

# de.NBI Quarterly Newsletter

The de.NBI Quarterly Newsletter in May 2019 informs about recent developments and current events in the project **German Network for Bioinformatics Infrastructure**.

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

## THE RENEWED SCIENTIFIC ADVISORY BOARD OF THE de.NBI

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From the beginning on, the development of the de.NBI network was accompanied by an international Scientific Advisory Board (SAB) consisting of six members. After four years of its existence, the de.NBI SAB has been partially renewed and expanded to eight members.

The following scientists were appointed members of the renewed de.NBI SAB:

- ✦ **Dr. Anne-Françoise Adam-Blondon**, Plant Biology and Breeding Department, INRA, Versailles, France
- ✦ **Dr. Ivo Gut**, Centro Nacional de Análisis Genómico, Barcelona, Spain
- ✦ **Prof. Dr. Ivo Hofacker**, Institute for Theoretical Chemistry, Vienna University, Austria
- ✦ **Prof. Dr. Connie R. Jimenez**, OncoProteomics Laboratory, VU University Medical Center, Amsterdam, Netherlands
- ✦ **Prof. Dr. Alice McHardy**, Helmholtz Centre for Infection Research, Braunschweig, Germany
- ✦ **Dr. Claudine Médigue**, l'Institut Français de Bioinformatique, CNRS, and LABGeM, GENOSCOPE, Evry, France
- ✦ **Prof. Dr. Bengt Persson**, National Bioinformatics Infrastructure Sweden, Uppsala University & Karolinska Institute, Uppsala, Sweden
- ✦ **Dr. Reinhard Schneider**, Luxembourg Centre for Systems Biomedicine, University of Luxembourg, Belvaux, Luxembourg

Four members of this group are well known to the de.NBI network since they agreed to continue the work in the board. The remaining four members have been newly recruited and complete the panel. It is evident that the de.NBI SAB consists of renowned experts accustomed to all aspects of bioinformatics infrastructure, is truly international and gender balanced. The task of the SAB is to advise the de.NBI CCU in technical, organizational and strategic matters.

The next SAB meeting will take place on 13-14 February 2020 in Berlin. During this meeting, the achievements of the de.NBI network will be presented in oral presentations and also in posters. Beforehand, the SAB members will receive a written statement demonstrating the recent developments of the de.NBI network.

In the past, it turned out that the de.NBI SAB was of greatest importance for the development of the de.NBI network. It is expected that the new de.NBI SAB will play a similar role in guiding the de.NBI network and also the German ELIXIR node into a successful future.



*The new Scientific Advisory Board: A.-F. Adam-Blondon, I. Gut, I. Hofacker, C. R. Jimenez, A. McHardy, C. Médigue, B. Persson, R. Schneider (from left to right)*

## de.NBI BRIDGING PHASE UNTIL THE END OF 2021

The de.NBI consortium will receive further project funding during a bridging phase planned from March 2020 to the end of 2021. Project funding of the de.NBI network by the BMBF started in March 2015 and was originally scheduled for five years. So far, the network has established a bioinformatics infrastructure in Germany that should be continued in the future. Since a sustainable continuation will not be possible before January 2022, the BMBF decided to continue the de.NBI project with a bridging phase until the end of 2021.

During the bridging phase the de.NBI network will be involved in new activities such as the formation of national communities focusing on specific life science topics, organized and maintained by an expanded de.NBI administration office. An important task of the extended de.NBI administration office in this context will be to introduce the de.NBI tools and services to new users and to help them find the right contact persons at the service centers.

In order to intensify the cooperation with ELIXIR, especially with regard to the interaction with the ELIXIR platforms Data, Tools, Compute, Interoperability and Training, a coordination and administration office for the German ELIXIR node will be established. The staff of the ELIXIR-DE coordination- and administration office will also be involved in the ELIXIR specific tasks such as the communities on the European level, implementation projects and EU third-party funding projects. In addition, the eight de.NBI service centers will apply for new positions to fulfil specific ELIXIR-DE tasks within their service center.

