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THEME/TRACK: ELIXIR

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Poster number	EasyChair number	Author list	Presenting author	Title	Abstract	Theme/track	Topics
P_EI001	714	Joan Segura, Daniel Tabas Madrid, Ruben Sanchez-Garcia, Jesús Cuenca, Carlos Oscar Sánchez Sorzano, Ardan Patwardhan and Jose Maria Carazo	Joan Segura	3DBIONOTES: Unifying molecular biology information	With the advent of next generation sequencing methods, the amount of proteomic and genomic information is growing faster than ever. Several projects have been undertaken to annotate the genomes of most important organisms, including human. For example, the GENECODE project seeks to enhance all human genes including protein-coding loci with alternatively splices variants, non-coding loci and pseudogenes. Another example is the 1000 genomes, a repository of human genetic variations, including SNPs and structural variants, and their haplotype contexts. These projects feed most relevant biological databases as UNIPROT and ENSEMBL, extending the amount of available annotation for genes and proteins.Genomic and proteomic annotations are a valuable contribution in the study of protein and gene functions. However, structural information is an essential key for a deeper understanding of the molecular properties that allow proteins and genes to perform specific tasks. Therefore, depicting genomic and proteomic information over structural data would offer a very complete picture in order to understand how proteins and genes behave in the different cellular processes.In this work we present the second version of a web platform -3DBIONOTES- that aims to merge the different levels of molecular biology information, including genomics, proteomics and interactomics data into a unique graphical environment. Current development offers a unified view of three of the most relevant protein databases: UniProt, PDB, EMDB, and ENSEMBL onto which other sources of biological annotations are also provided, such as PhosphoSitePlus, Immune Epitope DB, BioMuta and dSysMap.	ELIXIR poster	ELIXIR
P_EI002	647	Chao Zhang, Sanne Abeln, Jochem Bijlard, Christine Staiger, Youri Hoogstrate, Alexander Senf, Saskia Hiltemann, David van Enckevort, Remond Fijneman, Jan-Willem Boiten, Gerrit Meijer, Dylan Spalding, Jaap Heringa, Susanna Repo, Niklas Blomberg, Andrew Stubbs, Jordi	Chao Zhang	A Systematic Solution to Map Processed Data in tranSMART to Raw Data in Multiple Repositories	With the evolving of high-throughput experimental techniques, large amounts of molecular profiling data are becoming available for regular clinical studies. These data need to be stored, processed, archived, distributed and, more importantly, linked. In ELIXIR pilot project, we focus on connecting the archival storage of such data, with databases that store the processed data and visualised workflow systems that manage the computational pipelines. After perusing the processed data, users often come back to the raw data not only to reconfirm the data processing but also to further explore the raw data in workflow systems like Galaxy. In the Translational Research IT (TraIT) project of Center for Translational Molecular Medicine, raw data are stored in European Genome-phenome Archive (EGA); and processed data, tranSMART. In light of the distinct interpretations of data ontology structures in different repositories, we are aiming to establish the a systematic, flexible and sustainable mapping between the processed data and the corresponding raw data regardless of their repositories.We propose an ontology structure with a few stable mapping concepts -- Study, Sample Collected Experimental Data (SCED) and File -- to connect different repositories, separating the three essential processes: data uploading, data ontology structuring and data retrieving, in such a way that a general upload and structuring methodology can be used for malleable data retrieving. To demonstrate this ontology structure, we create a RDF graph demo using CTMM-TraIT Cell Line Use Case (CLUC) data.	ELIXIR poster	ELIXIR
P_EI003	811	Jon Ison and Registry-Core Bio.Tools Core Team	Jon Ison	bio.tools : tools & data services registry	bio.tools is a registry of bioinformatics software information, sustained by a community-driven curation effort, tailored to local needs and shared amongst a network of engaged partners. Life sciences yield huge data sets that underpin vital scientific discoveries. In support, a plethora of databases and tools are used, in technically complex and diverse forms, across a spectrum of scientific disciplines. The corpus of information for these resources is fragmented across the Web, with much redundancy, and has lacked a common information standard. The outcome is that scientists often struggle to find, understand, compare and use the best resources for the task at hand. bio.tools enables users to easily formulate precise queries and quickly retrieve tools and services that fulfill specific scientific functions and technical requirements. Ontologies are used, such as EDAM for scientific domains, functions, types of data, data formats and identifiers. These support the retrieval of concise, consistent and therefore comparable information, for the convenience of the user. bio.tools can provide a practical catalogue, that will help scientists not only find, understand, compare and select resources, but also use and connect them in workflows. It is anchored within a broader initiative, fostered by the European Infrastructure for Biological Information (ELIXIR), that includes community-driven performance benchmarking, training, and multi-faceted user support.	ELIXIR poster	ELIXIR
P_EI004	744	Carlos Horro, Manuel Corpas, Rafael Jiménez and John Hancock	Carlos Horro	BioCIDER: a Contextualisation InDEx for biological Resource discovery	Life-science resources (i.e., databases, tools, training materials, courses and event information) are many, diverse and dispersed. The 2016 Nucleic Acids Research (NAR) Database Issue reported 1,685 major databases in the molecular biology domain, while the latest NAR Web Server Issue presented 97 new resources for 2015 alone. It is thus difficult for researchers to be aware of and familiar with all current and relevant research assets, the utility of which is further compromised if these are scattered and difficult to find. Discoverability of resources and information can be significantly enhanced if a suggested list of resources is exposed to users in context with the information they are currently browsing. If sufficiently relevant, a list of potential resources placed in an unobtrusive way can provide users with new, advantageous information and save precious time browsing further. To date, there is no life science-focused service that provides contextualised information driving researchers to the discovery of relevant databases, tools, events and training materials. To address this gap, we have developed BioCIDER, a Contextualisation InDEx for biological Resource discovery. BioCIDER automatically collects information (metadata and source description) from a compendium of centralised registries, including the Bio.tools service registry, the iAnn collaborative event dissemination portal, and the ELIXIR training portal. BioCIDER provides an open source BioJS widget that can be embedded in any website.	ELIXIR poster	ELIXIR
