

Why should you be part of sbv IMPROVER?

Computational Challenge Crowdsourcing Systems Toxicology

Verification of Systems Biology Research in the age of Collaborative Competition

sbv IMPROVER stands for Systems Biology Verification combined with Industrial Methodology for Process Verification in Research.

The sbv IMPROVER project is designed to enable scientists to learn about and contribute to the development of a new crowd sourcing method, combined with Industrial Methodology, for verification of scientific data and results.

Publications

Species Translation Challenge

- Hoeng et al. **Where are we at regarding species translation? A review of the sbv IMPROVER challenge.** Bioinformatics. 2015
- Rhrissorrakrai et al. **Understanding the limits of animal models as predictors of human biology: lessons learned from the sbv IMPROVER Species Translation Challenge.** Bioinformatics. 2015
- Bilal et al. **A crowd-sourcing approach for the construction of species-specific cell signaling networks.** Bioinformatics. 2015
- Hormoz et al. **Inter-species inference of gene set enrichment in lung epithelial cells from proteomic and large transcriptomic datasets.** Bioinformatics. 2015
- Dayarianet et al. **Predicting protein phosphorylation from gene expression: top methods from the IMPROVER Species Translation Challenge.** Bioinformatics. 2015
- Biehl et al. **Inter-species prediction of protein phosphorylation in the sbv IMPROVER species translation challenge.** Bioinformatics. 2015

Diagnostic Signature Challenge

- Tarca et al. **Strengths and limitations of microarray-based phenotype prediction: lessons learned from the IMPROVER Diagnostic Signature Challenge.** Bioinformatics. 2013

Network Verification Challenge

- IMPROVER team et al. **Enhancement of COPD biological networks using a web-based collaboration interface.** F1000Res. 2015
- IMPROVER team et al. **Reputation-based collaborative network biology." Pac Symp Biocomput.** 2015
- Boué et al. **Causal biological network database: a comprehensive platform of causal biological network models focused on the pulmonary and vascular systems.** Database (Oxford) 2015
- IMPROVER team.et al. **On Crowd-verification of Biological Networks.** Bioinform Biol Insights. 2013
- Hoeng et al. **A network-based approach to quantifying the impact of biologically active substances.** Drug Discov Today. 2012

sbv IMPROVER Project

- Meyer et al. **Industrial methodology for process verification in research (IMPROVER): toward systems biology verification.** Bioinformatics. 2012
- Meyer et al. **Verification of systems biology research in the age of collaborative competition.** Nat Biotechnol. 2011

Your publication can be next...

The current challenges, website and biological network models were developed and are maintained as part of a collaboration among Philip Morris International, Selventa, OrangeBus, and ADS. The project is led and funded by Philip Morris International. Further information at www.pmi.com

SHARE

Become a best performer and present your approach in the challenge symposium.

PUBLISH

Co-author a scientific article describing the outcome of the challenge.

LEARN

Receive an independent assessment of your methods.

CONTRIBUTE

Develop the 21st century predictive systems toxicology.

COLLABORATE

Leverage the crowd wisdom.

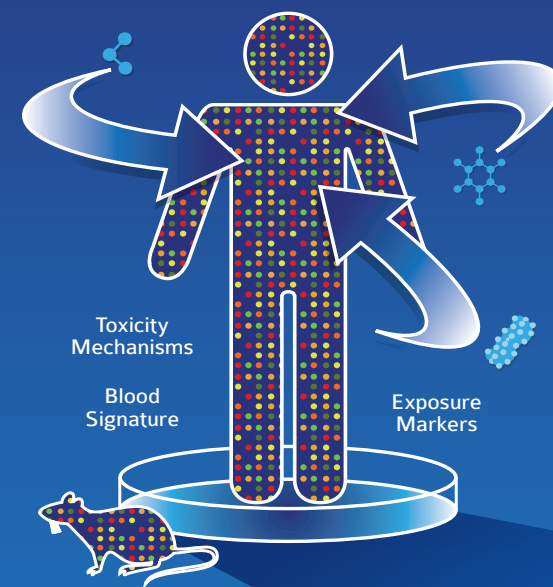
EXPLORE

Access new high quality data.

NETWORK

Grow your professional network and enhance your visibility.

www.sbvimprover.com/discover



Benchmark your methods !

- Identify specific markers for exposure response
- Predict toxicity mechanisms

2012 Diagnostic Signature Challenge

Designed to determine whether computational approaches and transcriptomics data could be used for phenotype prediction.

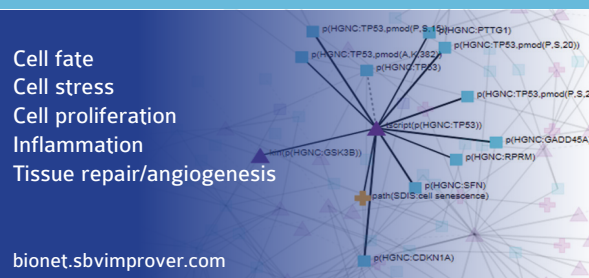
2013 Species Translation Challenge

Designed to address whether biological events observed in rodents were translatable to humans.

