

## Bioinformatics of Infectious Disease: Comparative Genomics of *M. tuberculosis*

Calling all biologists or computational biologists seeking advanced training in genome analysis



### 16-20 SEPTEMBER 2013

This course will present theoretical and practical aspects of the computational methods for carrying out comparative genomics using a variety of data types for bacterial pathogens with a focus on *Mycobacterium tuberculosis*.

Participants will learn the principles of bacterial comparative genomics including:

- Next generation sequencing and evaluating sequence data quality
- Retrieving information from biological databases
- Sequence alignment and assembly
- Gene annotation
- Polymorphism discovery and interpretation
- Phylogenetic analysis
- Integrating sequence data with biological information

Hands-on workshop to master the steps needed to carry out comparisons of genome sequences will take place in the afternoons.

Generously sponsored by the Broad Institute and the National Institute of Allergy and Infectious Diseases (NIAID), not including the funding for food and beverages.

**Eligibility:** Individuals needing to master current analytical methods to find and interpret similarities and differences between related genomes. Advanced programming skills are not needed.

**Location:** K-RITH Tower Building, Nelson R. Mandela Medical School, University of KwaZulu-Natal

**To Apply:** Please send a CV and cover letter to [bioinformatics@k-rith.org](mailto:bioinformatics@k-rith.org) by Monday 5 August 2013. For more information, go to [www.k-rith.org](http://www.k-rith.org).

**Cost:** Participation is free.

**Funding Opportunities:** Apply through the Connect Africa Scholarships Programme:

[www.k-rith.org/connect-africa-scholarships](http://www.k-rith.org/connect-africa-scholarships)

In collaboration with the University of KwaZulu-Natal, the University of Cape Town and the University of the Witwatersrand