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Verification of Systems Biology Research in the Age of Collaborative- Competition

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Copenhagen, Denmark

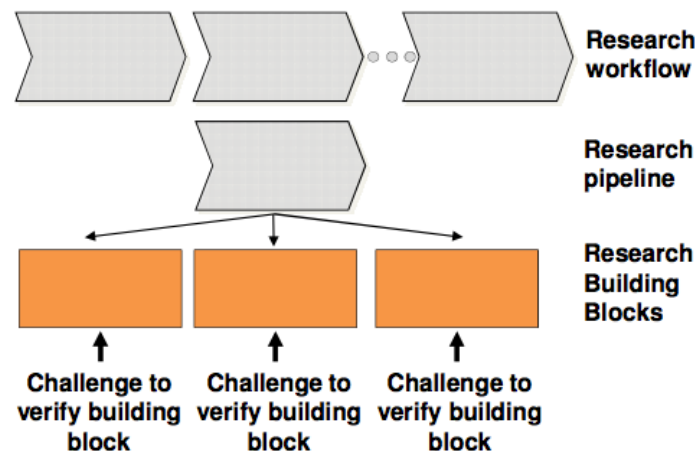
- sbv IMPROVER at a glance
- Need for sbv IMPROVER
- Crowdsourcing
- Network Verification Challenge

sbv IMPROVER: Industrial Methodology for Process Verification in Research

Aims to provide a measure of quality control in research and development efforts by identifying the building blocks that need verification in a complex industrial research pipeline

Crowdsourcing challenges with double blind performance assessment of building blocks

IBM collaborating on a project funded by Philip Morris International



Why do we need sbv IMPROVER?

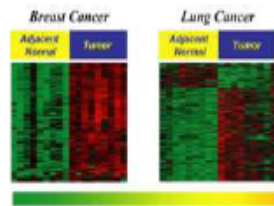
We are experiencing a data deluge...



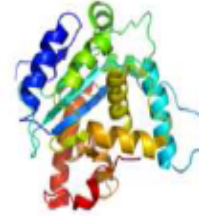
Genomic



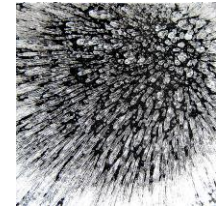
Literature



Molecular
Profiles

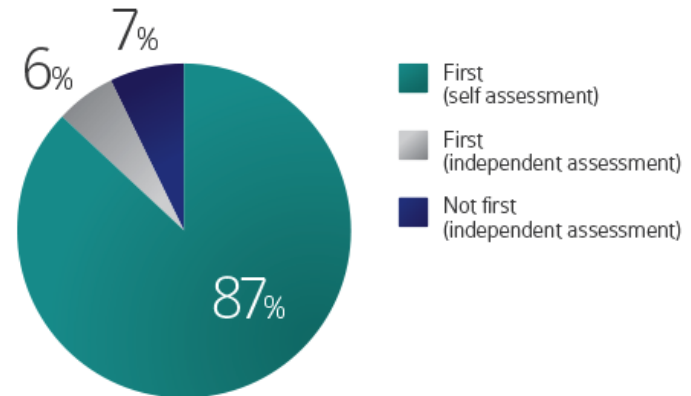


Structures



Explosion of data

But we lack the corresponding validation tools...



The self-assessment trap: can we all be better than average?

Molecular Systems Biology 7: 537; published online 11 October 2011; doi:10.1038/msb.2011.70

Develop a robust methodology that verifies systems biology-based approaches

- Many contributors with independent methods / knowledge
- Different solutions tackle various aspects of a complex problem
- The combination of solutions often outperforms the best performing submissions and is extremely robust → “Wisdom of Crowds”
- Nucleates a community around a given scientific problem
- Allows for unbiased benchmarking
- Establishes state-of-the-art technology and knowledge in a field
- Complements the classical peer-review process



Diagnostic Signature Challenge (completed)

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Diagnostic signature challenge

Aim to assess and verify computational approaches that classify clinical samples based on transcriptomics data.

