

Why should you be part of sbv IMPROVER?

sbv IMPROVER Datathon Japan

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 for verification of scientific data and results.

Key publications

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

Diagnostic Signature Challenge

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

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
- Poussin et al. **The species translation challenge - A systems biology perspective on human and rat bronchial epithelial cells.** Scientific Data. 2014

Network Verification Challenge

- sbv IMPROVER team et al. **Enhancement of COPD biological networks using a web-based collaboration interface.** F1000Res. 2015
- sbv IMPROVER team and NVC best performers. **Community-reviewed biological network models for toxicology and drug discovery applications.** Gene Regulation and Systems Biology. 2016

Systems Toxicology Challenge

- Poussin et al. **Crowd-sourced verification of computational methods and data in systems toxicology: a case study with a heat-not-burn candidate modified risk tobacco product.** Chem Res Toxicol. 2017

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, Douglas Connect, OrangeBus, and ADS. The project is led and funded by Philip Morris International. Further information at www.pmiscience.com and www.sbvimprover.com.

SHARE

Present the method applied in your submission at the Symposium.

PUBLISH

Co-author scientific articles describing the outcome of the challenge

LEARN

Receive an independent assessment of your methods.

NETWORK

Network with your peers and grow your professional network.

PRESENT

Your own research during a poster session at the Symposium.

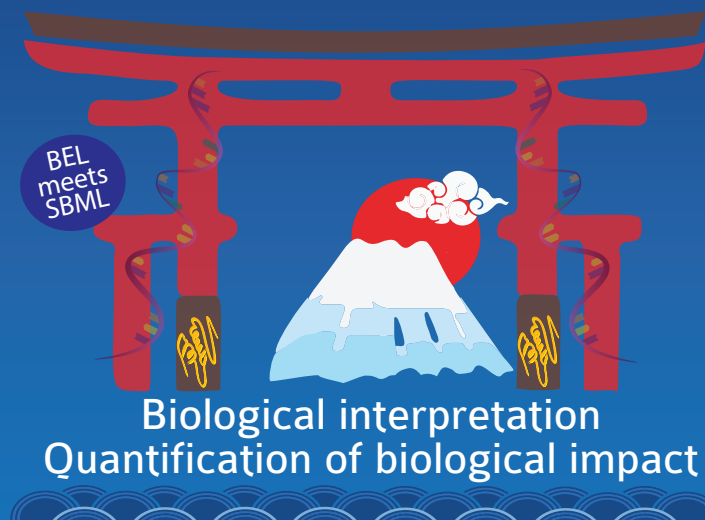
COLLABORATE

Have fun working with others.

MEET

Meet with worldwide experts.

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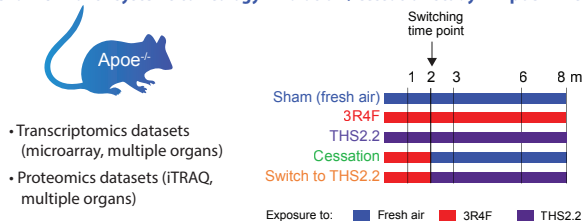
Symposium: 13th October 2017
Tokyo, Japan

sbv IMPROVER Challenges

- 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 Challenges**
Designed to verify previously built biological network models relevant to lung biology and responses to exposure.
- 2014 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.
- 2016 Singapore Datathon**
Designed to analyze big data in the field of epigenomics and extract biological knowledge.
- 2017 Israel Epigenomics Challenge**
Designed to predict class labels of different exposed groups based on epigenomics and transcriptomics information.
- 2017 Japan Biological Interpretation Datathon**
Designed to assess biological interpretation and quantification of biological impact based on omics datasets.

