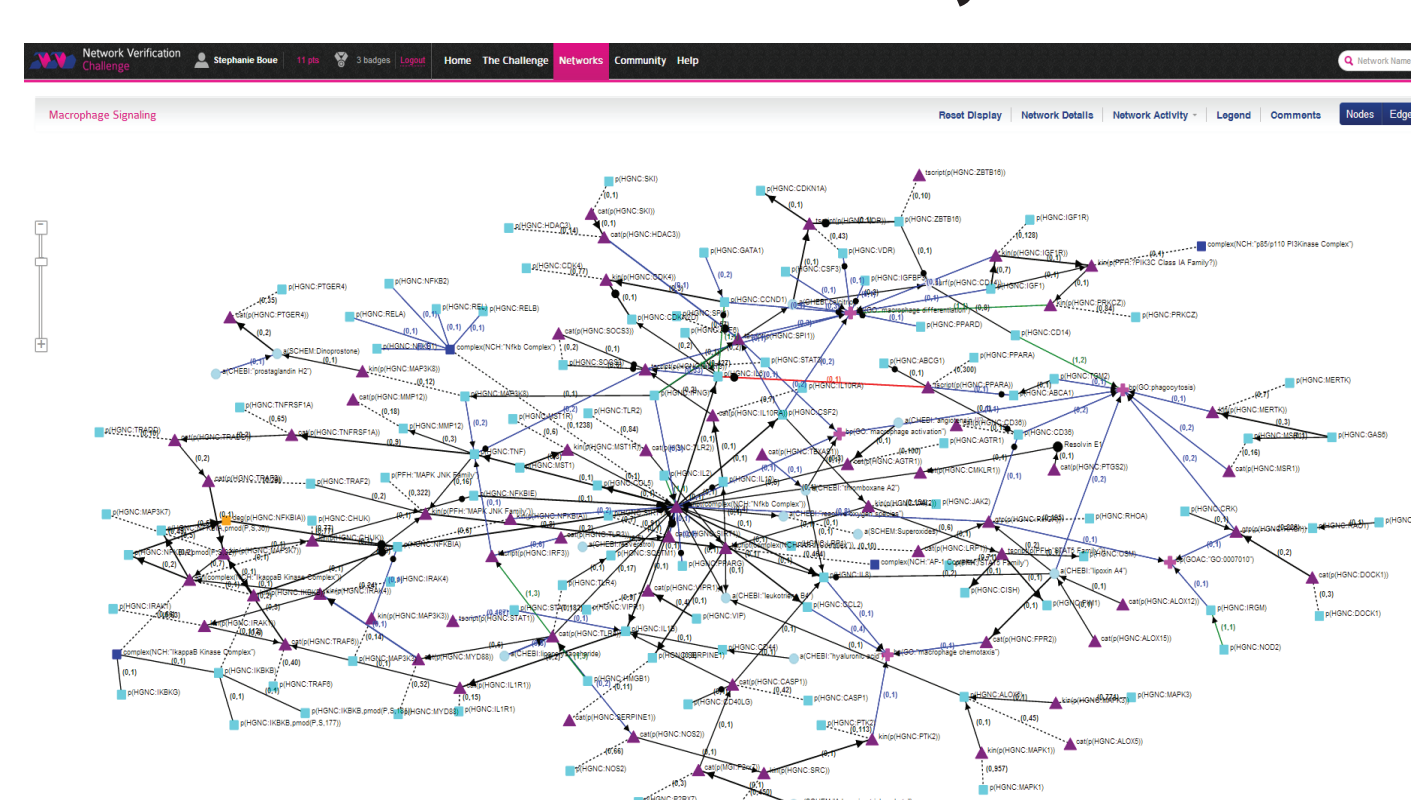
## 50 Network Models