2014 Network Verification Challenge

2015

Designed to verify previously built biological network models and ensure their relevance to lung biology and COPD.



NOW Systems Toxicology Computational Challenge

Designed to verify that a robust predictive signature can be extracted from gene expression data that differentiates smokers, former smokers, and never smoker subjects.

Who can be part of the Challenge?

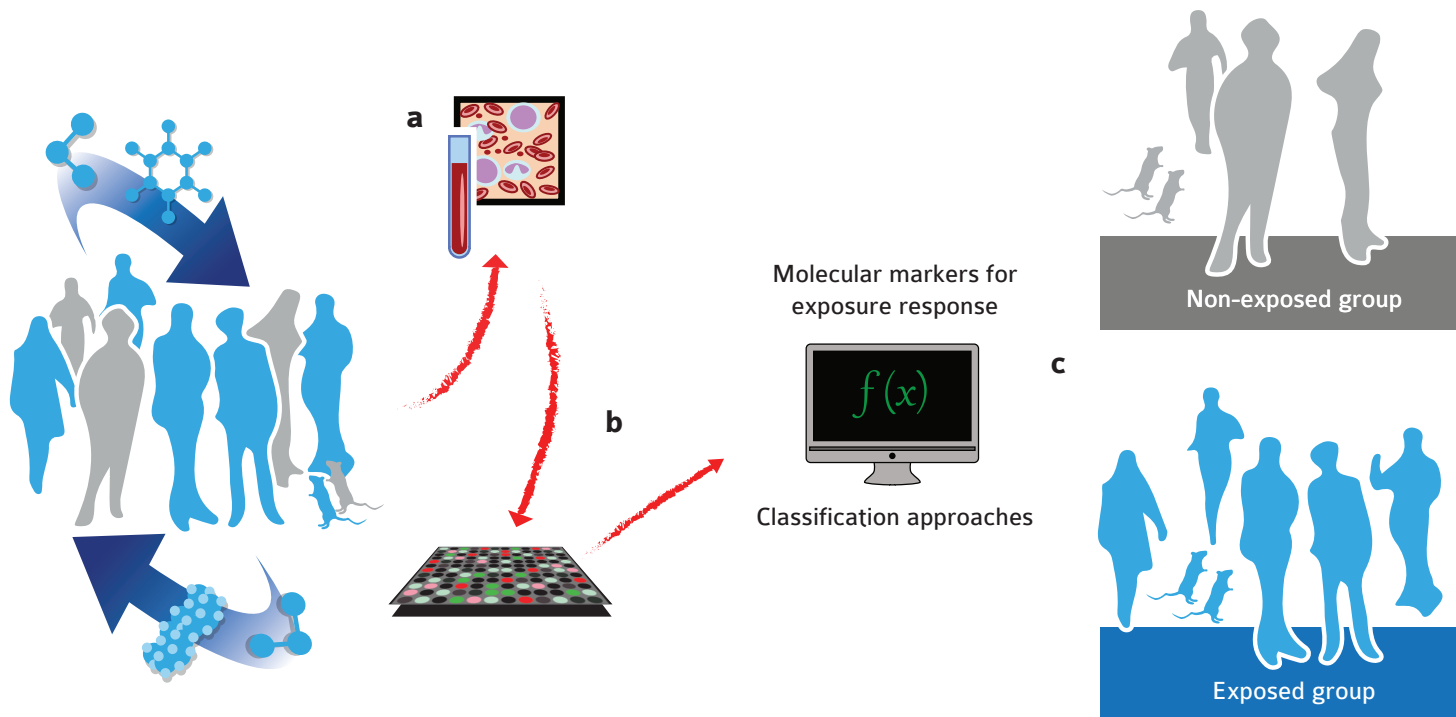
Everyone – Knowledge in computational science is an asset

When?

Fall 2015 - Spring 2016

Contact

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Markers of Exposure Response Identification

- a. Blood samples are collected from human and mouse subjects belonging to exposed or non-exposed groups.
- b. Gene expression profiles (GEX) are measured using microarray-based technology.
- c. Participants are provided with GEX and asked to develop a classification approach that identifies a gene signature capable of associating subjects to the correct exposure group.

The Two Sub-Challenges

Sub-challenge1: Human blood signature as exposure response marker

Humans are constantly exposed to individual or mixtures of chemicals (e.g. cigarette smoke, pollutants, pesticides, drugs) that may trigger molecular changes in their organism. The identification of specific response markers is important to assess the exposure status of an individual. The blood is an easily accessible matrix, however remains a complex biofluid to analyze.

Scientific Question

Are gene expression changes in blood sufficiently informative to extract a predictive gene signature for smoking exposure (Smoker vs Non-current smoker) or cessation (Former smoker vs Never smoker) in human?

Sub-challenge2: Species translatable blood signature as exposure response marker

Most of pre-clinical in vivo studies are conducted in rodents which raises the question of translatability and applicability of results to human.

Scientific Question

Are gene expression changes in blood of humans and rodents sufficiently informative to define a unique rule or classifier to extract a specific gene signature predictive of smoking exposure (Smoker vs Non-current smoker) or cessation (Former smoker vs Never smoker) in both species?