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Headline: Philips Morris International and IBM Launch Third 'Improver' Challenge

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Philips Morris International and IBM, organizers of the Systems Biology Verification: Industrial Methodology for Process Verification in Research, or SBV Improver, initiative, are now challenging the life sciences community to develop new methodologies for defining and verifying biological networks.

As part of the Network Verification Challenge, participants will have the opportunity to work on 50 biological networks associated with human lung diseases and comprising approximately 2,000 nodes and 2,500 edges and based on 75,000 pieces of scientific evidence in total.

According to the developers, the challenge has five phases. In the first, the organizers will construct biological network models based on the Biological Expression Language — a standard language and framework for capturing, storing, and sharing life sciences data that was initially developed by Selventa ([BI 4/1/2011](#)). In the second phase, participants will be asked to enhance and/or verify the network models using a high-performance online platform. This part of the process will be run as a collaborative competition where members of the community will be asked to review submissions and award points for various actions which help improve the network models.

In the third phase, the Improver project team will review participants' contributions and a subset of the contributors — those who create "controversial edges" in the second phase for which the community cannot come to a consensus — will be invited to participate in an international networking jamboree session planned for March 18-20, 2014 in Montreux, Switzerland, where their submissions will be discussed in detail. Once the networks models have been verified, they will then be shared with the scientific community at large.

“This challenge is uniquely placed to help us generate accurate, comprehensive and reliable models of biological networks,” according to Martin Hofmann-Apitius, head of the bioinformatics department at the Fraunhofer Institute for Algorithms and Scientific

Computing, which developed part of the online platform that participants will use to work on the networks. He further noted that it offers a new approach to network verification that “has a number of implications, including the potential to provide an accelerated mechanism for the dissemination and validation of scientific knowledge, better maps of disease, and improvements to therapeutic discovery and development.”

The challenge also addresses some of the most fundamental issues facing the scientific community today, such as how to cope with the explosive growth of data, David De Graaf, Selventa's president and CEO, said in a statement. “By providing high-quality data sets to any scientist who wishes to look at them, openly and for free, and then asking them to scrutinize that data as part of the crowd, we are helping to forge the way towards a more transparent, collaborative, and robust framework in which scientific research is conducted,” De Graaf said.

Submissions for this incarnation of the Improver will be accepted through February 2014. The challenge is open to scientists in both academia and industry. There is no financial reward for this challenge, although top participants may be eligible to receive a travel bursary to attend the jamboree session. These bursaries will be funded by Philip Morris International. Additional details about the challenge and how to participate are available [here](#).

The Improver team has organized other challenges including a Diagnostic Signature challenge launched last year, which aimed to assess and verify computational methods used to classify clinical samples based on gene-expression data in psoriasis, multiple sclerosis, lung cancer, and chronic obstructive pulmonary disease ([BI 10/5/2012](#)). The team has also organized a Species Translation challenge, which sought to refine current understanding of the limits of rodent models for predictors of human biology.

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