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**Headline:** Public Science Insights: Community verified biological network models

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Biological network models that are comprehensive, accurate and verifiable are valuable resources that can help facilitate a deeper understanding of the mechanisms underlying diseases. In addition, such resources have important real-world applications across a range of disciplines, including toxicology and drug discovery. One such set of models has recently been created, and made publically available, by the Network Verification Challenge (NVC), a global crowdsourcing initiative designed to draw on expertise from many scientific areas in order to enhance and verify our understanding of biological networks.

The NVC, which is led and funded by Philip Morris International, has involved collaborations between a global network of scientists (173 individuals from 26 countries in the latest iteration of the challenge) and comprised of two stages:
1) Previously published network models were made available for communal verification by the global scientific community via a bespoke online platform. Gamification principles were employed at this stage to encourage engagement, with users able to move up a leaderboard based on their contributions.
2) A sub-set of networks with controversial edges (i.e., those that did not obtain consensus from the community in stage one) were discussed at an in-person 'jamboree' meeting. Top active performers were invited to participate in the meeting to refine the models.

The models produced in the NVC offer a detailed and comprehensive representation of selected biological processes which is not seen in other available network resources (e.g. KEGG and Reactome.) NVC networks are open to the crowd for editing, thereby facilitating a peer-review process which helps to ensure that networks are both comprehensive and current. They are built using the Biological Expression Language (BEL), which captures relationships between biological entities and provides information on activation or inhibition. They contain many layers of information with direct causal, indirect causal, correlative and other non-causal relationships being captured.

NVC models aim to capture all existing knowledge of biological relationships across a range of mechanisms (calcium signaling, senescence and oxidative stress as just three examples). 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. 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 NVC 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 scientific methods and results based on the principles of crowd-sourcing and collaborative competition. In using this approach, sbv IMPROVER is facilitating enhanced dialogue within the scientific community, transparency of research processes and open innovation in scientific discovery.

Participants were motivated to take part in the NVC due to the opportunity to further their understanding of the biology involved in the networks, to share their knowledge, to learn and use BEL and to collaborate with leading experts in the fields of toxicology and systems biology. Due to the volume and complexity of the data involved, it is only through this structured, collaborative working that we are able to achieve the best understanding of biological pathways. In bringing the community together, the NVC has given us new insights into the relationships involved in these pathways, and provided us with a valuable resource with applications across a variety of scientific fields.

Dr Julia Hoeng and Professor Dr Manuel Peitsch are two authors of the recently published paper, [Community-reviewed biological network models for toxicology and drug discovery applications](), available for download now in [Gene Regulation and Systems Biology]().

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