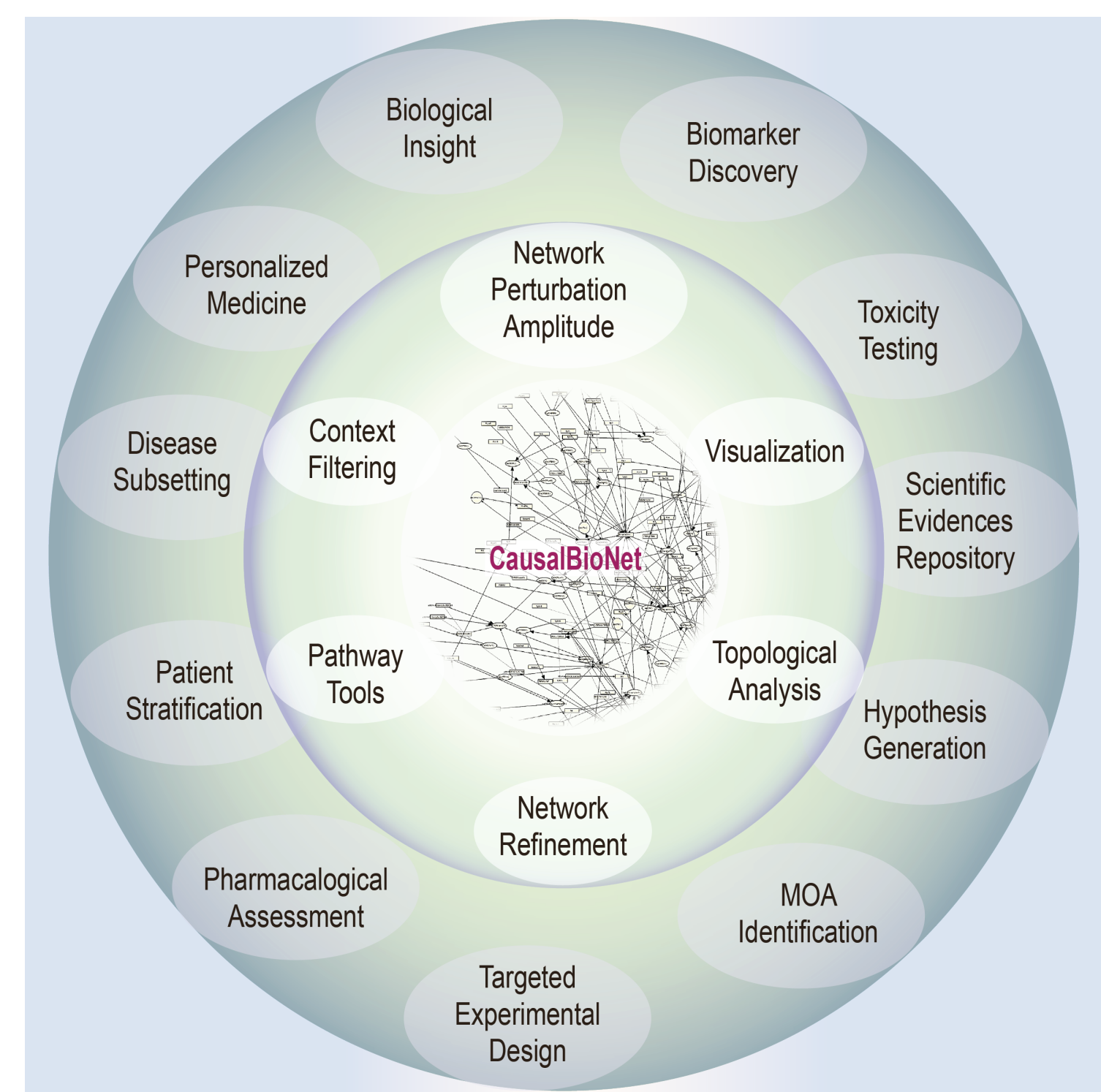
## Training Material: Videos and Webinars



