Tuesday 2nd July

8:00	Conference Desk Open
9:00	Talks - 1 plenary track

Plenary. Moderator: B. Grüning — *Greece*

- 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 & Sponsors
11:00	Talks - 2 parallel tracks

Admin & Dev. Moderator: H. Rasche — *Greece*

- 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

Outside the Genome & Community. Moderator: Y. Le Bras — *Germany*

- 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 & Birds-of-a-Feather

13:20	Trainings - 6 parallel workshops

Epigenetics.

- **ChIP-seq data analysis.** L. Rabbani, D. Ryan — *Italy*
- **EWAS data analysis for population epigenetics integrated into Galaxy.** K. Poterlowicz — *France*

Admin & Dev.

- **How to create a Galaxy Tool.** J. Chilton, N. Soranzo — *Greece*

Variation, Metagenomics & Assembly.

- **Variant calling I - from sequenced reads to variant lists.** W. Maier — *Spain*
- **16S analysis with Mothur.** S. Hiltemann — *Belgium*

General.

- **Quality control of HTS data.** TBA — *Germany*

14:50	Posters, Demos & Sponsors
15:50	Trainings - 5 parallel workshops

Epigenetics.

- **Hi-C analysis.** J. Wolff, L. Rabbani — *Italy*

Admin & Dev.

- **Scripting Galaxy through BioBlend.** N. Soranzo, M. van den Beek — *Greece*

Variation, Metagenomics & Assembly.

- **Variant Calling II - causative variant discovery.** W. Maier — *Spain*
- **Metatranscriptomics & multi-omics microbiome analysis.** T. Griffin, B. Batut, R. Sajulga, P. Jagtap — *Belgium*

General.

- **Machine learning with Galaxy.** A. Kumar, J. Goecks, A. Khanteymoori — *Germany*

17:20	Group picture

17:30	Talks - 2 parallel tracks

Epigenetics. Moderator: D. Ryan — *Greece*

- 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

Outside the Genome & Community. Moderator: A. C. Fouilloux — *Germany*

- 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	Dinner on your own & Birds-of-a-Feather

Legend:

- Outside the Genome & Community
- Epigenetics
- Variation, Metagenomics & Assembly
- Transcriptomics
- Proteomics & Metabolomics
- General
- Admin & Dev

Galaxy Community Conference