P_EI005	820	Matúš Kalaš, Sveinung Gundersen, László Kaján, Hervé Ménager, Jon Ison, Christophe Blanchet, Steve Pettifer, Rodrigo Lopez, Kristoffer Rapacki andInge Jonassen	Matúš Kalaš	BioXSD | BioJSON | BioYAML - Integrated formats for sequence data	BioXSD has been developed as a tree-based data model and an exchange format for basic bioinformatics data, centred around a bio-polymer sequence. BioXSD allows integration of diverse features, information, measurements, and inferred values about a biological molecule or its part, annotated with provenance and reliability metadata, ontology concepts, scientific remarks, and conclusions.BioJSON and BioYAML are the ongoing developments. These exchange formats are based on the same data model as BioXSD, but providing serialisations in JSON and YAML respectively. BioJSON and BioYAML thus enrich the BioXSD family with alternatives to the original XML.As tree-based data formats, BioXSD, BioJSON, and BioYAML are particularly suitable for programming in object-oriented languages, and for use with web applications and web APIs (Web services), while at the same time allowing a reasonable level of human readability.BioXSD|BioJSON|BioYAML are developed together with GTrack (the universal tabular format for sequence features; http://gtrack.no), by ELIXIR Norway and an international community of collaborators (http://bioxsd.org/#Contact). The BioXSD|GTrack family is going to support smooth interoperability between these alternative, universal formats, and between the tools that consume or provide them as inputs or outputs.	ELIXIR poster	ELIXIR
P_EI006	807	Aravind Venkatesan, Julien Gobeill, Jee-Hyub Kim, Francesco Talo, Michele Ide-Smith, Patrick Ruch and Johanna Mcentyre	Aravind Venkatesan	Bridging literature and data using text-mined annotations in Europe PMC	Bio-curation is essential in maintaining high quality information in biological databases. With the exponential growth in data, curators are faced with a challenging task of bridging the gap between raw data and the knowledge it represents. Curators are required to develop or extend structured vocabularies and tag data with functions, molecular interactions and gene-disease associations by manually extracting information from literature. Biological databases are both dependent and required for this process. Therefore, it is critical that the literature is linked effectively to underlying data and related biomolecular databases, aiding curators extract the essence from the articles. Some links to data are currently made available through data citations, however, deeper integration is required to make curation more scalable. To this end, text mining offers a solution by tagging entities, for instance, gene names, functions and ontological concepts, reducing the burden of manual curation.Here we present a new Europe PMC [1] service - SciLite - that allows text-mined annotations from any source or provider to be displayed on full text articles. The goal of this annotation system is to expose text-mining outputs from the community in useful ways for curators, as well as other interested stakeholders. In the context of ELIXIR, this system will support database curation processes and provide a mechanism to make deep links between the literature and data for clear provenance of curatorial statements.References:[1] Europe PMC Consortium (2015). Europe PMC: a full-text literature database for the life sciences and platform for innovation. Nucleic acids research, 43(D1), D1042-D1048 [PMC4383902].	ELIXIR poster	ELIXIR
P_EI007	836	Jose Borbinha, Pedro L. Fernandes, Inês Chaves, Bruno Costa, Daniel Faria, João Cardoso, Célia Miguel, Ahmad Nadali,Daniel Sobral, Arlindo Oliveira,Mário J. Silva and Cymon Cox	Arlindo Oliviera	Business Model Canvas for ELIXIR	A business is a system that creates value to customers. Accordingly, a business model defines the business concepts (core are value and resource, but others might also exist), their relationships (concepts interdependency) and their dynamics (how resources are acquired and spent, and value is created and delivered). A team representing the four laboratories integrating ELIXIR PT used the Business Model Canvas to define reference business models for the ELIXIR Hub and for its own context, using as sources of information the ELIXIR web sites. We believe this is a very efficient technique to reach a wide range of stakeholders at the business and political levels.According to the findings, the cost structures for the PT Node and the ELIXIR Hub are similar: value driven, with mainly fixed costs for coordination, technical support, development and maintenance. Human resources and IT infrastructure are also key resources common to both contexts.Specific to the ELIXIR Hub are the key resources of reference data models and vocabularies, related with knowledge management as key activity. Other Hub specific key activities are coordination of Nodes, outreach communication, and dissemination, while key activities specific of the PT Node are training and consulting. Key activities common to both contexts are brand value development.For the PT Node the main agreed costumer segment is the biomedical industry and R&D community, with a main value proposition on woody plants (key data resources for eucalyptus, cork oak, pine and grapevine). For key activities, it emerged the development of analytical software tools.	ELIXIR poster	ELIXIR
P_EI008	818	Niklas Blomberg, Friederike Schmidt-Tremmel, Andrew Smith and Manuela Schuengel	Andrew Smith	CORBEL - Harmonisation of access to Europe's biomedical research infrastructures	The Grand Challenges in health can only be met by translation of biomedical discoveries to new, innovative and cost effective treatments. Biological and medical research that addresses these challenges spans a broad range of scientific disciplines and user communities. The ESFRI Biological and Medical Science Research Infrastructures (BMS RIs) sit at the centre of this movement, providing pan-European access to the specialised research services, instruments, samples and facilities that underpin the revolution in life science research and translation.CORBEL, uniting 11 BMS RIs, aims to establish a collaborative and sustained framework of shared services between the participating RIs. CORBEL addresses the critical need of users - particularly those in large advanced research projects - to seamlessly integrate and leverage specialist services from multiple RIs and national centres. Provision of harmonized accession processes, unified ethical and legal support, joint data management, and coordinated user access to advanced research instruments, facilities and samples will boost R&D - from discovery of basic biological mechanisms to applied medical translation.An Open Call for research projects utilising several RIs will be launched in October 2016. These projects will serve as proof-of-concept studies for the envisaged streamlined access to European RIs and will demonstrate its added value for research as well as for the society.	ELIXIR poster	ELIXIR
