

Bioinformatician

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What does a Bioinformatician do?

Bioinformatics is a multidisciplinary science which applies computers to enhance our understanding of biology. Computational biology is changing the way we manage our health and the environment and how research in biological science is conducted.

What do you work in and what is your specialty?

I am a Research Bioinformatician at CSIRO Mathematics. I am conducting post-doctoral research at the CSIRO in the area of metagenomics, where DNA sequencing is applied to diverse communities of microbes, instead of homogeneous cultures, resulting in discoveries of new species, interactions and biochemical functions.

Metagenomics is an exciting but challenging new application of DNA sequencing. If analysing DNA sequences from an individual microbial genome can be considered akin to solving an individual puzzle, metagenome analysis is like trying to simultaneously solve thousands of different puzzles mixed together, with many of the pieces either shared between puzzles or outright missing. The outcomes of these studies often yield exciting results, such as the discovery of microbes linked with human disease, or new proteins with exciting industrial applications.

How did you become interested in this area and when did you first start?

At ten years of age, I began creating computer games inspired by an older brother, who taught me the basics of computer programming. While at high school I also discovered a love of biological science and on considering my university options, decided to find a program that fused these two strong interests together. Bioinformatics was a new degree when I started, but over the past decade, demand for trained bioinformaticians has grown rapidly as biologists generate larger and more complex datasets.

What study path have you taken to get here?

I studied a PhD (Bioinformatics) at the University of Queensland, graduating in 2013 and a Bachelor of Science (Bioinformatics), The University of Sydney, 2006.

What do you like most about your job?

I enjoy both the means and then ends of my job, developing algorithms to analyze data, and ultimately running this software to yield biological discoveries.

Do you have any particular career highlights?

As part of my PhD, I developed new software called Acacia, which finds errors in the DNA code of sequences produced during gene sequencing. In a simple analogy, the Acacia software works like a “computer spell checker” to automatically detect errors in the sequencing. In 2012, my discovery was published in the prestigious journal Nature Methods. It’s exciting to be published in a journal like Nature Methods but I get more satisfaction from hearing how my software is helping biologists fix sequencing errors.

The method, or algorithm, that Acacia uses took 18 months to fully develop and test and I now use it as part of my ongoing research career. I am now conducting post-doctoral research at the CSIRO.



What advice would you give to someone interested in working in this area?

Having access to world-class research facilities, brilliant academics and cutting-edge technologies were some of the best aspects of my program.