Introduction to Galaxy

Next Generation Sequencing Data Analysis and Visualization
April 29, 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.

Farrell Learning and Teaching Center
Training Room 602, 520 S. Euclid Ave.
Washington University in St. Louis

Register now:
http://bit.ly/WashU2013Reg

Time	Topic
9:00	Welcome, Intro
9:20	Basic Analysis with Galaxy
10:40	Break
11:00	Reusable Workflows
11:20	RNA-Seq Example part I
12:20	Lunch (on your own)
1:35	Galaxy Project Overview
1:55	RNA-Seq Example part II
2:45	Break
3:05	Sharing, Publishing, and Reproducibility
3:25	Run your own Galaxy Cloud
5:00	Done

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

No programming or Linux command line experience is required. Questions? Contact Kristi Holmes <holmeskr@wusm.wustl.edu> or Galaxy Outreach <outreach@galaxyproject.org>.

Washington University in St.Louis

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Galaxy Project
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