P_EI009	772	Rob Hooft, Niclas Jareborg, Frederik Coppens, Heinz Stockinger, Robert Pergl and Brane Leskosek	Rob Hooft	Data Management Planning in ELIXIR	The ELIXIR research infrastructure bundles not only the databases and tools of bioinformatics, but it also brings together life science data expertise. The assembled expertise can form a fantastic resource for researchers making a data management plan (DMP); currently, this expertise is hard to discover and access. Several of the ELIXIR nodes are looking for ways to offer DMP services to their communities. The technical coordinators in these nodes are planning to build these services together.First, we will expose the ELIXIR expertise through a web-based data management planning portal, using existing assets:A web technology platform (Czech Republic) to build and manage hierarchical (context-sensitive) questionnaires.A hierarchical analysis of the landscape of life science data management, in the form of a mind map, and associated explanatory text (Netherlands).The ELIXIR e-learning platform (Slovenia).We will also search for collaborations with others providing tools for data management planning across the sciences. Our portal will allow researchers who are making a DMP to find ELIXIR experts they could consult and appropriate learning resources that can help broaden their knowledge. For data stewards the portal will function as a checklist. Important motto will be: Data Management Planning not because we have to, but because it pays off.In addition to this resource, training is needed on many aspects of DMP and this has been prioritized for 2017 by the ELIXIR Training Platform. As a first step, skills needed for various target groups in the ELIXIR community will be identified.	ELIXIR poster	ELIXIR
P_EI010	770	Alba Gutiérrez-Sacristán, Janet Piñero, Núria Queralt-Rosinach, Emilio Centeno and Laura I. Furlong	Janet Piñero	disgenet2r: An R package to explore the molecular underpinnings of human diseases	DisGeNET is a discovery platform designed to answer questions concerning the molecular mechanisms underlying human diseases (http://www.disgenet.org/). DisGeNET follows the FAIR data principles (http://www.datafairport.org/), and can be explored using a suite of tools that includes a web interface, a Cytoscape app, and a SPARQL endpoint. We present disgenet2r, a novel R package for exploring and analyzing DisGeNET. disgenet2r contains a variety of functions for leveraging DisGeNET using the powerful visualization and statistical capabilities of the R environment. disgenet2r is specially designed to harness the large amount of information contained in DisGeNET, facilitating its analysis and interpretation. By integrating different disease vocabularies, disgenet2r eases the exploration of gene-disease associations from different perspectives. It offers different types of visualization, such as heatmaps and networks, and it is especially well suited to explore genes and variants associated to diseases. To allow answering more sophisticated research questions that need the interrogation of heterogeneous data resources, the disgenet2r package leverages the potential of Semantic Web technologies, without the need of special expertise in this area. This is achieved through a set of functions that connect DisGeNET with other resources present in the Linked Open Data, covering different information such as gene expression, gene function, drug activity, and biological pathways, among others. The disgenet2r package (https://bitbucket.org/ibi_group/disgenet2r) expedites the integration of DisGeNET data with other R packages, and allows the development of complex bioinformatic workflows.	ELIXIR poster	ELIXIR
P_EI011	838	Maxim Scheremetjew, Simon Potter, Dario Vianello, Hubert Denise, Alex Mitchell and Rob Finn	Maxim Scheremetjew	EBI's Metagenomics Pipeline: Moving towards cloud computing	EBI metagenomics (EMG, https://www.ebi.ac.uk/metagenomics/) is a free to use hub for the analysis and exploration of metagenomic, metatranscriptomic, amplicon and assembly data. The resource provides rich functional and taxonomic analyses of user-submitted sequences, as well as analysis of publicly available metagenomic datasets that are held within the European Nucleotide Archive (ENA).The pipeline is capable of providing analysis of extremely large datasets. For example, in 2015, we analysed the oceanographic dataset, Tara Oceans, which is the largest project to be processed by EMG to date, with ~10 Tb of sequence data (~29 billion sequences). The pipeline is also able to provide a high level of throughput: the number of analysed datasets within the resource has grown 6-fold in 2016 (as of 22 July 2016), and now comprises over 55,000 sequence runs, with over 200 billion sequences analysed in total.To address future analysis challenges, as metagenomic datasets grow ever larger, we have continued to refine the pipeline, with the aim of improving scalability and portability. As part of this process, we have begun to investigate ways to deploy the pipeline on computing clouds within the ELIXIR hub, as well as commercial clouds, such as Amazon or Google. Here, we give an overview of the analysis pipeline itself, outline a number of updates that we have made to ensure scalability and discuss the ongoing work to deploy it on the cloud.	ELIXIR poster	ELIXIR

P_EI012	785	Mikael Linden, Michal Procházka, Premysl Velek, Susanna Repo, Tommi Nyrönen and Ilkka Lappalainen	Premysl Velek	ELIXIR Authentication and authorization infrastructure	ELIXIR is developing and deploying ELIXIR authentication and authorisation infrastructure (ELIXIR AAI) - a set of general purpose services that support scientific services to authenticate their end users, and to decide what kind of access permissions users have in the services. The end users can benefit from a single login - no need to remember a multitude of usernames and passwords. A well-organised approach to service login and access also increases information security.The first release of ELIXIR AAI is deployed in the ELIXIR-EXCELERATE project, part of the ELIXIR compute platform and scheduled to be operational in the end of August 2016. ELIXIR AAI integrates to components on the ELIXIR compute platform, such as cloud and data transfer services.	ELIXIR poster	ELIXIR
P_EI013	867	José María Fernández González, Juergen Haas, Salvador Capella, Torsten Schwede and Alfonso Valencia	Alfonso Valencia	ELIXIR-EXCELERATE WP2 Activities	Critical benchmarking of scientific tools and services in the different research communities, like the ones registered in the ELIXIR tools registry bio.tools, provides added value to these communities and their developers. Critical benchmarking is based on objective quantitative quality measures, both in terms of technical reliability as well as scientific quality.At the same time, criteria agreed within a community in the form of periodic assessments is an effective way to encourage new developments by highlighting areas which require improvements and/or new solutions. Motivated by the success of CASP, a number of similar community driven benchmarking experiments have been organized e.g. CAPRI, BioCreative, CAGI, CAFA, etc. These experiments have great value in organizing community discussions around new developments and solutions.However, continuous benchmarking efforts are required to compare the tools performance in a steady way over large common data sets. Several efforts have been designed and implemented to address this need in different research areas e.g. EVA, CAMEO, LifeBench, BioCreative Metaserver, CAFASP, BECalm, etc. Note that some of them have been abandoned or superseded by newer ones.ELIXIR-EXCELERATE WP2 aims to bring together different communities needing periodic and/or continuous evaluation of their tools and services. The main targets are: learning from the different benchmarking efforts in order to find commonalities across different benchmarking experiments; trace guidelines and best practices for future research community efforts in order to avoid common problems and pitfalls; and, if possible, defining a standard workflow. infrastructure which is transferable to other scientific communities.	ELIXIR poster	ELIXIR
