

Introduction to Galaxy

Next Generation Sequencing Data Analysis and Visualization
February 4 + February 5

Are you a biomedical researcher who needs to do complex analysis on large datasets?

Galaxy is an open, web-based platform for data intensive biomedical research that enables non-bioinformaticians to create, run, tune, and share their own bioinformatic analyses.

These hands-on workshops will teach participants how to integrate data, and perform simple and complex analysis within Galaxy. They will also cover data visualization and visual analytics, and how to share and reuse your bioinformatic analyses, all from within Galaxy.

Rangos 490

725 North Wolfe Street

Register now:

<http://bit.ly/jhgalaxy13>

The agenda (for both days) is:

Time	Topic
9:00	Welcome, Intro
9:20	Basic Analysis with Galaxy
10:20	Reusable Workflows
10:40	Break
11:00	RNA-Seq Example part I
12:00	Galaxy Project Overview
12:20	Lunch
1:05	RNA-Seq Example part II
1:55	Persistence, Sharing and Publishing
2:15	Break
2:35	Run your own Galaxy Cloud
4:30	Done

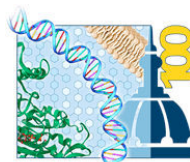
Registration is free, and open to anyone in the Johns Hopkins community. Space is limited and pre-registration is required. Reserve your spot now.

No programming or Linux command line experience is required. Questions? Contact Mo Heydarian <mheydar1@jhmi.edu> or Galaxy Outreach <outreach@galaxyproject.org>.



JOHNS HOPKINS

<http://jhmi.edu>



Biological Chemistry



Galaxy Project

<http://galaxyproject.org>