Participants were asked to establish predictive signatures on unlabeled gene expression data sets in 4 disease areas

Chronic Obstructive
Pulmonary Disease

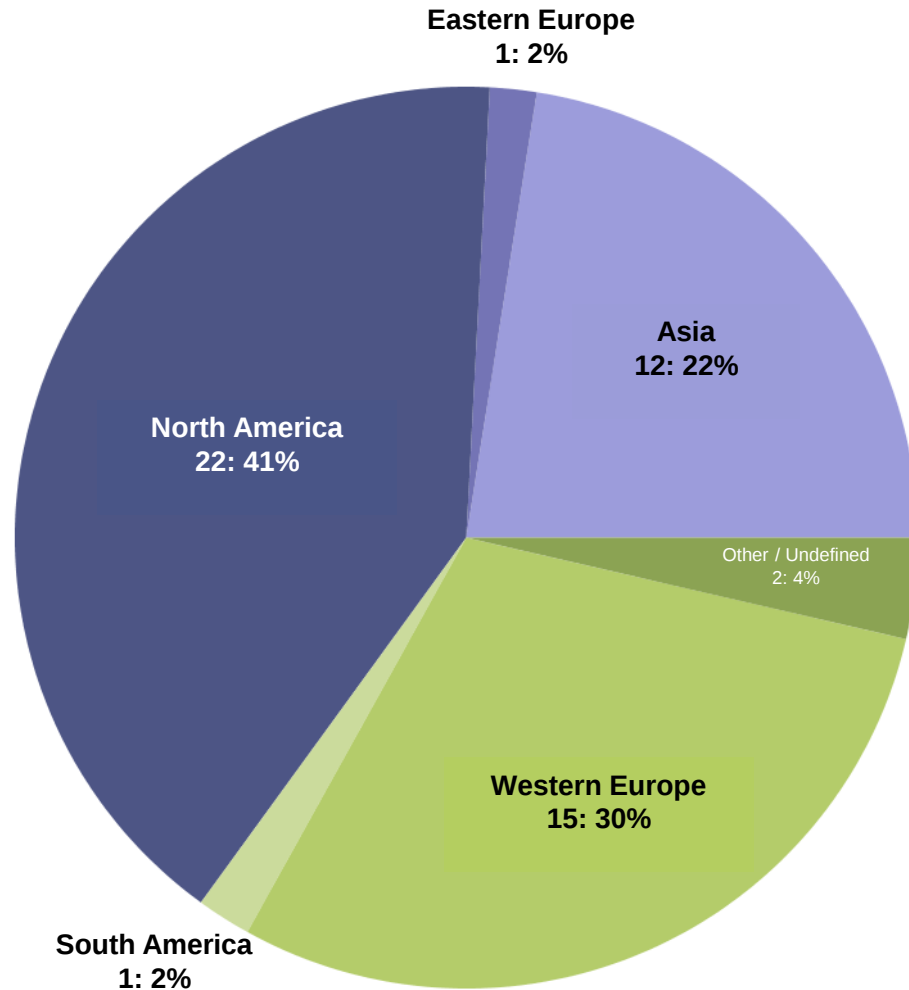
Multiple Sclerosis

Lung Cancer

Psoriasis

Diagnostic Signature Challenge: overall participation

54 Teams from
around the world
participated



Diagnostic Signature Challenge participation

Submissions were spread evenly across all five sub-challenges:

Psoriasis: 49 participants

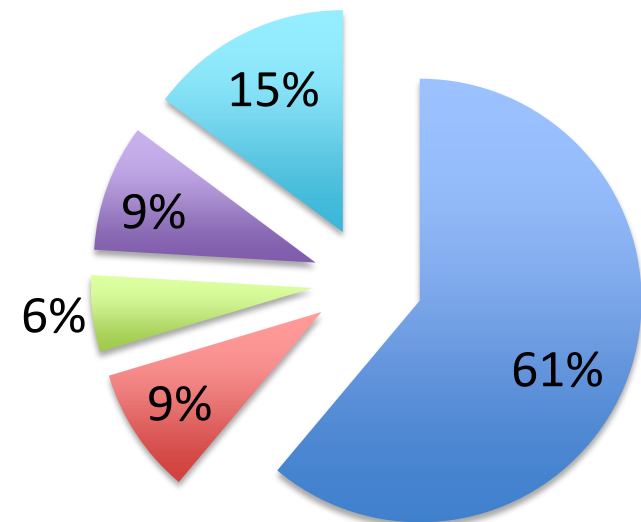
COPD: 40 participants

Lung Cancer: 46 participants

MS Diagnosis: 40 participants

MSS Staging: 39 participants

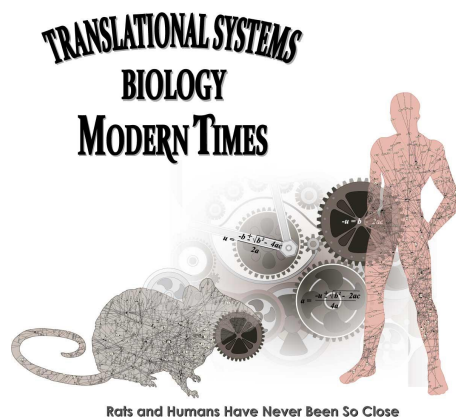
■ 5 ch ■ 4 ch ■ 3 ch ■ 2 ch ■ 1 ch



Most teams submitted predictions to all challenges (34/54)

