GERMAN NETWORK FOR BIOINFORMATICS INFRASTRUCTURE

de.NBI Quarterly Newsletter

EDITION MAY 2016

1) EDITORIAL

In the first year of funding of the German Network for Bioinformatics Infrastructure (de.NBI) all members of the consortium have established with great enthusiasm a very broad spectrum of excellent bioinformatics services and training courses that are increasingly used and attended by experimental research groups. In the near future, the de.NBI staff has to deal with additional exciting challenges, for instance the integration of de.NBI partner projects and the integration of de.NBI into ELIXIR.
To close thematic gaps in the bioinformatics services provided by the de.NBI consortium, the Federal Ministry of Education and Research (BMBF) published an additional call for proposals, named de.NBI partner projects, in November 2015. Eight excellent proposals for de.NBI partner projects, out of 39 submitted proposals, were selected by an international reviewer panel in March. The start of de.NBI partner projects is scheduled for November 2016. With this thematic extension, the de.NBI network is now the pre-eminent service provider in bioinformatics in Germany.

The current investment of more than 25 Million Euro into de.NBI has created a network which can function not only as a service provider in Germany. de.NBI now has the chance to collaborate on the international level by becoming a part of the ELIXIR program in Europe. Certain administrative and personnel requirements for the integration of de.NBI into the ELIXIR program are currently in the process of decision to ensure that Germany will become an excellent bioinformatics partner on the European level. de.NBI is the designated German ELIXIR node and, in this way, German bioinformaticians can in future contribute to and participate in the development of innovative technologies and international bioinformatics standards.

Another challenge for bioinformatics infrastructure and thus for the de.NBI consortium is to ensure the storage and integrative analysis of continuously increasing amounts of data in life sciences. Cloud solutions such as the Applied & Translational Genomics Cloud (ATGC) have been discussed recently during a workshop in Heidelberg that was initiated by Prof. Roland Eils and his team. This is another interesting topic selected by the de.NBI Administration Office for this Quarterly Newsletter. I hope you enjoy reading this new edition of the newsletter.

Yvonne Pfeiffenschneider

Yvonne Pfeiffenschneider
(Project Management Jülich)

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2) de.NBI PARTNER PROJECTS

The de.NBI consortium is currently composed of 23 academic and industrial partners from all over Germany that are organized in eight service centers according to their thematic priorities in bioinformatics services and training. The Project Management Jülich (PtJ) is processing an additional call for proposals by the Federal Ministry of Education and Research (BMBF), named de.NBI partner projects, to expand the current network. Eight proposals for de.NBI partner projects, out of 39 submitted applications, were selected by an international reviewer panel in March 2016 to provide bioinformatics services in areas of life science research that are not yet covered by de.NBI activities, for instance bioimaging, epigenetics, and lipidomics. The official start of the selected de.NBI partner projects is scheduled for November 2016. With this thematic extension, the de.NBI network will provide not only new services but also an extended repertoire of training courses in 2017.

3) de.NBI AND ELIXIR COLLABORATION

The international collaboration between de.NBI and the European ELIXIR initiative has been continued very successfully during the last three months. The RNA Bioinformatics Center (RBC) and the Heidelberg Center for Human Bioinformatics (HD-HuB) organized in April 2016 the first joint Galaxy DevOps workshop with the ELIXIR project to train people in deployment strategies of Galaxy and Galaxy tools. Bioinformaticians learned the internals of the multi-omics Galaxy workbench, how to set up and run a Galaxy server and how to develop Galaxy tools to perform reproducible and accessible research.

At the strategic level, an official meeting with representatives from BMBF, ELIXIR and de.NBI was held in Berlin in March 2016 to negotiate the requirements for a full German membership in ELIXIR. de.NBI now has the chance to become a part of the ELIXIR program in Europe as the German ELIXIR Node and to participate in the development of innovative technologies and international bioinformatics standards. Administrative, legal and personnel requirements for the integration of de.NBI into the ELIXIR program are currently in the process of decision.

4) ELIXIR ALL HANDS MEETING 2016

The ELIXIR All Hands Meeting 2016 took place in Barcelona 7-9 March 2016. As part of the de.NBI-ELIXIR collaboration Matthias Lange (IPK Gatersleben, GCBN) and Renzo Kottmann (MPI Bremen, Database Node) attended as de.NBI representatives. The meeting attended by 220 participants from all 17 ELIXIR partner countries featured strategic developments in the consortium and breakout sessions on EXCELERATE work packages.

