Issue 3/19

de.NBI Quarterly Newsletter

This de.NBI Quarterly Newsletter in August informs about events in the next three months in the project

German Network for Bioinformatics Infrastructure – de.NBI.

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

CONTENT:

FOUNDATION OF THE BIELEFELD INSTITUTE FOR BIOINFORMATICS INFRASTRUCTURE (BIBI)

As an essential step in the process to obtain a sustainable solution for the German Network for Bioinformatics Infrastructure (de.NBI), the Faculty of Technology of Bielefeld University founded the Bielefeld Institute for Bioinformatics Infrastructure (BIBI). Besides the two administration offices for the de.NBI network and the German ELIXIR node, respectively, the BIBI Institute harbors sections for a bioinformatics cloud, for microbial bioinformatics and for the Graduate School "Digital Infrastructure for the Life Sciences". The section "Bioinformatics Cloud" offers compute support for the analysis of big data generated in life science experiments. In the section "Microbial Bioinformatics", tools for genome and metagenome analyses will be developed. Finally, the Graduate School will help to educate data scientists.

The BIBI institute was officially founded 1 July 2019 with the publication of the administrative and user regulations (VBO). A festive event on 31 July 2019 celebrated the foundation in the presence of the prorector of Bielefeld University Prof Dr M. Egelhaaf and the dean of the Faculty of Technology, Prof Dr M. Nebel, who welcomed the start of the Bielefeld Institute for Bioinformatics Infrastructure as a new chance for the advancement of bioinformatics. The BiBi has already 30 members..

The institute is provisionally headed by Jens Stoye. In future, a newly appointed professor for "Service Science in the Life Sciences" will lead the institute. The appointment procedure is underway and it is expected that the new professor will join the Faculty of Technology of Bielefeld University during the winter term.

Further information at https://www.uni-bielefeld.de/fakultaeten/technische-fakultaet/bibi/
and the press releaseat https://ekvv.uni-bielefeld.de/blog/uninews/entry/a_center_for_big_data

GRADUATE SCHOOL "DIGITAL INFRASTRUCTURE FOR THE LIFE SCIENCES"

An important goal of the new Bielefeld Institute for Bioinformatics Infrastructure, in cooperation with researchers from the Cologne Information Centre for Life Sciences ZB MED, is to establish the new research profile "Service Science in the Life Sciences" on an international level. To set up a critical mass of research activities for successfully initiating and accomplishing new, bilateral projects, young researchers are important. The institute includes the graduate school "Digital Infrastructure for the Life Sciences" (DILS) with a focus on the development and advancement of bioinformatics methods and services. For starters Bielefeld University provides funding for four PhD positions for three years commencing October 2019 (application deadline was end of July) and further Bielefeld or ZB MED students are welcome to apply for affiliation. The faculty is jointly composed of ten professors from Bielefeld University and three from ZB MED ensuring co-supervision of the projects from both sides. Besides a broad research program with common focus, the graduate school offers a qualification program including dedicated courses, workshops, retreats, etc.

Spokesperson: Prof. Dr. Jens Stoye | Vice spokesperson: Prof. Dr. Andrea Bräutigam | Coordinator: Dr. Roland Wittler
Find more information at: https://www.uni-bielefeld.de/fakultaeten/technische-fakultaet/bibi/graduate-school-digital-i/

NEW CO-LEAD OF THE ELIXIR PLANT COMMUNITY


Photo: A. Junker

Astrid Junker, head of the Acclimation Dynamics and Phenotyping research group at IPK Gatersleben, has been elected as one of the new co-leads of the ELIXIR Plant Sciences Community. Together with Kristina Gruden (ELIXIR Slovenia) and Cyril Pommier (ELIXIR France) Astrid Junker will work on FAIR implementations for plant data management, in particular phenotypic data. The Plant Sciences Community of ELIXIR aims to establish a technical infrastructure to allow plant genotype-phenotype analysis, based on the widest available public datasets. By making data interoperable, in accordance with the FAIR principles, plant genotypic and phenotypic data will be easier to find, integrate and analyse. The most important standards are MIAPPE, which provides a minimum information standard for plant phenotyping, the Crop Ontology, a common framework for describing phenotyping variables, and the Breeding API (BrAPI). The Plant Sciences Community has been involved in a number of short-term, technical projects called Implementation Studies. The current study ELIXIR Germany is involved in is entitled “FONDUE - FAIR-ification of Plant Genotyping Data and its linking to Phenotyping using ELIXIR Platforms”. It will ensure an interoperable link with the phenotypic data that is stored in distributed institutional repositories which is crucial for excelerated crop breeding.

