



**Date:** October 2014

## **Headline:** Network Verification Challenge generates COPD network models

**Byline:** n/a

The Network Verification Challenge, part of the sbv IMPROVER project, has generated a comprehensive set of biological models relevant to chronic obstructive pulmonary disease (COPD) which are now available for review by the global scientific community. The models have the potential to enable improved understanding of lung biology as well as identification of clinically relevant COPD biomarkers and drug targets.

The sbv IMPROVER project (systems biology verification: Industrial Methodology for PROcess VERification in Research) led and funded by PMI Research and Development, aims to both establish methodological foundations for systems biology and to demonstrate that crowd sourcing is a viable strategy to verify scientific methods and concepts in an industrial context.

“Under the umbrella of the Network Verification Challenge, scientists from around the world are working together to build the most comprehensive and sophisticated models of COPD that we have ever known,” said Daniele Guardavaccaro Ph.D, Principal Investigator, Hubrecht Institute, The Netherlands. “These models will be invaluable in assessing the mechanistic action of new drug compounds, and thereby expedite the drug discovery and development process. Beyond COPD, many of the models are relevant to other diseases too, and the implications for the advancement of healthcare across a number of fields are thus far reaching.”

COPD is the fourth leading cause of death worldwide and, without interventions to cut risk, total deaths from COPD could increase by more than 30% in the next 10 years, according to the WHO. It is a progressive inflammatory disease induced by cigarette smoking as well as the inhalation of pollutants, dust, chemicals or other foreign matter. COPD ultimately manifests as tissue destruction in the alveolar compartments, leading to reduced oxygen exchange. Understanding the mechanisms involved in these processes is important in understanding the progression of the disease, identifying drug targets and developing effective COPD treatments.

Part one of the challenge, which is now completed, involved participants from over 60 institutions across 12 countries. It comprised of two phases; communal verification of previously published networks by the scientific community and a discussion of a sub-set of

networks with controversial edges in a Jamboree later. In total, novel information in the form of 451 new network edges incorporating previously uncaptured biological components and 885 new literature evidences were added in the first phase, while 167 nodes and 296 edges were added to the network models during the Jamboree.

One of the many outcomes from part one of the Network Verification Challenge is an improved understanding of T-helper cell activation of other immune cell types that promote COPD inflammation, additional granularity to the process of neutrophil chemotaxis, a key driver of tissue damage in COPD, and an expansion of the macrophage activation network, adding further clarity to its effect on other immune cell types active in COPD. While these three networks received the largest amount of crowd activity, many additional enhancements have also improved the granularity and connectivity within other network structures.

“We are delighted with the response to part one of the Network Verification Challenge and particularly with the quality of scientific submissions that we have received from the crowd so far,” said Manuel Peitsch Ph.D, Vice President Biological Systems Research, PMI R&D. “We are confident that the models we now have cover the majority of known COPD biology. However, the true value of this initiative lies in the ability for the crowd to continue to develop and refine these networks as more people get involved in the project and as new studies are published.”

-- ENDS --