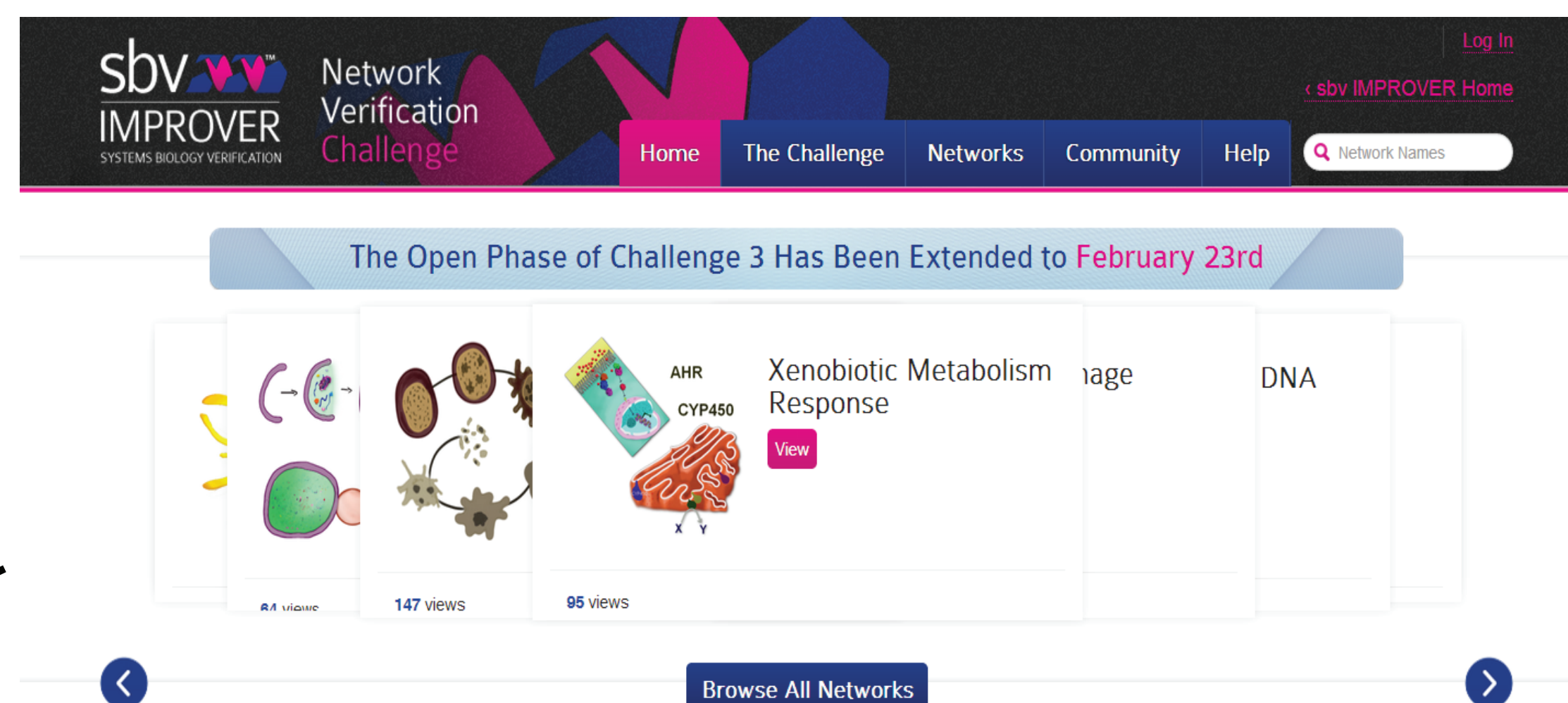
## Live Network Visualization including Crowd Activity