Keynote lectures informed on “The human genome phenome archive (EGA)” as a distributed data repository for human data. The focus was on the compatibility of this API accessible resource with data security considerations for person-related data. In a second keynote lecture the NIH presented strategies and implementation of the “Big data 2

Attendants of ELIXIR All Hands Meeting in Barcelona, Spain (Photo kindly provided by Premysl Velek, ELIXIR Communications and Community Outreach Officer) knowledge initiative”. This initiative has strong conceptional overlaps with the program of ELIXIR. Of special interest was a presented concept for long term financing of services via a credit system. A third keynote lecture on the Malaspina 2010 Expedition provided insights into diversity and genomics of marine microorganism and featured the feasibility of such big data projects on environmental analysis with the help of good informatics infrastructures.

Presentations of the EXCELERATE work packages. The “marine metagenomics” package focuses on homogenizing workflows and building of marine specific reference databases. The central challenge of the WP “plants is the accessibility of the existing heterogeneous and distributed data resources. First steps are taken in homogenization of meta data and data types, and unification of data set IDs. The WP “rare diseases” is based on the necessity of data integration in form of a portal based on the EGA. The ELIXIR panels of the core activities “tools and compute”, “training”, and “data and capacity building” reported on their advances and future developments.

Both de.NBI representatives emphasized their participation as an important and beneficial brick in the de.NBI - ELIXIR cooperation and the high value of information provided meeting in reference to standards, communication infrastructures and technologies.

5) LAUNCH OF THE NEW de.NBI LOGO

A visual identity has been created for de.NBI by the design agency LANGE+PFLANZ. The logotype is optimized for the use in web (RGB color space) as well as print media (CMYK). Additionally a de.NBI style guide was compiled, which will be continuously extended by the agency. This document specifies the exact fonts and colors and defines the correct usage of the logo. The overall aim is to create a coherent de.NBI look for all future products (e.g. web layout, flyer, posters).

All versions of the logo as well as the style guide can be downloaded from the de.NBI ownCloud online archive. The de.NBI office will be happy to answer any questions concerning the de.NBI design. The agency LANGE+PFLANZ is currently engaged in creating material for public relation activities. Working on these products will provide supplemental decorative and visual elements that will be embedded into a new website layout. Furthermore, the SIG 1 is preparing suggestions and concepts for an improved web presence of the network.

6) CLOUD WORKSHOP

BY C. LAWERENZ

The workshop “Towards Cloud Solutions For Life Sciences And Translational Medicine” was held 21-22 April 2016 at Heidelberg University. The workshop had been initiated in the context of de.NBI and the Applied & Translational Genomics Cloud (ATGC). ATGC is a cloud initiative for high-throughput data in life sciences in Germany. The event provided a platform for discussing comprehensive cloud solutions for computing and storage of various data types. 34 international experts from science and industry presented their state-of-the-art solutions. The workshop was already of great interest in advance. However, the number of participants had to be limited to 130 due to the capacity of the venue.

At the beginning of the meeting overviews of ATGC, the Heidelberg Next Generation Sequencing (NGS) approaches in science and personalized medicine, as well as the de.NBI network were presented. Here the basic requirements were derived for appropriate cloud approaches with respect to big data in the field of omics; with a special focus on the sensitivity of human genomic data. The crucial aspects for data protection within the scope of cloud storage, processing and access were presented in the


A brief impression of the Cloud workshop

following talks on applied ethics and law. Already existing solutions for storage and processing in cloud environments were introduced by the national and international academic speakers. The industry delegates focused on available professional cloud applications already deployed and proven to work elsewhere and, remarkably, not on high polished promises of solutions in some unknown future. There were presentations about the cloud approaches developed by, e.g., T-Systems, IBM, Hewlett Packard Enterprise, Intel, EMC, SAP, and Oracle - to name some prominent companies. The chosen organizations took the European conditions and regulations into account, thereby enabling discussions about further possibilities for cooperation. A joined de.NBI and industry workshop was announced to continue these discussions and foster the cooperation in the future.

The prominent ELIXIR cloud solutions were presented in seven talks by our European partners from France, Spain, UK, Finland, Sweden and Norway. The get-together on the first evening and breaks between the workshop sessions enabled all participants, especially the de.NBI members, to get in close contact with the ELIXIR cloud providers and benefit from the experience already gained by the ELIXIR network. As an outcome of the workshop regular video conferences are planned to continue exchanging and sharing ideas and experiences and to synchronize the ELIXIR and de.NBI cloud activities to the benefit of the projects.

