Crowdsourced enhancement of causal network models – new Network Verification Challenge enabling advanced xenobiotic metabolism models verification and refinement

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in the figure, scientific
network models, the overall biological impact of a perturbing agent, the Biological Impact Factor (BIF) [3], can be calculated

Implementation
models
enzymes that detoxify or activate xenobiotic compounds by catalyzing chemical reactions, such as oxidation, reduction or

alpha (Ppara) mediate this signal.

The phase I Xenobiotic Metabolism describes the activation of UDP-glucuronosyltransferases, sulfotransferases, N-acetyltransferases, glutathione S-transferases and the importance of nuclear factor, erythroid 2 like 2 (NQO2), and nuclear receptor subtype 3 group C member 1 (Nrf2) in the transcription process.

In the final step, the phase III Xenobiotic Metabolism Network Model describes the xenobiotic excretion from cells. It is mediated by the activation of molecular transporters, such as ATP-binding cassette subfamily B (ABCB), ATP-binding cassette subfamily G (ABCG), and ATP-binding cassette subfamily C (ABCC), and ATP-binding cassette subfamily A (ABCA).

The networks will be released for editing sequentially and the challenge will be open until end of December 2017.


Submit your work as they unite to verify and enhance the biological network models that will then be released to the community for use in research applications such as drug discovery, personalized medicine, and toxicological assessment.

Collaborate: have fun competing and collaborating with others.

• Test and expand your knowledge.
• Learn the Biological Expression Language, and use BEL, a curriculum tool to create BEL statements and annotations from scientific publications.
• Challenge your peers and see in real time how you rank and the challenge will be open until end of December 2017.

At the end of the challenge, the best performing participants will be rewarded with a travel grant of up to 2,000 USD (see Challenge rules on believ.com).