P_EI014	806	Stephanie Suhr, Susanna Repo and Niklas Blomberg	Susanna Repo	ELIXIR-EXCELERATE: accelerating the implementation of ELIXIR	ELIXIR-EXCELERATE is a major EU Horizon 2020 grant awarded to ELIXIR to help implement its scientific programme and integrate Europe's bioinformatics resources into a coherent infrastructure. It supports ELIXIR's early implementation phase by i) delivering world-leading data services for academia and industry, ii) increasing bioinformatics capacity and competence across Europe, and iii) completing the management and organisational processes for an efficient distributed ELIXIR infrastructure.Funded through a four year grant of nearly €20 million and including over 50 partners from ELIXIR Nodes, the grant will deliver services for users within five technical Platforms (Data, Tools, Interoperability, Compute and Training), which are informed by four domain-specific Use Cases: marine metagenomics, crop and forest plants, rare disease and human data. The technical and scientific activities are complemented by a Capacity building programme, which supports the organisational and scientific development of ELIXIR Nodes. A complimentary training programme is aimed at increasing competency within partner organisations.The successful implementation of ELIXIR-EXCELERATE will enable sustainable management and re-use of data for millions of users across the globe and improve the competitiveness of European life-science industries by providing academia, SMEs and multinationals with the tools to develop new knowledge, products and services.	ELIXIR poster	ELIXIR
P_EI015	861	Salvador Capella-Gutiérrez, Josep Ll. Gelpi and Alfonso Valencia	Salvador Capella-Gutiérrez	ELIXIR-Spain: Activities overview and future perspectives in the context of ELIXIR-EXCELERATE	The Spanish National Bioinformatics Institute (INB) joins ELIXIR in 2015. This virtual institute, created in 2003, is formed by 10 research nodes which altogether cover a broad range of bioinformatics areas. INB nodes have an internationally recognised expertise in the areas of genomics, proteomics, structural biology, and translational medicine. Moreover, INB has contributed to create and maintain a bioinformatics infrastructure through the involvement of the Barcelona Supercomputing Centre.As the ELIXIR node in Spain (ELIXIR-Spain), the INB coordinates the participation of its nodes in this European core infrastructure. INB brings to ELIXIR the experience of many years of distributed work aiming to design, implement and maintain different services from databases e.g. Apris, DisGeNet, etc; to tools e.g. Babelomics, JORCA, GEM3, FlexServ; etc; to databases such as 3D BioNotes, BIGNaSim, etc, to complex infrastructures like the INB-BSC Genomics Cloud.Specifically, INB is participating in the ELIXIR's tools platform helping to the curation of WP1's bio.tools ontology annotations, and developing a platform for continuous benchmarking of tools (WP2) such as text mining, paralogy and orthology predictions, or multiple sequence alignments, among others. In the context of ELIXIR-EXCELERATE, the INB is contributing to setting the foundations of collaborative long standing infrastructures. In fact, INB co-leads two of the four use cases, centered in human data, developing infrastructure for the management of rare-diseases data (WP8) and maintaining the European Genome-Phenome archive (WP9), the long term repository for sensitive human genomics data.	ELIXIR poster	ELIXIR
P_EI016	34	John Hancock	John Hancock	ELIXIR-UK	ELIXIR-UK is the UK Node of ELIXIR. ELIXIR-UK's current focus is on enhancing training capacity and capability both across ELIXIR and within the UK. Chris Ponting from the Node co-leads the ELIXIR Training platform and the UK's ELIXIR training grant. As part of this award ELIXIR-UK is developing the TeSS training portal, led by Terri Attwood. Carole Goble, ELIXIR-UK Interim Head of Node, co-leads the ELIXIR Interoperability platform and plays an important role in developing links internationally, and especially with the USA, in this area. Susanna-Assunta Sansone leads the BioSharing initiative which is central to ELIXIR's interopaerability activities. John Hancock, ELIXIR-UK's Node Coordinator, manages the Node's activities.	ELIXIR poster	ELIXIR
P_EI017	683	Magnus Palmblad, Arzu Tugce Guler, Anna-Lena Lamprecht, Kristian Davidsen, Jon Ison and Veit Schwämmle	Magnus Palmblad	Functional software annotation and automatic workflow generation for mass spectrometry data processing	Many software utilities operating on mass spectrometry (MS) data have been described in the literature. Finding that which one needs is often hard, however. We have added a number of MS-related terms to EDAM and annotated over 200 software tools currently in the public domain, including those on http://ms-utils.org, in the ELIXIR Tools and Data Services Registry http://bio.tools. The ms-utils.org tools emphasizes modular rather than monolithic design. Such small utilities performing one operation with well-defined inputs and outputs are ideally suited for assembly into scientific workflows. Annotating the ms-utils.org content with EDAM terms elevates it to the biotoolsXSD standard, supporting the exposure of these resources in the bio.tools registry, bringing the utilities to a broader audience. We used these annotations to automatically generate workflows in four use cases using loose programming and the jABC framework plugin PROPHETS. The use cases were selected to represent common data analysis tasks in MS-based proteomics: peptide retention time prediction, protein identification and enrichment analysis, localization of phosphorylation and protein quantitation using isotopic labeling. Automatically generating and running different but logically equivalent workflows allows the user to verify their analysis results. Software and service annotations are also useful to find a replacement for a workflow component that is no longer supported. This is the first demonstration of using the EDAM ontology to annotate mass spectrometry software utilities and generate workflows for MS data processing.	ELIXIR poster	ELIXIR
P_EI018	805	Michael Dondrup, Wei Zhang, Frank Nilsen, Zhaoran Zhou and Inge Jonassen	Michael Dondrup	LiceBase – a species focused resource for sea lice – including an RNAi LIMS and tools for data analysis and genome annotation	We present LiceBase, a model organism database and web-portal for genomics of sea lice and other economically relevant marine genomes. Sea lice are the major pathogens affecting the global salmon farming industry. The annual costs for sea lice management have recently been estimated to exceed €500 millions and the aquaculture industry relies on few medicines for lice control. We have recently sequenced and annotated the genome of the Atlantic salmon louse in collaboration with Ensembl and the EBI; large scale RNA-sequencing and reverse genomics experiments are constantly being conducted. The aim of LiceBase is to provide excellent bioinformatics resources for the analysis, retrieval, and visualization of the sea lice genome and related Omics data to the global research community. LiceBase is closely integrated with other Norwegian Elixir applications such as NeLS (Norwegian infrastructure for Life Sciences) Storage and NeLS Galaxy, allowing users to run computational pipelines.LiceBase is a Norwegian international deliverable to Elixir.LiceBase is freely accessible at https://licebase.org.	ELIXIR poster	ELIXIR