The workshop was well received by all participants independent of their affiliation in academia or industry and gave deeper insights into the challenges faced in the field of life science today as well as the solutions already applied. It provided everyone with ideas to solve the issues at hand and possible partners. More details about the workshop can be found online at http://www.applied-translational-genomics-cloud.de/joomla/index.php/en/workshop.

7) REVIEW OF THE SeqAn USER MEETING

From 30 March - 1 April 2016, 32 participants took part in the SeqAn User Meeting at the Institute for Computer Science in Berlin. The training course was organized by the team of Knut Reinert, a member of the de.NBI service unit "Center for Integrative Bioinformatics (CIBI)". The SeqAn User Meeting was aimed at mainly two groups of bioinformaticians: tool developers and end users of sequencing related problems. Both groups of participants were split into small learning groups. Guided tutorials for tool developers and programmers were offered to get programmers acquainted with the programming paradigms as well as the content and the structure of the SeqAn template library. For end users, courses in selected SeqAn applications (e.g. Yara or Lambda), talks by research groups using SeqAn and tutorials of workflow integration into KNIME were presented.

8) THE 11TH CEBITEC SYMPOSIUM WITH de.NBI MINISYMPOSIUM

The Center for Biotechnology at Bielefeld University is organizing the **11th CeBiTec Symposium** “Microbial Genomics and Metagenomics in Human Health and Disease”, which will be held at the Center for Interdisciplinary Research (ZiF) of **Bielefeld University** from **4-6 July 2016**. The conference highlights the impact of the genomics revolution on medical microbiology.

The de.NBI contribution consists of **the minisymposium “Bioinformatics for Metagenome Analysis”** scheduled for **6 July 2016.** It features two sessions, chaired by P. Bork and A. Sczyrba, dealing with **bioinformatics tools for analyzing metagenome sequences** and **human microbiomes in health and disease**. Members of the de.NBI


de.NBI
CeBiTec
11th CeBiTec Symposium
July, 4 - 6 2016
Microbial Genomics and Metagenomics in Human Health and Disease
including the de.NBI mini symposium Bioinformatics for Metagenome Analysis
at the Center for Interdisciplinary Research of Bielefeld University

CONFIRMED SPEAKERS:
Mark Achtman (Warwick/UK)
Peer Bork (Heidelberg/DE)
Carmen Buchrieser (Paris/FR)
Ulrich Dobrindt (Münster/DE)
Marc-Emmanuel Dumas (London/UK)
Edward Feil (Bath/UK)
Jörg Hacker (Halle, Saale/DE)
Dirk Haller (München/DE)
Dag Harmsen (Münster/DE)
Jay C.D. Hinton (Liverpool/UK)
Alexander Mellmann (Münster/DE)
Björn Nielsen (Lyngby/DK)
Ulrich Nübel (Braunschweig/DE)
Jörg Overmann (Braunschweig/DE)
Alexander Sczyrba (Bielefeld/DE)
Jörg Vogel (Würzburg/DE)
Georg Zeller (Heidelberg/DE)
http://www.cebitec.uni-bielefeld.de

Topics

- **genomics of major bacterial pathogens**
- **microbial population genetics and genomic nomenclature**
- **host-pathogen interactions as assessed by transcriptomics approaches**
- **epidemiology and surveillance of pathogenic microorganisms**
- **novel sequencing techniques as a tool in human medicine**
- **bioinformatics tools for analyzing metagenome sequences**
- **human microbiomes in health and disease**

network will receive a discount on the registration fee for the 11th CeBiTec Symposium.

Furthermore, two Distinguished Lectures will be included into the Symposium: **J. Hacker**, president of the Leopoldina, Halle, will focus on **“Antibiotics and Antibiotic resistances: Scientific and Social Implications”** and **P. Bork**, EMBL Heidelberg, will give a lecture on **“My Gut Microbes and Me: A Long-Term yet Fragile Relationship”**. Both lectures are without doubt highlights of the symposium and should not be missed. For more details and registration please see: http://www.cebitec.uni-bielefeld.de/events/

9) UPCOMING EVENTS

The calendar of upcoming events lists quite a number of events scheduled for the next six months. All offers are accessible via the de.NBI homepage http://www.denbi.de. The de.NBI training programme is continuously updated on our homepage.

