de❤NBI
GERMAN NETWORK FOR BIOINFORMATICS INFRASTRUCTURE

# de.NBI Quarterly Newsletter

The de.NBI Quarterly Newsletter informs about recent developments and current events in the project **German Network for Bioinformatics Infrastructure.**

Further information at: https://www.denbi.de/

## REVIEW OF THE de.NBI and ELIXIR GERMANY PLENARY MEETINGS IN NOVEMBER 2018

In combination with the de.NBI SAB meeting, the plenary meetings of the de.NBI network and of ELIXIR Germany took place at the Seminaris Campus Hotel in Berlin on 30 November 2018. Around 110 de.NBI members participated in these two meetings. The de.NBI plenary meeting focused on flash talks presented by service centers and special interest groups. These flash talks responded to the detailed reviewer recommendations provided during the de.NBI midterm review at the end of the establishment phase I. The plenary meeting of ELIXIR Germany took place in the afternoon of 30 November. The main purpose of this meeting was an introduction to the ELIXIR Programme 2019-2023 and a discussion on the further collaboration between de.NBI and ELIXIR with a focus on platforms, communities and implementation projects. Impressions of the SAB conference and the plenary meetings have been summarized in a video clip.

Find the video at https://www.denbi.de/news/560-impressions-of-the-sab-and-plenary-meeting-2018



## AN ENTHUSIASTIC REPORT FROM THE SAB ON THE de.NBI DEVELOPMENT

The 3rd Scientific Advisory Board Meeting of the network took place at the Seminaris CampusHotel in Berlin on 29-30 November 2018. The de.NBI coordinator and the de.NBI Administration Office prepared the de.NBI Status Report 2018 entitled "The de.NBI network in its 2nd funding phase". The oral presentations focused on benefits and visions of

*The SAB in an internal meeting with PtJ representatives and de.NBI coordination*

human, plant, and microbial bioinformatics. These were supplemented by lectures on the service, training and data management cases as well as recent developments of the de.NBI cloud, workflow engines, the ELIXIR cooperation, and, finally, the sustainable continuation. In particular, the sustainable continuation of the de.NBI network was intensively discussed in an internal meeting between SAB and CCU members. The SAB evaluated the network in a very positive way and summarized their response as follows:

*"It is our view that de.NBI is now a mature established and functional bioinformatics network, working to raise standards and expertise in handling life sciences data and providing user-friendly tools, hardware/software solutions, and access to compute to scientists in Germany and beyond. In total eight service centres and 37 different projects are now operational, including the successful extension in 2016 to include 17 new partner projects. This has created a dynamic distributed infrastructure, with a community of dedicated scientists, devoted to making it work well. We commend the achievements of the Director – Alfred Pühler, the Administrative Office and the Central Coordination Unit (CCU) for making this happen. de.NBI is now a mature community providing state-of-the art infrastructure and services to the life science community, in particular at four levels: provision of tools, community building, training, and the de.NBI Cloud. In addition, by running the ELIXIR-DE operation, de.NBI is well integrated in international activities and especially the bioinformatics community in Europe."*

# OLIVER STEGLE IS A NEW ASSOCIATED PARTNER IN HD-HUB

*by Ulrike Trojahn & Oliver Stegle*

In October 2018, Dr Oliver Stegle applied to join the de.NBI network as an associate member within the Heidelberg Center for Human Bioinformatics (HD-HuB). The decision has now been ratified when the CCU convened in Gatersleben on 23 January 2019. Oliver Stegle is holding a joint appointment between the European Molecular Biology Laboratory (EMBL), Genome Biology Unit and the German Cancer Research Center (DKFZ), Division of Computational Genomics and System Genetics in Heidelberg.

O. Stegle's work will contribute to the Single Cell Data Analysis activities that are part of the HD-HuB service portfolio. These contributions include widely-used bioinformatics tools for



- single-cell RNA-seq analysis,
- single-cell epigenetics and multi-omics methods, as well as
- spatial transcriptomics.