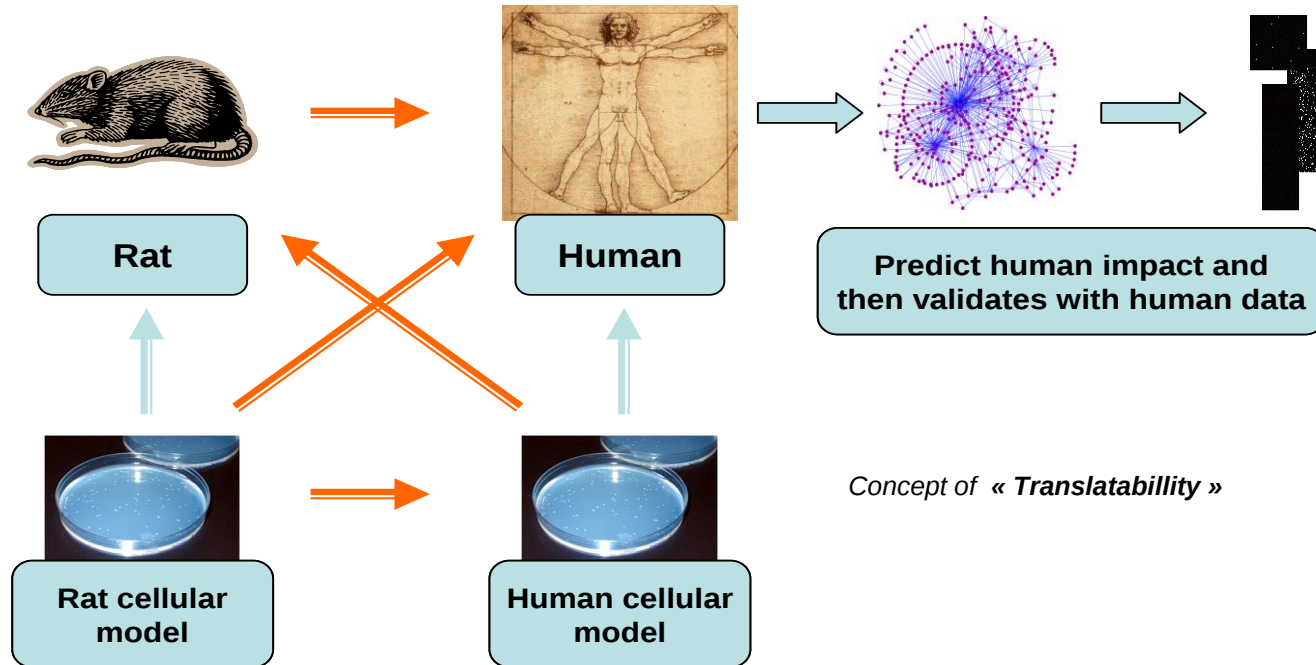
Species Translation Challenge

From Rat To Human: Understanding the Limits of Animal Models for Human Biology



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Species Translation Challenge: Background and Goal



Goal: Verify the translation of biological effects of perturbations in one species given information about the same perturbations in another species.

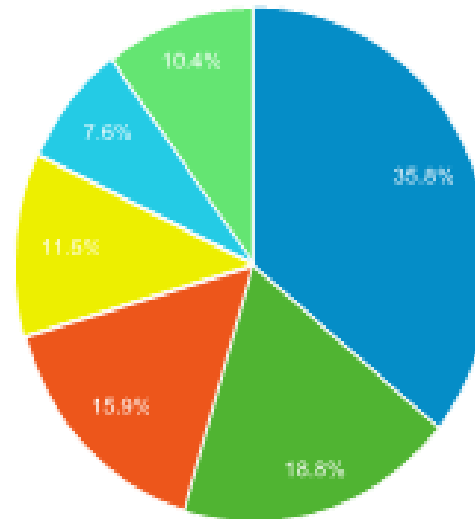
The **Species Translation Challenge** involves four sub-challenges that aim to shed light on important questions faced by the field:

- Can the perturbations of signaling pathways in one species predict the response to a given stimulus in another species?
- Which biological pathway functions and gene expression profiles are most robustly translated?
- Does translation depend on the nature of the stimulus or data type collected such as protein phosphorylation, gene expression and cytokine responses?
- Which computational methods are most effective for inferring gene, phosphorylation and pathway responses from one species to another?

