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Headline: Sometimes You Can Trust a Rat

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The results from the sbv IMPROVER Species Translation Challenge, [launched in February](#), were announced at a symposium in Athens last week. The [sbv IMPROVER program](#), a collaboration between IBM Research and Philip Morris International, was designed to validate commonly-used bioinformatics research techniques, by issuing incentivized challenges to research organizations who will attempt to show that their computational tools, working with public datasets, can accurately predict hidden experimental results.

The Species Translation Challenge, the second to emerge from the program, asked how reliable rodent models are as predictors of genetic pathways in humans. Participants were given public information about gene activation and expression in rat models, and asked to predict the expression patterns of homologous molecular pathways in experiments on human cells. Four sub-challenges provided data at different junctures in the molecular pathway; for instance, Sub-Challenge 2 gave researchers gene expression data and protein phosphorylation data across 16 proteins in rat models, plus analogous gene expression data from human cells, and invited predictions on the activation status of the relevant human phosphoproteins.

Judges were surprised at the high accuracy of the winners in these challenges, suggesting that rodent models can be used with reasonable confidence to understand genetic pathways in humans on the molecular level, when the best computational techniques are applied. In a statement at the symposium, Michael Biehl, a professor from the University of Groningen and a member of challenge team AMG, said, “Based on our work in the second Sub-Challenge, it seems that there may well be a closer relationship between rat and human than what is currently acknowledged. This is an exciting discovery, with potential implications across a number of fields, and one we look forward to exploring further.” Team AMG, which also included representatives from Rutgers University and UCSB, was declared the winner of Sub-Challenges 2 and 3 and joint winner of Sub-Challenge 1.

Added Professor Gyan Bhanot, a member from Rutgers, “It is crucial that we continue to take steps to improve modeling capabilities as a complement to in vivo systems, and we

would like to see how we could improve our predictions now that the challenge is closed and the full dataset has been unblinded.”

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