

Talks	
10:00	Using Galaxy <b>Introduction to Using Galaxy (Galaxy 101).</b> M. Heydarian, J. Hillman-Jackson
12:00	Break
13:00	Using Galaxy <b>Beyond the Intro: Further Adventures in Using Galaxy.</b> M. Heydarian, J. Hillman-Jackson
15:00	Break
15:30	Using Galaxy <b>Analyzing Large / Complex Experimental Designs with Galaxy.</b> D. Blankenberg, M. van den Beek, M. Heydarian, J. Hillman-Jackson
17:30	



Talks	
10:00	Admin & Dev <b>Introduction to Galaxy Administration I.</b> M. Čech, E. Afgan, S. Gladman, M. van den Beek, J. Chilton, N. Coraor, H. Rasche
12:00	Break
13:00	Admin & Dev <b>Introduction to Galaxy Administration II.</b> M. Čech, E. Afgan, S. Gladman, M. van den Beek, J. Chilton, N. Coraor, H. Rasche
15:00	Break
15:30	Admin & Dev <b>Introduction to Galaxy Administration III.</b> M. Čech, E. Afgan, S. Gladman, J. Chilton, N. Coraor, H. Rasche
17:30	



10:00

**BeerDEcoded, Here and Now!**

**Nanopore Loading Zone!**

18:00



9:00	Talks
	Plenary. Moderator: B. Grüning
9:00	<b>Opening and Welcome.</b> A. Erxleben, B. Grüning
9:10	Invited Talk <b>Evolution of X chromosome recognition during Drosophila Dosage Compensation.</b> C. I. Keller Valsecchi
9:40	<b>Galaxy Australia - inside the national vision of a data commons</b> G. Price
10:00	<b>A Machine Learning Tool Suite for Galaxy.</b> J. Goecks
10:20	<b>An Update on Galaxy Workflows: More Accessible, Expressive, Robust, and Scalable.</b> J. Chilton, M. van den Beek
10:30	Break
11:00	Talks
	Admin & Dev. Moderator: H. Rasche
11:00	<b>GalaxyCloudRunner: Streamlined Cloud Bursting for Galaxy.</b> N. Goonasekera
11:07	<b>Laniakea: A Galaxy-on-demand Provider Platform Through Cloud Technologies.</b> M. A. Tangaro
11:27	<b>Enabling Single Sign-On for Multiple Galaxy Instances.</b> E. Afgan
11:34	<b>How - And How not - to manage successful local Galaxies.</b> P. Mabon
11:54	<b>Building a Pulsar Network across Europe.</b> G. Cuccuru
12:00	Break

13:20	Training
	Admin & Dev. <b>How to create a Galaxy Tool.</b> J. Chilton, N. Soranzo
14:50	Break
15:50	Training
	Admin & Dev. <b>Scripting Galaxy through BioBlend.</b> N. Soranzo, M. van den Beek
17:20	Break
17:30	Talks
	Epigenetics. Moderator: D. Ryan
17:30	<b>HiCEXplorer 3: A toolbox for Hi-C data analysis.</b> J. Wolff
17:50	<b>Histone Deacetylases 1/2 In Microglia Function During Development And Neurodegeneration.</b> M. Frosch
17:57	<b>Analysis and visualization of the human cardiac myocyte epigenome using Galaxy.</b> R. Gilsbach
19:00	



11:00	Talks
	Outside the Genome & Community. Moderator: Y. Le Bras
11:00	<b>Galaxy Computational Chemistry.</b> C. Barnett
11:20	<b>Climate Analysis with Galaxy.</b> A. Fouilloux
11:40	<b>Galaxy Image Analysis: Web-based microscopy image analysis and cellular phenotyping.</b> T. Wollmann
12:00	Break
13:20	Training
	General.
	<b>Quality control of HTS data.</b> TBA
14:50	Break
15:50	Training
	General.
	<b>Machine learning with Galaxy.</b> A. Kumar, J. Goecks, A. Khanteymoori
17:20	
17:30	Talks
	Outside the Genome & Community. Moderator: A. C. Fouilloux
17:30	<b>Using Galaxy for Creation and Execution of Text Mining Workflows in the OpenMinTeD platform.</b> D. Galanis
17:50	<b>To Better Benefit from Shared Tasks in Biomedical Text Mining.</b> M. Ba
17:57	<b>The LAPPS Grid/Galaxy Platform for Mining Scientific Publications.</b> A. Mahmoud
18:17	<b>Infrastructure for Healthier Living: Galaxy at Quadram Institute Bioscience.</b> T. Le Viet
18:24	<b>How Usable is Galaxy? A Usability Evaluation of Galaxy.</b> N.-H. Truong
19:00	



