Preparing for Next Generation Sequencing Data Analysis 101

We invite you to attend an introductory course for researchers entering the field of Next Generation Sequencing (NGS) applied to Health Sciences.

The course aims to teach researchers with limited experience in NGS to access various resources related to the theory and analysis of NGS data.

Who will be offering the course?

Anelda van der Walt has an MSc in Bioinformatics and 4 years experience in dealing with a variety of NGS data sets – including RNA-seq, microRNA-seq, genome sequencing, and targeted approaches such as amplicon sequencing. She has analysed data from 454, Illumina, Ion Torrent, and SOLiD. Anelda currently works as an eResearch Analyst at the newly established UCT eResearch Centre.

Armin Deffur is an infectious disease physician and computational biologist. He is actively involved in research relating to disease mechanisms in TB-HIV co-infection. Armin has 4 years' experience in using R and other tools for analysis of transcriptomic data, as well as experience in using UNIX-based systems and the command line.

Who should attend?

Researchers in Health Sciences with limited knowledge or experience of NGS theory and practice, who are embarking on projects where data is already being generated.

When?

The course will run over four weeks with 3 hour sessions scheduled on Mondays 10:00 – 13:00. The first session will start on 15 September 2014.

Where?

The course will run in the newly launched BIRTH lab in Groote Schuur, Old Main Building, Room L51

What should I bring?

Bring your own laptop to ensure the skills you learn are transferable to your own environment. Please contact us if you are unable to bring your own laptop.

How can I register?

An online registration form is available here http://goo.gl/1Cpw9X

For enquiries about the course or registration, please contact

Anelda van der Walt – anelda.vanderwalt@uct.ac.za

What topics will be covered?

We will start of with a very basic introduction to some theory of NGS and discuss how to use resources available on the WWW to inform study design and data analysis decisions. This will be followed by an extremely basic introduction to Linux using your Windows machine, and a session on how to access the UCT High Performance Computing Cluster.

How will attending this course benefit me?

We aim to provide researchers who are completely new to the application of NGS with a course that can prepare them for more applied courses on Metagenomics, Transcriptomics or Genome assembly offered by other groups. It will also provide an opportunity to stimulate conversation about other NGS courses being offered locally and abroad, NGS service providers, different analysis platforms and tools and more.

What next?

The course organisers plan to follow up with a more in-depth 4-week course in the use of Linux and the UCT HPC facilities. This will be in close collaboration with IT specialists running the HPC. The second course will be run in October/November 2014. Participants who successfully completed the first course, will be eligible to attend the second course.