More information at https://elixir-europe.org/communities/plant-sciences

FIRST EXTERNAL DE.NBI TRAINING PARTNER @ UNIVERSITY MEDICAL CENTER HAMBURG-EPPENDORF

The Central Coordination Unit of de.NBI approved the application by Malik Alawi to become associated to the network as an external training partner. Malik Alawi is head of the Bioinformatics Core Facility at University Medical Center Hamburg-Eppendorf since 2011. He is mainly involved in the analysis of high-throughput sequencing data and the development of bioinformatic workflows and tools. He also conducts training in bioinformatics. Malik Alawi and his working group will contribute to the de.NBI training program especially by offering introductory courses on high-throughput sequencing data analysis and the Linux operating system. The first two courses already took place in Hamburg in June and July 2019.

THIRD DAIS LEARNATHON 2019 AT CSBD


Photo: CSBD

The third de.NBI “Learnathon” of DAIS (Dresden Analysis-of-Images Suite) choose the hottest June ever measured in Dresden to take part at theCSBD. From 24-28 June, the hands-on course introduced 32 participants from 10 countries to developing within and for the **Fiji**, **ImageJ2**, and **KNIME** ecosystems. These open-source software applications can advance bioimage analysis for scientific projects. The attendees learned about the core libraries and concepts behind these analysis tools, the software engineering infrastructure commonly used, and how the existing community collaborates and communicates. During “hack-time” the attendees brought in their own ideas and/or solved their problems with the help of experienced leaders in the field.
Integrating newcomers into the existing community and presenting the synergetic exchange within the group was another declared goal of the meeting. A hot summer night out in Dresden's famous nightlife quarter added to this aspect of the agenda. “The Learnathon is a great place for beginners and experts to get together, learn and exchange ideas. Also learning how to contribute back to the community.”

The DAIS Learnathon series was first launched in 2017. Since then, it is repeated in annual intervals. We are already looking forward to hosting the fourth edition in 2020, maybe at slightly more moderate temperatures.

Find the review at: http://www.csbdresden.de/news-events/news/article/2019/07/03/not-too-hot-to-code/

2ND de.NBI CLOUD USER MEETING

CLOUD
USER
MEETING²
HEIDELBERG

The de.NBI Cloud User Meeting program is finalized. Join us in Heidelberg on September 3-5, 2019 and learn about current de.NBI Cloud projects and participate in multiple hands-on sessions.

This year, multiple large scale services will be presented such as Usegalaxy.eu (Björn Grüning) and SILVAngs (Alan Beccati). Usegalaxy.eu offers an easy-to-use-service for running bioinformatic tools and pipelines whereas SILVAngs is a data analysis service for ribosomal RNA gene (rDNA) amplicon reads from high-throughput sequencing. Both applications are using the power of the de.NBI Cloud to offer services to researchers not only in Germany.

Further talks are about systems medicine of the liver (Matthias König), big data analytics with Nextflow & nf-core (Alexander Peltzer), environmental microbial bioinformatics (Johannes Werner), and automatic deployment and management of containerized applications for scientific service groups (Jens Preussner). Based on the services and tools that are already running in the de.NBI Cloud, workshops will train users to develop or extend their own services and tools to the cloud computing environment in de.NBI Cloud.

Workshops:
- Kubernetes
- OpenStack Introduction
- Extensible Cluster Setup in the Cloud with BibiGrid and Ansible
- Using, building and exploring (bio)containers
- Getting Started with Nextflow & nf-core
- Virtual cluster deployment with Terraform

We invite researchers and developers with or without background and experience in cloud computing!
The registration is open until 23rd August 2019

More information and registration at: https://cloud.denbi.de/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 respective publications:

- **Vienna RNA package 2.4.13 -** Global und local RNA structural prediction with soft constraints. 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 2.4.13 from 31 May 2019. Link to the service: https://www.denbi.de/services/361-bioinformatics-leipzig-various-webservices-and-tools-for-transcriptomics

- **EggNOG v5.0:** A database of orthology relationships, functional annotation, and gene evolutionary histories. New Publication: *EggNOG 5.0: a hierarchical, functionally and phylogenetically annotated orthology resource based on 5090 organisms and 2502 viruses*, J. Huerta-Cepas et al., Nucleic Acids Res. 2019. https://doi.org/10.1093/nar/gky1085
  Find the service at: https://www.denbi.de/services/273-eggnog-database-of-nested-orthologous-gene-groups-nogs

