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Headline: Community-Verified Biological Network Models Show Promise for Toxicology, Drug Discovery

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A new set of community-produced biological network models allows a greater understanding of the mechanisms underlying a range of diseases. The models have been shown to have important applications in toxicology and drug discovery in a new paper in Gene Regulation and Systems Biology. These models are the latest output of the Network Verification Challenge (NVC), a global crowdsourcing initiative designed to draw on expertise from many scientific areas in order to verify and enhance understanding of biological networks.

According to Borislav Simovic, Quality Control at FM Pharma and one of the challenge best performers, “The Network Verification Challenge represents a powerful new approach in the identification and validation of new drug targets. Due to the volume of data involved, only through structured, collaborative working are we able to achieve the best understanding of biological pathways. In bringing together leading experts in toxicology and systems biology, the Network Verification Challenge gives us valuable new insights into the complex relationships involved in these pathways.”

The NVC, which is led and funded by Philip Morris International, has involved online and in-person collaborations between a global network of scientists (173 individuals from 26 countries in the latest iteration of the challenge). Networks were built using the Biological Expression Language (BEL), which captures relationships between biological entities and provides information on activation or inhibition. Applications for toxicology and drug discovery come through the overlay of data onto pathways of interest and/or the use of computational inference techniques.

The networks produced in the NVC offer a detailed and comprehensive representation of selected biological processes that is not seen in other available network resources. NVC networks are open to the crowd for editing, facilitating a peer-review process that helps to ensure that networks are both comprehensive and current. They also contain many layers of information with direct causal, indirect causal, correlative and other noncausal relationships being captured. The networks explored in the NVC relate to lung biology and respiratory disease, but many also apply to other tissues and disease contexts and can be built on according to scientists’ specific needs.

The NVC is the third challenge under the sbv IMPROVER umbrella. For more information about the sbv IMPROVER project, please visit <http://www.sbvimprover.com>.

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