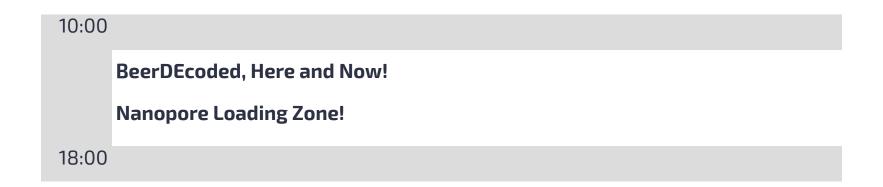
	Talks
10:00	Using Galaxy Introduction to Using Galaxy (Galaxy 101). M. Heydarian, J. Hillman-Jackson
12:00	Lunch
13:00	Using Galaxy Beyond the Intro: Further Adventures in Using Galaxy . M. Heydarian, J. Hillman-Jackson
15:00	Break
15:30	Using Galaxy Analyzing Large / Complex Experimental Designs with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







9:00		Talks
	Plena	ry. 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
	Admir	n & 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	
17:20	Talks
17:30	
	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. NH. Truong
19:00	



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Using Galaxy in automated production setups.
P. Moreno

Training
Epigenetics.
ChIP-seq data analysis. L. Rabbani, D. Ryan

14:50
Break
Training
Epigenetics.
Hi-C analysis. J. Wolff, L. Rabbani

17:20
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13:20	Training
6	Epigenetics.
(EWAS data analysis for population epigenetics
i	ntegrated 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



Training
Variation, Metagenomics & Assembly.

16S analysis with Mothur. S. Hiltemann

14:50
Break

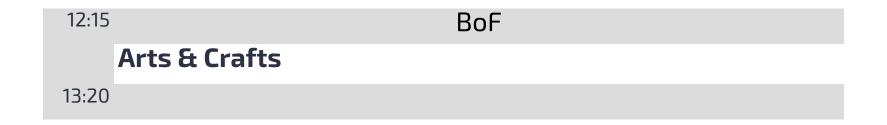
15:50
Training
Variation, Metagenomics & Assembly.

Metatranscriptomics & multi-omics microbiome analysis.

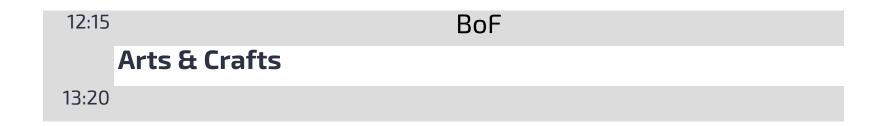
T. Griffin, B. Batut, R. Sajulga, P. Jagtap

17:20











9:00		Talks
	Trans	criptomics & 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
	Trans	criptomics & 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
	Admir	n & 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
	Admir	a & 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 highthroughput 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. 7. 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
Gener	al.
	n the Galaxy Trainer. S. Gladman, A. Syme, B. Batut, emann, 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
15:25 15:45	Tool Prediction in Galaxy Workflows using Deep
	Tool Prediction in Galaxy Workflows using Deep Learning. A. Kumar
15:45	Tool Prediction in Galaxy Workflows using Deep Learning. A. Kumar Break Training
15:45 15:50 Gener	Tool Prediction in Galaxy Workflows using Deep Learning. A. Kumar Break Training



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



9:00		Talks
	Prote	omics & 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
	Prote	omics & 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
	Admir	n & Dev.
	CVMF	S and Pulsar. H. Rasche, S. Gladman, N. Coraor, G. Cuccuru
14:50		Break

15:50		Training
	Variat	ion, Metagenomics & Assembly
		mic assembly and data analysis in Galaxy with Nanopore ONT long sequencing. S. Hiltemann, M. Miladi, W. de Koning
17:30		Talks
	Plena	ry. 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
	Outsid	de 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
	Variat	ion, 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. Khanteymoori
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

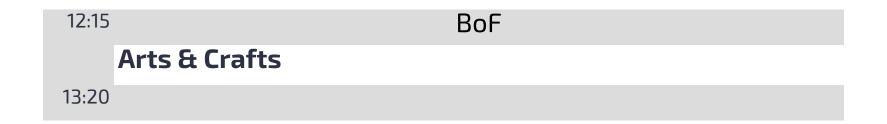


13:20 Training Proteomics & Metabolomics. Proteomic data analysis. M. Föll, M. Fahrner, M. Stillger 14:50 Break 15:00 Demo Galaxy on Kubernetes. S. Golitsynskiy, E. Afgan, A. Mahmoud, N. Goonasekera 15:45 Break 15:50 **Training** Proteomics & Metabolomics MALDI imaging of peptides data analysis. M. Föll, 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 **Training** 15:50 Admin & Dev. ELIXIR Galaxy AAI. K. Klepper 17:20







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	

