Network Verification Challenge open for Scietists

THE Network Verification Challenge recently opened for submissions from the global scientific community. The Challenge uses a crowd-verification process (an approach also known as "Wisdom of the Crowds") to fine-tune and verify sophisticated biological networks. The resulting models represent the current status of scientific knowledge as related to a given set of networks, and provide a framework by which other biological networks can be visualized, expanded and verified.

"The Network Verification Challenge is uniquely placed to help us generate accurate, comprehensive and reliable models of biological networks," said Professor Martin Hofmann-Apitius, Head of Department of Bioinformatics at the Fraunhofer Institute for Algorithms and Scientific Computing SCAI, which developed part of the online platform that Challenge participants use to work on the networks. "This is an exciting new approach to network verification which has a number of implications, including the potential to provide an accelerated mechanism for the dissemination and validation of scientific knowledge, better maps of disease and improvements to therapeutic discovery and development."

The Challenge is part of the sbv IMPROVER project (systems biology verification: Industrial Methodology for PROcess VErification in Research), a collaborative initiative by IBM Research and Philip Morris International R&D which is designed to develop a robust, transparent and practical process for assessing complex scientific data. Within this framework, it also provides an approach for the verification of systems biology data and with implications for human healthcare and other scientific and industrial areas.

"The sbv IMPROVER project is addressing some of the most fundamental issues facing the scientific community today, including: how can we cope with the explosive growth of data confidently, thoroughly and practically," said Dr David De Graaf, President and CEO of Selventa, which has played an important role in the development of the biological networks used in this challenge and also developed the software that allows visualization of the models.

Participants in the Network Verification Challenge have the opportunity to work on 50 biological networks based on 75,000 individual pieces of scientific evidence. In total, the networks comprise approximately 2,000 nodes and 2,500 edges.

The Challenge consists of five phases:

1. Initial biological network models (related to human lung disease) are constructed based on literature and data-driven hypotheses. These models are encoded in Biological Expression Language (BEL), a human-readable and machine-computable language that captures causal and correlative relationships between biological entities.

2. Challenge participants are asked to enhance and/or verify the network models using a high-performance online platform. This process is set-up as a collaborative competition where points are awarded for various actions contributing to the improvement of the models.

3. The contributions made by the participants will be carefully reviewed by the sbv IMPROVER project team against the supporting evidence provided. The most controversial edges (i.e., those that did not obtain a consensus from the community in phase two) will be selected for further review and discussion in phase four.

4. The participants that contributed most effectively in phase two will be invited to participate in an international networking jamboree session (planned for 18-20 March 2014 in Montreux, Switzerland). The objective of the jamboree is to reach a consensus among the experts of how best to formulate the network models.

5. The verified networks models are then shared with the scientific community.

Challenge participants will have early access to curated network models of signaling pathways, downloadable networks for participants who perform a certain number of actions (which are likely to help scientists generate new hypotheses for their own research) and early expertise in BEL, which is increasingly being adopted as a biological syntax conducive to computational manipulation. There is no financial reward for this challenge, although top participants may be eligible to receive a travel bursary to attend the jamboree session to discuss controversial edges. Travel bursaries will be funded by Philip Morris International.

The Network Verification Challenge is the third in a series of four challenges in sbv IMPROVER. The first, the Diagnostic Signature Challenge, asked participants to identify robust diagnostic signatures across four disease areas. The second, the Species Translation Challenge, sought to refine understanding of the limits of rodent models for predictors of human biology.

The Network Verification Challenge is open to scientists from commercial entities as well as academic and research institutions. Submissions will be accepted through to February 2014. Those interested can visit http://www.sbvimprover.com.