

POSTER LIST  
ORDERED ALPHABETICALLY BY POSTER TITLE  
GROUPED BY THEME/TRACK

THEME/TRACK: TRAINING  
Poster numbers: P\_T001 - 017

Poster number	EasyChair number	Author list	Presenting author	Title	Abstract	Theme/track	Topics
<b>P_T001</b>	591	Oscar Torrefo Tirado, Oswaldo Trelles, Michael T. Krieger and Alex Upton	Michael T. Krieger	An overview of training in the Spanish ELIXIR node	The Spanish National Bioinformatics Institute (Instituto Nacional de Bioinformática) (INB) is part of the Carlos III Health Institute (Instituto de Salud Carlos III, ISCIII). The mission of the INB is to provide bioinformatics support to Spanish research institutions and companies. The INB has actively participated in the creation of ELIXIR. It acts as a transmitter of ELIXIR developments for the benefit of national projects, and promotes the use of INB systems and tools at European level. The Bilbao group, part of the Computer Architecture Department of the University of Malaga, is one of the INB nodes and acts as the training coordinator of Spain in ELIXIR. The INB is heavily involved in training, providing its expertise in organising training events. The training collaboration is bidirectional, with ELIXIR providing materials and certifying them to ensure the quality of the training sessions. A wide range of training courses have been offered in the last year across the whole node. This includes courses in NGS, R programming, proteomics, genomics, and Galaxy. This highlights the breadth in the training offer, with a number of training courses planned in the node for the coming year. This includes a two-day High Performance Computing (HPC) workshop at the University of Malaga in October 2016. The first day will provide an introduction to HPC with introductory practical exercises, whilst the second day will present HPC use cases from the bioinformatics and biomedicine domains. Along with the other planned courses, this demonstrates INB's continued commitment to bioinformatics training.	Training poster	Training
<b>P_T002</b>	445	Vera Matser, Cath Brooksbank, Rossen Apostolov, Adam Carter, Alexandre Bonvin, Mark Abraham and Emiliano Ippoliti	Vera Matser	Applying competency profiling of user groups to develop a training programme in Computational Biomolecular Research	Life Science research has become increasingly digital and has a direct influence on our daily life in areas such as health and medical applications, drug discovery, agriculture and food industry. It is one of the largest and fastest growing communities in need of high-end computing, leading to an increasing number of life science researchers who are not computing experts but who need to use complicated computationally intensive biomolecular modeling tools. BioExcel is a newly launched Centre of Excellence for Biomolecular Research aimed at supporting these academic and industrial researchers in the use of high-performance computing (HPC) and high-throughput computing (HTC). To make sure that the biomedical research communities can fully profit from the training offered through the new Centre of Excellence we will be determining the training needs for three user groups (Entry Level Users, Expert Users and System Administrators) by drafting a competency profile. The competencies have been determined with the aid of the community and sent out for wider consultation. To enrich the competency profile we will, for each competence, define what an individual will need to know and what skills they need to have to exhibit competence in a specific area, as well as list what behaviours are suited and unsuited to an individual with that particular competency - so that individuals can assess their own competence in each area and select appropriate training. The competencies will be mapped against existing training and new training courses and material will be developed where gaps are revealed.	Training poster	Training
<b>P_T003</b>	746	Janick Mathys, Christof De Bo and Alexander Botzki	Janick Mathys	Bioinformatics Training at VIB: laying the cornerstones for life scientists to survive in data-intensive biotech research	Set up in response to the increasing importance of bioinformatics in biotechnology research, VIB's Bioinformatics Training and Service (BITS) facility provides trainings, software support and services that contribute to the generation of useful biological knowledge. The facility gives basic and intermediate trainings to the life sciences research community in Belgium, focusing on the fields of bioinformatics, statistics, omics data analysis, programming and support of the software that the VIB offers to its members. Most trainings are part of a training track that teaches researchers to perform complete bioinformatics analyses of the data