- **SILVAngs** is now running in the de.NBI Cloud. A 400 CPU cluster has been set up and is providing valuable compute power for your analysis projects https://www.denbi.de/services/344-silvangs-a-data-analysis-service-for-ribosomal-rna-gene-rdna-amplicon-reads-from-high-throughput-sequencing-next-generation-sequencing-ngs-approaches

- **Galaxy Genome Annotation project (GAA)** is focused on supporting genome annotation inside Galaxy. It consists of several teams, projects, and tool suites that are working closely together to deliver a comprehensive, scalable and easy to use Genome Annotation experience. This blog post will highlight a few of the recent developments and the new Genome Annotation subsection of the European Galaxy server.
  Find the service at : https://galaxy-genome-annotation.github.io
  Find the blog at: https://galaxyproject.eu/posts/2019/08/05/gga/

Publications
- **SIG 6 de.NBI Cloud:** *de.NBI Cloud federation through ELIXIR AAI*, Belmann P, Fischer B, Krüger J et al.. F1000Research 2019, 8:842; https://doi.org/10.12688/f1000research.19013.1

de.NBI @ CONFERENCES

de.NBI partners and CAU members have been present on a variety of conferences

ELIXIR All Hands meeting 2019

The 5th ELIXIR All Hands meeting took place 17-20 June 2019 in Lisbon. This meeting again brought together members of the European ELIXIR community from across the national ELIXIR Nodes and collaborators from partner organisations to review ELIXIR's achievements and to discuss plans for the future. The plenary session provided lectures about the scientific work of the ELIXIR Platforms and newly founded ELIXIR Communities. About 30 workshops focussed on specific topics relevant for the ELIXIR community, complemented by a poster session with almost 100 contributions from the ELIXIR Nodes. Numerous de.NBI members participated in the various formats of the conference: The de.NBI Administration Office presented the de.NBI Industry Forum in ELIXIR's Industry engagement workshop; Björn Grüning and Bérénice Batut (RBC Freiburg) talked about the Galaxy Community Project. Posters were presented by IPK Gatersleben ("Digital resources for plant genomics and phenomics at ELIXIR-Germany partner IPK Gatersleben") and by de.NBI SIG 3 – Training ("The de.NBI / ELIXIR-DE Training Network"). The 6th ELIXIR All Hands meeting will take place 2020 in Amsterdam.

Slides and posters are available on the ELIXIR F1000R channel: https://f1000research.com/gateways/elixir

Galaxy Community Conference (GCC 2019)

The Galaxy Community Conference (GCC) is the annual gathering of users as well as developers of the Galaxy computational platform. This year's GCC took place in Freiburg from 1-8 July 2019 covering data-intensive research and supporting compute infrastructure Galaxy. 65 talks, 39 training modules, 14 demos, 54 Posters, and other networking opportunities brought together users and developers. With around 230 participants this GCC has been the largest so far. The de.NBI network was present with a booth to increase its visibility by offering direct contact to the network's service, training and cloud capabilities. The Galaxy project is supported by de.NBI in multiple ways. Next to the support of GCC, de.NBI enables the European Galaxy Server Galaxy.eu, which is run by the de.NBI Cloud infrastructure. Furthermore, the development of the Galaxy RNA Workbench 2.0 was also supported by de.NBI, to further improve the transcriptomic analysis pipeline.

A summary with full program and conference book can be found at: https://galaxyproject.eu/posts/2019/08/06/gcc/

ISMB/ECCB 2019

The 27th Conference on Intelligent Systems for Molecular Biology (ISMB) and the 18th European Conference on Computational Biology (ECCB) took place in Basel 21-25 July 2019. It is the largest meeting of scientists working in computational biology in Europe and provides an intense multidisciplinary forum for disseminating the latest developments in computational tools for data driven biological research. The de.NBI Administration Office presented the de.NBI training program, the network's activities, the de.NBI Cloud and ELIXIR Germany on its poster. Furthermore, de.NBI member Björn Grüning (RBC) offered a workshop on "Tools for reproducible research". In addition, several de.NBI members gave lectures, e.g. Nikolaus Rajewsky (MDC Berlin/RBC) opened the conference with the Welcome & Opening Keynote "Principles of gene regulation in space and time by single-cell analyses". Other de.NBI members were active in or even lead COSIs (Communities Of Special Interest), like Oliver Kohlbacher (CIBI) – CompMS COSI, Alexander Sczyrba (BiGi) – Microbiome COSI, Rolf Backofen und Uwe Ohler (RBC) – RNA COSI. In the frame of the BOSC (Bioinformatics Open Source Conference) Malvika Sharan (HD-HuB) contributed a talk on "Inclusiveness in Open Science Communities"

