

# Introduction to Galaxy

Next Generation Sequencing Data Analysis and Visualization

April 30, 2013

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.

This hands-on workshop 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.

Caroline Building  
Room 204  
Saint Louis University

Register now:

<http://bit.ly/slu2013reg>

<u>Time</u>	<u>Topic</u>
9:00	Welcome, Intro
9:20	Basic Analysis with Galaxy
10:30	Reusable Workflows
11:00	RNA-Seq Example part I
11:30	Lunch (on your own)
1:00	RNA-Seq Example part II
1:30	Galaxy Project Overview
2:00	RNA-Seq Example part III
2:30	Sharing, Publishing, and Reproducibility
2:50	Break
3:10	ChIP-Seq Example
5:00	Done

Registration is free, and open to anyone.

However, space is limited and pre-registration is required. Reserve your spot now.

No programming or Linux command line experience is required. Questions? Contact Marureen Donlin <[donlinmj@slu.edu](mailto:donlinmj@slu.edu)> or Galaxy Outreach <[outreach@galaxyproject.org](mailto:outreach@galaxyproject.org)>.



SAINT LOUIS UNIVERSITY

Edward A. Doisy Department of  
Biochemistry and Molecular Biology

at Saint Louis University School of Medicine



Galaxy Project

<http://galaxyproject.org>