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Making Sense of Complex Disease

Marylyn Ritchie's lab at Vanderbilt is focused on pinpointing susceptibility genes for common, albeit complex, human diseases. These run the gamut from hypertension and cardiovascular disease to diabetes and cancer. To make sense of the gene and protein expression data that fuels her search, Ritchie resorts to a home-grown arsenal of statistical techniques and computational tools to make meaning of gene-gene interaction or whole genome association data.

One such tool in development is a research platform designed to integrate multiple analytical techniques at the same time. "The idea is that no one method is going to work best for all data," Ritchie says, "so we're trying to combine the successes of lots of different groups … so that we can intelligently do analyses of whole genome association data." The tool — known as the Platform for Analysis, Translation, and Organization (PLATO) of large scale data — exists as a prototype and is capable of discovering gene-gene interactions in genome-wide data.

The hard part isn't just a matter of taming algorithms or applying statistics, according to Ritchie. "I think a lot of what we work on is kind of cutting-edge — sometimes bleeding-edge — so trying to make other people understand the techniques we're using can be a challenge," she says. So far, though, response to Ritchie's posters and talks on the whole genome association research platform has been enthusiastic.

Ritchie, now an assistant professor, knew she wanted to do biomedical research even as an undergrad, though she didn't have a specific focus at the time. That came when a turn in Vanderbilt's interdisciplinary graduate program brought her to Jason Moore's lab, where she found a research program that capitalized on her talents in mathematics and statistics to resolve biological questions. Moore, who is now at Dartmouth, remains a collaborator and one whom Ritchie credits as having a major impact on how she approaches her own research.

Looking ahead

Ritchie sees cost-effective whole genome sequencing as likely in the not-too-distant future, although she's hesitant to hazard a date. However, she does predict that the data analysis challenges of whole genome-level data will be immense. Ritchie also cites the integration of data across fields — from microarrays to protein and biomarkers — as another research trend.

In terms of genetics proper, Ritchie says that researchers are starting to realize that genes don't work in isolation, and that the environment plays a large role in their expression. "There's a lot of grumbling about looking for gene-environment interactions," she says, "and I think that a lot of that is going to take off." In fact, she's already involved in a proposal researchers at Vanderbilt are putting together for the NIH's Genes and Environment Initiative. "It's certainly a high-risk, high-payoff type of proposal," Ritchie says, "but we figured that even the effort we put into planning how we would do it is helpful for how we are facing these studies in our own research."

And the Nobel goes to...

If Ritchie ever receives an early morning call from Stockholm notifying her of a certain prize, she would want it to be "for developing a methodology to dissect the genetic architecture of complex disease."

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Education: *PhD, Vanderbilt University, 2004*

Recommended by: *Jonathan Haines*

Great scientists communicate

Ritchie says that being an organized, creative thinker with a gift for communication is key to being a great scientist. "The nature of science these days is very collaborative," she says, "and if you can't communicate with people — both in your field and in other fields — you're not going to go far very fast."

— *JC*