The complete programme is available at: https://www.iscb.org/ismbeccb2019

COMBINE 2019, Heidelberg, 15-19 July 2019

The tenth annual COMBINE forum was organized by Martin Golebiewski, Wolfgang Müller and Dagmar Waltemath at HITS in Heidelberg (Germany) from 15 to 19 July 2019.
More than 100 guests from around the globe celebrated the anniversary and exchanged their ideas, approaches and implementations for improved data and modelling standards in the life sciences. The Keynote Talks on "Computational Physiology and the Physiome Project" (Peter Hunter), "Implementing Open Science in publishing" (Thomas Lemberger), "Modeling projects across platforms - the reality and how reality should be" (Ursula Kummer) and "Let's go on a FAIR asset management safari" (Carole Goble) opened the conference. A dedicated de.NBI session featured lectures by Judith Wodke, HU Berlin, "How (not) to Apply (COMBINE) Standards in Agent-Based Modeling", Matthias König, HU Berlin, "Computational modeling of liver function tests - Stratification and individualization based on semantic annotations of models and data", and Heidi Seibold, LMU München, "Research software engineers and their role for open and reproducible research". The complete interesting abstract book is available online.

Further information is available at: http://co.mbine.org/events/COMBINE_2019

de.NBI supported conferences in the next time

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 five tutorials:

- de.NBI showcase: Combining Workflows, Tools and Data Management (W. Müller, de.NBI-SysBio, HITS and partners)
- SeqAn3 – a modern C++ library for efficient sequence analysis (R. Rahn, CIBI, Berlin)
- Getting started with the de.NBI Cloud (A. Sczyrba, BiGi, Bielefeld)
- Proteomics and metabolomics with OpenMS and pyOpenMS (T. Sachsenberg, CIBI, Tübingen)
- Integrating computational meta-omics for microbiome research (D. Benndorf, BiGi, Magdeburg, T. Muth, Robert Koch Institute)

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

ICRC 2019 – International CeBiTec Research Conference, Bielefeld, 23-25 September 2019

The 2019 International CeBiTec Research Conference "*Advances in Industrial Biotechnology*" focuses on "*Renewable feedstocks and synthetic pathways for production of fine chemicals*". The major topics to be addressed are:

- Aroma Biotechnology
- Synthetic pathways
- Podium discussion on white biotechnology
- Alternative Feedstocks
- C1 Utilization

The conference will promote scientific excellence in microbial biotechnology by providing leading scientists and young researchers with a platform to present their work, to discuss current scientific understanding along with recent developments in key areas of industrial biotechnology, and to identify the priorities for further research.

General information and registration at: https://www.cebitec.uni-bielefeld.de/events/conferences/555-2019-09-23-9th-int-cebitec-research-conference-bielefeld

CytoData 2019 – 4th CytoData Symposium and Hackathon, Heidelberg, 28-30 October 2019

CytoData brings together the community of researchers mining microscopy image data at the DKFZ in Heidelberg. The CytoData Society (CytoDS) was recently formed to build and maintain an active community around image-based profiling of biological phenotypes induced by genetic, chemical or other perturbations of biological systems. The conferencen will be a great venue to connect with this community, exchange ideas, and learn from experts in the field. General information and registration at: https://cytodata.org/

de.NBI WORKSHOPS @ CONFERENCES IN AUTUMN 2019

de.NBI partners will teach a variety of workshops at conferences in the next months:

- **64. GMDS-Jahrestagung 2019, Deutsche Gesellschaft für Medizinische Informatik, Biometrie und Epidemiologie GMDS e.V., Dortmund, 8-11 September 2019**
  - NGS data analysis with Galaxy for clinical applications; A. Bagnacani, M. Wolfien (RBC)
- **20. International Conference on Systems Biology, ICSB 2019, Okinawa, Japan, 1-5 November 2019**
  - COMBINE & de.NBI Tutorial: Modelling and Simulation Tools in Systems Biology; A. Weidemann, M. Golebiewski, F. Bergmann, J. Pahle, S. Sahle (de.NBI-SysBio) and international partners.
  - Advanced modeling with COPASI; S. Sahle, F. Bergmann, Ursula Kummer, J. Pahle (de.NBI-SysBio/de.NBI-ModSim) and international partners.
- **Lipidomics Forum 2019, Borstel, 10-12 November 2019**
  - Lipidomics MS Data processing, identification & quantification - What is it and how much? J. Miranda Ackermann, N. Hoffmann (BioInfra.Prot)
  - Statistical analysis & qualitative and quantitative comparison of lipidomics data - How do I compare? Fancy graphics & convincing plots; F. al Machot, N. Hoffmann (BioInfra.Prot)