The Stegle laboratory is also a member of the Human Cell Atlas project, and hence will bring the required expertise to establish community standards and workflows for single-cell analytics.

*Photo: Oliver Stegle*

- The group will establish workflows for the first-line analysis of single-cell RNA-seq data, which includes read alignment, quality control, data normalization and batch adjustment. These workflows will leverage the parallel compute capacities available on the de.NBI Cloud and support common data formats and protocols, including Smart Seq 2 and the 10X Genomics Chromium platform. The workflows will build on standards established by the Human Cell Atlas project, which will be extended to support non-human data, as well as multiplexed pooled experimental designs. In addition, O. Stegle will establish and maintain elementary analysis tools for scRNA-seq on the de.NBI Cloud.
- Building on his own prior work in this area, O. Stegle will provide methods and workflows for processing sparse single-cell DNA methylation data (DeepCpG), as well as tools for interpreting and visualizing single-cell epigenome data (scNMT-seq software suite).
- Finally, the group will deliver bioinformatics methods for emerging data types and new technologies. They recently developed the first generation of analysis methods for data from spatial single-cell expression assays and will provide and support software such as SpatialDE.

Within the de.NBI training program, the Stegle lab will offer a training course for single-cell data analysis, which will be run on an annual basis. These training activities will be coordinated with the newly established Single-cell Biology Center Heidelberg.

Find further information at https://single-cell-center-hd.de

## NEW ELIXIR-DE TECHNICAL AND TRAINING COORDINATORS

From the start of ELIXIR Germany in 2016, Rolf Backofen (RBC, Freiburg) and Oliver Kohlbacher (CIBI, Tübingen) have been active in the German ELIXIR Node as technical and training coordinator, respectively. As both resigned from their ELIXIR-DE position this year, the Central Coordination Unit (CCU) of de.NBI unanimously elected new representatives from the national node as members of ELIXIR's Technical Coordinators Group (TeCG) and the Training Coordinators Group (TrCG). Briefly, the former deputies will take over: Björn Grüning (RBC, Freiburg) is the new technical coordinator and thus responsible to explore technical opportunities and issues to promote connections among the ELIXIR nodes and platforms. Daniel Wibberg (de.NBI Administration Office, Bielefeld) is the new training coordinator and thus involved in coordinating and implementing the ELIXIR training strategy across Europe. New deputies will be elected by the Central Coordination Unit later this year. In addition, Rolf Backofen and Alexander Goesmann (BiGi, Gießen) have been reappointed as ELIXIR Board members by the German Federal Ministry of Education and Research.

## PUBLICATION AWARD FOR MANUSCRIPT *PiGx: REPRODUCIBLE GENOMICS ANALYSIS PIPELINES WITH GNU Guix*　　　by Altuna Akalin
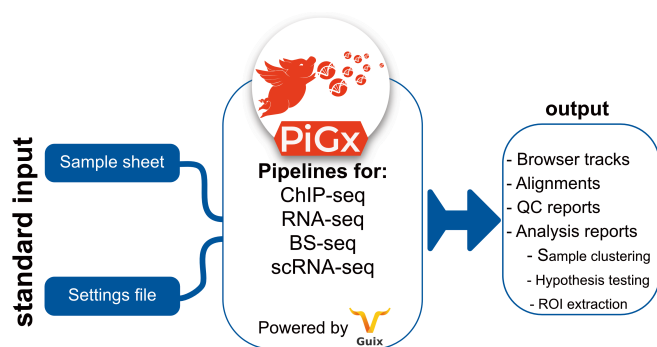
The Akalin lab/Bioinformatics Platform at the Berlin Institute of Medical Systems Biology (BIMSB), Max Delbrück Center (MDC) published a paper about a collection of reproducible genomics pipelines called **PiGx**. The team created these highly reproducible pipelines for the analysis of RNA-seq, ChIP-seq, BS-seq, and single-cell RNA-seq. All pipelines process raw experimental data and generate reports containing publication-ready plots and figures, with interactive report elements and standard observables. Their dependencies are managed with GNU Guix, which also provides the high reproducibility. All the pipelines have a similar interface and installable via one line command including all their dependencies.