## de.NBI MEMBERS PARTICIPATE IN THE EOSC-LIFE PROJECT



The EOSC-Life project started recently with a kick-off meeting (20-21 March 2019) in Amsterdam that brought together over 120 participants from 13 ESFRI Research Infrastructures in the Health and Food domain. The project duration covers 48 months, from March 2019 to February 2023, with a public funding resource of 23.7 million €. The EOSC-Life project aims at creating an open collaborative digital space for life science in the European Open Science Cloud (EOSC). The contributing research infrastructures will publish data from facilities and data resources in the EOSC and will link these FAIR databases to open tools and workflows accessible to users via national and international life-science clouds. The de.NBI partner Charité - Berlin (Chris Lawrence, HD-HuB) is co-leading a work package entitled 'Cloud Deployment Services' that will deliver a set of cloud resources integrated through the life science Authentication and Authorization Infrastructure (AAI) and discoverable through the EOSC service registry. The de.NBI partner University of Freiburg (Björn Grüning, RBC) will be involved in two work packages to assist in developing the integration of tools and data sources into the Galaxy analysis system (<https://usegalaxy.eu/>). Two partners of the de.NBI Service Center BiGi, Bielefeld University (Alexander Sczyrba) and Giessen University (Alexander Goemann), will participate in a demonstrator project to provide metagenomics services in the cloud.

Find further information at <https://www.eosc-portal.eu/eosc-life> (under construction)

Find further information at <https://elixir-europe.org/news/eosc-life-start> (press release)

## NEW ELIXIR-DE TRAINING COORDINATOR DEPUTIES



Daniel Wibberg from the de.NBI Administration Office in Bielefeld has been elected recently by the Central Coordination Unit (CCU) of de.NBI as the new ELIXIR Germany Training Coordinator (see Issue 1/2019). The team responsible for training coordination of the German Node in Europe has been completed by the CCU during the April Meeting in Heidelberg. The CCU unanimously elected two new representatives from the national node as deputy members of ELIXIR's Training Coordinators Group: Bérénice Batur from RBC Freiburg and Malvika Sharan from HD-HuB Heidelberg (EMBL). ELIXIR Training is organized through the Training Platform, a European network of experts in their scientific domains and in adult learning. The members of the Training Platform meet regularly to share information and expertise and to coordinate and lead the implementation of the ELIXIR training strategy across Europe.



Malvika Sharan (l.), Bérénice Batur (r.)

More information at: <https://www.denbi.de/elixir-germany>

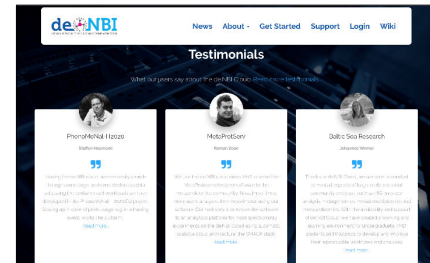
## NEW de.NBI CLOUD WEB PAGE



The de.NBI Cloud web page (<https://cloud.denbi.de>) has now a new design with a theme that uses official de.NBI colors and is well adapted to the main de.NBI website.



The cloud portal also provides new content. The two project types currently offered, Open-Stack and SimpleVM, are described in more detail and a comparison of the project types is included. User testimonials describe specific projects running in the de.NBI Cloud (<https://cloud.denbi.de/testimonials/>).



## GATERSLEBEN RESEARCH CONFERENCE – APPLIED BIOINFORMATICS FOR CROPS & SPRING SCHOOL “COMPUTATIONAL BIOLOGY STARTER” SUPPORTED BY de.NBI






by: Sebastian Beier, Uwe Scholz & Mary-Ann Blätke



The **15th Gatersleben Research Conference 2019** took place 18 -20 March at the Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben. The organization of this event was planned by the Service Center GCBN (in particular by Uwe Scholz) and besides de.NBI also supported by Deutsche Forschungsgemeinschaft (DFG), KWS Saat SE, SGS-TraitGenetics, ELIXIR Germany, Green Gate Gatersleben and the IPK.

The conference was able to attract 112 participants from 15 different countries from all over the world. In the course of these three days, the audience saw 32 talks and 36 posters about cutting-edge plant science. With Barend Mons (Leiden University,NL) a prominent figure in the GO FAIR initiative gave a fascinating keynote lecture on Social Machines and the implications on human-computer interactions. Also, of particular interest to the de.NBI community, Björn Grüning (University of Freiburg) presented a lecture titled “Integrative Bioinformatics with Galaxy Building Frameworks to Serve the 21st Century Data Science Problems” and could give insight into Galaxy, Bioconda and BioContainers in the frame of the Galaxy Training Network.

### Main topics

-  Image-Based Data Analyses and Data Visualization
-  Distributed Computing, Tools and Infrastructures
-  Systems Biology and Modeling
-  Biodiversity and Information Systems
-  Breeding Informatics



*Impression of the GRC2019 (Photo: IPK Gatersleben)*

One highlight was without question a tour through the old town of Quedlinburg, a UNESCO World Heritage Site since 1995. For the physical well-being participants of the conference were invited afterwards to the conference dinner at the Hotel Schlossmühle.

