

# Introduction to Galaxy

Next Generation Sequencing Data Analysis and Visualization

July 22, 2013

Are you a life sciences 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.

## Location

3503 Thomas Hall (Stephens Room)  
North Carolina State University

Register now:

<http://bit.ly/ncsu2013>

Time	Topic
9:00	Welcome, Intro
9:20	Basic Analysis with Galaxy
10:40	Break
11:00	Reusable Workflows
11:30	RNA-Seq Example part I
12:30	Lunch (on your own)
1:30	RNA-Seq Example part II
2:20	Galaxy Project Overview
2:50	Break
3:10	Sharing, Publishing, and Reproducibility
3:30	Run your own Galaxy Cloud
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 Trudy Mackay <Trudy\_Mackay@ncsu.edu> or Galaxy Outreach <outreach@galaxyproject.org>.



**NC STATE UNIVERSITY**



**Galaxy Project**

<http://galaxyproject.org>