MAJOR DE.NBI EVENTS - SAVE THE DATES

➢ **de.NBI Symposium “Bioinformatics in Human Health an Disease” (7-9 November 2016), Heidelberg.** Lead by HD-HuB the de.NBI Symposium 2016 focused on human bioinformatics is open for the public and de.NBI members.

➢ **2nd SAB meeting including Workshop and Plenary Meeting, (28-29 November 2016), Berlin.** This internal de.NBI Meeting for all de.NBI members will take place at the Seminaris Campus Hotel, Berlin.

de.NBI TRAINING COURSES

➢ **Kinetics on the move: practical workshop on data and tools for quantitative modelling (30-31 May 2016), Heidelberg.** The NBI-SysBio team celebrates the 10th anniversary of SABIO-RK with talks and practical trainings relating to the publication, curation, retrieval, and usage of kinetic data in SABIO-RK. The goals of this workshop are using SABIO-RK to access and export structured reaction kinetics data and basic modeling with kinetic data, publishing, publishing data in a standard-ised and reusable manner as well as application of existing models with own data. http://www.denbi.de/index.php/22-training-cat/training-courses/105-move

➢ **Hackathon - KNIME & Image Processing (05-14 July 2016), Konstanz.** The CIBI crew will bring together KNIME experts and expert users working with KNIME Image Processing and ImageJ2. The course is addressed to attendees with a background in Java and KNIME and ImageJ development. http://www.denbi.de/index.php/22-training-cat/training-courses/125-knime3

➢ **CSAMA 2016 - Statistics and Computing in Genome Data Science (10-15 July 2016), Bressanone, Italy.** HD-HuB staff is engaged in a one-week intensive course on statistical and computational analysis of multi-omics studies in biology and biomedicine. The course covers theory and state of the art lectures and practical hands-on exercises based on the R / Bioconductor environment. Main topics are the primary analysis of high-throughput sequencing based assays in functional genomics and integrative methods including efficiently operating with genomic intervals, statistical testing, linear models, machine learning, bioinformatic annotation and visualization.
http://www.denbi.de/index.php/22-training-cat/training-courses/135-csama

➢ **Computational genomics approaches to precision medicine (12-23 September 2016), Berlin.** The RBC team at MDC offers a hands-on computational course covering fundamental topics in computational genomics and its applications in precision medicine. There will be theoretical lectures by international experts followed by practical sessions where students directly apply what they have learned. The programming will be mainly done in R and Unix. The course will be beneficial for first year computational biology PhD students and experimental biologists who want to begin data analysis or are seeking a better understanding of computational genomics and precision medicine. http://www.denbi.de/localmedia/flyer/2016/genprecmed_poster_version1_4.pdf

➢ **Software Carpentry Workshop (19-21 September 2016), Heidelberg.** This HD-HuB workshop will teach the key skills required to practise robust computational science effectively and efficiently, and provide an overview of some of the tools and resources available for modern computational biology. The topics covered include an introduction to scripting in Python and using the language for scientific applications and biological data handling. The effective use of the Unix command line and compute cluster job submission will be another subject. Besides version control with git and GitHub, the analysis pipeline management with SnakeMake will be covered. http://www.denbi.de/index.php/22-training-cat/training-courses/138-scw

➢ **2nd Galaxy Workshop on HTS data analysis (19-23 September 2016), Freiburg.** RBC offers a Galaxy workshop on High-Throughput-Sequencing (HTS) data analysis. The one week full-day hands-on workshop offers an introduction into Galaxy, RNA-seq data analysis, ChIP-seq data analysis, Exome-seq data analysis, and Methyl-seq data analysis. http://www.denbi.de/index.php/22-training-cat/training-courses/133-2nd-galaxy-workshop-on-hts-data-analysis

➢ **9th OpenMS User Meeting (21-23 September 2016), Tübingen.** CIBI welcomes participants to present the capabilities of OpenMS, and discuss user needs and future directions in mass spectrometry. An optional OpenMS tutorial session on the first day (Wednesday) precedes the general conference starting on Thursday, September 22. Participants can bring their own data, an OpenMS wish list, ideas for collaboration projects, or also give a talk on project. http://open-ms.sourceforge.net/um2016/