The article won one of the GigaScience ICG-13 Prizes. ICG is a yearly genomics conferences organized by BGI. Representing the authors, Ricardo Wurmus was invited to present the work on PiGx and GNU Guix in Shenzhen, China at ICG-13 and received the award on behalf of the team.

Find the tool at http://bioinformatics.mdc-berlin.de/pigx
Find the publication at https://academic.oup.com/gigascience/article/7/12/giy123/5114263

## de.NBI LINKEDIN CHANNEL

After the success of using the Twitter channel @denbiOffice for public relations, de.NBI is now also active via LinkedIn. The de.NBI profile name is Tom Denbi, and a company page called "de.NBI" has been established. The new LinkedIn channel currently features about 150 followers and 100 posts. We will use this channel to network with professionals in academia and industry and with industrial partners, e.g. members of the recently founded de.NBI Industrial Forum. Using LinkedIn, we will announce training courses and all news related to de.NBI events. Interested to network with us? Follow or connect us on LinkedIn!

The channel can be found at https://www.linkedin.com/company/de-nbi

## EUROPEAN BIOCONDUCTOR MEETING 2018

With over 100 participants, the European Bioconductor Meeting 2018 took place in Garching near Munich from 6–7 December 2018. Bioconductor is a bioinformatics software collection for the R programming language and is widely used in Life Science research. The meeting addressed software developers and users at the same time. Developers presented the latest tools and analysis techniques for Bioconductor. Users had the opportunity to get in contact with developers and

discussed recent trends in the Life Sciences. The conference sessions covered recent topics in data visualization, epigenomics, proteomics, multiomics and RNA. As members of the Bioconductor core developer team were also present at the meeting, software developers and users were able to actively discuss and shape the future of Bioconductor. de.NBI supported the meeting by inviting the keynote speakers Keegan Korthauer (Dana-Faber Cancer Institute, Boston, USA) and Fanny Perraudeau (Whole Biome, Inc, USA). Furthermore, Bioinformaticians as well as Life Science Researchers were able to get hands-on experience of the de.NBI Cloud at a conference stand. Independently of the meeting de.NBI supports the development and maintenance of the Bioconductor packages BiocWorkflowTool and Protein Array Analyzer (PAA).

Read more about the event at https://www.denbi.de/events-archive/514-european-bioconductor-meeting-2018

## 3rd METAPROTEOME SYMPOSIUM 2018 – A REVIEW          by Dirk Benndorf

In December 2018, about 80 scientists from 14 countries participated in the 3rd International Metaproteome Symposium. The leading event in the field of metaproteomics was organized by Helmholtz-Centre for Environmental Research‑UFZ and the German Network for Bioinformatics Infrastructure - de.NBI*.

The number of publications examining microbiomes is currently exploding and results are providing new perspectives on human health and global nutrient cycles as well as on technical application of microbial communities in biotechnology. Multi-omics analysis is accepted as the gold standard to assess the microbiome samples, but the data integration is still challenging. The symposium offered a great opportunity to broaden the discussion on the integration of different datasets. Besides results from all areas of microbial ecology, first results of collaborative multi-omics study of a human gut microbiome sample and of a defined microbial community were presented. First insights demonstrated the reliability of metaproteomics regarding the assignment of major phyla and functions. The ongoing analysis of data from multiple labs will provide more detailed knowledge on reliability of metaproteomic data obtained with different experimental and bioinformatic pipelines and will reveal aspects for further improvement of the different workflows.
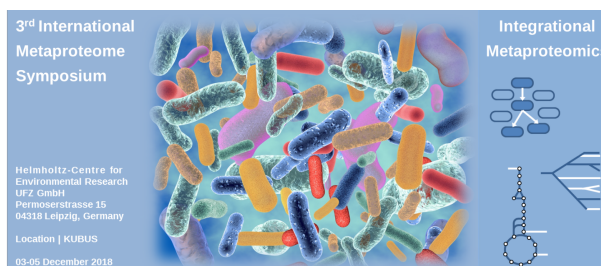
The symposium provided a good platform for oral and poster presentations of young passionate scientists in the interdisciplinary field of microbiome research. Three posters representing well the range of scientific contributions were priced.