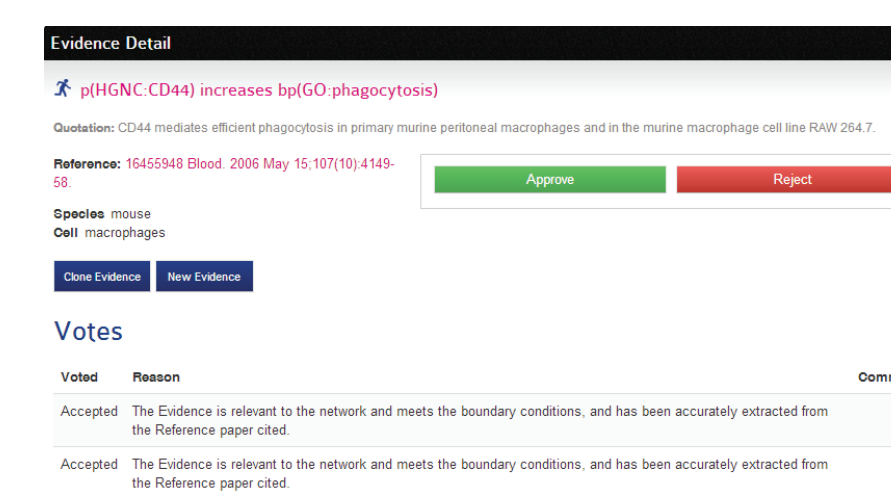
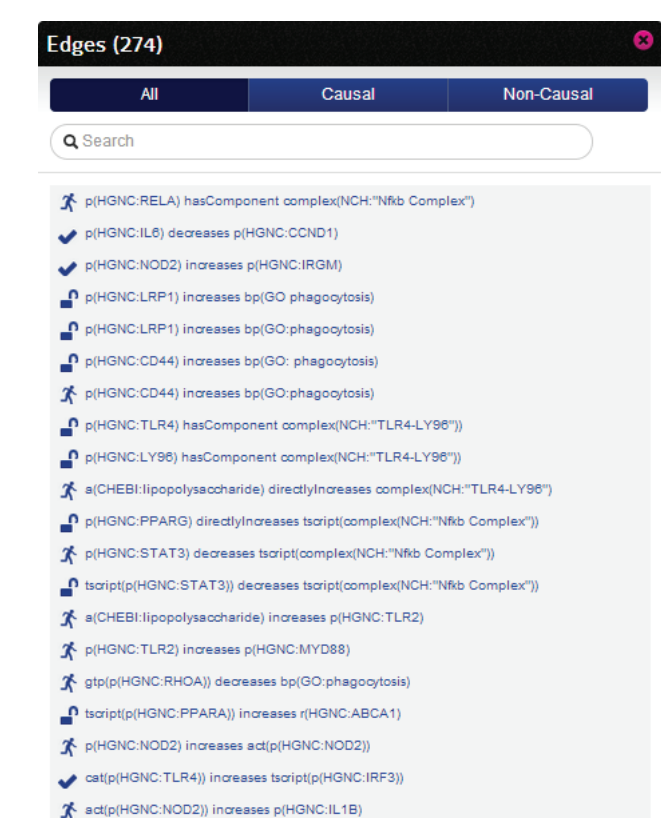
## Numerous Possible Applications of the Network Models



## A Single Web-interface



Filter the Network  
See Evidences  
Vote  
Comment



## Leaderboard: Possibility of Self-moderating Crowd-sourced Network Verification

## Earn Reputation

You can gain reputation points by verifying and enhancing the biological networkmodels in several ways: you can extend networks with new edges, provide additional evidence for edges and approved evidence that has been posted in support of network edges. The responses from the scientific community to your actions will define how you rank in the leaderboard and, ultimately, your success.

## Earning Reputation Points

If the scientific community participating in the challenge builds a consensus around your submissions, you will earn the following amount of points:

Your submission	Consensus criteria	Reputation points earned
Create new edge	At least 1 piece of evidence associated with edge is approved by 4 other participants	100
Add new evidence	4 other participants vote to approve the evidence	50
Approve evidence vote	3 other participants also approve the evidence	Up to 13
Reject evidence vote	3 other participants also reject the evidence	Up to 13

Up to 5 votes can be received per piece of evidence.