Following right after the Gatersleben Research Conference the **International Spring School “Computational Biology Starter”**, took place from 20–22 March at IPK. The Spring School was organized by the IPK Postdoc Board and supported by de.NBI and the IPK. Sessions were in part held by speakers of the Gatersleben Research Conference, e.g. Andrea Bräutigam and Jędrzej Jakub Szymanski, and researchers at IPK Gatersleben.

From a large number of excellent applications, 25 participants were chosen to learn about the basics of computational biology and bioinformatics in the context of plant sciences. The program covered an introduction to Linux and R, statistics and data visualization, applied phenomics, working with Galaxy and metabolic modelling. Each session was a mixture of lecture and hands-on training, which was well perceived by the participants. In the evenings, participants were invited to attend social events for further discussions and networking.

To celebrate the 4444<sup>th</sup> de.NBI training course participant Daniel Wibberg (de.NBI Administration Office, Head of Training, Web and Social Media Coordination) surprised the lucky participant (Vanessa Paffrath from the IPK) with a gift.

Following up this successful event, the IPK Postdoc Board plans similar training opportunities in the near future.



Impressions from the Computational Biology Starter (Photos: M.-A. Blätke & IPK Gatersleben)

Further information at:

[https://www.ipk-gatersleben.de/uploads/media/190318\\_PM\\_2019\\_07\\_Pflanzenbioinformatikertagung.pdf](https://www.ipk-gatersleben.de/uploads/media/190318_PM_2019_07_Pflanzenbioinformatikertagung.pdf)

## 2<sup>ND</sup> de.NBI CLOUD USER MEETING



### CLOUD USER MEETING<sup>2</sup> HEIDELBERG


The 2nd de.NBI Cloud User Meeting is an upcoming 3-day event (03-05 Sep 2019) in Heidelberg for scientists interested in bioinformatics, cloud computing or big data. Due to the diversity of approaches that arise in this exciting and rapidly evolving cloud computing technology niche, this meeting should help to exchange ideas and approaches in the growing de.NBI Cloud Community.

We aim to equip our attendees, from beginner to expert, with comprehensive understanding of the very broad applications and benefits of the de.NBI Cloud. This event is your chance to meet users, developers and administrators of the de.NBI Cloud. We feature topics from introduction or use case talks to simply introduce different technologies (OpenStack, Docker, Kubernetes, Nextflow, ...) to tutorials and workshops that will help understand how to actually apply the technology in your research.

More information will follow soon at: <https://www.denbi.de/training/622-2nd-de-nbi-cloud-user-meeting>

## 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:

-  **Edgar:** Public and free to use EDGAR database has been updated. The public databases provided by the EDGAR platform for comparative genomics as part of the BIGI node in the German Network for Bioinformatics Infrastructure (de.NBI) has again been updated and significantly extended. A new project type was added that consists of all type strains of a certain family. In this project type also draft genomes are included. More than 4400 genomes in 226 new family-based projects are now available. This extends the public EDGAR database to 548 genera and families with 12479 genomes.



The EDGAR web server can be found at the URL: <http://edgar.computational.bio>

### Publications

-  **RBC: The RNA workbench 2.0: next generation RNA data analysis,** J. Fallmann, P. Videm, A. Bagnacani, B. Batut, M.A. Doyle, T. Klingstrom, F. Eggenhofer, P.F. Stadler, R. Backofen, B. Grüning; Nucleic Acids Research, gkz353, <https://doi.org/10.1093/nar/gkz353>, published 10 May 2019. *Abstract:* RNA has become one of the major research topics in molecular biology. As a central player in key processes regulating gene expression, RNA is in the focus of many efforts to decipher the pathways that govern the transition of genetic information to a fully functional cell. As more and more researchers join this endeavour, there is a rapidly growing demand for comprehensive collections of tools that cover the diverse layers of RNA-related research. However, increasing amounts of data, from diverse types of experiments, addressing different aspects of biological questions need to be consolidated and integrated into a single framework. Only then is it possible to connect findings from e.g. RNA-Seq experiments and meth-

