He later introduced me to researchers at The University colleague and Nobel Prize winner Hamilton Smith, a Johns Hopkins University researcher. He was interested in the restriction enzymes. He was interested in natural language processing to the problem of gene finding. Around the same time, I started applying methods I knew from work in my area. Our efforts focused on genome assembly, as well as finding and annotating genes using statistical techniques developed in my group. We created a number of successful and widely adopted computational biology techniques. Even today, 14 years after its publication, our GlimmerM program is still the most accurate gene finder for bacteria and archaea.

Currently, we are focused on aligning short reads from next-generation sequencing datasets, including RNA-Seq, which involves alignment of intron spanning transcripts to multiple locations on the genome, assembly of the reads, and quantification of the transcripts. I think it is fair to say that the software we developed, Bowtie, TopHat, and Cufflinks, have become the standard in the field.

What has been your most significant scientific contribution so far?
My group at TIGR was responsible for the computational analysis of the bacterial, archaeal, viral, parasitic, and Arabidopsis genomes first sequenced and published during the late 1990s and early 2000s. Each of those papers was a landmark in its own area. Our efforts focused on genome assembly, as well as finding and annotating genes using statistical techniques developed in my group. We created a number of successful and widely adopted computational biology techniques. Even today, 14 years after its publication, our GlimmerM program is still the most accurate gene finder for bacteria and archaea.

I write about topics for the scientific community as well, voicing my opposition to gene patents as well as my support for open access publishing, open source software, and sharing scientific data as freely and quickly as possible. As scientists, you have a significant number of editorials addressing misleading health claims. What motivated you to devote your efforts here?
In 2004, my group at TIGR began to sequence thousands of strains of the influenza virus in an effort to track sequence changes so that we could improve the design of new vaccines. Through an interaction with a journalist, I became aware of the anti-vaccine movement, which is based on several beliefs that are wildly inaccurate. While we were working day and night to improve influenza vaccines, a growing movement was simultaneously advocating avoiding vaccination.

The overarching goal of doing biomedical research is to develop better treatments so people live longer, healthier lives. I decided that in addition to my research, another way I might achieve this goal was to educate the public on the benefits of vaccines and counter the pseudoscience promoted through the anti-vaccine movement, starting with the thoroughly discredited theory that vaccines cause autism. Once I started writing about this, I encountered other kinds of quack treatments offered by true believers and scam artists alike. My hope is that I can reach people while they are still open minded so they will look at the evidence and stop doing things to harm themselves.

I write about topics for the scientific community as well, voicing my opposition to gene patents as well as my support for open access publishing, open source software, and sharing scientific data as freely and quickly as possible. As scientists, our goal is to solve scientific problems and move our fields ahead; the best way to do that is to be open and share.

Interviewed by Kristie Nybo, Ph.D. Image courtesy of Steven Salzberg.

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