

Why should you be part of sbv IMPROVER?

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

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
- sbv IMPROVER team and NVC best performers. **Community-reviewed biological network models for toxicology and drug discovery applications.** Gene Regulation and Systems Biology. 2016

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

DEVELOP

Have your method published as a Garuda gadget.

WIN

Win a USD 150 Amazon gift card.

SHARE & LEARN

Exchange on computational methods.

NETWORK

Network with your peers and grow your professional network.

PUBLISH

Co-author the event outcome publication.

COLLABORATE

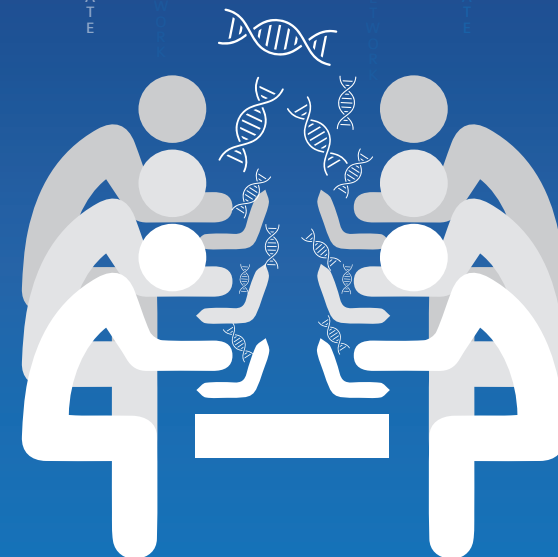
Have fun working with others.

MEET

Meet with worldwide experts.

www.sbvimprover.com/datathon

sbv IMPROVER Datathon



September 23rd-24th
Park Avenue Rochester
Hotel, Singapore

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 Challenge

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

2015 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.

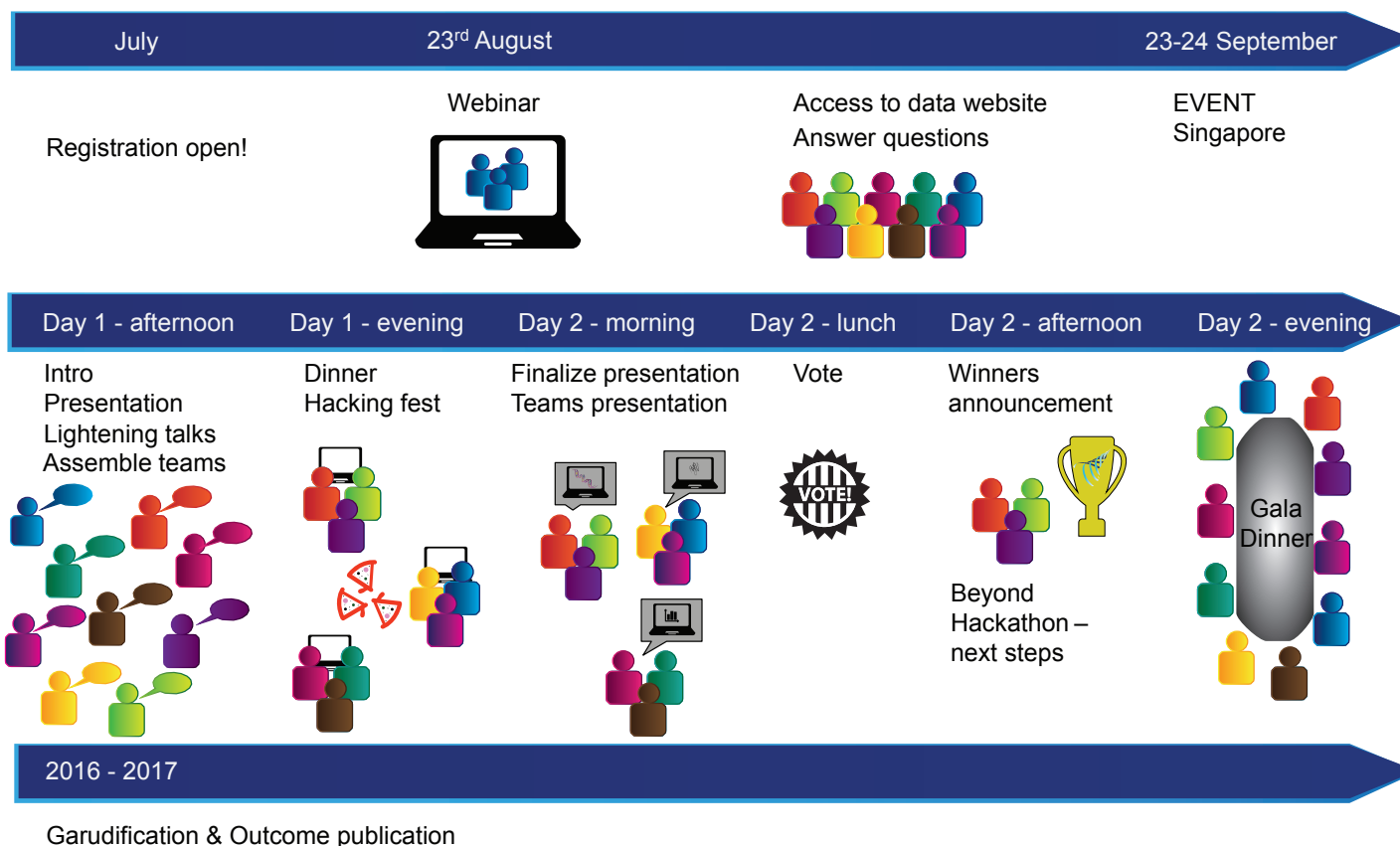
2016 Dataathon

The Dataathon in a Nutshell



POWERED BY GARUDA

Dataathon

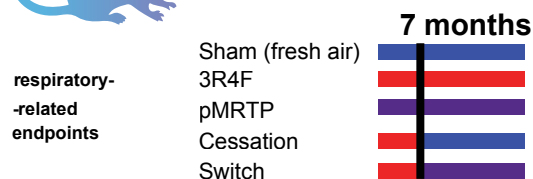


The data

Omics and functional measurements from a 7-month inhalation toxicology study.



Switching Study



Questions examples

- Is methylation of CpG islands only sufficient or does whole genome methylation bring additional value to discriminate between the exposure groups?
- Do you find enrichment of DNA methylation status within specific genome features (e.g. TSS, promoter, TEs, ...)?
- How much of the transcriptomics changes may be correlated with the methylation of associated sites?
- Is there an enrichment on specific gene class(es)?
- From the list of differentially expressed genes at month 7 in 3R4F, how many have associated differential methylation? On which genomic feature do those fall? (promoter/...). Do you find differential methylation in the same genes in other groups?