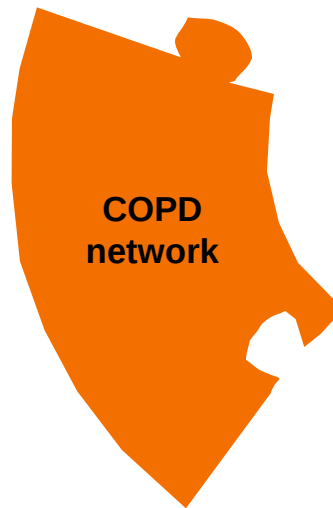
Challenge participant overview

Visits by subcontinent

■ Northern America ■ Western Europe ■ Eastern Asia ■ Southern Europe
■ Southern Asia ■ Other



Network Verification Challenge

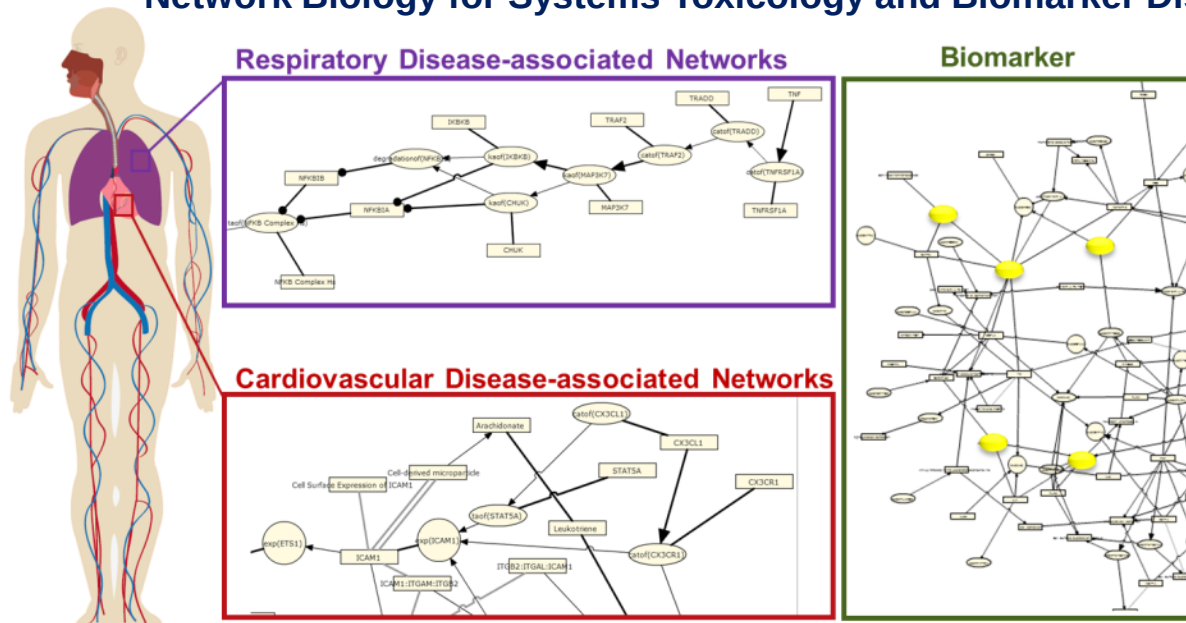


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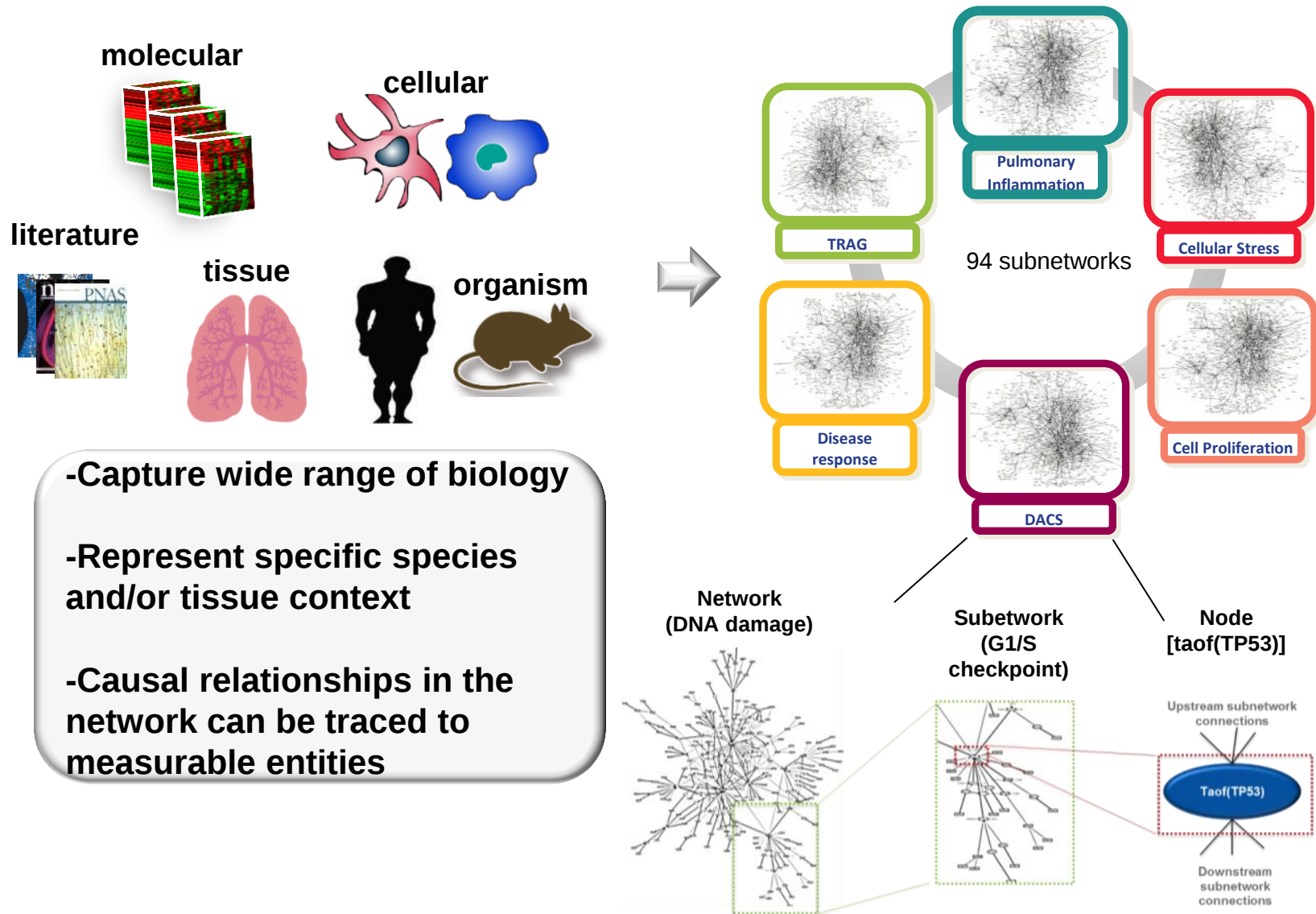
Overview of Network Verification Challenge

- The disparate information on molecular mechanisms of the respiratory system has been organized and captured within a coherent collection of network models.
- The purpose of the Network Verification Challenge is to engage the scientific community to review, challenge, and make corrections to the conventional wisdom
- The verified network will be used in the “COPD Grand Challenge”