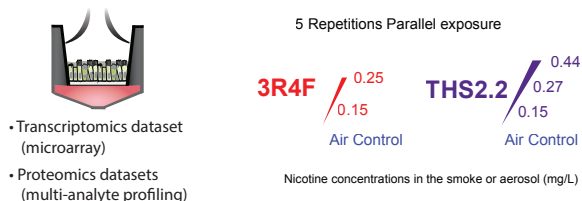
The data

THS2.2 - 8-month systems toxicology inhalation / cessation study in Apoe^{-/-} mice



- Transcriptomics datasets (microarray, multiple organs)
- Proteomics datasets (iTRAQ, multiple organs)

Assessment of acute THS2.2 aerosol exposure in Human nasal epithelial cultures

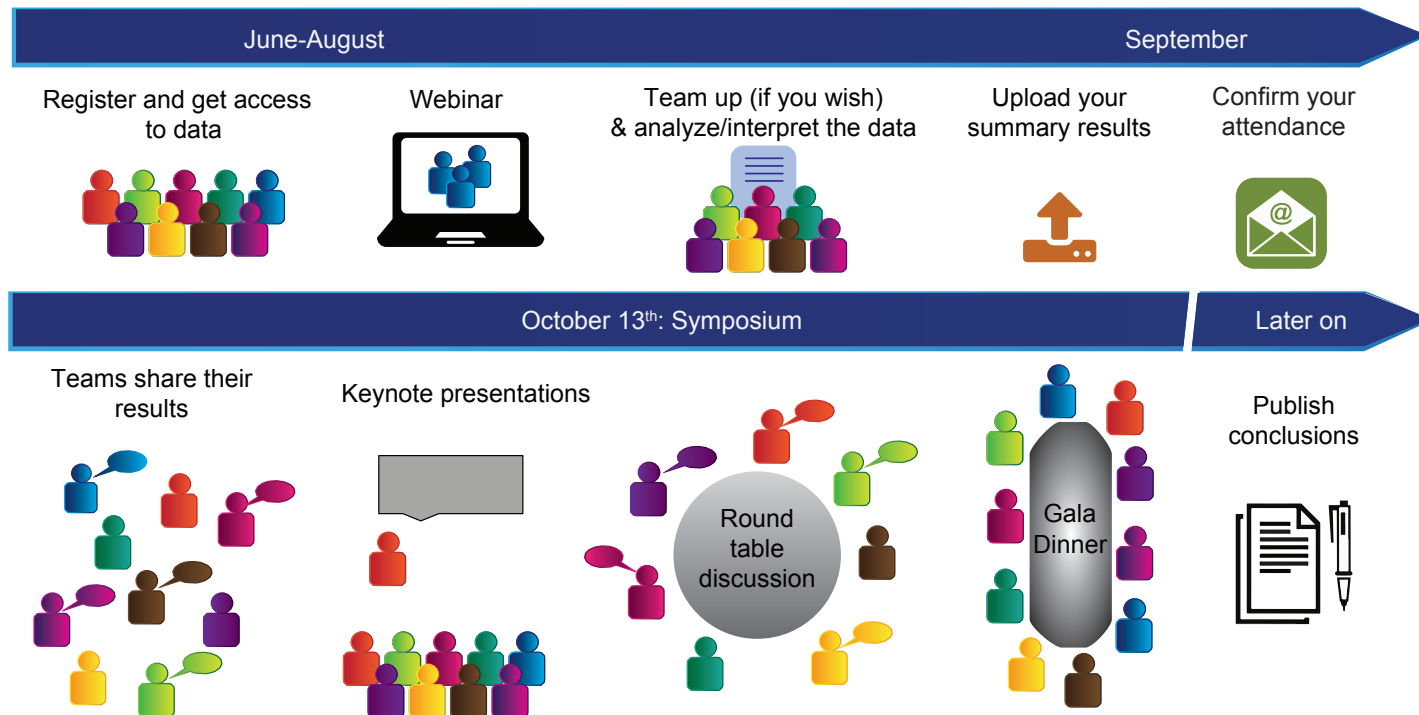


- Transcriptomics dataset (microarray)
- Proteomics datasets (multi-analyte profiling)

The Datathon in a Nutshell



Biological interpretation of omics data & Quantification of biological impact



Questions

- **What are the pathways/biological processes perturbed by exposure to cigarette smoke or to THS2.2 aerosol, a heat-not-burn product? After smoking cessation? After switching to THS2.2 aerosol?**
—> Participants are expected to submit a write up with their biological interpretation
- **How would you quantify relative perturbations in the respective groups?**
—> Innovative proposals will be conversed during the round table discussion



Biological network models are at the center of systems biology. The Biological Expression Language (BEL) is a language for representing scientific findings in the life sciences in a computable form. SBML is a data format for encoding models of biological processes. What are the proposals/interfaces one might consider to convert between BEL statements and SBML models?