



**Date:** 5 November 2013

## **Headline:** IMPROVER Species Translation Challenge Results Released

**Byline:** n/a (Uduak Grace Thomas)

**Article online at:** <http://www.genomeweb.com/informatics/improver-species-translation-challenge-results-released>

Last week, Philips Morris International and IBM, organizers of the Systems Biology Verification: Industrial Methodology for Process Verification in Research, or SBV Improver, initiative, released the results of the Species Translation Challenge.

The organizers launched the challenge earlier this year to better understand the limits of using rodent models to understand biological events in humans. The results, which were presented last week at the SBV Improver Symposium 2013 in Athens, Greece, showed that rodent models can be used to generate predictions of biological process in humans to a greater extent than may be expected based on species similarity alone.

A total of 28 teams, comprising 51 scientists from 14 countries submitted predictions for the challenge, which began accepting participants in March this year. It was made up of four sub-challenges that explored whether perturbations of signaling pathways in one species predict the response to a given stimulus in another species; and which biological pathway functions and gene expression profiles are most robustly translated.

It also addressed whether translation depends on the nature of the stimulus or data type collected such as protein phosphorylation, gene expression and cytokine responses; and which computational methods are most effective for inferring gene, phosphorylation and pathway responses from one species to another.

Three best-performing teams were recognized in the first sub-challenge. The first, team AMG, has scientists from University of California Santa Barbara, University of Groningen, and Rutgers University — this group was also the best performer in sub-challenges two and three. The other best-performers in this category came from Clemson and Wayne State universities.

Five teams were recognized as joint best-performers in sub-challenge four: one from Max Planck Institute for Dynamics of Complex Technical Systems, a team from University of

Lausanne and Institute of Bioinformatics, one from Pacific Northwest National Laboratory, and two separate teams from University of Pittsburgh.

Commenting on the results, Pablo Meyer, a member of the SBV Improver project team from Computational Biology Center at IBM Research, said in a statement that participants submitted "a diverse set of approaches" that make it possible to "see without any biases or limitations what computational techniques work best when using different data sets to predict translatable biological processes."

Manuel Peitsch, vice president of PMI's Biological Systems Research arm, added that the results "may have far reaching implications for scientists in many fields that use animal models to understand more about human biological system." Based on the results of this challenge, "it is clear that from a computational biologists' perspective, rodents and humans are indeed closer than we think," he said.

The results of the challenge will be published in a series of peer-reviewed papers at a later date. The dataset used in the challenge will also be made available to the broader scientific community for further analysis.

Last month, Improver's organizers launched a new challenge focused on developing new methodologies for defining and verifying biological networks. Participants in the Network Verification challenge will have access to 50 biological networks associated with human lung diseases and comprising approximately 2,000 nodes and 2,500 edges and based on 75,000 pieces of scientific evidence in total ([BI 10/18/2013](#)). Submissions will be accepted until the end of January 2014.

-- ENDS --