



Data intensive biology for everyone



Galaxy is an open, web-based platform for data intensive biological research. Whether on the free public server, or your own instance you can perform, share, and reproduce complete bioinformatic analyses.

To learn more about how Galaxy can help you gain insight from your data, please attend one of these Galaxy related presentations at PAG 2012:

Sunday	The Galaxy Platform: Running analysis in the cloud 1:40-2:10, Town and Country, Dannon Baker Need high-end computation, but lack the infrastructure? This session (part of the <i>Cloud Computing</i> workshop) will show you how to use Galaxy on the cloud to run your analysis.	
Monday	Poster Sessions	P698: Developing Tools for Genomic Analysis in a Wide Bulb Onion (<i>Allium Capsa L.</i>) , John A. McCallum Galaxy pipelines were developed to enable large-scale design of PCR-based markers for validation and mapping of polymorphisms identified between transcriptomes of parent lines.
	Grand Exhibit Hall	P936: DDBJ Sequence Read Archive and cloud-computing based annotation tool for new-generation sequencing data , Hideki Nagasaki This DDBJ resource provides analysis support using Galaxy.
	Even: 10:00-11:30 Odd: 3:00- 4:30	P87: GMOD in the Cloud , Scott Cain Galaxy is a part of the GMOD consortium and is just one of many GMOD components that are cloud enabled.
Wednesday	Galaxy 10:30-11:30, Golden West, Dave Clements <i>Want to learn about Galaxy, and how to use it? This is the session for you.</i> This is the first session of a workshop on GMOD components that also covers tools for genome annotation (MAKER), visualization (JBrowse, GBrowse_syn), and online database construction (Tripal).	
	MAPHiTS: an efficient workflow for SNP detection 11:35-11:50, California Room, Marc Bras MAPHiTS has been integrated into INRA URGI's local Galaxy instance, allowing biologists without Unix skills to easily analyse short-reads sequences with a user-friendly interface.	