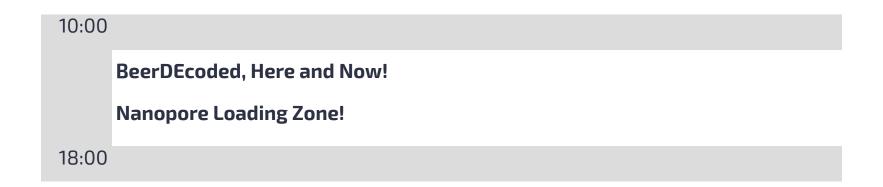| Talks		
10:00	Using Galaxy **Introduction to Using Galaxy (Galaxy 101)**. M. Heydarian, J. Hillman-Jackson	
12:00	Lunch	
13:00	Using Galaxy **Beyond the Intro: Further Adventures in Using Galaxy**. M. Heydarian, J. Hillman-Jackson	
15:00	Break	
15:30	Using Galaxy **Analyzing Large / Complex Experimental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

Galaxy Community Conference

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	

Galaxy Community Conference

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	

Galaxy Community Conference

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	

Galaxy Community Conference

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

Galaxy Community Conference

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	

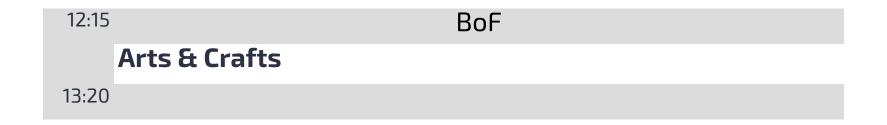| 13:20	Training
	Variation, Metagenomics & Assembly.
	16S analysis with Mothur. S. Hiltemann
14:50	Break
15:50	Training
	Variation, Metagenomics & Assembly.
	Metatranscriptomics & multi-omics microbiome analysis.
	T. Griffin, B. Batut, R. Sajulga, P. Jagtap
17:20	

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	

Galaxy Community Conference

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	

Galaxy Community Conference

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. Hiltemann, 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. Khanteymoori

14:50	Break
15:50	Training

General.
Handling integrated biological data using Python, Jupyter, and InterMine. Y. Yehudi

17:20	

Galaxy Community Conference

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
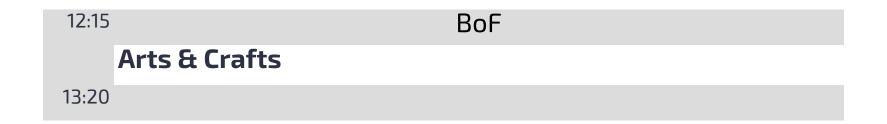
17:20	

Galaxy Community Conference

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	

Galaxy Community Conference

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	

Galaxy Community Conference