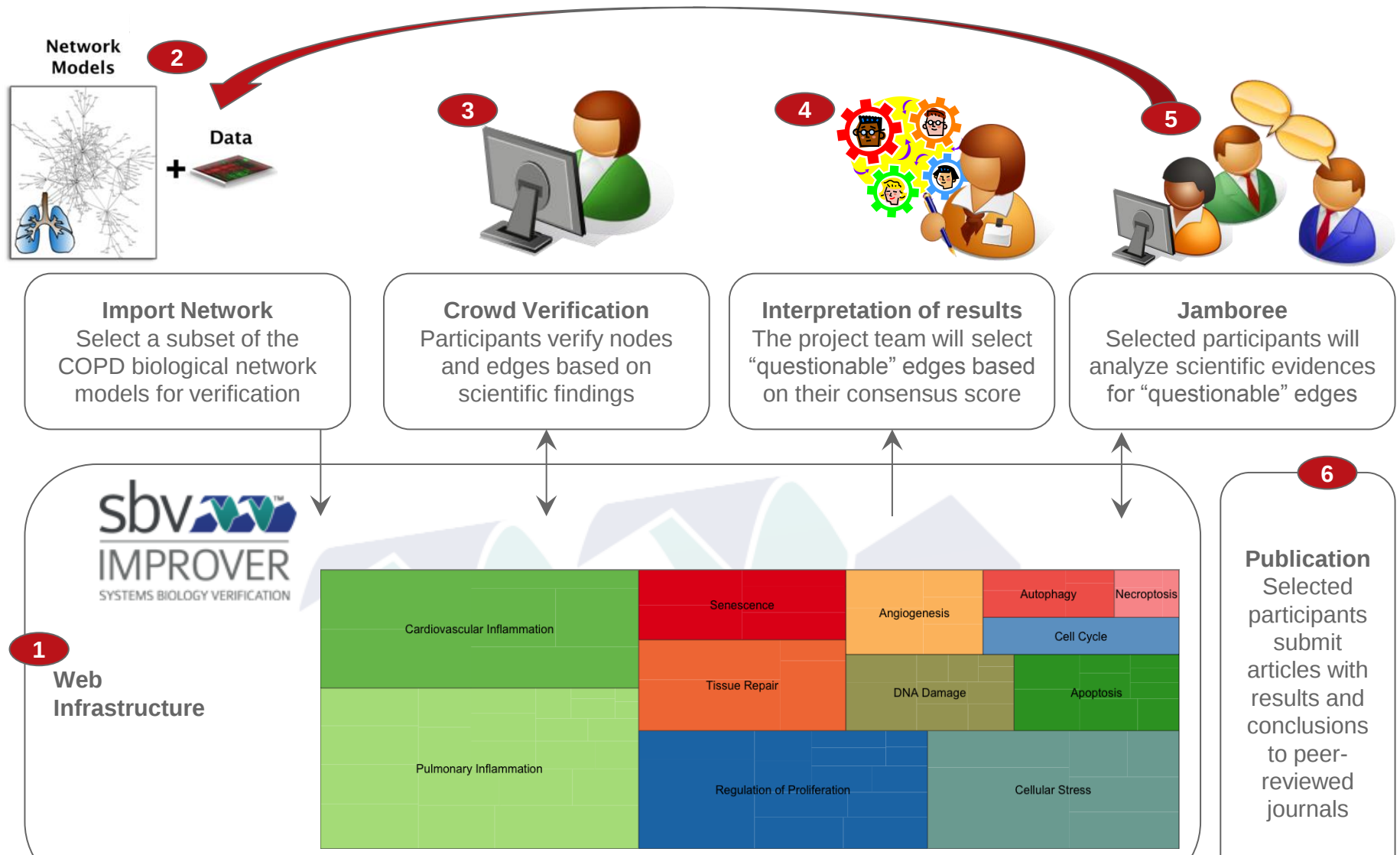
Network Biology for Systems Toxicology and Biomarker Discovery



