



Date: November 2013

Headline: sbv IMPROVER Symposium 2013 in Athens

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Article online at:

http://www.scienceview.gr/imported/files/Newsletters/2013/Newsletter_SV_11_2013.pdf

The results of the challenge entitled “The Species Translation Challenge: Understanding the Limits of Rodent Models for Human Biology”, at the sbv IMPROVER Symposium 2013 was held at the Grand Resort Lagonissi Athens, Greece, on 29 – 31 October 2013.

The sbv IMPROVER Symposium 2013 was held at the Grand Resort Lagonissi Athens, Greece, on 29 – 31 October 2013. sbv (systems biology verification) IMPROVER (Industrial Methodology for Process Verification in Research) is a collaborative project designed to enable scientists to learn about and contribute to the development of new methods for verification of scientific data and results. sbv IMPROVER is a collaborative effort involving scientists from IBM Research and Philip Morris International. The project is funded by PMI.

This challenge focused on understanding the limits of rodent models for human biology. Teams were scored using a gold standard where predictions were compared to unreleased experimental data.

Open to academic and industrial researchers and data-mining experts around the world, the challenge calls on participants to design the most effective computational method for inferring cellular response in humans, based on high-throughput biological data in rats. While studies in rats have been instrumental in understanding a range of human ailments, translating those findings to humans remains a fundamental challenge in biomedical research.

The Athens symposium included:

- The results and presentation of awards for the Species Translation Challenge
- Keynote presentations on systems biology
- Workshops on Network Verification and Network Inference
- Poster Session

A team of researchers from UC Santa Barbara's Kavli Institute for Theoretical Physics (KITP) has taken first place honors in the Species Translation Challenge. Adel Dayarian and Sahand Hormoz, postdoctoral researchers at the KITP, and their collaborators Gyan Bhanot, professor of physics and molecular biology and biochemistry at Rutgers University, and Michael Biehl, professor of computer science at the University of Groningen in the Netherlands, reported their findings.

The team named AMG formed by Bhanot, Biehl, Dayarian and Hormoz achieved first rank performance in three of the four sub-challenges. A research grant of US\$ 20000 is awarded per sub-challenge, which is divided among three best performing teams for one of the sub-challenges while for two other sub-challenges, AMG was the only rank one performing team.

As an integral part of this interdisciplinary effort, the design and application of machine learning techniques in the analysis of gene expression and other biological data was instrumental in achieving accurate predictions. Michael Biehl's recent research interests focus on the development of efficient machine learning methods and their application in the bio-medical domain.

Studies on rodents have been a necessary part of modeling various diseases in humans," KITP's Dayarian said. "Due to the lack of sufficient data, it has been common to assume that biological processes in mice or rats can be translated to processes in humans. The Species Translation Challenge was designed to verify the accuracy and limitations of this assumption."

Providing some answers to whether biological processes in mice or rats can correspond to biological processes in humans under analogous conditions is invaluable to the biomedical research community as rodent models continue to be a central tool in that field of study. To that end, the Species Translation Challenge consisted of four subchallenges that together sought to shed light on several important questions faced by researchers, with each question addressing a different aspect of translatability:

- » Can the perturbations of signaling pathways in one species predict the response to a given stimulus in another species?
- » Which biological pathway functions and gene expression profiles are most robustly translated?
- » Does translation depend on the nature of the stimulus or data type collected, such as protein phosphorylation, gene expression and cytokine responses?
- » Which computational methods are most effective for inferring gene, phosphorylation and pathway responses from one species to another?

KITP's Hormoz emphasized the important role that theoretical physicists can play in the changing field of computational biology. "Physicists are used to dealing with large and noisy data sets," he said. "Our background in statistical physics was particularly useful. We used fluctuations in the measured data to correct for biases introduced by the measurement process."

The next sbv IMPROVER project, the Network Verification Challenge, runs until January. NVC, which aims to verify and enhance existing biological network models, is expected to increase the networks' value and promote their use in such research applications as drug discovery, personalized medicine and toxicological risk assessment.

More info: <https://www.sbvimprover.com>

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