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NEUCHÂTEL, Switzerland— A newly published paper has highlighted the potential of scientific crowdsourcing to illuminate the mechanisms underlying a range of diseases. The paper in *Gene Regulation and Systems Biology* showed that a crowdsourced biological network model focused on lung and chronic obstructive pulmonary disease has important applications in toxicology and drug discovery. The community-produced biological network model was the latest product of the Network Verification Challenge (NVC), a global initiative that allows scientists from many areas to contribute to the verification of biological networks.

NVC, an effort originally spearheaded by IBM and Philip Morris International (PMI) (IBM hasn't been involved in the past couple years), is one phase of a broader project referred to as sbv IMPROVER (Systems Biology Verification—Industrial Methodology for Process Verification in Research). sbv IMPROVER is designed to allow scientists to compete and collaborate both in an online platform and in person through a structured crowdsourcing process. The overall goal of sbv IMPROVER is to create better verification of methods and concepts in systems biology research.

Marja Talikka, a senior scientist with PMI leading the development of the network models, tells DDNews that the collaborative nature of the effort allowed for an enormous amount of data to be thoroughly verified and analyzed with a high degree of precision. The result, she says, is a model that offers a deeper understanding of the complex relationships involved in the relevant biological pathways.

“Scientists are very interested in working together to tackle common challenges and questions,” Talikka tells DDNews. “When people are evaluating their own work they are not necessarily unbiased and do not always have expertise in all areas relevant to their research, so crowdsourcing can bring greater accuracy and greater insight.”

The project’s networks were built using the Biological Expression Language (BEL) to capture relationships between biological entities and provide information on activation or inhibition. When data is overlaid onto biological pathways that are of interest, it becomes possible to identify applications for toxicology and drug discovery. The networks explored through the NVC relate to lung biology and respiratory disease, but many also apply to other tissues and disease contexts and can be built upon according to scientists’ specific needs.

Biological network models can help scientists gain deeper insights into diseases through describing the relationships between the molecular mechanisms involved in the regulation of a particular biological process. Several network models are widely used within the scientific community, including the Kyoto Encyclopedia of Genes and Genomes (KEGG) and Reactome, which are open-access pathway databases. But these general pathway databases have important differences from the networks developed through NVC.

Talikka says that unlike KEGG and Reactome, NVC has developed a set of networks within defined boundaries relevant to chronic obstructive pulmonary disease that are available to the public for viewing and downloading on the Bionet website. Moreover, NVC networks are open to any user for editing and discussion in order to facilitate a peer-review process aimed at ensuring the networks are comprehensive and current. The networks also contain many layers of information that capture direct causal, indirect causal, correlative and other non-causal relationships.

At least 173 individuals from 26 countries have been involved in NVC. Participants have been motivated to contribute by the opportunity to collaborate with leading experts in the fields of toxicology and systems biology, as well as the chance to gain greater knowledge of BEL and lung biology. NVC also used gamification to incentivize activity on the networks. Participants were able to move up a leaderboard based on their contributions. Best-performers had further opportunities for collaboration, including contributing to peer-reviewed papers.

“As part of the Network Verification Challenge community I have been able to contribute to state-of-the-art research in network biology,” said Aravind Tallam, postdoctoral fellow at TWINCORE Centre for Experimental and Clinical Infection Research. “As well as improving my own understanding of disease mechanisms and underlying biology, on a personal level the challenge has also allowed me to meet and collaborate with a diverse group of scientists who are working at the cutting edge of research.”

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