- Data-independent acquisition mass spectrometry enables reproducible characterization of microbiota function (Sami Pietilä, University of Turku)
- Exploring new small proteins in a simplified human gut microbiome (Hannes Petruschke, Helmholtz-Centre for Environmental Research‑UFZ)
- Prediction-based reduction of the search space leads to increased identifications in metaproteomics without impacting sensitivity (Tim van den Bossche, VIB - Ghent Center for Medical Biotechnology)

The scientific committee of the symposium agreed to continue this symposium series at one and a half year. Intervals. The next symposium will be take place in Summer 2020 in Luxembourg (organized by Paul Wilmes, University of Luxembourg).

Microbiome researchers interested in the emerging field metaproteomics are invited to join the Applied Metaproteomics Workshop (Magdeburg, June 2019) providing hands-on training for the complete workflow starting from design of experiments via sample preparation to measurement and bioinformatics (MetaProteomeAnalyzer Software) analysis of high-resolution MS data.

More information on the workshop at: https://www.denbi.de/training/576-applied-metaproteomics-workshop-2019

*de.NBI partner project MetaProtServ, Otto-von-Guericke-University Magdeburg within BiGi - Bielefeld-Gießen Resource Center for Microbial Bioinformatics

## BeerDEcoded: RBC FREIBURG AND THE STREET SCIENCE COMMUNITY          by the Street Science Community Freiburg

The Street Science Community (https://streetscience.community/) is a volunteer-based non-profit group that aims to bring science to the public. The group organizes workshops to teach pupils, students and citizens molecular biology and genetics, data-analysis, and open science by extracting, sequencing and analyzing DNA. The current project, **BeerDEcoded**, uses the beer to sensitize the public to molecular biology and genome-related research. Beer contains DNA that comes from its ingredients and over hundreds of microbes. In Freiburg, the group developed a first prototype of the DNA extraction and sequencing

protocols using the Nanopore MinION, a portable real-time device for DNA sequencing. The results are very promising! The group has successfully identified specific brewing yeast strains from the DNA that was extracted out of bottled beer. For the bioinformatic data analysis, a workflow using Galaxy (https://streetscience.usegalaxy.eu) has been created. This open source, web-based and easy to use platform makes reproducible computational biology and bioinformatics accessible to interested citizens. Therefore, all proof-of-principle preparations are finished to start workshops and spread science into the community. The Street Science Community is supported by Bérénice Batut and Björn Grüning from RBC Freiburg and received financial support from de.NBI.

## LATEST FIGURES ON de.NBI TRAINING

The fourth de.NBI year was very successful in the training area. In 2015, de.NBI started with 17 training courses and with 329 participants and in 2016 (40 courses with 882 participants) and 2017 (69 courses with 1,489 participants) the numbers increased dramatically. In the last year, we further increased the numbers to 77 training courses with 1,520 participants. The largest course was attended by 73, the smallest one by four scientists. Approximately, 75% of the participants were PhD students or Postdocs. The remaining 25% were PIs, undergraduates, and participants from industry. The gender ratio of the students was 59% male and 41% female. About 30% of the participants came from outside Germany. In general, the user survey shows satisfaction values around 90% with only a small number of exceptions. In the ELIXIR context, de.NBI belongs to the leading providers bioinformatics training courses in Europe in 2018. Already 50 training courses are announced for 2019.

