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.

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 by Monday 5 August 2013. For more information, go to www.k-rith.org.

Cost: Participation is free.

Funding Opportunities: Apply through the Connect Africa Scholarships Programme: www.k-rith.org/connect-africa-scholarships

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