**Personal History | Ben Haley | 2009**

I gained an appreciation for the complexity of information processing in microbiology as an undergraduate learning about transposons, signaling, ncRNA, and HGT. I realized that human thought was the macro scale tip of a network of biological information processing that extended into life's nano-chemical codes. I was excited to learn that many fundamental processes of biology, including RNAi, induced pluripotency, and prions were discovered in my lifetime, and the prospect of future upheavals enticed me to pursue biological research.

The realities of research at the Tischkau lab contrasted these broad fascinations. The demands of Real Time PCR and cell culture compelled me to focus on detail. I left my undergraduate training with a strong desire to find techniques that would help me to explore information processing in biology.

Following graduation, I became a technician in the Woloschak Lab at Northwestern University. There, I contributed to the lab’s titanium dioxide nanocomposite project by refining an RNA cleavage experiment and developing a centrifuge-based nanoparticle separation technique that is now regularly used in the lab. I performed prostate, liver, and heart dissection and flow-cytometry assays. Over several summers, I oversaw six high school and undergraduate students as they performed real time PCR to study the response of PCNA-negative mice to irradiation. These experiences taught me how community, education, administrative support, and funding placed constraints on research. In training students and coordinating with my manager, I discovered the critical role that the communication of results and methods played in the productive functioning of an individual lab. I became interested in how this communication might be automated, organized, and improved.

I was exposed to the related challenge of communication between laboratories when I was given the opportunity to write a review paper on the effects of ionizing radiation on hnRNP proteins. It was difficult to exhaust PubMed, Google Scholar, OMIM, and other web resources, and I became familiar with the frustrations of parsing poorly annotated data from its inconsistent presentation in published source materials. Still, there was a reward for this struggle; I was able to produce a paper that merged the results from those unfocused sources to find a novel role for hnRNP proteins in the regulation of DNA damage response pathways following ionizing radiation1. I became excited by the outcome of data integration in biology but frustrated by the difficulty of performing such meta-analyses. Again I found myself wondering how the communication of results might be automated, organized, and improved.

In the winter of 2008, I felt that I needed to refocus my energies and I took time off for a bike trip up the coast of California. During that time, I discovered a new focus, discipline, and joy in computer science. I read about HTTP protocols, memory hierarchies, and Python in the libraries where I stopped to rest. These subjects were gratifying to study because they were designed to be comprehensible as opposed to the undescribed depths of biology.

Over the next year, my newfound interest in computer science and my longstanding passion for biology led me to turn my attention to computation in biological systems. I taught myself discrete mathematics, compiler theory, and algorithms while studying biocomputation in the hope of discovering an avenue of research where I could contribute. I found like-minded thinkers who were studying computation in DNA and proteins2. I learned that DNA could be used as a computing molecule3 and that gene regulatory networks have an immense capacity for parallel computation4. I also learned of the gap between the theory of biocomputation and the reality of its accessibility. While attending the DNA 15 biocomputation conference, I heard presentations from theoretical mathematicians who had designed Turing-complete DNA compilers5 juxtaposed against bench workers who struggled to implement simple DNA logic circuits6. It became obvious to me that the computational potential of microbiology was too subtle for our current biochemical techniques to mimic and control. I realized that without the ability to precisely manipulate the information-carrying molecules of biology, the study of biocomputation would be inherently limited. I resolved myself to find a way to contribute to the nanotechnology work that is swiftly advancing biology’s ability to manipulate and measure individual molecules.

At the Woloschak Lab I accepted a promotion to the role of information manager as a chance to exercise my interests in programming. I was commissioned to build a website to present the data from the radiobiology tissue archive that our lab had inherited from Argonne National Lab7. When my PI put me in contact with similar efforts at the European Radiobiological Archives (ERA), we began to collaborate.

A practical outlet emerged for my research ambitions while pursuing this collaboration. I was introduced to various methods of data sharing through controlled vocabularies, web services, information-rich linking, and the semantic web8. I realized that these concepts were applicable to the challenges I had encountered in biology: culling sources for the hnRNP review, sharing data from the biological archives, and providing an information platform that could accelerate the advance of nanotechnology. I joined the local Semantic web group and began the process of putting the tissue archive data into semantic RDF formats linked to accepted ontologies.

Meanwhile, volunteer work in education helped me to realize the value of remote access to sophisticated tools. AAAZs a Saturday-school teacher, I taught under-served middle school students how to build websites, start blogs, and use web resources like Google Maps and Wikipedia. The students were empowered by remote access to advanced programs and I wondered how education researchers could be empowered by remote access to students. So, I began collaborating with a friend at Stanford’s social psychology program to develop a web platform for the delivery of research-proven motivational exercises to students9. I also realized that remote accessibility could contribute to the development of nanotechnology in biology by exposing new hardware to a larger audience of interested researchers.

My research over the coming years will focus on these problems, developing methods and tools to promote remote access to instrumentation and results in nanotechnology work aimed at manipulating biomolecules. The aim of this effort is to develop remotely accessible cellular interfaces. I hope that these interfaces will advance the pace of biological discovery by involving more researchers in its cutting edge technologies and results.

**References**

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