

Genome Technology

Inside Integrated Biology

December 2006/January 2007



special issue

Tomorrow's PIS

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



Genome Technology

Inside Integrated Biology

table of contents

in every issue

- 5 Primer
- 50 Blunt End

systems biology

- 7 **Nathan Price:** A Bioengineer Gone Astray
- 8 **Manolis Kellis:** Elucidating Evolution with Model Orgs
- 9 **Hiroki Ueda:** He's Seen the Light

gene expression

- 11 **Kimberly Stegmaier:** Screening for Cures
- 12 **Adolfo Ferrando:** The Rise and Fall of Oncogenes

sequencing

- 13 **John Fondon:** Evolution and the Slippery Genome
- 15 **Elliott Margulies:** Finding Function in Genomes
- 16 **Babak Parviz:** Nanotech Meets Genomics
- 17 **Steven Cannon:** Leading the Legume Charge

rnai

- 19 **Jens Kurreck:** Turning Silencing into Therapy
- 20 **Michael Hemann:** Using RNAi to Fight Cancer

bioinformatics

- 28 **Joshua Akey:** Explorer of Evolutionary Forces
- 29 **Adam Siepel:** Conquering Comparative Genomics
- 30 **Atul Butte:** Reclassifying Medicine with Genomics
- 31 **Ben Raphael:** Computation Takes on Cancer

cytogenetics

- 27 **Frank Grützner:** Unraveling Platypus Genes

proteomics

- 23 **Michael MacCoss:** Tackling Targeted Proteomics
- 24 **Alexey Nesvizhskii:** From Physics to Proteins
- 25 **Martin Røssel Larsen:** Methods to His Mass Spec
- 26 **Joshua Coon:** Mass Spec, But Better

pharmacogenomics

- 32 **Heidi Rehm:** Moving Toward Personalized Medicine
- 33 **Tera Newman:** From Duplication to Disease Variants
- 34 **Holger Kirsten:** Genotyping for the Clinic
- 35 **Marylyn Ritchie:** Making Sense of Complex Disease

bioimaging

- 36 **Taekjip Ha:** FRET and the Single Molecule
- 37 **Anne Carpenter:** Imaging Breakthrough by Necessity

epigenetics

- 38 **Pablo Rabinowicz:** Unlocking the Methylation Mystery
- 39 **Bradley Bernstein:** Understanding Embryonic Stem Cells

metagenomics

- 40 **Mya Breitbart:** Watching Over Communities

structural genomics

- 41 **Andy Sharp:** Structure Is the New SNP

resources

- 43 Get Your Career on Track
- 45 Young Investigator Awards
- 46 Deadlines
- 48 Early-Career Grant Opportunities
- 49 Thanks to Today's Pls

Profiles written by Jennifer Crebs, Matthew Dublin, and Meredith Salisbury

Genome Technology

Inside Integrated Biology

Issue No. 67

125 Maiden Lane, Second Floor
New York, NY 10038
Tel +1 212 269 4747 Fax +1 212 269 3686
Genome-Technology.com

Editor

Meredith W. Salisbury
msalisbury@genomeweb.com

Senior Editor

Jennifer Crebs
jcrebs@genomeweb.com

Reporter

Matthew Dublin
mdublin@genomeweb.com

Design

Elena Coronado
ecoronado@genomeweb.com

Production

Three Bears gweb@threebears.com

GenomeWeb News

Bernadette Toner, *Editorial Director*
and *BioInform Editor*
btoner@genomeweb.com

Kirell Lakhman, *Deputy Editorial Director*
klakhman@genomeweb.com

Justin Petrone, *BioArray News Editor*
jpetrone@genomeweb.com

Ed Winnick, *BioCommerce Week Editor*
ewinnick@genomeweb.com

Ben Butkus, *Cell-Based Assay News Editor*
bbutkus@genomeweb.com

Turna Ray, *Pharmacogenomics Reporter Editor*
tray@genomeweb.com

Tony Fong, *ProteoMonitor Editor*
tfong@genomeweb.com

Doug Macron, *RNAi News Editor*
dmacron@genomeweb.com

Julia Karow, *Contributing Editor*
jkarow@genomeweb.com

Matt Jones, *GenomeWeb*
mjones@genomeweb.com

Chairman and Publisher

Dennis P. Waters, PhD
dwaters@genomeweb.com

Associate Publisher/Director of Advertising

Judy Block jblock@genomeweb.com
+1 212 651 5629

Margarita Serrano, Assistant

Director of Publishing Operations

Greg Anderson
ganderson@genomeweb.com
+1 212 651 5632

Director of Subscription Sales

Allan Nixon anixon@genomeweb.com

Copyright ©2006 GenomeWeb LLC.

The GenomeWeb Intelligence Network



No portion of this publication may be reproduced in whole or in part without written permission from GenomeWeb.

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

pharmacogenomics

marylynritchie

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 Van-

derbilt'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



Title: Assistant Professor, Department of Molecular Physiology & Biophysics, Vanderbilt University

Education: PhD, Vanderbilt University, 2004

Recommended by: Jonathan Haines

to dissect the genetic architecture of complex disease."

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