12:15	BoF
	<b>Using Galaxy in automated production setups.</b> P. Moreno
13:20	Training
	Epigenetics.
	<b>ChIP-seq data analysis.</b> L. Rabbani, D. Ryan
14:50	Break
15:50	Training
	Epigenetics.
	<b>Hi-C analysis.</b> J. Wolff, L. Rabbani
17:20	



13:20	Training
	Epigenetics. <b>EWAS data analysis for population epigenetics integrated into Galaxy.</b> K. Poterlowicz
14:50	Break
15:00	Demos
15:00	<b>Analysing and organising large-scale metabolome annotation studies with Django, ISA and Galaxy.</b> T. Lawson
15:25	<b>GalaxyCloudRunner: Streamlined Cloud Bursting for Galaxy.</b> N. Goonasekera
15:45	Break



13:20	Training
	Variation, Metagenomics & Assembly. <b>Variant calling I - from sequenced reads to variant lists.</b> W. Maier
14:50	Break
15:00	Demos
15:00	<b>Galaxy Computational Chemistry.</b> C. Barnett
15:25	<b>Climate Analysis with Galaxy.</b> A. Fouilloux
15:45	Break
15:50	Training
	Variation, Metagenomics & Assembly. <b>Variant Calling II - causative variant discovery.</b> W. Maier
17:20	





13:20	Training
	Variation, Metagenomics & Assembly. <b>16S analysis with Mothur.</b> S. Hiltmann
14:50	Break
15:50	Training
	Variation, Metagenomics & Assembly. <b>Metatranscriptomics &amp; multi-omics microbiome analysis.</b> T. Griffin, B. Batut, R. Sajulga, P. Jagtap
17:20	



12:15

**Arts & Crafts**

13:20



12:15

**Arts & Crafts**

13:20



9:00	Talks
Transcriptomics & Genomics. Moderator: A. Syme	
9:00	Invited Talk <b>Pou5f3, SoxB1 and Nanog control the Zygotic Genome Activation in Zebrafish.</b> M. Veil
9:30	<b>Single-cell RNA Analysis in Galaxy on 10X Datasets.</b> M. Tekman
9:50	<b>Biology-driven classification of Single-Cells RNAseq data in Galaxy.</b> C. Antoniewski
10:10	<b>Improving Transcriptome Analysis with Molecular Indices and Galaxy.</b> B. W. Langhorst
10:17	<b>Transposon Insertion Sequencing Analysis in Galaxy.</b> D. Larivière
10:30	Break
11:00	Talks
Transcriptomics & Genomics. Moderator: A. Bhardwaj	
11:00	<b>Aequatus.js: a plugin to visualise gene trees in Galaxy.</b> A. Thanki
11:20	<b>Visual Refinement of Genome Annotations with Apollo in a Community Environment.</b> N. Dunn
11:27	<b>Architectural and Systems Improvements to G-OnRamp, a Collaborative Eukaryotic Genome Annotation Platform.</b> L. Sargent
11:34	<b>ChiRA: an integrated framework for Chimeric Read Annotation.</b> P. Videm
11:54	<b>Training experience on "Data analysis and interpretation for clinical genomics" using Galaxy.</b> G. Cuccuru
12:00	

13:20	Training
Transcriptomics & Genomics.	
<b>Single cell RNA-seq analysis I.</b> M. Tekman, A. Ostrovsky	
14:50	Break
15:50	Training
Transcriptomics & Genomics.	
<b>Single cell RNA-seq analysis II.</b> M. Tekman, A. Ostrovsky	
17:30	



9:00	Talks
	Admin & Dev. Moderator: S. Gladman
9:00	<b>Containerizing Galaxy server as a Singularity application on HPC clusters for GenAP.</b> D. Morais
9:20	<b>Galaxy on Kubernetes: where we are and future challenges.</b> P. Moreno
9:40	<b>A Minimal Docker Image for Galaxy.</b> S. Golitsynskiy
9:47	<b>CVMFS-CSI for Galaxy: Efficient Access to Read-only Data in Kubernetes.</b> A. Mahmoud
9:54	<b>gxadmin: usegalaxy.* administration wisdom.</b> H. Rasche
10:14	<b>Galaxy container for Hinxton Single Cell Interactive Analysis Portal (HiSciAP).</b> J. Manning
10:30	Break
11:00	Talks
	Admin & Dev. Moderator: D. Morais
11:00	<b>Working Effectively with Remote Data in Galaxy - A Progress Report.</b> J. Chilton
11:07	<b>Testing and Visualizing the State of Galaxy Tools and Workflows.</b> M. Čech
11:27	<b>Setting up a Galaxy Platform in a HPC Infrastructure for Genomics Implementation into Diagnosis Routines for a Health Reference Center.</b> M. Juliá
11:34	<b>RealTimeTools: Integrating, Customizing, and Accessing UI-based Tools in Galaxy.</b> D. Blankenberg
11:54	<b>Creating a Universe of Galaxies: The UseGalaxy.* Project.</b> N. Coraor
12:00	