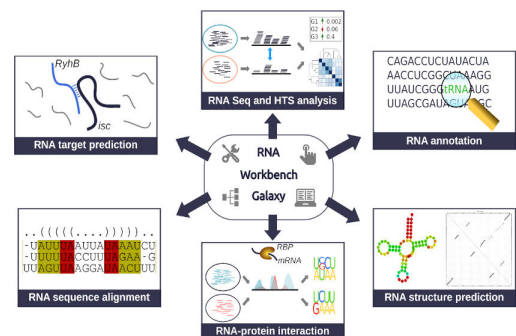


Figure taken from Nucleic Acids Research, gkz353, <https://doi.org/10.1093/nar/gkz353> [creativecommons.org/licenses/by-nc/4.0/](https://creativecommons.org/licenses/by-nc/4.0/)

ods for e.g. target predictions. To address these needs, we present the RNA Workbench 2.0, an updated online resource for RNA related analysis. With the RNA Workbench we created a comprehensive set of analysis tools and workflows that enables researchers to analyze their data without the need for sophisticated command-line skills. This update takes the established framework to the next level, providing not only a containerized infrastructure for analysis, but also a ready-to-use platform for hands-on training, analysis, data exploration, and visualization. The new framework is available at <https://rna.usegalaxy.eu>, and login is free and open to all users. The containerized version can be found at <https://github.com/bgruening/galaxy-rna-workbench>.

## de.NBI @ CONFERENCES

The network has been presented at major national conferences in the first Quarter of 2019.

### de.NBI at the Annual Conference 2019 of the Association for General and Applied Microbiology (VAAM) in Mainz

During 17-20 March 2019, a representative from the de.NBI administration office attended the Annual Conference 2019 of the Association for General and Applied Microbiology (VAAM) that took place at the Johannes Gutenberg University, Mainz, Germany.

The conference this year was co-organized by the two major universities, Mainz and Kaiserslautern, and hosted over 500 participants from academia in addition to extensive industrial exhibitions. During the poster session, the de.NBI network was presented to a big audience of graduate researchers in the field of microbiology. Participants were introduced to the wide range of de.NBI services and training offers in addition to the de.NBI Cloud and its capacity to serve the need of researchers in multiple fields of life science. The conference represented a chance for networking and increasing the visibility of the de.NBI network for a large audience of scientists and industry representatives.



Further information: <http://www.vaam-kongress.de/>

### de.NBI supported conferences

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

#### **Galaxy Community Conference, Freiburg, 1-6 July 2019**

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!

1 July: Training day featuring parallel introductory training tracks.

2-4 July: Core conference

5-6 July: CollaborationFest, two tracks on

- *Galaxy development (Galaxy Dev):*
- *Galaxy documentation, analysis, and training (Galaxy DAT)*

**Advance registration ends 7 June, Poster and demo submissions are due 10 June.**

General information and registration at:

<https://www.denbi.de/events/12-galaxy-community-conference-2019-gcc2019>

Doing or supporting data intensive research?  
Wanting to connect with a global community?  
The 2019 Galaxy Community Conference is for you.



# GCC 2019

## Freiburg, DE

### 1-6 July

[galaxyproject.org/events/gcc2019](http://galaxyproject.org/events/gcc2019)



Training for data analysis  
Accepted and lightning talks,  
posters and demos  
Birds-of-a-feather gatherings  
Collaborative work  
Networking with a worldwide  
community

Significant discounts for early registration, students, post-docs,  
faculty and other academics and non-profits

### **COMBINE 2019, Heidelberg, 15-19 July 2019**

This year's meeting is organized by the de.NBI-SysBio team at HITS Heidelberg. The "Computational Modeling in Biology Network" (COMBINE) is an initiative to coordinate the development of the various community standards and formats in systems biology, synthetic biology and related fields. COMBINE 2019 will be a workshop-style event with invited lectures, oral presentations and posters, but also reserving enough time for afternoon breakout sessions. The five meeting days will include talks about the COMBINE standards and associated or related standardization efforts, as well as presentations of tools using these standards and similar topics. Some oral presentations will be selected from the abstracts submitted by the attendees. In addition, poster sessions will allow people to inform each other about their software and other projects in a setting that fosters interaction and in-depth discussion. The first day (Monday 15 July) will be a colloquium day celebrating the 10<sup>th</sup> anniversary of the COMBINE network. One of these is a de.NBI colloquium. Abstract submission closes on 31 May 2019, **registration is possible until 15 June 2019**.



General information and registration at: [http://co.mbine.org/events/COMBINE\\_2019](http://co.mbine.org/events/COMBINE_2019)

### **GCB 2019 – German Conference on Bioinformatics, Heidelberg, 16-19 September 2019**

*Precision Medicine-where Bioinformatics & Medical Informatics meet* is the main topic of this year's conference. The organizers have compiled an attractive panel of speakers that makes the attendance of the meeting attractive. The first day is dedicated to a number of interesting workshops.



de.NBI Partners will teach four tutorials:

- de.NBI showcase: Combining Workflows, Tools and Data Management (W. Müller, de.NBI-SysBio, HITS gGmbH and partners)
- SeqAn3 – a modern C++ library for efficient sequence analysis (R. Rahn, CIBI, FU Berlin)
- Getting started with the de.NBI Cloud (A. Sczyrba, BiGi, Bielefeld University)
- Proteomics and metabolomics with OpenMS and pyOpenMS (T. Sachsenberg, CIBI, University of Tübingen)

General information and registration at: <https://www.denbi.de/events/548-gcb-2019>










## 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.

### **Major de.NBI events – Save the Dates**

- **de.NBI SAB Meeting and Plenary Meeting 2020, 13-14 February 2020 in Berlin.** The venue is the Seminaris Campus Hotel Berlin. This meeting is the obligatory annual assembly of the de.NBI consortium. The meeting will simultaneously celebrate 5 years of de.NBI. Registration will open by the end of September.

### **Overview of upcoming de.NBI events**

Date	Event	City	Organizer
 20-22 May 2019	<a href="#">5th de.NBI Genomics training course</a>	Gießen	BiGi
 21 May 2019	<a href="#">Introduction to Version Control with Git &amp; GitHub</a>	Heidelberg	HD-HuB
 22 May 2019	<a href="#">Phylogenetic reconstruction course</a>	Kiel	Associated Partner Kiel
 22-24 May 2019	<a href="#">Computational genomics course for hands-on data analysis</a>	Berlin	RBC
 23-24 May 2019	<a href="#">DNA Methylation: Design to Discovery 2019</a>	Saarbrücken	HD-HuB
 27-29 May 2019	<a href="#">12th Annual International Conference on Systems Biology of Human Disease - SBHD 2019</a>	Berlin	HD-HuB
 27-29 May 2019	<a href="#">Single cell RNA-seq data analysis with R</a>	Espoo	HD-HuB
 11-12 Jun 2019	<a href="#">RNA-seq workshop for beginners: from sequences to visualization using Galaxy</a>	Freiburg	RBC
 13 Jun 2019	<a href="#">The Linux Command Line: From Basic Commands to Shell Scripting</a>	Hamburg	Training Partner UKE

Date	Event	City	Organizer
 17-21 Jun 2019	<a href="#">Applied Metaproteomics Workshop 2019</a>	Magdeburg	BiGi
 23-29 Jun 2019	<a href="#">dais Learnathon 2019</a>	Dresden	CIBI/DAIS
 03 Jul 2019	19. CCU Meeting	Bremen	CAU/BioData
 01-06 Jul 2019	<a href="#">Galaxy Community Conference 2019 – GCC2019</a>	Freiburg	RBC
 15-19 Jul 2019	<a href="#">Combine 2019 Conference</a>	Heidelberg	de.NBI-SysBio
 16 Jul 2019	<a href="#">An Introduction to ChIP-seq Data Analysis</a>	Hamburg	Training Partner UKE
 21-26 Jul 2019	<a href="#">CSAMA 2019 - Statistical Data Analysis for Genome-Scale Biology</a>	Bressanone/Brixen	HD-HuB
 02-06 Sep 2019	<a href="#">de.NBI Summer School 2019 - (Bio)Data Science</a>	Gatersleben	GCBN et al.
 03-05 Sep 2019	<a href="#">2nd de.NBI Cloud User Meeting</a>	Heidelberg	all cloud locations/CAU
 16 Sep 2019	<a href="#">Combining Workflows, Tools and Data Management - GCB 2019</a>	Heidelberg	de.NBI-SysBio
 16 Sep 2019	<a href="#">SeqAn3 – a modern C++ library for efficient sequence analysis - GCB 2019</a>	Heidelberg	CIBI
 16 Sep 2019	<a href="#">Getting started with the de.NBI Cloud - GCB 2019</a>	Heidelberg	BiGi
 18 Sep 2019	<a href="#">Introduction to genome-wide association studies (GWAS) 2019</a>	Kiel	Ass. Partner Kiel
 19 Sep 2019	<a href="#">Eukaryote genome annotation workshop 2019</a>	Kiel	Ass. Partner Kiel
 23-24 Sep 2019	<a href="#">Protein Structure Fundamentals: Searching – Analyzing – Modeling</a>	Hamburg	BioData
 23-27 Sep 2019	<a href="#">8th Galaxy workshop on HTS data analysis</a>	Freiburg	RBC
 22 Oct 2019	20. CCU Meeting	Bielefeld	CAU/BiGi
 23-24 Oct 2019	<a href="#">Introduction to BRENDA and EnzymeStructures</a>	Braunschweig	BioData

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

## IMPRESSUM

### RESPONSIBLE FOR CONTENTS

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### SUBSCRIPTION

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