➢ **de.NBI Summer School 2016 - From Big Data to Big Insights (26-30 September 2016), Schloss Dagstuhl (Wadern).** This year's de.NBI Summer School featuring computational methods for the analysis and interpretation of mass-spectrometric high-throughput data is jointly organized by Bio-Infra.Prot, CIBI and BiGi. The de.NBI summer school aims at providing deeper insights into the details of existing algorithms or software systems in proteomics and metabolomics. Participants will use – instructed by international keynote and de.NBI speakers – existing tools to analyse and visualize real-world datasets (data specifically prepared for the tutorials as well as the participants' own data). Beyond that, the end users will be put into a position to be able to combine their own existing and future algorithms or tools with other solutions as well as to integrate them into a sustainable software system. To this end the summer school will also contain hackathons to quickly prototype novel tools. http://www.denbi.de/index.php/news/100-lss2016-2 or https://goo.gl/ZRgxuV

➢ **Differential analysis of proteomic data using R (21 November 2016), Bochum.** The BioInfra.Prot staff will impart knowledge about how to conduct a differential analysis of high-throughput data using R. Starting point is a basic introduction to the popular statistical programming language, no prior knowledge on R is required. The statistical background on utilized methods is explained in order to enable the participants to assess their own as well as published workflows critically. In this regard the course will touch upon statistical inference: hypotheses, type I and II error, location tests (t-test and ANOVA), and multiple testing. http://www.denbi.de/index.php/22-training-cat/training-courses/101-r

➢ **From Primer to Paper: Training in Biodiversity Analysis using NGS Amplicon Data (22-25 Nov 2016), Bremen.** The Database Node will introduce into the principles of marker-gene-based sequence analysis using NGS technologies. This training course explains all necessary steps researchers need to take when performing amplicon-based investigations using the rDNA as a marker gene. The course starts with experimental design, including an overview of relevant sequencing technologies, and the selection, design, and evaluation of primers for the amplification of rDNA. It teaches the importance of contextual data and standards for data analysis and integration. It provides examples and best practice solutions for data pre-processing and quality assurance up to the contextualized submission of the NGS data to public repositories. It finishes with a framework for statistical analysis of the data including a short LINUX and R crash course. http://www.denbi.de/index.php/22-training-cat/training-courses/120-p2p

OVERVIEW OF UPCOMING de.NBI EVENTS

	Date	Event	City	Organizer
➢	21-22 Apr 2016	**“Towards Cloud Solutions For Life Sciences And Translational Medicine” workshop**	Heidelberg	HD-HuB, DKFZ, EMBL, CAU
➢	30-31 May 2016	**Kinetics on the move: practical workshop on data and tools for quantitative modelling**	Heidelberg	NBI-SysBio
➢	01 July 2016	**Special CCU-Meeting with reviewers**	Braunschweig	CAU, DB Node
➢	4-6 Jul 2016	**“Microbial Genomics and Metagenomics in Human Health and Disease” 11. CeBiTec-Symposium including de.NBI Minisymposium “Bioinformatics for Metagenome Analysis”**	Bielefeld	CAU, BiGi,
➢	05-14 Jul 2016	**Hackathon - KNIME & Image Processing**	Konstanz	CIBI
➢	10-15 Jul 2016	**CSAMA 2016 - Statistics and Computing in Genome Data Science**	Bressanone/Brixen, IT	HD-HuB
➢	15 Jul 2016	**7th CCU-Meeting in Tübingen**	Tübingen	CAU, CIBI
➢	12-23 Sep 2016	**Computational genomics approaches to precision medicine**	Berlin	RBC, MDC
➢	21-23 Sep 2016	**9th OpenMS User Meeting**	Tübingen	CIBI
➢	19-21 Sep 2016	**Software Carpentry Workshop**	Heidelberg	HD-HuB
➢	19-23 Sep 2016	**2nd Galaxy Workshop on HTS data analysis**	Freiburg	RBC
➢	26-30 Sep 2016	**de.NBI Summer School 2016- From Big Data to Big Insights**	Schloss Dagstuhl (Wadern)	BioInfra.Prot, CIBI, BiGi
➢	18 Oct 2016	**8th CCU-Meeting in Gatersleben**	Gatersleben	CAU, GCBN
➢	7-9 Nov 2016	**de.NBI Symposium “Bioinformatics in Human Health and Disease**	Heidelberg	HD-HuB, CAU,
➢	21 Nov 2016	**Differential analysis of proteomic data using R**	Bochum	BioInfra.Prot
➢	22-25 Nov 2016	**From Primer to Paper: Training in Biodiversity Analysis using NGS Amplicon Data**	Bremen	Database Node
➢	28-29 Nov 2016	**2nd SAB meeting including workshop and plenary meeting**	Berlin	CAU

IMPRESSUM:

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