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Network Verfication Challenge gains momentum

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Singapore: Scientific consensus in the *Network Verification Challenge*, conducted in Spain from 15-18 June 2015, has exhibited positive growth as project continues to develop verified biological network models for use in toxicological risk assessment.

Network Verification Challenge is part of the SBV IMPROVER project (Systems Biology Verification: Industrial Methodology for PROcess VErification in Research), which aims to develop a robust methodology for verifying systems biology methods and results based on the principles of crowd-sourcing and collaborative competition. SBV IMPROVER is designed as a series of open scientific challenges and is a collaborative effort led and funded by Philip Morris International Research and Development (PMI R&D).

Part two of the challenge attracted over 173 scientific participants from 26 countries. They have contributed 2,225 new evidences, 1,289 new edges and 1,000 new nodes to the networks. As part of the process used to reach consensus, the community of scientists participating in the challenge cast 9,286 votes either verifying or rejecting elements of the networks compared to 2,456 votes in Part One, representing an overall consensus increase of 278 percent. The resulting models, which will be made freely available, are set to have far reaching implications for toxicological risk assessment.

"The Network Verification Challenge is helping to shift the paradigm of toxicological risk assessment," said Dr Rajesh Mandarapu, research associate, Prakhya Research Laboratories and one of the challenge best performers. "The models being produced are both comprehensive and verifiable, allowing us to make toxicity predictions based on biological mechanisms. It is a privilege to be part of the SBV IMPROVER community and to be contributing to these exciting developments in computational biology."

The models being produced aim to capture all existing knowledge of biological relationships across a range of mechanisms (calcium signaling, senescence and oxidative stress as just three examples). As well as being highly relevant for computation-based approaches to toxicological risk assessment, the models also have applications in drug discovery and personalized medicine. They may further assist in placing in vitro assays into a regulatory context, creating toxicological testing strategies

and frameworks.

"As well as being useful in the biological context, the models proded by initiatives such as the Network Verification Challenge also have important regulatory implications, providing a verifiable framework for data analysis and improving the human-relevance of regulatory test methods," said Dr Kristie Sullivan, Director of Regulatory Testing Issues, Physicians Committee for Responsible Medicine (USA).

"It is fantastic to see how the Network Verification Challenge has grown," said Professor Manuel Peitsch, vice president, biological systems research, PMI R&D. "The increasing interest in the challenge from around the world is testament to the value the scientific community places on the models being produced and the robustness of the SBV IMPROVER methodology. To take part in an SBV IMPROVER challenge is to be part of pioneering community that is driving innovation and working together to improve how scientific research is conducted and verified."

PMI is currently developing a portfolio of innovative products for adult smokers that have the potential to reduce the risk of smoking-related diseases as compared to the continued use of conventional cigarettes. A comprehensive scientific assessment program is being conducted to test and evaluate the reduced-risk potential of these products and it is hoped that the set of models being produced in the Network Verification Challenge prove to be a valuable tool within that program.

The Network Verification Challenge is the third in a series of 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 as predictors of human biology.