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Headline: sbv IMPROVER Launches Species Translation Challenge

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sbv IMPROVER announced its next challenge today at the Molecular Medicine Tri-Conference in San Francisco. The Species Translation Challenge is an open scientific challenge that will use crowdsourcing to help define the limits of rodent models as predictors of human biology. The challenge will launch later in 2013.

"We still lack a profound understanding of the extent to which we can use animal models to understand human biology," says Gustavo Stolovitzky, manager of Functional Genomics and Systems Biology, IBM Computational Biology Center. "The Species Translation Challenge is an important step to elucidate some of the limitations of the animal to human translation, as well as a verification of the biological processes in which such translation is meaningful."

The challenge is part of the sbv IMPROVER project—systems biology verification Industrial Methodology for PROcess VErification in Research; recently rebranded from IMPROVER—a collaborative effort by IBM Research and Philip Morris International R&D designed to develop a transparent and robust process for assessing complex scientific data in systems biology (see, IMPROVER-ing Data Verification for Systems Biology).

"The Species Translation Challenge will give participants access to data sets of remarkable quality," says Hugh Browne, director of scientific communications, PMI. "We believe that the outcomes of the challenge will enable the scientific community to re-define the boundaries of rodent models as predictors of human biology. This may have relevance and potentially far reaching implications for a host of industries including pharmaceuticals, biotechnology, food and many other consumer products."

Challenge participants will verify that translational mapping allows accurate prediction of the biological effects of stimulus-induced genetic alterations in one species given information about the same alterations in another species.

The Species Translation Challenge will be divided into four sub-challenges, each posing a specific question: 1) Can rodent phosphorylation status be inferred from rodent gene expression data? 2) Can human phosphorylation status be inferred from rodent gene expression and phosphorylation data, as well as human gene expression data? 3) Can rodent gene expression data be used to infer responsive gene sets and pathways in humans? 4) Can a consensus network be constructed from gene expression, phosphorylation and cytokine data?

"There is a growing demand for genomic approaches to personalized medicine," said John Quackenbush, Dana-Farber Cancer Institute, in a statement. "While our knowledge of the link
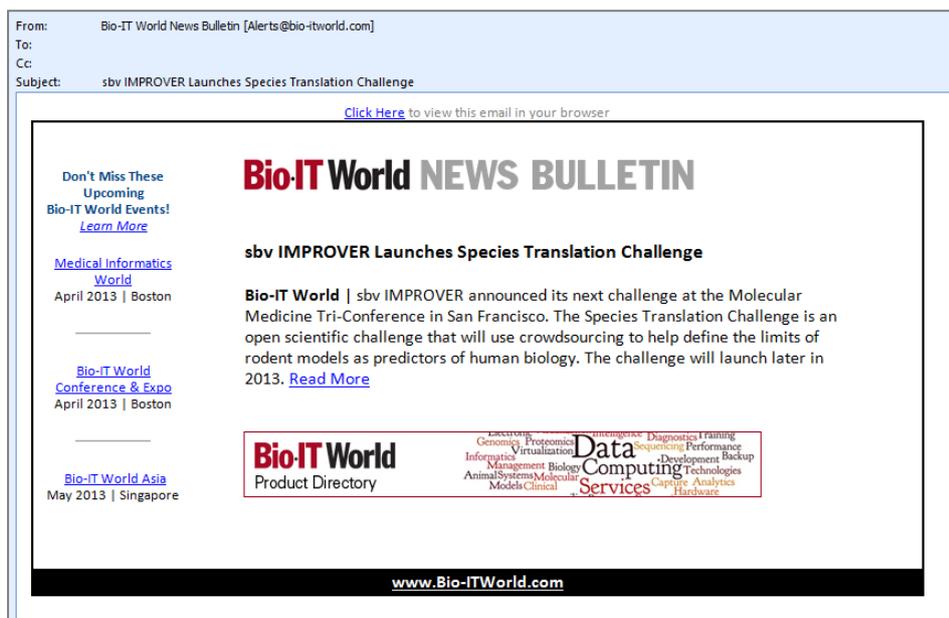
between genotype and phenotype is constantly growing, we are still in the early days of developing models that can be used to make meaningful predictions and improve outcomes for patients. Projects like sbv IMPROVER are important because they challenge scientists to develop systems biology methods to integrate data and develop a better understanding of disease."

The Species Translation Challenge will be the second of four planned challenges in sbv IMPROVER. The first, the Diagnostic Signature Challenge, asked participants to identify robust diagnostic signatures in four disease areas: chronic obstructive pulmonary disease (COPD), lung cancer, multiple sclerosis (MS) and psoriasis. The challenge attracted the participation of 54 teams from around the world, many of whom subsequently applied the sbv IMPROVER methodology to their own research in different disease areas.

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