Networks Contain Relevant Biology Expressed in a Causal Framework

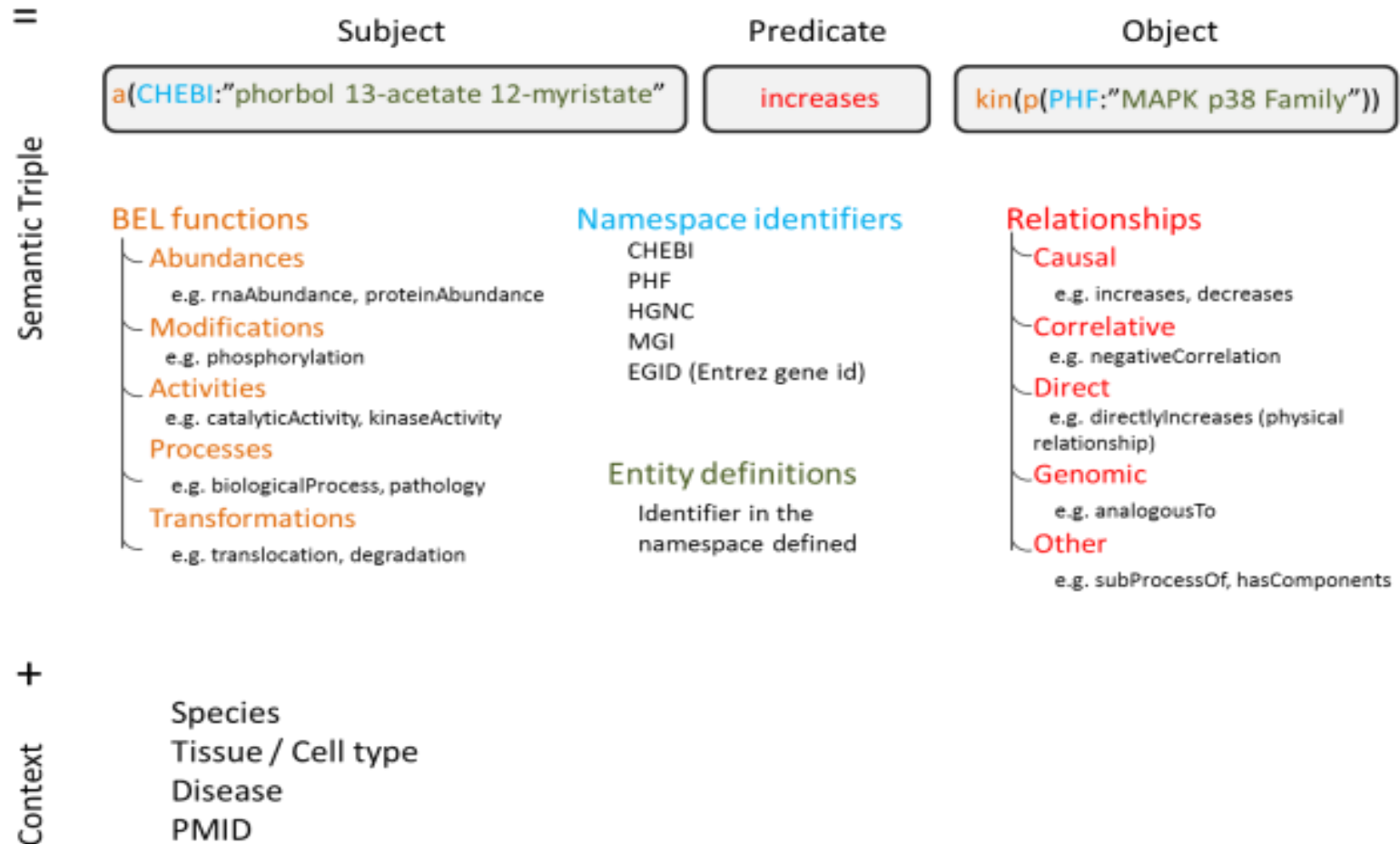


Network Verification Challenge in a nutshell



BEL (Biological Expression Language) Statement

BEL Statement



Who can participate

- Any biology researcher / student
- Researchers / students working on inflammation / lung tissues / COPD
- Researchers / students interested in pathways verification
