EDITORIAL

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Biophysical Review's 'meet the editors series'— a profile of Joshua W. K. Ho

Joshua W. K. Ho[1]

Abstract
It is my pleasure to write a few words to introduce myself to the readers of *Biophysical Reviews* as part of the 'meet the editors' series.

A portrait of Dr. Joshua Ho

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Early life

Perhaps I am an unusual breed of 'biophysicist', at least in a traditional sense. I was born and raised in Hong Kong to a physician father and a medicinal chemist mother. After completing my high school diploma in Hong Kong, I went to an overseas education and career fair, and came across a unique opportunity to study abroad for university, without doing the A-level examination (which would have taken another 2 years of studies). As a young man who were seeking independence and excitement, I packed my bag and headed to Australia in a few weeks after that first encounter. After completing a short 'foundation studies' (university preparation) course at La Trobe University, I had to choose a degree programme. At that time, I was mostly thinking of doing a professional degree, such as pharmacy or physiotherapy. While I flipped through the course prospectus, I came across a word that I did not recognise—bioinformatics. Given my parent's medical and scientific background, I was no stranger to science, but I have never heard of this word. The idea of using computers and mathematics to decode the secret of life sounded like science fiction! This excited me. I decided to choose bioinformatics at La Trobe—which was one of the few universities at that time to have an undergraduate bioinformatics programme.

After 1 year of study, wanting to be closer to some of my relatives who lived in Sydney, I transferred to the University of Sydney in 2004 to enrol in the BSc (Advanced) programme, majoring in Biochemistry and Computer Science—a combination that was essentially the same as a bioinformatics degree. The more I studied, the more I enjoyed the beauty and intellectual stimulation of studying this two seemingly different disciplines. At the University of Sydney, I was fortunate enough to be able to undertake research projects as an undergraduate student,

resulting in quite a few peer-reviewed publications in the area of data visualisation (Ho and Hong 2006; Ho et al. 2006a), phylogenetics (Ho et al. 2006b), protein sequence mining (Ho et al. 2005) and mass spectrometry data analysis (Ho et al. 2007).

PhD

After completing my honours project in my BSc degree, I decided that bioinformatics research was so exciting that it would be a waste not to do a PhD. At the time, my supervisor of my honours project was Dr. Michael A Charleston. We previously worked on modelling the evolution of gene regulatory networks. Michael understood my interest in working on some 'real' biomedical data. He introduced me to Professor Cris dos Remedios, who was based in the Medical School. I vividly remembered my first meeting with Cris in his basement office at the Anderson Stuart Building—an old sandstone building which housed the School of Medical Sciences. Cris stared at me with a gentle grin on his face, seemingly giving a stamp of approval, saying 'So you want to work on some real data, we have a lot of them here'. Then, he went onto showing me many of his ongoing projects, including many 'omic' projects related to the Sydney Heart Bank, and some exciting data generated from his antibody microarray. I was captivated by his infectious passion for science and his seemingly endless energy in pursuing such a diverse array of projects that sometimes involves very different techniques, ranging from genomics, biophysical methods, immunological methods and even computational methods. This encounter made a strong impression on me. Looking back in my career, perhaps this was a defining moment that shaped the way I opened my arms to interdisciplinary projects.

In the next three years, I had the honour of working on a diverse array of projects under the supervision of Cris and Michael. Together, we worked on developing statistical methods for differential variability analysis of gene expression data (Ho et al. 2008b, 2009) and computational methods to analyse data generated from a novel antibody microarray platform with applications to autoimmune diseases and cardiovascular diseases (Ho et al. 2008a, 2010; Lin et al. 2013). Cris even sent me to his collaborator Dr. Bill Pu's laboratory at the Harvard Medical School, where I had the opportunity to work on discovering alternative splicing in ischemic cardiomyopathy (Kong et al. 2010). My PhD experience with Cris and Michael opened my eyes to the power of using big data in biomedical applications.

Time at Harvard

After completing my PhD in 2010, I moved to Boston to take up a postdoctoral position with Professor Peter J. Park and Professor Richard L. Maas. This was the period in which I matured as a research scientist. I was recruited to work on the Systems-based Consortium on Organ Design and Engineering (SysCODE), which aimed to use systems biology to understand the molecular pathways involved in organogenesis, and subsequently used this knowledge to inform regenerative medicine and tissue engineering strategies. In particular, I was tasked to identify the gene regulatory networks (GRNs) for tooth organogenesis. Working with a PhD student Daniel O'Connell, together we realised that it was insufficient to infer a meaningful GRN from gene expression data alone, we needed to capture and incorporate the vast amount of genetic and molecular perturbation experimental data into the GRN inference process. This was a critical insight. This led us to develop a statistical method that uses diverse perturbation data to infer a GRN. Using this approach, we identified a cross-tissue cross-pathway signalling interaction network that underlies tooth organogenesis (O'Connell et al. 2012). This project gave me a deeper appreciation of the challenges and power of using a systems biology approach to uncover molecular mechanisms.