Further information is available at https://www.denbi.de/training
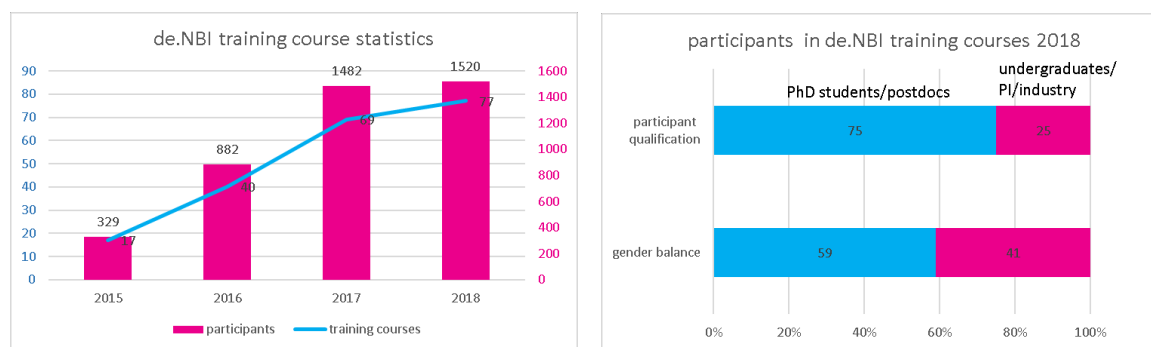




## A successful Galaxy RNA-seq workshop in Belgrade   by Bérénice Batut

The Freiburg Galaxy team (RBC) regularly organizes training workshops such as the bi-annual Galaxy HTS data analysis workshop in Freiburg. In the past year, we have also been invited to teach worldwide: Cape Town, Melbourne, Oslo, etc.

In January, Nevena Veljkovic from the Institute of Nuclear Sciences Vinča in Belgrade, Serbia organized and hosted a 2-day course. The Freiburg Galaxy team offered an introductory course to Galaxy and RNA-seq data analysis, using the online training material from the Galaxy Training Network and the European Galaxy server. Details of the schedule and links can be found on our dedicated event page.



*Pictures from Bérénice Batut - CC BY SA*

With 50 participants, this workshop was the largest we have taught using interactive hands-on training, and the most intense one: A fully packed room, where it was difficult to walk, a high heterogeneity of trainees, few internet, and server issues. Nevertheless, the participants seem to have enjoyed this workshop, given the feedback, when we asked them to write a positive one on green and a negative one on red stickers. Based on this positive experience and the high demand (more than 80 people registered), more training will be organized in the near

future in Serbia, probably with fewer participants and longer programs. We would like to thank Novena and Vlada for the invitation and the sightseeing, de.NBI for supporting this type of event, usegalaxy.eu and the Galaxy Training Network!
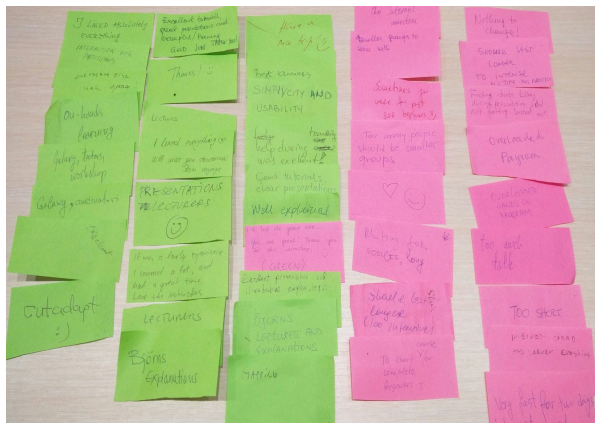


