PROFILE OF A SCIENTIST: ALEX PICO, PhD

Alex Pico recently completed a postdoctoral fellowship in the laboratory of Bruce Conklin and is now developing bioinformatics software. He received a BS in biochemistry from the University of Oregon and a PhD in molecular neurobiology and biophysics from Rockefeller University. His research involves developing software to help navigate the deluge of genomic, proteomic and SNP data with a focus on using biological pathways to provide intuitive context.

Were you interested in science as a child?

Looking back, I suppose there were early signs that I was destined to be a nerd. I was expressing scientific and engineering tendencies early in development. I had the popular chemistry set as a kid (see inset) and kept an expandable folder of invention ideas. I recall a do-it-yourself Ferris wheel kit for the backyard and magnetic closures for clothing in place of buttons (patent still pending). And, I'll never forget programming my Atari 400 to participate in simple dialogue...yes, I was an only child.

Did any person influence your decision to go into science?

Beyond his obvious genetic influence, I have always been fascinated by my father's work as a neuroscientist, and I could tell early on that we saw the world in the same way. Nevertheless, I started college as a music and literature major (I think Jim Morrison was my biggest influence at that point). Then, during my second year, I stumbled into an honors chemistry class and was immediately hooked. Professor Catherine Page let me work in her synthetic inorganic chemistry lab at the end of my first term in her class. In the lab, I remember feeling like I had found "my people."

What were your early research experiences?

I worked in research labs every quarter for the next 4 years, including summers. That first year in the inorganic chemistry lab, I worked on the synthesis and characterization of high-temperature superconductors. I went on to work in a behavioral neuroscience lab focusing on attention systems and then in two structural biology labs looking at the effects of mutations on protein structure and ligand binding. Much like Ms. Goldilocks, I found the first experience with inorganic chemistry to be a bit dry, the work with in vivo neurobiology was too wet, but structural biology seemed just right. So, by this time, I knew exactly what I wanted to do in grad school: study the structure and function of neurobiologically relevant molecules.

How would you characterize your time in graduate school?

Five long years studying one domain of one protein... what more could you ask for! It was truly an exceptional time, even more so in retrospect. I studied the calcium-activation mechanism in large-conductance voltage-gated potassium channels (a.k.a. BK channels) in Rod MacKinnon's lab at Rockefeller. I joined the lab in 1998, just months after they published the first crystal structure of an ion channel protein, which led to his 2003 Nobel Prize in Chemistry. My thesis work involved a combination of structural biology, electrophysiology and bioinformatics. I was beginning to realize that I really enjoyed wearing multiple hats in my research career and still had a few more to try on. Oh yeah...living in Manhattan was also great.

What brought you to Gladstone?

What I was looking for in a postdoc position was the opportunity to formalize my computer programming skills. I have always had a natural affinity for computers (ever since those early conversations with my Atari), but I had never taken a programming class or really applied it to my research. So, in Bruce Conklin's lab I found the opportunity to work on software engineering projects that were being designed and applied by biologists. It is rare to find software development and wet lab experiments being conducted under the same roof, and it's an ideal setting for making effective software for biologists. At Gladstone, I also found the unique balance of stability and adaptability, and of independence and community, that I came to appreciate at Rockefeller, which also operates more like a research institute than a university.

How does working on software compare to wet lab biology? Do you miss the bench?

You know, I thought I would. But I don't. The biggest differences are the pace of the work and reproducibility. When writing code, you can continuously test as you go, without having to wait weeks or months for a result, and you can trust that it will run the same way every time. If it doesn't, if there is an anomaly or bug, you know there is a logical solution because, ultimately, you know all of the variables. Biology is a little more messy. But that is also part of what makes it more interesting. So, being able to address interesting biological problems with reliable, (somewhat) intelligently designed software tools is yet another Goldilocks sweet spot that I've found.

How do you see the interface between biology and computation evolving?

It is an exciting time to be working at this particular interface. Unprecedented volumes of data are flooding countless archives and databases. The key is to develop software to access, organize, and integrate across these data in multiple dimensions and then present the resulting cross-sections and comparisons as interactive visualizations to biologists for interpretation and new hypotheses. Another exciting aspect of this interface is evolving online through new web-based tools that facilitate scientific collaboration and community efforts. Such tools include wikis (OpenWetWare, TOPSAN, WikiPathways), multimedia data presentations (SciVee, JoVE), social networks (LinkedIn), social bookmarking (delicious, CiteULike), and open access publishing (PLoS, Nature Precedings). I am convinced that everyone working in science should be using one or more of these tools, especially grad students. Participation in the communities formed by these tools may very well become an important measure of your career, rivaling that of your publication record.

Alex as a young scientist.