P_EI019	726	David Sehnal, Karel Berka, Lukáš Pravda, Radka Svobodová-Vařeková, Michal Otyepka and Jaroslav Koča	Karel Berka	MOLE 3.0 – remastered tool for detection and analysis of functionally important "void spaces" within biomacromolecules	MOLE is a gold standard in quick geometrical detection of channels and tunnels within biomacromolecular structures. MOLE 2.0 (www.mole.upol.cz) was first tool to come with automatic and user–defined detection of channels and tunnels using Voronoi diagram and Delaunay tesselation representations. New version of MOLE 3.0 also enables detection of pores and better description of individual types of important void spaces within protein structures together with additional increase of speed. Alpha version of MOLE 3.0 is available at http://webchemdev.ncbr.muni.cz/MOLE3/.	ELIXIR poster	ELIXIR
P_EI020	666	Klaas Vandepoele	Klaas Vandepoele	PLAZA 3.0: an access point for comparative and regulatory genomics in plants	Comparative sequence analysis has significantly altered our view on the complexity of genome organization and gene functions in different kingdoms. PLAZA 3.0 is designed to make comparative genomics data for plants available through a user-friendly web interface. Structural and functional annotation, gene families, protein domains, phylogenetic trees, and detailed information about genome organization can easily be queried and visualized. Compared with the first version released in 2009, the number of integrated genomes is more than four times higher, and now covers 37 plant species. The new species provide a wider phylogenetic range as well as a more in-depth sampling of specific clades, and genomes of additional crop species are present. The functional annotation has been expanded and now comprises data from Gene Ontology, MapMan, UniProtKB/Swiss-Prot, PlnTFDB and PlantTFDB. Furthermore, we improved the algorithms to transfer functional annotation from well-characterized plant genomes to other species. Recently, more than 1 million of conserved non-coding sequences were added for ten dicot species, which provide detailed information about conserved transcription factor (TF) binding sites for 642 TFs covering 35 TF families. These new data and features make PLAZA 3.0 (http://bioinformatics.psb.ugent.be/plaza/) a versatile and comprehensible resource for users wanting to explore genome information to study different aspects of plant biology, both in model and non-model organisms.PLAZA 3.0: an access point for plant comparative genomics. Proost et al., Nucleic Acids Res. 2015A Collection of Conserved Non-Coding Sequences to Study Gene Regulation in Flowering Plants.Van de Velde et al., Plant Physiol. 2016	ELIXIR poster	ELIXIR
P_EI021	429	Konstantinos D. Tsirigos, Arne Elofsson and Pantelis G. Bagos	Konstantinos D. Tsirigos	PRED-TMBB2: Improved topology prediction and detection of beta-barrel outer membrane proteins	PRED-TMBB was presented for the first time in 2004 and is one of the most cited methods regarding the topology prediction and detection of beta-barrel outer membrane proteins. Here, we present an update to this method, PRED-TMBB2, which contains several new features that improve its performance significantly. The major difference is the incorporation of evolutionary information in the form of Multiple Sequence Alignments (MSAs), which drastically improves the topology prediction capability and makes it able to achieve higher performance compared to all other available methods. At the same time, the single-sequence version of PRED-TMBB2 manages to perform better than almost all methods regarding detection of beta-barrel proteins in large datasets, outperforming even methods that use MSAs and are much slower. The combination of single- and multiple-sequence version of PRED-TMBB2 is something unique and we anticipate it will be of great interest to researchers in this field.	ELIXIR poster	ELIXIR
P_EI022	713	Andrew Nightingale, Jie Luo, Leyla Jael García Castro, Maria Martin and Uniprot Consortium	Andrew Nightingale	Protein Data Services and Feature Viewer Enabling Knowledge Driven Research	Complex biological processes, such as rare heterogenetic diseases, are difficult to discover and interpret. Coupled with the continuous growth and complexity in Biological data there is a requirement to develop tools for data linkage, integration and visualization to facilitate scientific progress that can contribute to essential infrastructures such as those provided by Elixir.In order to respond to this challenge and contribute to the Elixir effort, we have developed REST services and a BioJS component for accessing and visualizing protein data, while also ensuring interoperability with other tools and resources. This will enable users to fully transition from the genome, to the transcriptome and to the proteome and thus facilitate knowledge driven biomedical research. These services use a number of resources including UniProtKB as the source for proteins and functional information and Ensembl for genomic information and have a flexible design that can be extended to incorporate data from further resources.For example, our services include protein mappings to genomic coordinates and variation data, enhanced with proteomics experiments. Following simple instructions a novice user can quickly learn to carry out advanced searches tailored to their scientific needs. Based on these services, we have developed a new interactive visualization BioJS component depicting sequence functional annotations from UniProtKB such as domains, sites, PTMs and variants from multiple sources. This 'Feature Viewer' presents curated and large-scale experimental data in an intuitive compact picture with related protein annotations grouped together in zoomable tracks in a similar way to tracks in genome browsers.	ELIXIR poster	ELIXIR
P_EI024	534	Margarita C. Theodoropoulou, Konstantinos D. Tsirigos, Stavros Hamodrakas and Pantelis G. Bagos	Pantelis Bagos	Recent updates in the Database of Outer Membrane Proteins (OMPdb) in 2016	Beta-barrel outer membrane proteins (OMPs) are crucial for the life of Gram-negative bacteria, since they participate in many diverse procedures. OMPdb (http://www.ompdb.org/) is the largest, most complete and well characterized collection of OMPs from Gram-negative bacteria. Our database contains extensive information for each protein (entry) including protein description and classification, sequence, organism name, taxonomy, links to other databases, accompanied with annotation for TM segments and signal peptides. All proteins are classified into families based on function and sequence similarity. Each family (family entry) is extensively described and the information provided are the function of protein members, literature references, a list of proteins with 3D-structure (if any), and the respective seed and full protein alignments. Currently, OMPdb contains 91 families and more than 400,000 proteins. Out of the 91 families, 15 families were built completely from scratch, 16 do not belong to the respective clan of Pfam, while 6 of them are annotated as DUF in Pfam. OMPdb follows the monthly updates of Uniprot through a semi-automated procedure. Users may search the database using Text, Domain and/or BLAST Search and the database can be downloaded in several formats (text, FASTA, XML) through the Download page. We are now in collaboration with Pfam and TCDB in order to cross-link our databases. Finally, our database is coupled with PRED-TMBB2, the best performing algorithm for the topology prediction and detection of OMPs. We believe that OMPdb is valuable tool in the hands of researchers working with this important superfamily of transmembrane proteins.	ELIXIR poster	ELIXIR