- Researchers / students interested in applying text mining to an applied biological case

Why should you participate?

- Gain access to high quality and novel data
- Enhance your visibility and gain recognition
- Engage with peers to advance the field
- Get invited to the Jamboree (top performers)

Apoptosis-Caspase cascade--Merged

Detail My Activity Dropdown

Nodes Edges

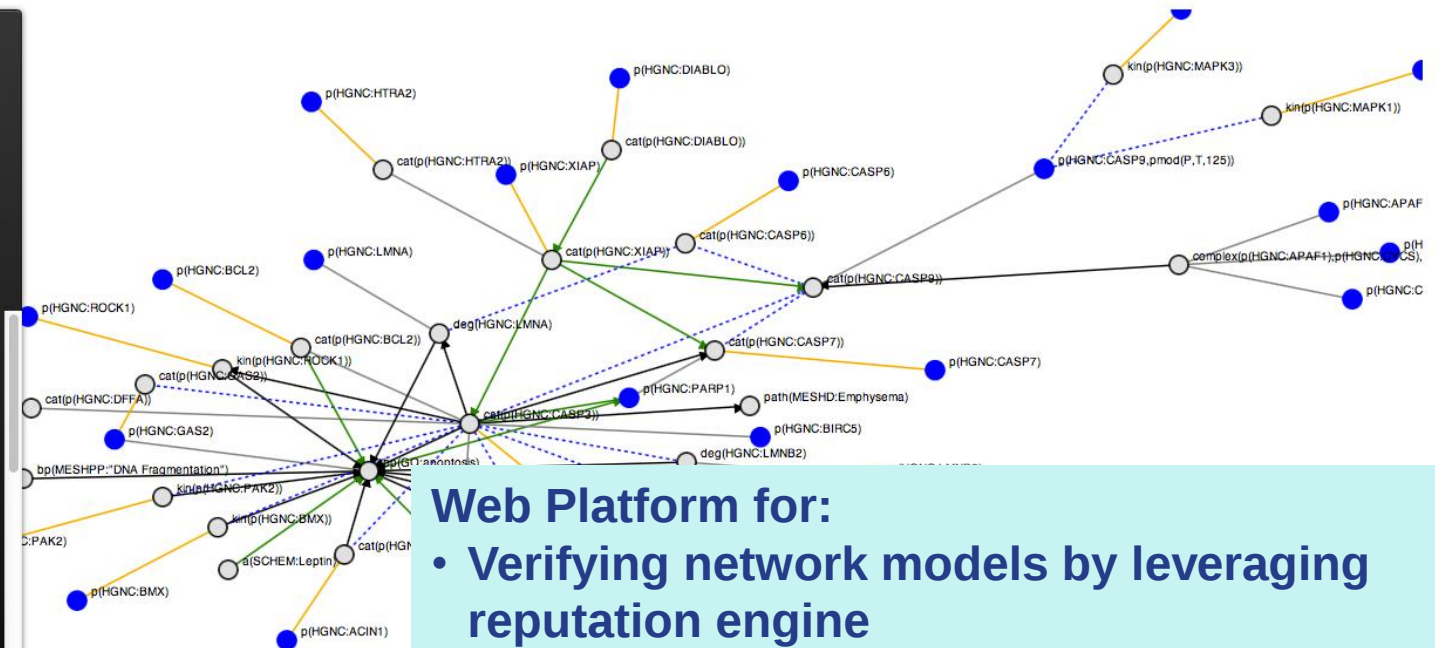
Node List

Search

Select Filter...

