Illumina Seminar Series

Next Generation Sequencing:
How you can apply it to your research

The economic availability of multiple gigabases of data from 40+ million templates (1.5 Gb in 3 days) enables new approaches to genomic characterization. The Illumina Genome Analyzer$_{II}$ empowers prior genome center-like studies to be accomplished at the individual laboratory level. This single technology workflow is readily capable of supporting genome-wide analyses as disparate as DNA sequencing, gene expression and expression control including small RNA discovery, protein-DNA interactions and CpG methlyation status.

WEDNESDAY, JUNE 11TH, 2008
1:30 p.m. – 4:30 p.m.

Refreshments will be provided

HOSTED BY

The Centre for Applied Genomics
The Hospital for Sick Children
MaRS Center – East Tower
101 College St., Room 14-701
Toronto, ON M5G 1L7
www.tcag.ca

Ontario Genomics Institute
MaRS Centre, Heritage Building
101 College St., Suite HL50
Toronto, ON M5G 1L7

AGENDA

1:30PM – 1:45PM
Opening remarks: Richard Wintle, PhD, Assistant Director, The Centre for Applied Genomics

1:45PM – 2:30PM
Next Generation Sequencing Technology Overview and Applications
Speaker: Haley Fiske, Sequencing Specialist, Illumina, Inc.

2:45PM - 3:30PM
Implementation of the Illumina sequencing platform at the Washington University Genome Center
Guest Speaker: Matt Hickenbotham, Washington University, Department of Genetics, Genome Center

3:45PM – 4:30PM
No Read Left Behind: A Unique Hybrid Templated/De Novo Assembly Algorithm for Illumina Genome Completion, SNP Detection, and Comparative Expression Analysis
Speaker: Jeff Engelking, Next-Gen Application Scientist, DNASTAR, Inc

SEMINAR LOCATION

The Hospital for Sick Children, Room 1250, 555 University Ave, Toronto, ON M5G 1X8

Questions? Contact your local sales representative, Grace Murray, gmurray@illumina.com , ph 416-565-0013

www.tcag.ca

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