*Selected remarks*

*Positive feedback*: "Interactive with participants", "on-hands learning", "Excellent tutorials, great presentations and examples/training. Good job. THANK YOU", "It was a lovely experience. I learned a lot, and had a great time. Love the instructors.", "Excellent presentation and illustrative explanations", "Björn's lectures and explanation"

*Negative feedback*: "the Internet connection", "smaller groups to work with", "sometimes you were too fast for beginners", "Too many people. Should be smaller groups", "Should last longer (too intensive)", "Too short course for complete beginners"

Further Information on this course at https://galaxyproject.eu/event/2018-12-07-Announcement-Galaxy-course/

# RECENT UPDATES OF de.NBI SERVICES

New versions of various de.NBI services and tools have been released in the last months accompanied by the respective publications:

- 🐍 **Vienna RNA package 2.4.11.** The Vienna RNA Package consists of a C code library and several stand-alone programs for the prediction and comparison of RNA secondary structures. Latest Version 2.4.11 from 18 December 2018. Link to the service: https://www.denbi.de/services/361-bioinformatics-leipzig-various-webservices-and-tools-for-transcriptomics

- 🐍 **Mitos 2.0** – New version of the Webserver for Automated Annotation of Metazoan Mitochondrial Genomes - multiple structure-based RNA alignment and folding. MITOS implements a pipeline for the automated annotation of Metazoan mitochondrial genomes. The method is based on an automatic consistent re-annotation of protein coding genes and non-coding RNAs using BLASTX and co-variance models. https://www.denbi.de/services/361-bioinformatics-leipzig-various-webservices-and-tools-for-transcriptomics, http://mitos.bioinf.uni-leipzig.de/index.py, or http://mitos2.bioinf.uni-leipzig.de/index.py

- 🐍 **MapMan4** and **Mercator:** A redesigned and significantly enhanced MapMan4 framework, together with a revised version of the associated online Mercator annotation tool have been published in: *Mapman4: a refined protein classification and annotation framework applicable to multi-omics data analysis*, R. Schwacke et al., Molecular Plant, 9 Jan 2019. https://doi.org/10.1016/j.molp.2019.01.003
  The new version is part of http://www.plabipd.de/portal/mercator-sequence-annotation

- 🐍 **HiCExplorer Version 2.2**: Set of programs to process, analyze and visualize Hi-C data. New version released in November 2018, https://github.com/deeptools/HiCExplorer

- 🐍 **BacDive:** Several novel features added to the strain detail view. Related publication: *BacDive in 2019: bacterial phenotypic data for High-throughput biodiversity analysis*, Reimer LC[1] et al., Nucleic Acids Res. 2019 Jan 8;47(D1):D631-D636, https://doi.org/10.1093/nar/gky879

**Publications**

- 🐍 **GCBN**: In a proof-of-concept study based on deep genotyping-by-sequencing (GBS) of the entire IPK barley collection of more than 20,000 accessions, comprehensive and coherent information has been generated on genetic diversity and population structure. Systematic valorization of these genomics data is facilitated by building an innovative and intuitive diversity informatics and data warehouse infrastructure for accommodation and analysis of BIG DATA sets. BRIDGE portal, http://bridge.ipk-gatersleben.de/
  The corresponding paper is *Genebank genomics highlights the diversity of a global barley collection,* Nature genetics, vol2 issue 2, February 2019, https://www.nature.com/articles/s41588-018-0266-x

- 🐍 **de.STAIR Rostock**: Two chapters on non-coding RNA bioinformatis published in Computational Biology of Non-Coding RNA pp 199-214, Part of the Methods in Molecular Biology book series (MIMB, volume 1912), First Online 12 January 2019, https://link.springer.com/book/10.1007%2F978-1-4939-8982-9
  1) *Workflow Development for the Functional Characterization of ncRNA*, M. Wolfien, D. L. Brauer, A. Bagnacani, O. Wolkenhauer
  2) *Tools for Understanding miRNA–mRNA Interactions for Reproducible RNA Analysis*, A. Bagnacani, M. Wolfien, O. Wolkenhauer