UPCOMING EVENTS

The calendar lists the de.NBI training courses and events scheduled in the next months. All courses 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

- **1st de.NBI Industrial Forum, 26 November 2019, Berlin.** This is the kick-off event of the de.NBI Industrial Forum. An ideal place for community building, networking, learning from each other and to discuss mutual needs in bioinformatics between academia and industry. Registration will open soon.
- **de.NBI SAB Meeting and Plenary Meeting 2020, 13-14 February 2020, 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
02-06 Sep 2019	de.NBI Summer School 2019 - (Bio)Data Science	Gatersleben	GCBN et al.
03-05 Sep 2019	2nd de.NBI Cloud User Meeting	Heidelberg	all cloud locations/CAU
09-13 Sep 2019	Dresden Deep Learning Hackathon	Dresden	CIBI/DAIS
16 Sep 2019	Combining Workflows, Tools and Data Management - GCB 2019	Heidelberg	de.NBI-SysBio
16 Sep 2019	SeqAn3 – a modern C++ library for efficient sequence analysis - GCB 2019	Heidelberg	CIBI
16 Sep 2019	Getting started with the de.NBI Cloud - GCB 2019	Heidelberg	BiGi
16 Sep 2019	Integrating computational meta-omics for microbiome research - GCB 2019	Heidelberg	BiGi
18 Sep 2019	Introduction to genome-wide association studies (GWAS) 2019	Kiel	Ass. Partner Kiel
19 Sep 2019	Eukaryote genome annotation workshop 2019	Kiel	Ass. Partner Kiel
19-20 Sep 2019	Microscopy Image Analysis Course 2019	Heidelberg	HD-HuB
23-24 Sep 2019	Protein Structure Fundamentals: Searching – Analyzing – Modeling	Hamburg	BioData
23-27 Sep 2019	8th Galaxy workshop on HTS data analysis	Freiburg	RBC
25-27 Sep 2019	de.NBI - CeBiTec Nanopore Best Practice Workshop 2019	Bielefeld	BiGi, GCBN
9-11 Oct 2019	4th de.NBI Training Course on Metagenome Analysis	Bielefeld	BiGi

Date	Event	City	Organizer
10-12 Oct 2019	Software Carpentry Workshop	Heidelberg	HD-HuB
22 Oct 2019	20. CCU Meeting	Bielefeld	CAU/BiGi
23-24 Oct 2019	Introduction to BRENDA and EnzymeStructures	Braunschweig	BioData
31 Oct 2019	COMBINE & de.NBI Tutorial: Modelling and Simulation Tools in Systems Biology – ICSB 2019	Okinawa	de.NBI-SysBio
10 Nov 2019	Lipidomics MS Data processing, identification & quantification - Lipidomics Forum 2019	Borstel	BioInfra.Prot/ LIFS
10 Nov 2019	Statistical analysis & qualitative and quantitative comparison of lipidomics data - Lipidomics Forum 2019	Borstel	BioInfra.Prot/ LIFS
18 Nov 2019	4th Differential analysis of quantitative proteomics data using R	Bochum	BioInfra.Prot
19 Nov 2019	Advanced analysis of quantitative proteomics data using R	Bochum	BioInfra.Prot
26 Nov 2019	de.NBI Industrial Forum	Berlin	CAU

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

IMPRESSUM

RESPONSIBLE FOR CONTENTS
A. Pühler, A. Tauch, T. Dammann-Kalinowski
de.NBI - German Network for Bioinformatics Infrastructure
c/o Center for Biotechnology (CeBiTec)
Bielefeld University
33594 Bielefeld
Germany

Phone: +49-(0)521-106-8750
Fax: +49-(0)521-106-89046
email: puehler@cebitec.uni-bielefeld.de
web: http://www.denbi.de
email: contact@denbi.de
twitter: #denbi, @denbiOffice

For questions and remarks please contact contact@denbi.de
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