**Applied GWAS Using R**

**Dates**

23-27 October 2017

**Course Overview**

Over the past decade, genome wide association studies (GWAS) has been widely used to identify and characterise genetic variants underlying traits and disorders in human and other species. This is possible with the ability to generate, to process large quantity of genetic polymorphisms and to integrate with other information such as gene expression and methylation. There are many established and evolving methods and techniques to tackle challenges via efficient implementation.

**Targeted audience and assumed background**

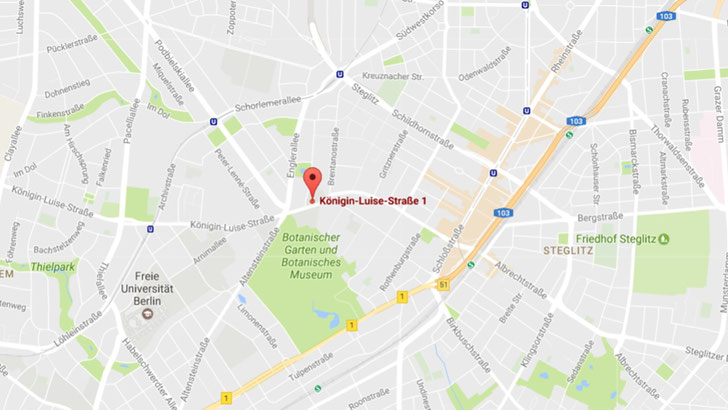
The purpose of this course and workshop is to provide broad pictures as with details of GWAS to researchers in diverse fields. It sets to explore the biological, statistical, and computational concepts, methodology and practice involving a variety of established software but with highlights on Linux and R. The lectures and exercise will bring tremendous benefit to the participants.

**Workshop structure**

The workshop will consist of both lectures and practical classes. Background information will be provided to help workshop attendees to understand the background and statistical analysis methods. Practical tutorials will be conducted on a step-by-step basis to guide the student for data analysis.

**WHERE**

Freie Universität Berlin, Institute of Biology, Königin-Luise-Str. 1-3, 14195 Berlin-Dahlem.



**Curriculum**

The workshop consists of the following modules.

Module 1. Overview

Module 2. Genetic association

Module 3. GWAS

Module 4. Advanced topics

Module 5. Additional topics

Each takes approximately a day.

**INSTRUCTOR**

Dr Jing Hua Zhao

He had studied and worked on statistical and computational methods at various institutions until 2005, when he joined the MRC Epidemiology Unit, University of Cambridge, with a focus on design and analysis of GWASs such as the EPIC-Norfolk, the Fenland and the InterAct. He has also participated in a number of genetic analysis workshops involving simulated and real data as from the Framingham heart study.

Besides local activities, he has also had tutorials on genetic dissection of complex traits with focus on GWAS at UseR! 2009, 2010, and 2011 Conferences and contributed one Henry-Stewart talk on genetic association with R.