13:20	Training
	Admin & Dev.
	<b>Galaxy Code Architecture.</b> J. Chilton, N. Coraor
14:50	Break
15:50	Training
	Admin & Dev.
	<b>Running Galaxy on Kubernetes.</b> E. Afgan, N. Goonasekera, A. Mahmoud, S. Golitsynskiy, P. Moreno
17:20	Break
17:30	Talks
	Plenary. Moderator: F. Coppens
17:30	Invited Talk
	<b>Galaxy Community Update.</b> J. Goecks, D. Blankenberg, A. Nekrutenko, J. Taylor
18:00	<b>Tool Prediction in Galaxy Workflows using Deep Learning.</b> A. Kumar
18:07	<b>Street Science Community: make science tangible &amp; accessible by bringing it to the "street" with open science workshops.</b> T. Müller
18:30	



12:15	BoF
	<b>Multi-omics.</b> T. Griffin, P. Jagtap
13:20	Training
	Transcriptomics & Genomics. <b>The RNA workbench, best practices for RNA and high-throughput sequencing bioinformatics in Galaxy.</b> J. Fallmann, F. Eggenhofer
14:50	Break
15:00	Demo
	<b>Mining hot topics in stem cells by combining text mining and scientometrics.</b> Z. Hu
15:20	Break
15:50	Training
	Admin & Dev. <b>Visualisation development in Galaxy.</b> A. Guerler, J. Goecks, A. Kumar
17:20	



12:15	BoF
	<b>Galactic Visualisation!</b> S. Hiltmann, P. H. Rasche, A. Thanki
13:20	Training
	General.
	<b>Visualization of HTS data.</b> TBA
14:50	Break
15:50	Training
	General.
	<b>Beyond the Intro: Further Adventures in Using Galaxy?</b> M. Heydarian, J. Hillman-Jackson
17:30	



13:20	Training
	General. <b>Train the Galaxy Trainer.</b> S. Gladman, A. Syme, B. Batut, S. Hiltemann, H. Rasche
14:50	Break
15:00	Demos
15:00	<b>Knockdown Effects of MAGOHB on Alternative Splicing Via RNA-Seq Analysis.</b> G. Basumata
15:25	<b>Tool Prediction in Galaxy Workflows using Deep Learning.</b> A. Kumar
15:45	Break
15:50	Training
	General. <b>Making your open source project awesome.</b> Y. Yehudi, B. Batut
17:20	





15:00	Demos
15:00	<b>Combat-tb Workbench, A Customizable Platform For Variant Discovery And Annotation, Phylogeny Construction And Variant Prioritisation.</b> Z. Mashologu
15:25	<b>ProteoRE, a Galaxy-based platform for the annotation and the interpretation of proteomics data in biomedical research.</b> F. Combes
15:45	

9:00	Talks
	Proteomics & Metabolomics. Moderator: M. Föll
9:00	<b>Metaproteomics Powered By Metatranscriptomics: Towards a Multi-omic Functional Microbiome Analysis Within Galaxy.</b> P. Jagtap
9:20	<b>Interactive Galaxy Visualizations for Multi-omics Research.</b> R. Sajulga
9:27	<b>ProteoRE, a Galaxy-based platform for the annotation and the interpretation of proteomics data in biomedical research.</b> F. Combes
9:47	<b>Galaxy Wrapper for MaxQuant.</b> D. Glätzer
9:54	<b>Application of Halogen Bonding in Molecular and Drug Design Facilitated by a Galaxy Webserver.</b> F. M. Boeckler
10:30	Break
11:00	Talks
	Proteomics & Metabolomics. Moderator: P. Jagtap
11:00	<b>Analysing and organising large-scale metabolome annotation studies with Django, ISA and Galaxy.</b> T. N. Lawson
11:20	<b>Reproducible and accessible analysis of spatially resolved proteomics and metabolomics data.</b> M. Föll
11:40	<b>Workflow4Metabolomics: an international computing infrastructure for Metabolomics.</b> G. Le Corguillé, M. Petera, R. Dallet
12:00	Break
13:20	Training
	Admin & Dev.
	<b>CVMFS and Pulsar.</b> H. Rasche, S. Gladman, N. Coraor, G. Cuccuru
14:50	Break

15:50	Training
	Variation, Metagenomics & Assembly
	<b>Genomic assembly and data analysis in Galaxy with Nanopore ONT long read sequencing.</b> S. Hiltemann, M. Miladi, W. de Koning
17:30	Talks
	Plenary. Moderator: A. Lonie
17:30	Invited Talk <b>UseGalaxy: Elucidating chromatin biology of mouse cardiomyocytes.</b> S. Nothjunge
18:00	<b>Galaxy and Training: 2019 updates from the Galaxy Training Network.</b> B. Batut
18:20	<b>Closing.</b> B. Grüning, A. Erxleben, D. Clements
18:30	



