

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



Talks	
10:00	Admin & Dev Introduction to Galaxy Administration I. M. Čech, E. Afgan, S. Gladman, M. van den Beek, J. Chilton, N. Coraor, H. Rasche
12:00	Lunch
13:00	Admin & Dev Introduction to Galaxy Administration II. M. Čech, E. Afgan, S. Gladman, M. van den Beek, J. Chilton, N. Coraor, H. Rasche
15:00	Break
15:30	Admin & Dev Introduction to Galaxy Administration III. M. Cech, 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	Opening and Welcome. A. Erxleben, B. Grüning
9:10	Invited Talk Evolution of X chromosome recognition during Drosophila Dosage Compensation. C. I. Keller Valsecchi
9:40	Galaxy Australia - inside the national vision of a data commons G. Price
10:00	A Machine Learning Tool Suite for Galaxy. J. Goecks
10:20	An Update on Galaxy Workflows: More Accessible, Expressive, Robust, and Scalable. J. Chilton, M. van den Beek
10:30	Break
11:00	Talks
	Admin & Dev. Moderator: H. Rasche
11:00	GalaxyCloudRunner: Streamlined Cloud Bursting for Galaxy. N. Goonasekera
11:07	Laniakea: A Galaxy-on-demand Provider Platform Through Cloud Technologies. M. A. Tangaro
11:27	Enabling Single Sign-On for Multiple Galaxy Instances. E. Afgan
11:34	How - And How not - to manage successful local Galaxies. P. Mabon
11:54	Building a Pulsar Network across Europe. G. Cuccuru
12:00	Lunch

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



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



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



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



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



13:20

Training

Variation, Metagenomics & Assembly.

16S analysis with Mothur. S. Hiltemann

14:50

Break

15:50

Training

Variation, Metagenomics & Assembly.

Metatranscriptomics & multi-omics microbiome analysis.

T. Griffin, B. Batut, R. Sajulga, P. Jagtap

17:20



12:15

BoF

Arts & Crafts

13:20



12:15

BoF

Arts & Crafts

13:20



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

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



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

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



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



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



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



15:00

Demos

15:00

Combat-tb Workbench, A Customizable Platform For Variant Discovery And Annotation, Phylogeny Construction And Variant Prioritisation. Z. Mashologu

15:25

ProteoRE, a Galaxy-based platform for the annotation and the interpretation of proteomics data in biomedical research. F. Combes

15:45



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

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



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

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



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



13:20

Training

Proteomics & Metabolomics.

Proteomic data analysis. M. Föll, M. Fahrner, M. Stillger

14:50

Break

15:00

Demo

Galaxy on Kubernetes. S. Golitsynskiy, E. Afgan, A. Mahmoud, N. Goonasekera

15:45

Break

15:50

Training

Proteomics & Metabolomics

MALDI imaging of peptides data analysis. M. Föll, M. Fahrner, M. Stillger



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



12:15

BoF

Arts & Crafts

13:20



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