During the same period, I was involved in another large collaborative consortium, the model organism Encyclopedia of DNA Elements (modENCODE) project. During a 3-year period, under the supervision of Professor Peter Park, I processed and analysed a large amount of ChIP-seq data to define and compare the histone modification landscape of *Drosophila melanogaster* (fruitfly) and *Caenorhabditis elegans* (round worm). Together with many wonderful national and international collaborators, we discovered the role of an active chromatin context in transcription factor binding in *Drosophila*'s dosage compensation process (Alekseyenko et al. 2012) and performed one of the first large-scale comparison of the chromatin landscape of human, fly and worm (Ho et al. 2014). We also made contributions to the experimental design and bioinformatics analysis of ChIP-seq data (Ho et al. 2011; Jung et al. 2014; Sohn et al. 2015). This experience gave me a real taste of consortium-based collaborative big data research. Importantly, it showed me how a large amount of well-annotated big data can be used to solve various long-standing biological problems.

Back to Australia

After spending 3 years in the USA, I moved back to Australia to take up a Faculty position at the Victor Chang Cardiac Research Institute (VCCRI) in Sydney. In this role, I established the Bioinformatics and Systems Medicine Laboratory and began my independent research journey. My laboratory focused on methodological innovation in bioinformatics, which meant development of new computational

methods to answer a range of biological or biomedical problems. Some of our representative contributions include the followings: a statistical method for cross-species gene set analysis (Djordjevic et al. 2016), a scalable cloud-based single-cell RNA-seq (scRNA-seq) data processing big data framework (Yang et al. 2017, 2019), a web-based real-time collaborative genome browser (Szot et al. 2017), a fast dimensionality reduction and clustering method for scRNA-seq data (Lin et al. 2017), a fast clustering method for millions of single cells in flow cytometry data (Ye and Ho 2019), and a method to mine meta-data in public gene expression repositories (Djordjevic et al. 2019). These works were only possible thanks to all the postdoctoral fellows, students and interns in my laboratory over the years. I am particularly proud to have been the colleague of Dr. Eleni Giannoulatou (currently a Division Head at VCCRI), and Dr. Paul Lin, who both worked as a postdoctoral fellow in my laboratory. I am also proud to be the supervisor of former PhD students Dr. Djordje Djordjevic, Dr. Andrian Yang, Dr. Xin Wang and Dr. Tomasz Szczesnik. I was also fortunate to have worked with over 20 undergraduate students and interns during my time at VCCRI.

Building community

One thing that I enjoyed the most while I was at VCCRI was the ability to be involved in building up the local and national bioinformatics community. In collaboration with colleagues such as Professor Jean Yang at the University of Sydney, we ran an annual local event called the Sydney Bioinformatics Research Symposium, in which we gather all the bioinformatics and computational biology researchers and students in the greater Sydney region to share their latest research work. I have also been involved in the Australian Bioinformatics and Computational Biology Society (ABACBS), in which I served as the secretary in the executive committee between 2016 and 2018. During this period, I facilitated ABACBS to become a regional affiliate of the International Society for Computational Biology (ISCB), further strengthening the place of Australian bioinformatics research in the world stage.

In 2019, ABACBS was the host of the joint International Conference on Genome Informatics (GIW) and the ABACBS annual conference. I served as the chair of the programme committee for this joint conference. In this role, I organised the peer review process of research papers submitted by researchers from around the world and facilitated the publication of the accepted papers in various journals. All these effort was done to build a community—with the idea that good science comes out of open sharing of scientific ideas and data. I was glad to be able to play a role.

Big data and the biophysics reviews

I was invited to join the editorial board of *Biophysical Reviews* by the then chief editor Professor Cris dos Remedios in 2013. I was excited about this opportunity as it was a way to serve the scientific community. *Biophysical Reviews* is a wonderful journal, since it encompasses a wide range of interdisciplinary topics, with the use of mathematics, physics, computer science and novel technology to solve various biological problems across different scale in time and space—from atomic, molecular, cellular, physiological, ecological and evolutionary scale. Cris encouraged me to lead the effort in promoting the role of big data to the biophysics community. Taking this opportunity, I co-chaired the 'Modelling, inference, and big data in biophysics' session in the 2017 IUPAB International Biophysical Congress in Edinburgh (Ho and Grant 2017). In 2019, I co-edited a special issue on 'Big Data' in *Biophysical Reviews* with Dr. Eleni Giannoulatou (Ho and Giannoulatou 2019).

Currently, I work at the University of Hong Kong. On the invitation of Dr. Damien Hall, I was asked to serve as an Executive Editor of *Biophysical Reviews*, with a focus on identifying and promoting exciting scientific ideas in the Asia region, and in the big data field. In this capacity, I welcome anyone who has an exciting idea to share to approach me if you think your work would fit this journal. I look forward to interacting with many of you!

Compliance with ethical standards

Conflict of interest The author declares that there is no conflict of interest.

Ethical approval This article does not contain any studies with human participants or animals performed by any of the authors.

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