

Plant breeding models could aid toxicological research

By Ernie Hood

New computer modeling techniques, already in commercial use to enhance grain, fruit, and vegetable crops, may offer insights for animal modeling related to toxicology and toxicogenomics, according to Russell Wolfinger, Ph.D., the director of scientific discovery and genomics at SAS Institute, Inc., in Cary, North Carolina. Wolfinger spoke Dec. 16, in the latest offering from the NIEHS Data Science Seminar Series, hosted by the Office of Scientific Information Management (OSIM).

In a talk titled “Genomic Selection in Plant and Animal Breeding with Potential Applications to Toxicological Research,” Wolfinger showcased predictive models for quantitative biological traits. These models were developed for plant breeding and are now in heavy use by scientists at SAS’s commercial partner, General Mills, one of the largest food companies in the world. In a demanding marketplace, these models help breeders fine-tune desired traits in advance through sophisticated computational methods that have been validated and proven successful.

Computing firepower helps

Cross-validation of the models is critical. “There are literally millions of ways you can build these predictive models, so the question becomes, which models are going to do best, and which will work best in the future?” Wolfinger said. “We use the cross-validation approach to tackle those questions.”

“Once we have these predictive models in hand, they can be used effectively to accelerate progress around the breeding cycle,” he said. The plant breeders at General Mills use genotyping to improve and accelerate the breeding cycle, particularly in oats, which are the key ingredient of one of their flagship products, Cheerios.

In recent years, dramatic improvements in computing speed, memory, and cost have enhanced the ability of statisticians to crunch big data quickly. “Though some of these algorithms have been out in the literature for a while, they haven’t been very useful because they took too long to run,” Wolfinger observed. “Now, a breeder can sit at the computer and simulate literally years of potential work in just an afternoon,” he continued. “It’s really changing the game.”

Crossover possibilities

OSIM Director Allen Dearry, Ph.D., said the take-home message of Wolfinger’s talk was that the statistical methods he described could be applied to development of animal models used in toxicology. “In NTP [the National Toxicology Program], for example, researchers could carry out this same kind of quantitative modeling of genomic selection to better define or develop rodent models,” he said.

Wolfinger agreed. “For anything that you’re interested in measuring for potential use as a trait, if you think there’s a genomic component, a model could be built to predict it.” (See sidebar for examples.)

Potential applications of predictive models to toxicological research

- Build genomic selection predictive models on mouse or rat lines
- Optimize animal line selection and potentially create new breeds for desired traits
- Optimize for microbes and viruses that interact with the environment, perhaps building in interaction with the microbiome



Wolfinger, who has worked at SAS since 1989, leads a research team developing software solutions in the genomics and clinical research fields. (Photo courtesy of Steve McCaw)

Wolfinger's talk was co-sponsored by NTP and the NIEHS [predictive toxicology and disease](#) faculty.

(Ernie Hood is a contract writer with the NIEHS Office of Communications and Public Liaison.)



Richard Paules, Ph.D., senior scientist for the Toxicogenomics and Genetics Group, and OSIM Data Scientist Rebecca Boyles were especially interested in Wolfinger's ideas. (Photo courtesy of Steve McCaw)



"Wolfinger is a major star in the genomics and data science constellation," said Dearry, above, in his introduction. (Photo courtesy of Steve McCaw)



A full house of NIEHS and NTP researchers turned out for Wolfinger's Data Science Seminar Series lecture. (Photo courtesy of Steve McCaw)

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