All Nodes (57)

p(HGNC:ACIN1)
p(HGNC:DIABLO)
cat(p(HGNC:BCL2L1))
p(HGNC:LEPR)
p(HGNC:PAK2)
deg(HGNC:LMNA)
cat(p(HGNC:DFFA))
p(HGNC:LMNB1)
p(HGNC:BMX)
p(HGNC:MAPK1)
p(HGNC:BCL2L1)
p(HGNC:PARP1)
cat(p(HGNC:CASP7))
deg(HGNC:LMNB2)
kin(p(HGNC:MAPK3))
p(HGNC:CASP6)
p(HGNC:CASP9)



Web Platform for:

- Verifying network models by leveraging reputation engine
- Managing network models collaboratively
- Generating BEL knowledge
- Developing network models

Current sbv IMPROVER Project Team

IBM

Ajay Royyuru
Elise Blase
Erhan Bilal
Gustavo Stolovitzky
Jeremy Rice
Kahn Rhrissorakrai
Pablo Meyer
Raquel Norel

Chaturika Jayadewa
Claudia Frei
Jörg Sprengel
Joanna Taylor
Peter Curle
Timothy Kilchenmann

PMI

Bruce O'Neil	Julia Höng
Carine Poussin	Lionel Schilli
Carole Mathis	Manuel Peitsch
Filipe Bonjour	Marja Talikka
Florian Martin	Nikolai Ivanov
Hugh Browne	Stephanie Boué
Jean Binder	Yang Xiang

External collaborators

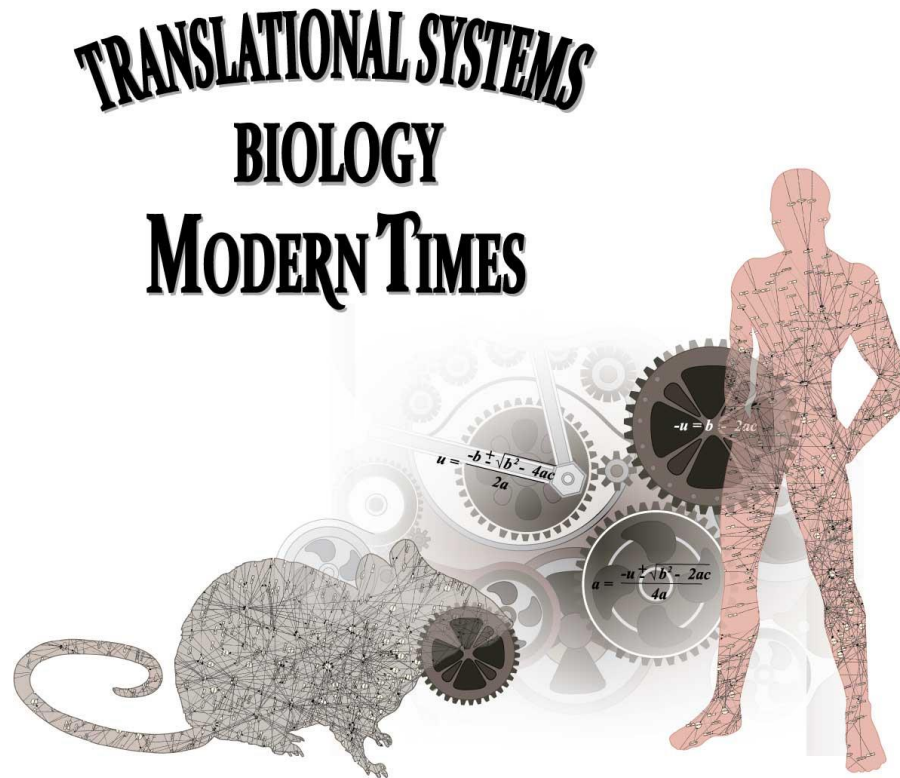
Protatonce

Selventa

The sbv IMPROVER project, the website and the Symposia are part of a collaborative project 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.

For more details on **sbv IMPROVER** and the Species Translation Challenge, visit www.sbvimprover.com



Are rats and humans maybe closer than we think?