- 🐍 **de.NBI** and **GFBio**: Zwei dezentrale Infrastrukturprojekte unterstützen Wissenschaft und Forschung, *Big Data in der Biologie: kein Problem mehr*, B. Gemeinholzer, J. Nieschulze, A. Tauch, A. Goesmann, Biologie in unserer Zeit, Vol. 49, 58-67, 4 February 2019, https://doi.org/10.1002/biuz.201910668

# de.NBI @ CONFERENCES

## ❊ de.NBI Workshops at upcoming conferences

de.NBI partners will be teaching a variety of workshops or tutorials at conferences in March:

### ♐ DGMS 2019 - 52. Jahrestagung der Deutschen Gesellschaft für Massenspektrometrie, Rostock, 10-13 March 2019

**Targeted Lipidomics with Skyline and LipidCreator**, R. Ahrends, N. Hoffmann (ISAS Dortmund). The course will cover the challenges and necessary precautions of designing and conducting a targeted LC-MS lipidomics experiment. It will be demonstrated how to analyze such data using the Skyline software and the targeted lipidomics plugin LipidCreator. In combination, these tools can be used for targeted assay development and optimization and for customized targeted lipidomics studies, including identification and quantification of lipids.
Further information at: https://www.denbi.de/training/552-lipidomics-workshop-dgms-2019

### ♐ Proteomic Forum 2019, Potsdam 24-28 March 2019

**Tool training for proteomics**, M. Turewicz, J. Uszkoreit, K. Schork, T. Sunny, D. Kopczynski (Ruhr Unversity Bochum and ISAS Dortmund). In this one-day course, four proteomics software tools will be introduced, PIA, PeptideShaker, SearchGUI and BIONDA. This course is a common teaching event of the EuBIC initiative and the de.NBI/ELIXIR Germany service center BioInfra.Prot.
Further information at: https://www.denbi.de/training/550-tool-training-for-proteomics-proteomic-forum-2019
and https://www.eupa2019.org/program/tool-training-for-proteomics/

## ❊ de.NBI supported conferences

de.NBI will support the following conferences co-organized by de.NBI partners:

### ♐ 15th Gatersleben Research Conference on Applied Bioinformatics in Crops, 18–20 March 2019 at the Leibniz Institute of Plant Genetics and Crop Plant Research (IPK) in Gatersleben.

This conference will be of interest to Life Scientists, Bioinformaticians, Computer Scientists, Systems Biologists, Synthetic Biologists and others working or interested in the developing area of Applied Bioinformatics for crops. The meeting will provide an excellent environment and a range of opportunities to present and discuss methods, theoretical approaches, and their practical applications. Topics: • Image-Based Data Analyses and Data Visualization, • Distributed Computing, • Tools and Infrastructures, • Systems Biology and Modeling, • Biodiversity and Information Systems, • Breeding Informatics. Two keynote lectures will be invited by de.NBI.
General information and registration at: https://meetings.ipk-gatersleben.de/grc2019-abc/
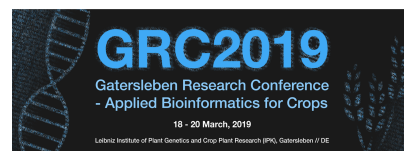
### ♐ Galaxy community conference, Freiburg, 1-6 July 2019.

We are pleased to announce that GCC2019 will be held in Freiburg, Germany, 1-6 July. Like previous Galaxy Community Conferences, GCC2019 will feature invited keynotes, accepted talks, posters, and demos, birds-of-a-feather gatherings, multiple days of collaborative work, and plenty of opportunities to network with your fellow data-intensive researchers and practitioners. If you are working in data-intensive life science, there is no better place to be.
General information and registration at: at: https://www.denbi.de/events/12-galaxy-community-conference-2019-gcc2019

# UPCOMING EVENTS

The calendar lists the de.NBI training courses and events scheduled in the next months. All offers are accessible via the de.NBI web page. A number of training events are in the pipeline but not yet scheduled. Please consult the de.NBI training program for the actual dates.