P_EI025	740	Diana Domanska and Abdulrahman Azab	Diana Domanska	Software Provisioning Inside a Secure Environment as Docker Containers using STROLL File-system	TSD (Tjenester for Sensitive Data), is an isolatedinfrastructure for storing and processing sensitive research data,e.g. human patient genomics data. Due to the isolation ofthe TSD, it is not possible to install software in the traditionalfashion. Docker containers is a platform implementinglightweight virtualization technology for applying the build-oncerun-anyware approach in software packaging and sharing. Thispaper describes our experience at USIT (The University Centreof Information Technology) at the University of OsloWith Dockercontainers as a solution for installing and running softwarepackages that require downloading of dependencies and binariesduring the installation, inside a secure isolated infrastructure.Using Docker containers made it possible to package softwarepackages as Docker images and run them smoothly inside oursecure system,TSD. The paper describes Docker as a technology,its benefits and weaknesses in terms of security, demonstratesour experience with a use case for installing and running theGalaxy bioinformatics portal as a Docker container inside theTSD, and investigates the use of STROLL file-system as a proxybetween Galaxy portal and the HPC cluster.	ELIXIR poster	ELIXIR

P_EI026	866	Jiri Vondrasek	Jiri Vondrasek	Structural Bioinformatics and Cheminformatics - the major focus of the Czech ELIXIR Node	Building sustainable infrastructure for biological data involves synergy of compatible resources as well as corresponding tools and services. The Czech ELIXIR Node comprises several high level solutions for structural bioinformatics, cheminformatics and genomic data available at the national as well as international level. The portfolio of these tools and services represents advanced scientific methods and results available via progressive technical solutions. A small number of selected tools are presented.For Cheminformatics we introduce solution utilizing Resource Description Framework (RDF) and the SPARQL query language applied on Integrated Database of Small Molecules. In the field of Structural Bioinformatics we present 4 complex tools including PatternQuery – a tool for detection structural fragments in biomacromolecules, (Multi)SETTER – SEcondary sTructure-based TERtiary structure superposition tools, program MOLEonline 2.0 which determines channels and pores in 3D structures of proteins and finally the DNATCO – a tool for DNA conformers assignment.Frequently used tool developed and curated by the Czech Node is Repeat Explorer which is dedicated to discover and identify repeats in NGS data. RepeatExplorer as well as other presented tools are a part of services provided by ELIXIR CZ - Czech research infrastructure for biological information. For other services provided by ELIXIR's Czech Republic Node visit www.elixir-czech.cz/services	ELIXIR poster	ELIXIR
P_EI027	829	Niall Beard, Aleksandra Nenadic, Susanna-Assunta Sansone,Terri Attwood,Carole Goble, Rafael Jiminez,Milo Thurston, Norman Morrison, Celia. Van Gelder and Fredrick Coppens	Niall Beard	Structured Data for Life Science using Schema.org	ELIXIR explicitly supports the FAIR Principles - Findable, Accessible, Interoperable, Reusable - for its data, software, tools, events and training resources. “Finding” has the significant challenge of effective discovery and indexing of web-based resources across all ELIXIR information providers - this is an issue because there has been no agreement within ELIXIR about how to expose such resources in order to make them discoverable.One solution to this problem is to adopt Schema.org mark-up. Schema.org is a community initiative supported by four major search-engine providers: Google, Bing, Yahoo and Yandex. It provides a simple way to publish data in a standard format.If websites publishing life-science training materials, data, tools, profiles etc. were to use Schema.org mark-up, then their websites could be crawled, and the data could be indexed and exposed in searchable portals. However, this approach has challenges. Bioschemas is a newly formed community group in the life sciences to address these challenges, aiming to make the adoption of Schema.org part of a powerful way to discover and collect life-science information. It produces specifications, one for each information type (‘Training Course’, ‘Event’, etc.). Each specification lists the Schema.org minimum properties expected, and the contraints for each property: for example, the ‘Events’ specification that the property ‘topic’ should be an EDAM ontology topic. The specifications are developed openly and are available on GitHub, with the support of existing communities of domain experts. Bioschemas also identifies the types or properties that are needed in the life sciences but not present in Schema.org, and works with the community to encourage the adoption of these types and properties into Schema.org.	ELIXIR poster	ELIXIR
P_EI028	831	Herve Menager and Edam-Core Edam Core Team	Herve Menager	The EDAM Ontology	EDAM is an ontology of well established, familiar concepts that are prevalent within bioinformatics, including types of data and data identifiers, data formats, operations and topics. EDAM is a simple ontology - essentially a set of terms with synonyms and definitions - organised into an intuitive hierarchy for convenient use by curators, software developers and end-users.EDAM is suitable for large-scale semantic annotations and categorization of diverse bioinformatics resources, and also suitable for diverse application including for example within workbenches and workflow-management systems, software distributions, and resource registries. Version 1.15 of EDAM has been released. Contributions and suggestions are welcome!	ELIXIR poster	ELIXIR
P_EI029	786	Ilkka Lappalainen, Jordi Rambla, Serena Scollen, Mikael Linden, Macha Nikolski, J. Dylan Spalding and Susanna Repo	Serena Scollen	The ELIXIR Beacon Project	ELIXIR has partnered with the Global Alliance for Genomics and Health (GA4GH) to light ELIXIR Beacons as primary data-discovery services for genomics. The Beacon will provide a single point of access to the data stored within the Node resources by promoting interoperability and standard technical data access interfaces. The ELIXIR Beacon project defines the Beacon query interface, user authentication and authorization mechanisms and the service security requirements together with the GA4GH. The ELIXIR Beacon reference implementation is fully integrated with the ELIXIR authentication and authorization services. It is designed to work with research consented sensitive human data as well as data from other organisms.The ELIXIR Beacon service has three distinct data access tiers. These tiers are designed to provide increased level of information for Beacon users with access rights based on data security and consent requirements.The Public Access Tier does not require user to authenticate before querying on data such as allele frequencies on national population or non-human data. Registered Access Tier covers allele frequencies on individual cohorts used for constructing national level allele frequencies. Data that require Data Access Committee approval is provided only to approved researchers through Controlled Access Tier. This open web service is designed to be technically simple, easy to implement, and to not return privacy violating information.The ELIXIR Beacon project includes partners from EMBL-EBI, Belgium, Finland, France, Netherlands, Spain, Sweden and Switzerland.	ELIXIR poster	ELIXIR