9:00	Talks
	Outside the Genome & Community. Moderator: B. Batut
9:00	Invited Talk <b>Data visualisation by citizen science participants: the case of birds and bats monitoring schemes and Galaxy-E.</b> R. Lorrillière, Y. Bas
9:30	<b>Galaxy-Bricks a Tool for Data Literacy and Scientific Approach Education in the Context of Citizen Science.</b> S. Bénateau
9:37	<b>Citizen Science Project in Ecology with the Galaxy-E Platform.</b> B. Yguel
9:44	<b>Galaxy-E project: 2019 news.</b> Y. Le Bras
10:04	<b>The ChemicalToolBox - Computational Chemistry in Galaxy.</b> S. Bray
10:11	<b>Improved Reference Data Management in Galaxy: Towards a Plant Data Analysis Platform.</b> I. Eguinoa
10:18	<b>Use Galaxy, Right Now!</b> D. Clements
10:25	<b>Galaxy Publication Library.</b> D. Clements
10:30	Break
11:00	Talks
	Variation, Metagenomics & Assembly. Moderator: S. Hiltmann Germany
11:00	<b>The IRIDA Platform for Microbial Genomics.</b> A. Petkau
11:20	<b>Combat-tb: Workbench, A Customizable Platform For Variant Discovery And Annotation, Phylogeny Construction And Variant Prioritisation.</b> Z. Mashologu
11:27	<b>High throughput HIV next generation sequence analysis in Galaxy.</b> D. Bouvier
11:47	<b>NanoGalaxy: A Galaxy toolkit and workflows for long-read sequencing.</b> W. de Koning
11:54	<b>MITOLINK: An integrated Web-based Workflow System to Evaluate Genotype-Phenotype Correlations in Human Mitochondrial Diseases.</b> A. Bhardwaj
12:00	Break

13:20	Training
	General. <b>Machine learning with Galaxy.</b> A. Kumar, A. Khanteymoore
14:50	Break
15:50	Training
	General. <b>Handling integrated biological data using Python, Jupyter, and InterMine.</b> Y. Yehudi
17:20	



12:15	BoF
	<b>Galaxy containers.</b> E. Afgan, M. van den Beek, N. Goonasekera, B. Grüning, P. Moreno
13:20	Training
	Proteomics & Metabolomics.
	<b>Metabolomics data analysis I.</b> G. Le Corguillé, M. Petera, R. Weber, T. Lawson
14:50	Break
15:00	Demos
15:00	<b>Visual Refinement of Genome Annotations with Apollo in a Community Environment.</b> N. Dunn
15:25	<b>The IRIDA Platform for Microbial Genomics.</b> A. Petkau
15:45	Break
15:50	Training
	Proteomics & Metabolomics
	<b>Metabolomics data analysis II.</b> G. Le Corguillé, M. Petera, R. Weber, T. Lawson
17:20	



13:20	Training
	Proteomics & Metabolomics. <b>Proteomic data analysis.</b> M. Föll, M. Fahrner, M. Stillger
14:50	Break
15:00	Demo
	<b>Galaxy on Kubernetes.</b> S. Golitsynskiy, E. Afgan, A. Mahmoud, N. Goonasekera
15:45	Break
15:50	Training
	Proteomics & Metabolomics <b>MALDI imaging of peptides data analysis.</b> M. Föll, M. Fahrner, M. Stillger



12:15	BoF
	<b>Galaxy containers.</b> E. Afgan, M. van den Beek, N. Goonasekera, B. Grüning, P. Moreno
13:20	Training
	Variation, Metagenomics & Assembly.
	<b>Assembly, annotation and analysis of bacterial genomes.</b> D. Larivière, A. Syme, S. Gladman
14:50	Break
15:50	Training
	Admin & Dev.
	<b>ELIXIR Galaxy AAI.</b> K. Klepper
17:20	



12:15

**Arts & Crafts**

13:20



13:20	Training
	Outside the Genome & Community. <b>Import, handle, visualize and analyze biodiversity data in Galaxy.</b> Y. Le Bras, S. Bénéteau
14:50	Break
15:00	Demos
15:00	<b>Interactive Galaxy Visualizations for Multi-omics Research.</b> R. Sajulga
15:25	<b>NanoGalaxy: A Galaxy toolkit and workflows for long-read sequencing.</b> A. de Konig
15:45	Break
15:50	Training
	Outside the Genome & Community. <b>Populations genomics with RADseq.</b> Y. Le Bras, S. Bénéteau
17:20	