Activate Network Download by adding 10 evidences and voting 20 times. Download links will show up on each Network page.

For more detailed information [click here](#)

## Badges

A vertical list of achievement badges. Each badge consists of an icon and a text label. The badges are:
 

- Badges Earned**: A header with a ribbon icon.
- Earn More Badges**: A ribbon icon with a plus sign.
- Comments**: A speech bubble icon.
- Teams**: A group of three people icon.
- Evidence**: A document icon with a checkmark.
- Edge**: A blue crown icon.
- Votes**: A blue crown icon.
- Experience**: A blue crown icon.
- Help**: A question mark icon.
- Downloads**: A document icon with a download arrow.

## Add New Edge

Step 1 - Create the Edge Step 2 - Add Evidence to the Edge Step 3 - Verify your work

Create a new edge for Myosin Stress

New Edge:  This is not a valid statement

Use the active node (HGNOC:CDK4) for:

From:  To:

Information Help Connect Text to BEL (Data)

This form can be used to create one or several BEL statements (or BEL Statement fragments) based on an record from an academic paper (evidence). Our text mining service will process the evidence and send you a call with information that can be used to create Network Edges. If you do not receive a result, please check your identifier and make sure that you have a correct email address in your account information.

Create

Step 2 - Add Evidence to the Edge Step 3 - Verify your work

including text mining tool to convert free text to BEL statement

## Add New Evidence

Evidence Create

Reference Type: PubMedID URL

Reference

PubMedID:

Literature Reference: e.g. <challenge> (YEARS), Title, <journalName>, <Vol.Issue>, <pages>

Context

Species: Human Mouse Rat

Tissue:

Disease:

Cell: Cell Line

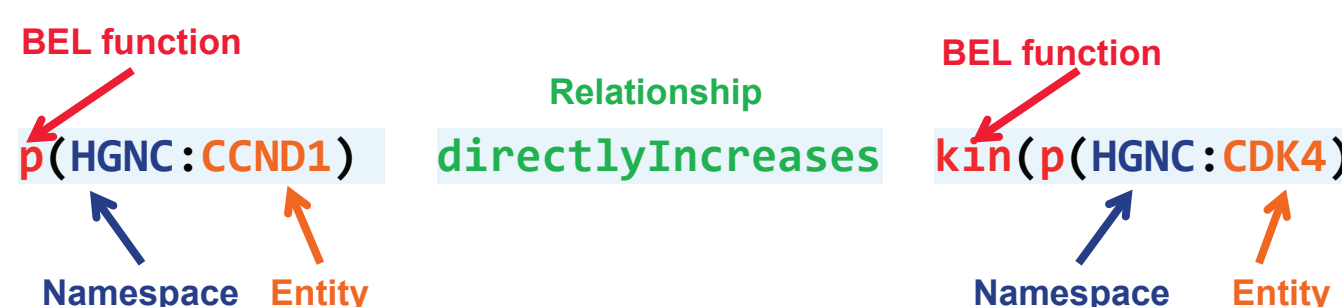
Quotation: Quotation from the reference that directly and obviously illustrates the edge and its context

Save

## BEL Terms and Statements

BEL functions	Namespace identifiers	Entity definition
Abundances Modifications Activities Processes Transformations	CHEBI PHF HNG MGI EGID	Gene symbol Protein symbol Biological process

PubMed ID 11278443  
"The CCND1 protein serves to directly increase the kinase activity of CDK4 to regulate cell cycle progression."



bionet.sbvimprover.com



sbvimprover.com

The sbv IMPROVER project and www.sbvimprover.com are part of a collaboration designed to enable scientists to learn about and contribute to the development of a new crowd sourcing method for verification of scientific data and results. The project team includes scientists from Philip Morris International's (PMI) Research and Development department and IBM's Thomas J. Watson Research Center. The project is funded by PMI.