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Headline: Systems Toxicology Computational Challenge Results Announced

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The Systems Toxicology Computational Challenge results have been announced from the fourth challenge launched by sbv IMPROVER, an international scientific crowdsourcing initiative. The latest challenge was [announced in December of last year](#), and sought to demonstrate how transcriptomics information present in the blood can be used to predict whether people have been exposed or not exposed to specific toxicants.

Teams from Wayne State University; Shanghai Jiao Tong University-Yale Joint Center for Biostatistics, China; Istanbul Technical University, Turkey; and La Jolla Institute for Allergy & Immunology took top honors. Challenge participants used their own computational techniques to make their predictions, with best-performers achieving accuracy of up to 95%.

Philip Morris International funds the sbv IMPROVER projects, and [the most recent challenge](#) aimed to verify that robust markers could be extracted from blood gene expression data that would distinguish current tobacco smokers from non-smokers, and then discriminate non-smokers as former smokers and never smokers. This question was addressed in two sub-challenges, the first one looking at human data only, the second one investigating human and mouse data together. Anonymized participants' submissions were scored against a gold-standard dataset. Final results and team rankings were reviewed and approved by an independent expert scoring review panel.

“The real-world application of models based on blood gene expression markers for predictive classification in toxicology is uniquely challenging,” said Carine Poussin, a computational biologist at Philip Morris International. “The difficulty resides in the identification of relevant markers in blood after chemical exposure and the low success of correct classification when predictive models are applied on new individual blood samples. Furthermore, most pre-clinical toxicological in vivo studies are conducted in rodents, adding a degree of complexity when applying the results to humans. The Systems Toxicology Computational Challenge has explored these questions and helped to increase our understanding of what is necessary to reach higher levels of predictability and robustness in both humans and across species.”

Participants were very successful in developing models with a high level of predictive performance in distinguishing current tobacco smokers from non-smokers; the best performers could identify the two groups near-perfectly. Predicting whether non-smokers were former smokers or never smokers was more challenging.

“Assessing toxicant exposure from blood data alone is a complex and fascinating undertaking. The tasks set in the Systems Toxicology Computational Challenge allowed us to address this issue, while objectively testing our computational methodologies. As computational biologists we are always looking for new data to work with, and it is of huge value to have access to the high quality datasets provided by sbv IMPROVER,” said Ismail Bilgen, a research assistant at Istanbul Technical University in Turkey. Bilgen’s team was the best performer in the second sub-challenge.

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