

HMS ChIP-Seq Analysis Workshop

December 15th, 2014

When: Monday, **December 15th**, 2014 from 9:00 AM to 5:00 PM

Where: **Countway Library, Room 403**, 10 Shattuck St, Boston, MA 02115

No prior programming experience or command line knowledge is required.

ChIP-Seq has become a valuable and widely used approach to map where DNA-binding proteins bind to DNA using massively parallel "Next Generation" sequencing (NGS). The ability to read protein-bound DNA sequences directly makes it possible to study model and non-model organisms with unprecedented sensitivity and reproducibility. The workshop will cover best practices for quality control, read alignment, peak calling, motif detection and functional enrichment using ChIP-Seq data.

Registration site (available 9:00 AM on December 1st):

<https://hms-chipseq-dec15-2014.eventbrite.com>

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 ChIP-Seq data
- want to use a simple, graphical interface to analyze their results
- want to analyze their results in a reproducible fashion

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

Requirements

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

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

Format and Schedule

ChIP-Seq using Galaxy (9am - 5pm, includes a break for lunch* and short breaks in the morning and afternoon): Introduction to basic concepts and illustration of 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 ChIP-Seq data, without using the command line.

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

Registration is mandatory and will open at **9:00 AM on December 1st** at:

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