

## Southern African Human Genome Programme

### Workshop 2 28 to 31 July 2014

SBIMB, University of the Witwatersrand

The NGS data from the 24 genomes have arrived and we are now planning two workshops to build capacity to understand the data, manipulate the data, characterise the genomes and formulate research questions. A policy for the storage of the data and access to the data will be formulated by the Core SAHGP group in accordance with the expectation from the DST.

The workshop participants are limited to 20 individuals. They will be chosen to represent geographical and institutional distribution. One to two people may be nominated from each of the 7 participating Institutions and 6 or more individuals from other institutions will be included to total not more than 20 people.

**Please complete the application form at the following URL:**

[https://docs.google.com/forms/d/1U3ST1Ab2ECj\\_6VVVAI46FJ40GQVfF1IxPH1AC0OulteQ/viewform?c=0&w=1&usp=mail\\_form\\_link](https://docs.google.com/forms/d/1U3ST1Ab2ECj_6VVVAI46FJ40GQVfF1IxPH1AC0OulteQ/viewform?c=0&w=1&usp=mail_form_link)

For assistance you may contact Freedom Mukomana ([freedom.mukomana@wits.ac.za](mailto:freedom.mukomana@wits.ac.za))

**Deadline for applications: Monday 7 July at 12 noon.**

**Accommodation and travel** will be funded by the SAHGP and arrangements will be made by Martie Madgwick ([martie.madgwick@up.ac.za](mailto:martie.madgwick@up.ac.za)) from Michael Pepper's Office.

### **Workshop 2 – Understanding and characterising Southern African genomes**

**Date and venue:** 28-31 July (4 days) at SBIMB, Wits

**Lead organisers:** Michèle Ramsay & Kate Theron

**Format:** Lectures/Tutorials and discussion groups (computers not required)

**Note:** Data will be pre-analysed and the outputs will be examined. A bioinformatics group will be on hand to perform additional analysis during the workshop should this be necessary.

#### **Objectives:**

1. To gain an understanding of the data provided on individual genomes
2. To interrogate SNP and indel data sets from whole genome sequences
  - a. Functional characterisation of SNP variants
  - b. Examining unique variants
3. To examine and critique population data
  - a. Principle component analysis (including multiple populations)
  - b. Admixture (STRUCTURE)
4. To discuss potential projects and further data analysis

#### **Participants:**

1. Mostly with a biological background
2. No hands on computer skills for data manipulation required

#### **Outcomes:**

1. Building capacity to interpret genome-wide data
2. Awareness of analysis tools and their capabilities
3. Potential projects with defined biological questions
4. A small writing group to pursue the descriptive characterisation of the genomes