## ❊ Overview of upcoming de.NBI events

| Date | Event | City | Organizer |
|------|-------|------|-----------|
| ♐ 12-13 Feb 2019 | Linux Command Line & Basic Scripting course 2019 | Heidelberg | HD-HuB |

| | Date | Event | City | Organizer |
|---|---|---|---|---|
| | 21 Feb 2019 | GTN CoFest on Galaxy Training Material | Online | RBC |
| | 25 Feb-01 Mar 2019 | 7th Galaxy workshop on HTS data analysis | Freiburg | RBC |
| | 06-08 Mar 2019 | Galaxy for linking bisulfite sequencing with RNA sequencing | Rostock | RBC/de.STAIR |
| | 10 Mar 2019 | Targeted Lipidomics with Skyline and LipidCreator - DGMS 2019 - DGMS 2019 | Rostock | BioInfra.Prot/LIFS |
| | 13-14 Mar 2019 | Miracum whole-exome sequencing pipeline workshop | Freiburg | RBC |
| | 18 Mar 2019 | SeqAn & OpenMS (CIBI/de.NBI) Integration Workshop | Berlin | CIBI |
| | 18-22 Mar 2019 | Summer school on Integration of Large Scale Lipidomics Data in Systems Medicine Research (LipoSysMed) | Leipzig | BioInfra.Prot/LIFS |
| | 19 Mar 2019 | Tools for Systems biology modeling and data exchange: COPASI, CellNetAnalyzer, SABIO-RK, FAIRDOMHub/SEEK | Heidelberg | de.NBI-SysBio |
| | 20-22 Mar 2019 | Spring School "Computational Biology Starter" | Gatersleben | GCBN |
| | 22-31 Mar 2019 | SeqAn3 Developer Retreat 2019 | Escala | CIBI |
| | 2019-03-28 | Tool-Training for Proteomics – Proteomic Forum 2019 | Potsdam | BioInfra.Prot |
| | 01-03 Apr 2019 | de.NBI CompMS metaRbolomics Hackathon | Lutherstadt Wittenberg | CIBI/MASH |
| | 09 April 2019 | 18. CCU Meeting | Heidelberg | CAU, de.NBI-SysBio |
| | 23-26 Apr 2019 | Galaxy training and hackathon | Roscoff | RBC |
| | 29 Apr – 01 May 2019 | Proteomics and Metabolomics with OpenMS | Boston | CIBI |
| | 22 May 2019 | Phylogenetic reconstruction course | Kiel | Associated Partner Kiel |
| | 22 May 2019 | Computational genomics course for hands-on data analysis | Berlin | RBC |
| | 27-29 May 2019 | 12th Annual International Conference on Systems Biology of Human Disease - SBHD 2019 | Berlin | HD-HuB |
| | 17-21 Jun 2019 | Applied Metaproteomics Workshop 2019 | Magdeburg | BiGi |
| | 01-06 Jul 2019 | Galaxy Community Conference 2019 – GCC2019 | Freiburg | RBC |
| | 15-19 Jul2019 | Combine 2019 Conference | Heidelberg | de.NBI-SysBio |
| | 03 Jul 2019 | 19. CCU Meeting | Bremen | CAU/BioData |
| | 21-26 Jul 2019 | CSAMA 2019 - Statistical Data Analysis for Genome-Scale Biology | Bressanone/Brixen | HD-HuB |
| | 02-06 Sep 2019 | de.NBI Summer School 2019 - (Bio)Data Science | Gatersleben | GCBN et al. |
| | 23-24 Oct 2019 | Introduction to BRENDA and EnzymeStructures | Braunschweig | BioData |

Further information at: http://www.denbi.de/training

# IMPRESSUM

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