HMS RNA-Seq Analysis Workshop

February 6th, 2015

When: Friday, **February 6th**, 2015 from 9:00 AM to 5:00 PM

Where: **Countway Library, Room L2-025**, 10 Shattuck St, Boston, MA 02115

No prior programming experience or command line knowledge is required.

RNA-Seq is replacing microarrays as a new tool to study transcriptome changes through massively parallel "Next Generation" sequencing (NGS). The ability to read cDNA sequences directly makes it possible to study non-model organisms as well as model organisms with unprecedented sensitivity and reproducibility. This introductory workshop will cover best practices for quality control, read alignment, and expression analysis using RNA-seq data.

Who should attend?

Harvard Medical School-affiliated researchers from the **Harvard NeuroDiscovery Center** or the **Basic and Social Science Departments on the Quad** who:

- are generating or hope to generate RNA-Seq data
- want to use a simple, graphical interface to analyze their results
- want to analyze their results in a reproducible fashion

Registration site (available 9:00 AM on January 23rd):

https://hms-rnaseq-feb6-2015.eventbrite.com

Sponsored by Harvard Medical School Tools and Technology Committee (TnT) and Harvard NeuroDiscovery Center (HNDC)

Format and Schedule

RNA-Seq using Galaxy (9am - 5pm, includes a break for lunch* and short breaks in the morning and afternoon): Introduces basic concepts and illustrates an end-to-end data analysis workflow through live tutorials using the Galaxy analytical framework. At the end of this activity, participants will be able to set up their own Galaxy servers using Amazon's EC2 environment to analyze their data, without using the command line.

* Lunch will not be provided, but there are a number of cafeterias and restaurants in the immediate vicinity.

Requirements

Participants must be Harvard Medical School-affiliated researchers from the Harvard NeuroDiscovery Center (HNDC) or the Basic & Social Science Departments on the Quad. Preference will be given to participants who are conducting or planning studies using RNA-Seq data.

No prior experience using the Galaxy framework or the command line required.

Registration is mandatory and will open at **9:00 AM on January 23rd**:

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