BIOINFORMATICS WORKSHOPS AT GSA/NZSBMB '17

Presented by The Bioinformatics Institute (University of Auckland)

All participants of GSA/NZSBMB '17 in Dunedin 2-6 July are welcome to participate in three fantastic bioinformatics workshops held over the course of the conference.

A. INTRODUCTION TO *R* AND *R SHINY* (2hr 45m)

With just a little guidance, you can wield the power and expressivity of R to make awesome paper-ready images for scientific publication, AND turn your analyses into elegant interactive web applications without requiring HTML, CSS, or JavaScript knowledge.

The R language has become the most important scripting language for experimental and computational biologists. R is great for beginners because it's free, well-documented, and runs almost everywhere. R's large library of external packages perform diverse tasks. With R you can easily make many graphical outputs, especially those super paper-ready images you need for top scientific publications.

While R's great power and expressivity may at first seem difficult to approach, just a little guidance can set even those new to programming on the road to great things. This workshop will introduce R Studio and how to use R to analyse your data.

Additionally, we will introduce you to *R Shiny*, an open source R package that provides an elegant and powerful web framework for building web applications. Shiny helps you turn your analyses into interactive web applications without requiring HTML, CSS, or JavaScript knowledge.

Who should attend? What Equipment Do I need?

- Please bring your own laptop, as this is a hands-on workshop. If you do not have a laptop, we will try to pair you with someone who does.
- No prior coding knowledge required. Knowledge of unix and basic command-line text editors is a plus.

B. BEST PRACTICE IN RNASEQ (1hr)

Want to design, analyse and visualise RNA-seq experiments? Wish you knew how to solve bioinformatics issues when manipulating large datasets?

Transcriptomics is fast-moving and continues to see developments in data analysis, experimental design, and sequencing technologies. High-throughput sequencing of RNA libraries (RNA-seq) is increasingly common and has largely supplanted gene microarrays for transcriptome profiling. When processed appropriately, RNA-seq data has the potential to provide a considerable amount of detail of the transcriptome.

This workshop introduces you to the design, analysis and visualisation of an RNA-seq experiment, with a focus on the bioinformatics issues that arise from large datasets and their manipulation.

Focusing primarily on an overview of the tools and approaches used to conduct RNA-seq analyses, the workshop will give you a basic understanding of Next-Generation Sequencing data formats and how to handle potential problems and errors. Following the talk, there will be time for questions and answers with the team of experts from the Bioinformatics Institute at the University of Auckland.

Who should attend? What Equipment Do I need?

- The course has been adapted to the needs of beginners in the field of NGS bioinformatics and allows scientists with no or little background in computer science to get a first hands-on experience in this new and fast evolving research topic.
- No laptop necessary.

BEST PRACTICE IN METAGENOMICS (1hr)

Novice observing the incredible world of metagenomics with excitement, but not sure where to start? Meet the experts and get an overview of metagenomics tools and approaches.

Metagenomics is the catch-all phrase used for bulk sequencing of DNA (next generation sequencing) directly from a sample without first culturing and isolating the organisms. This technique is primarily used to explore the diversity, function, and ecology of microbial communities. In other words, metagenomics allows for rapid analysis of the species diversity present in populations. This has many different applications across medical, agricultural, and environmental research.

You can meet the experts, who will outline tools and approaches used to conduct metagenomic analyses. Following the talk, there will be time for questions and answers with the team of experts from the Bioinformatics Institute.

Who should attend? What Equipment Do I need?

- This course is designed to be understood by novice scientists with no or little background in computer science as a way to get a basic knowledge in this incredible field of novel discoveries.
- No laptop necessary.

Who is Running these Great Workshops?

The workshops will be delivered by the Bioinformatics Institute, a research and education centre bringing together biosciences, health sciences, computer science, mathematics, and statistics to understand complex

datasets. The Institute is based at the University of Auckland. The Institute's scientists aim to help early career researchers, medical students, and/or postgraduate students to understand the value of bioinformatics in research collaborations, emphasizing the importance of work that translates results from lab to clinic, pasture, or field.

Workshop Team

William Schierding, PhD
Bioinformatician and Programmer Analyst

William came to New Zealand from the United States, where he worked as a Programmer Analyst at the McDonnell Genome Institute at Washington University in St. Louis. In New Zealand, William recently completed his PhD at the University of Auckland, where he focused on the functional consequences of the three-dimensional structure of genome organization. Genetic changes can alter genome structural relationships, altering regulatory patterns, resulting in disease risk in humans. William's PhD research relates disease associations in non-coding regions of the genome to their regulatory impact to implicate novel genes in several different diseases. Currently, William's interests still involve analysis of genomic data and development of bioinformatics tools to enable more precise understanding of the role of genetics in human disease. William's areas of expertise involve genome mapping, variant detection, RNA-sequencing, epigenetics, and analysing of environmental metagenomics data. William's teaching role has centered around developing, delivering, and promoting a consistent bioinformatics infrastructure for the New Zealand research community.

Vicky Fan, MSc Hons
Bioinformatician and Programmer Analyst

Vicky completed her MSc (Hons) in biological sciences, specialising in bioinformatics, at the University of Auckland in 2009. Her MSc thesis focused on the genomic and proteomic analysis of New Zealand triplefin fish. Currently, Vicky's research includes microarray analysis, developing software for R, and analysis of deep read sequence data. Vicky's role is to forge a path for NZGL and the Auckland Bioinformatics Institute to be able to contribute to New Zealand's diverse scientific resources encapsulating

the work done on native species. Vicky's teaching roles have included travels around New Zealand and Australia, learning from and teaching to the scientific community in a process that promotes maximum researcher enablement, through both services and education.

Nooriyah Poonawala, MSc Hons
Bioinformatician and Programmer Analyst

Nooriyah completed her MSc (Hons) in bioinformatics in 2014, combining genomic and clinical data to improve our understanding of pathology. This research aimed to improve outcomes of the diagnosis and treatment of complex genomic diseases, such as cancer. Currently, Nooriyah is interested in improving the capabilities of researchers to better understand novel technologies such as RNAseq on single cells, and the analysis of data from the novel frontiers of genetic technologies. Nooriyah's areas of expertise include tools for extracting and using feature table information for genomic sequences. She also has worked extensively with genome mapping, variant detection, and RNA-sequencing. Nooriyah's teaching is focused on leveraging the relationships, skills, knowledge, and experience of the Bioinformatics Institute to lead New Zealand researchers towards world-first capabilities in their fields, through data exploration and data-driven science.