P_EI030	871	Sveinung Gundersen, Matúš Kalaš, Boris Simovski, Brynjar Rongved, Henrik Skifjeld, Sivert Kronen Hatteberg, Abdulrahman Azab, Osman Abul, Arnoldo Frigessi,Geir Kjetil Sandveand Eivind Hovig	Sveinung Gundersen	The GTrack ecosystem - expressive file formats for analysis of genomic track data	GTrack, BTrack and GSuite are file formats designed to handle genomic track data of heterogeneous types. The file formats are designed to complement each other and work jointly as a complete ecosystem for representation and analysis of most types of data that can be located along a reference genome.GTrack is a tabular format that was developed to provide a uniform representation of most types of genomic datasets, being able to replace common formats such as WIG, GFF , BED, BED-like formats, and even FASTA. GTrack supports all possible track types, mathematically defined as a delineation of possible genomic datasets into 15 different basic informational structures. In addition to common track types such as points or segments, this includes 8 types of tracks usable for analysis of the three-dimensional aspects of DNA.The BTrack format supports the same variety of informational content as GTrack, but in a binary form. BTrack is unique in supporting a collection of multiple tracks stored together in one (possibly compressed) HDF5-based binary file, while still supporting a high level of efficiency.The GSuite format is a unique tabular format that binds together the whole chain of multi-track analysis, from search and retrieval of genomic tracks, through intermediate processing, to analysis.A Python library supporting parsing, conversion and operations is available with a rudimentary API. The BTrack format is supported only in a prototype version.The GTrack ecosystem has, together with BioXSD, been selected as one of four main national deliverables from Norway towards the ELIXIR project.	ELIXIR poster	ELIXIR
P_EI031	762	Frederic B. Bastian, Julien Roux, Mathieu Seppey, Komal Sanjeev, Valentine Rech de Laval, Philippe Moret, Panu Artimo, Séverine Duvaud, Vassilios Ioannidis, Heinz Stockinger and Marc Robinson-Rechavi	Frederic B. Bastian	TopAnat : a new way to understand genomics results using gene expression enrichment in anatomy	TopAnat is an innovative tool to discover where a set of genes is preferentially expressed, and it represents a completely new kind of enrichment analyses. TopAnat is quite similar to a Gene Ontology (GO) enrichment test, which determines the GO terms preferentially associated to a set of genes. In our case, however, the test is applied to terms from an anatomical ontology (Uberon ontology), mapped to genes by expression patterns. This allows to study a new type of property of gene sets, regarding their expression domains. TopAnat is both highly sensitive for detecting organs where genes have an expression biais, and specific to provide the most relevant and precise terms. For instance, we used TopAnat to analyze the expression domains of genes associated with autistic end epileptic disorders in human, from Jabbari and Nürnberg, 2016; TopAnat succesfully determined that these genes were preferentially expressed in some specific brain regions, likely to be associated with these disorders (see http://bgee.org/?page=top_anat#/result/8fce889da7b4519c5792573ed3933032c8122819/). Note that TopAnat is not to be confused with a differential gene expression analysis, where gene expression levels are compared between two conditions, to detect changes in expression. Rather, TopAnat retrieves the anatomical structures where genes are expressed, and for each anatomical structure, tests whether genes from the list of interest are over-associated with this structure, as compared to a background list of genes. TopAnat is available as a webtool (http://bgee.org/?page=top_anat), and as a Bioconductor R package (https://bioconductor.org/packages/release/bioc/html/BgeeDB.html).	ELIXIR poster	ELIXIR
P_EI032	784	Ian Sillitoe, Natalie Dawson, Paul Ashford, Sayoni Das, Su Datt Lam, Jon Lees, Millie Pang and Christine Orengo	Natalie Dawson	Using CATH-Gene3D to explore the impacts of disease-induced genetic variations	CATH classifies 3D structures from the PDB into superfamilies of protein domains that are evolutionarily related. Since protein structure tends to be much more highly conserved than sequence, CATH superfamilies are often able to trace further back in evolution than sequence methods alone. Currently, CATH classifies more than 300,000 domain structures (from ~80% of PDB structures) into ~2700 evolutionary superfamilies.Once these distant structure-based evolutionary relationships have been established, the Gene3D resource uses start-of-the-art sequence comparison technology to augment these superfamilies with more than 50 million protein domain sequences from ~20,000 cellular genomes. Many of these superfamilies contain protein sequences with detailed functional annotations, which enable a deep understanding of the evolutionary mechanisms by which functions evolve. A recent development is the identification of functional families within CATH superfamilies and the establishment of a new function prediction protocol, which has been highly ranked by the CAFA independent assessment.CATH-Gene3D is an endorsed resource of the UK ELIXIR Node and our HMM libraries are used to provide structural and functional annotations in the ELIXIR marine metagenome infrastructure use case. CATH-Gene3D is also a member of the Genomics England Functional Effects Domain, for which we are using our function family data to explore the impacts of disease-associated residue mutations and identify the specific protein domains that are enriched in such mutations. CATH-Gene3D is a member of a consortium of UK structural bioinformatics groups contributing to an ELIXIR training initiative that is developing web-based training workflows to analyse the impacts of mutations.	ELIXIR poster	ELIXIR
P_EI033	477	Eric Bonnet, Yimin Shen, Xavier Benigni, Nizar Touleimat, Jorg Tost, Jean-François Deleuze and François Artiguenave	Eric Bonnet	WBS: a computational pipeline for the treatment of whole-genome high-throughput bisulfite sequencing data	DNA methylation is an important epigenetic mechanism used by higher eukaryotes and is involved in several key physiological processes, including regulation of gene expression, X-chromosome inactivation, imprinting and silencing of germline-specific genes and repetitive elements. Patterns of methylation are maintained through somatic cell divisions and may be inherited across generations. These patterns are altered in many complex human diseases, such as imprinting disorders and cancer. Understanding methylation patterns is therefore of great importance for many biomedical questions.Bisulfite treatment of DNA is method of choice to analyse these patterns. Bisulfite treatment leaves methylated cytosines unaffected. Thus, bisulfite treatment introduces specific changes in the DNA sequence that depend on the methylation status of individual cytosine residues, yielding single-nucleotide resolution information about the methylation status of a segment of DNA. Various analyses can be performed on the altered sequence to retrieve this information. Especially, rapidly falling costs of high-throughput sequencing have made the global analysis of DNA methylation at the whole genome level a viable option.However, there are significant computational challenges associated with the computational treatment of bisulfite generated reads. Here we describe WBS (Workflow Bisulfite), a computational pipeline set-up at the Centre National de Génotypage (CNG) for the analysis of bisulfite whole genome sequencing data. The pipeline is built around standard state-of-the-art tools and workflows for the treatment of bisulfite reads. We describe the organization of the pipeline, performance and possible evolutions in the framework of the analysis of mammalian (mostly human) whole genome DNA methylation patterns.	ELIXIR poster	ELIXIR
