Genome Technology
Inside Integrated Biology
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special issue

Tomorrow's PIs

Genome Technology's special year-end issue profiling rising young investigators

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Inside Integrated Biology

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A special issue for special scientists

You're a busy person. If you're like most of our readers, you probably spend your day scrambling from one meeting to the next, squeezing in experiments and data analysis whenever you can, and after your long, hard day, you finally go home — where you catch up on all of your work e-mail. Sound familiar?

In a field where speed is essential — you need results *now*, you have to release your data immediately, and there's always a grant application or project presentation looming — it's a rare thing indeed to step back and actually take a moment to appreciate what you and your colleagues have accomplished.

It's that rare moment we offer to you with this issue of *Genome Technology*, aimed at celebrating the accomplishments of a select group of researchers in this community. In the past several months, readers have asked me for more profiles of up-and-coming scientists. So when we decided to add a bonus tenth issue to our calendar, choosing the theme was simple: who would be the PIs of tomorrow's labs? Who are the rising stars people should be watching right now?

We tapped today's leading PIs to find out, and they had no shortage of names to share with us. The tough part was narrowing the field to the 30 most promising scientists whose profiles you will find on the following pages. Our criteria were simple: they had to be involved in the disciplines that comprise systems biology, and could be no more than five years into their first faculty or equivalent post.

In what has been perhaps the most fun issue we've ever put together, the *GT* staff got to spend hours talking with these bright researchers not only about what they're doing today, but also about where they see the field going in the years to come (we did get mocked soundly, though, for my own favorite question: "If you were to one day win the Nobel Prize, what accomplishment would you like that to be for?"). What we found was that these scientists are already fluent in some key attributes: if you read the profiles carefully, you'll notice a theme of highly collaborative people who understand the importance of networking and surrounding themselves with other very smart people.

I'd like to thank all of the current lab heads who recommended people for inclusion in this issue, and also *GT* reporter Matt Dublin for heading up this project. And though we keep our editorial and advertising departments completely separate, I will take a moment to thank our advertisers, whose contributions for this issue have allowed us to give travel stipend honoraria to our profiled investigators.

You'll notice that this issue doesn't look like a typical *Genome Technology*. With different content comes a different designer, and GenomeWeb's own Elena Coronado has done an outstanding job in giving our bonus issue a very special look. We'll be back to our usual designers, the talented folks at Three Bears, with our next issue.

Finally, for those of you who thought we'd forgotten about the cartoon caption contest we offered earlier this year, don't miss the Blunt End. We held results till now since so many entries were plays on the PI/postdoc dynamic. Check out p. 50 for the winning caption and our honorable mention.

Meredith W. Salisbury

systems biology

nathanprice

A Bioengineer Gone Astray

By all accounts, Nathan Price had a pretty successful career as a graduate student. Upon finishing his PhD in bioengineering with Bernhard Palsson at the University of California, San Diego, where he published some 20 papers in computational biology, Price was offered a faculty position in the department of Chemical and Biomolecular Engineering at the University of Illinois at Urbana-Champaign. The majority of Price's grad work was centered on metabolic systems, mitochondria, and red blood cells, but he wanted to do something more relevant to disease research, specifically cancer. So Price decided to defer the job offer and applied instead for a fellowship to work with systems bio guru Lee Hood.

"The rationale for that is that Lee is one of the best persons in the world for thinking about systems approaches to medicine," says Price. "What I wanted to do was to harness computational models and high-throughput technologies to [be] able to get a better grasp of understanding of cancer from [the] systems perspective."

In Hood's lab, Price has set about developing algorithms that harness information external to the cell. "What we really want to learn is how to read secreted protein patterns in blood, not only to distinguish between health and disease at various stages, but also we hope to be able to link that back into causal perturbations and networks to use these patterns to identify states," he says.

He sees blood as a window into human health and disease that's just teeming with data. The problem, of course, is getting it. Price notes that one of the biggest challenges is measuring protein concentration in the blood. "It's very important that you identify your candidate markers in advance because when you go into the blood, it's much easier to measure proteins that you know you're looking for," he says.

And although Price says that researchers often refer to "deluges" of data in biology, that's not a problem he faces. "Relative to what we want to do, and the kind of algorithms that we want to run and the kinds of predictive capabilities that we want to generate, we often find that we have much less data than we would like," says Price. "That's a fairly universal problem that almost anyone in modeling faces."

Looking ahead

In the future, Price would like to see small microchips that can measure 1,000 to 2,000 proteins in the blood. His vision is to be able to take blood measurements, run them through various algorithms, and detect patterns that will essentially read out a person's health, what kind of diseases that individual might have, and the state of those diseases. "So we hope that eventually, the blood can be used as a window to track the development of various diseases and even to assess drug efficacy," says Price. "We hope to be able to see those kinds of things very early on." Price sees the blood not only as a way to monitor network perturbations and screen for diseases like brain cancer, but also as a means to determine how well a particular treatment will work.

Publications of note

Price and his colleagues recently submitted a paper entitled "Highly accurate two-gene classifier to differentiate gastrointestinal stromal tumors and leiomyosarcomas." Using a novel classifier based on a simple relative expression reversal between the expression of two genes, the paper reported 100 percent accuracy in differentiating between GIST and LMS in all patients tested.

And the Nobel goes to ...

Price says if he were to win the Nobel Prize, he would want it to be for developing good systems models and algorithms that could assess vulnerability in cancer as a dynamic system and effectively treat it in a variety of settings. *—MD*

Title: *Postdoctoral Fellow, Institute for Systems Biology*

Education: *PhD, University of California, San Diego, 2005*

Recommended by: *Harris Lewin*