# Galaxy @ 3DSIG BOSC

VIENNA ISMB ECCB 2011

## Friday

*Enacting Taverna Workflows through Galaxy*, 11:55-12:05, BOSC, Kostas Karasavvas

*Applying Visual Analytics to Extend the Genome Browser from Visualization Tool to Analysis Tool*, 14:50-15:10, BOSC, Jeremy Goecks

*CADDSuite: A flexible and open framework and workflow system for computer-aided drug design*, 12:10-15:00, 3DSIG Poster/Laptop Session, Marcel Schumann and Marc Röttig

## Sat

*Enabling NGS Analysis with(out) the Infrastructure*, 12:05-12:15, BOSC, Enis Afgan

*SymD server: a platform for detecting internally symmetric protein Structures,* 12:10-15:00, 3DSIG Poster/Laptop Session, Chin-Hsien (Emily) Tai, *et al.*

## Monday

*Enacting Taverna Workflows through Galaxy,* 12:15-12:40, Tech Track, Kostas Karasavvas

*Statistical Tests for Detecting Differential RNA-Transcript Expression from Read Counts,* Poster, 12:40-14:30, J43, Phillipp Drewe, *et al.*

*SymD server: a platform for detecting internally symmetric protein Structures,* Poster, 12:40-14:30, V7, Chin-Hsien (Emily) Tai, *et al.*

## Tuesday

*NGS Best Practices through Galaxy: Cloud-based variant discovery with visual analytics*, Tech Track, 10:45-11:10, Daniel Blankenberg

*From Sets to Graphs: Towards a Realistic Enrichment Analysis of Transcriptomic Systems,* Proceedings Track, 12:15-12:40, Ludwig Geistlinger

*CADDSuite: A flexible and open framework and workflow system for computer-aided drug design*, Poster, 12:40-14:30, Z04, Marcel Schumann and Marc Röttig

*Genomics for Non-Model Organisms*, a Galaxy organized workshop, 14:30-16:25
   *Using RAD-seq for genomic and transcriptomic studies of non-model organisms*, Julian Catchen

   *Using RNA-seq for gene annotation, quantitation, and function in non-model organisms*, Jeremy Goecks

   *Development of a workflow for SNP detection in grapevine species: MAPHiTS*, Marc Bras

   *Repeatable plant pathology bioinformatic analysis: not everything is NGS data,* Peter Cock

*Oqtans: A Galaxy-integrated workflow for Quantitative Transcriptome Analysis from NGS data,* Tech Track, 14:30-14:55, Géraldine Jean and Sebastian Schultheiss

*EMBOSS: New developments and extended data access,* Tech Track, 14:30-14:55, Peter Rice

*The Galaxy Track Browser: Transforming the Genome Browser from Visualization Tool to Analysis Tool*, Tech Track, 16:00-16:25, Jeremy Goecks

Galaxy is an open, web-based platform for *accessible, reproducible and transparent* computational biomedical research.

Use the public Galaxy server now at http://usegalaxy.org or download from http://getgalaxy.org.