

# 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.

## 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
- Rhrissorakkrai 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](http://www.pmiscience.com)

### SHARE

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# sbv IMPROVER Epigenomics Challenge



**Symposium: May 4<sup>th</sup>, 2017**  
**Tel Aviv, Israel**

# 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 Datathon

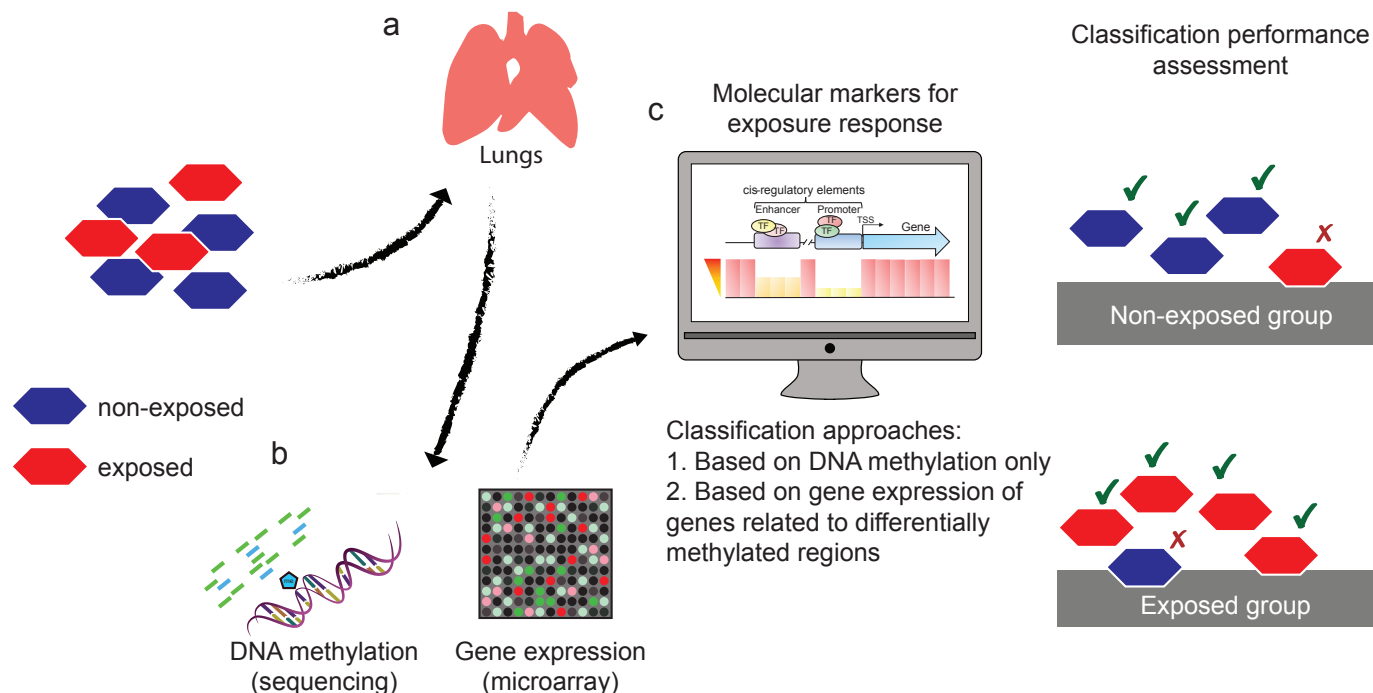
Designed to predict class labels of different exposed groups.

## 2017 Epigenomics Challenge

# The Challenge in a Nutshell

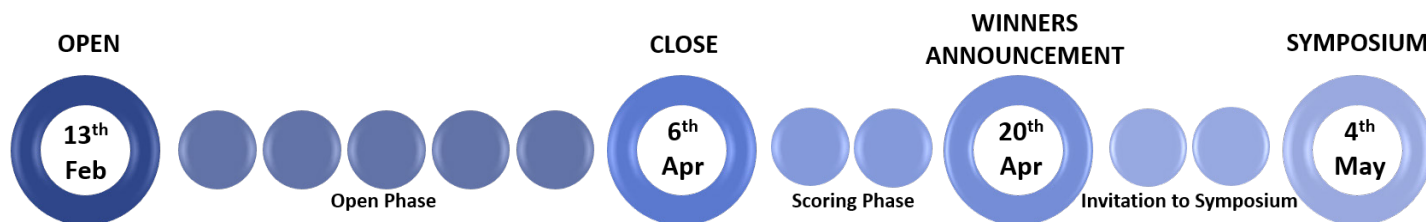
## Scientific Questions

- Can a smoke exposure signature be extracted from DNA methylation levels of DNA cis-regulatory elements (CRE)?
- Can a smoke exposure signature be extracted from expression data of genes controlled by differentially methylated DNA cis-regulatory elements?



- Samples of lung tissue are collected from mice belonging to the exposed or non-exposed groups.
- Gene expression profiles (GEX) and DNA methylation are measured using microarray based technology and Illumina sequencing by synthesis technology, respectively.
- Participants are provided with GEX and DNA-Methylation and asked to develop a classification approach capable of associating subjects to the correct exposure group.

## Timeline



## The data