				ELIXIR/TRAINING			
P_EI/Tr034	339	Teresa K. Attwood, Louisa Bellis, Cath Brooksbank, Pedro L Fernandes, Valerie Florance, Rita Hendricusdottir, Lee Larcombe, Patricia M. Palagi, Celia W.G. van Gelder, Allegra Via, Sarah L. Morgan, Gabriella Rustici and Rochelle E. Tractenberg	Louisa Bellis	Assessing the impact(s) of international bioinformatics & computational biology training within ELIXIR & BD2K	Two large-scale initiatives have recently been created – one in the USA (Big Data to Knowledge, BD2K) and one in Europe (ELIXIR) – with emphasis on training and capacity building to promote, respectively, biomedical and life science research in the current, dynamic context of big data and bioinformatics. Definitions and metrics of success and impact for the training being developed (ELIXIR) and marshalled (BD2K) are needed. These should include quantitative and/or qualitative indicators of whether, how and to what extent the training delivered is: (1) successful, based on its stated goals, and (2) aligned with the driving strategies of the above-mentioned initiatives.Determining the impact of training is a challenging task that requires: 1) a definition of "impact"; 2) concrete understanding of the purposes and the corresponding stakeholders to which "demonstrating training impact" might be useful (i.e., how will the outcome of our analyses be used, and how will this affect future decisions); 3) articulation of what types of indicator/metric/measurement of impact are best to use; and 4) determination of the most appropriate strategies to collect such data.BD2K and ELIXIR share a commitment to identify the most reliable and robust indicators, to collect and analyse the relevant data, and to develop and publish guidelines. The two groups have already met, and continue to work to align their efforts, to share and discuss their results, and to promote globally useful definitions and metrics for training impact and success.	ELIXIR/Training poster	ELIXIR Training
P_EI/Tr035	841	Brane Leskosek, Eija Korpelainen and Jure Dimec	Maja Zagoršćak	Node collaboration through the ELIXIR e-learning platform – follow up	The eLearning platform developed by ELIXIR-SI (EeLP) enables remote execution of the f2f courses, so that teacher can be in one location and students on remote and distributed locations. EeLP offers secure access to the training materials, presentations, exercises and assessment systems in the form of online lessons, discussion forums for teacher and students, as well as single-sign-on using eduGain authentication (ELIXIR AAI is in preparation).In order to gain experience and to develop best practises, we transformed the popular ELIXIR-FI course "RNA-seq data analysis with Chipster" into e-learning format, and successfully executed the course with the teacher in FI, students in CZ and e-learning materials and video conference system (VC) in SI. The communication between the teacher and students was conducted through a two-way VC. Students downloaded the analytics software and data sets from the ELIXIR-FI servers. Guided online by the teacher, the students performed their data analysis tasks and were constantly assessing themselves in the EeLP that also allow the teacher to follow their progress.We are planning the EeLP and e-learning services to be a long-term activity. With simple web based system (https://elixir.mf.uni-lj.si/elearning/) we collect information about f2f courses for which authors are interested in transformation to appropriate e-learning formats. The courses from SE and IT nodes are already being transformed.Experiences so far shows that EeLP combined with lectures over VC is a scalable and cost-effective way complementary to f2f training and capacity building, and it could be used for training researchers, developers and infrastructure specialists.	ELIXIR/Training poster	ELIXIR Training
P_EI/Tr036	822	Niall Beard, Terri Attwood and Aleksandra Nenadic	Terri Attwood	TeSS - The Life Science Training Portal	TeSS [1] (ELIXIR's life science training portal) has been in development since early 2015. Following a proof-of-concept (pilot) phase, funding was received (as part of ELIXIR-EXCELERATE) to harden the product and bring it to a production-level service.TeSS aggregates links to disparate training materials and events scattered around the institutional websites of ELIXIR Nodes and other content providers (GOBLET [2], Software and Data Carpentry [3, 4], EBI TrainOnline [5], Genome3D [6], on-course [7], etc.), making them centrally discoverable and searchable. Training resources within TeSS can be collected and arranged into packages and/or training workflows, which are graphic representations of scientific pipelines to organise resources into easily navigable views. Aggregation of training content happens automatically through a set of custom-made nightly-run scraper scripts. Scrapers use a number of techniques to extract information: HTML-scraping and APIs had been the predominent methods, but more recently we have focused on parsing structured schema.org mark-up data. The TeSS team has been heavily involved in the specification definition and promotion of the adoption of a schema.org standard for describing training materials and events online through the BioSchemas [8] group. We are currently developing an integration strategy with other ELIXIR registries (e.g., BioTools [9] and BioSharing [10]) to link training materials to relevant tools, databases, standards and policies.[1] https://tess.elixir-uk.org[2] http://mygoblet.org[3] http://software-carpentry.org[4] http://www.datacarpentry.org[5] http://www.ebi.ac.uk/training/online/[6] http://genome3d.eu/[7] https://www.on-course.eu/[8] http://bioschemas.org	ELIXIR/Training poster	ELIXIR Training
P_EI/Tr037	617	Bjoern Gruening and The De.Nbi Special Interest Group Training And Education	Bjoern Gruening	The de.NBI Training Network	The German Network for Bioinformatics Infrastructure (de.NBI) provides a nationwide infrastructure for bioinformatics tools, resources, and training for these tools funded by the German Ministry for Research and Education. Consequently, de.NBI develops and collects educational materials related to bioinformatics. Training activities are focused on supporting and training end users through training courses, webinars, and online training. Life science researchers will thus be enabled to exploit their data more effectively by applying tools, standards and compute services provided by de.NBI. The network has been offering a number of training activities ranging from summer schools, hands-on trainings, hackathons to online teaching activities. In 2016, de.NBI will organize around 40 training courses and thus aims to train around 500 participants.The different training courses are adapted to different levels of users. The range goes from beginners’ courses up to expert meetings. Thematically, these courses provide expertise in the application of de.NBI tools and databases, programming skills, data management as well as data interpretation.de.NBI has developed internal standards for monitoring the quality of its educational events. Standardized survey forms permit the comparison of the quality of individual training events and yield invaluable feedback to instructors. In order to scale up the training efforts, we providing its training materials online. de.NBI will join the European ELIXIR network in 2016 and will thus integrate its training activities into the ELIXIR activities. de.NBI training activities are accessible online on the network’s website at http://www.denbi.de.	ELIXIR/Training poster	ELIXIR Training