they generate. The trainings are very hands-on with a focus on applications, many allow participants to work on their own data. To support this practical approach we work in small groups on laptops provided by VIB. The training material (slides, tutorials and exercises) are available on our wiki web site for consultation and we capture the lessons of some courses as videos. To increase the visibility of the BITS training courses, all training web sites are systematically tagged according to 'biochemia' Life Science training material specification. In collaboration with the ELIXIR training coordinator group, these metadata are scraped from our web site and deposited in the TeSS training portal ( <a href="https://tess.elixir-uk.org/">https://tess.elixir-uk.org/</a> ). Currently, the BITS training team is setting up a Belgium ELIXIR training network and participates in organising some ELIXIR-BE training courses like Data Carpentry course in November 2016. To even further grow our training network, we organise experience and trainer exchanges within the Core For Life alliance ( <a href="http://coreforlife.eu">http://coreforlife.eu</a> ).	Training poster	Training
<b>P_T004</b>	615	Sandrine Perrin, Victoria Dominguez Del Angel, Jonathan Lorenzo, Jean-François Gibrat and Christophe Blanchet	Victoria Dominguez Del Angel	Cloud Computing Training at French ELIXIR node (French Institute of Bioinformatics)	Cloud Computing presents a new approach to allow the development of elastic, distributed and highly scalable resources. The French Institute of Bioinformatics set up a Cloud Computing Infrastructure which offers services, software, database and computing resources. Education and Training are key components of the IFB-infrastructure. IFB-core, the national hub of IFB, offers training courses to educate the community on how to use the IFB-Cloud for analyses and methodological developments in bioinformatics. IFB-core offers 3 training modules to teach life-science scientists to adopt the IFB-Cloud. The modules build progressively to cater for the needs of general and advanced audiences. 1) In the "Cloud basic usage" module, the attendees learn to deploy the appropriate application in the cloud for analyzing their data. This module is dedicated to non-users of the command line interface. Demonstration on available applications e.g. Galaxy, RStudio and Virtual-desktop technology. 2) In the "Cloud advanced usage" module, the attendees learn to deploy complex bioinformatics applications, including multiple virtual machines in a cluster, to install new integrate public data collection, and manage data with NFS virtual disks. We demonstrate automatic installation tools, such as Approver, Docker and how to build a cluster with SGE, Spark or Torque. 3) In the "development of the appliances" module, developers learn how to create appliances according to a guideline of good practices. All created appliances will increase the Catalogue. Developers are accompanied during the creation of the appliance. The modules are regularly scheduled throughout the year.	Training poster	Training
<b>P_T005</b>	837	Kim Gurwitz, Shaun Aron, Sumit Parjli, Suresh Maslamoney, Pedro Fernandes, David Judge and Nicola Mulder	Kim Gurwitz	Distance-based online Bioinformatics training in Africa: the H3ABioNet experience	Africa is not unique in its need for basic Bioinformatics training for individuals from a molecular biology background. However, unique logistical challenges in Africa, most notably access to administrative and academic support. Classroom selection was based on certain infrastructure criteria, including computer resources, Internet access, and availability of local teaching assistants. Although lectures are delivered live to remote sites via an online platform, to ensure that classroom success does not rely on stable Internet, classrooms can watch pre-recorded and pre-downloaded lecture videos, as well as work through practical assignments on the lecture content, during biweekly contact sessions. Lecture recordings are available on the course website <a href="http://training.h3abio.net/IT_2016/">http://training.h3abio.net/IT_2016/</a> . While trainers are available via video conferencing to take questions and participate in discussion forums, hosted on the course management platform, are also available. This distance based model, developed for a resource limited setting, could easily be adapted to other settings.	Training poster	Training
<b>P_T006</b>	685	Teresa K Attwood, Pamela Black, Marie-Claude Blatter, Cath Brooksbank, Pedro L. Fernandes, Nicola Mulder, Patricia M Palagi, Gabriella Rustici, Maria Victoria Schneider and Celia W Van Gelder	Pedro L. Fernandes	GOBLET's Bioinformatics Learning, Education and Training Activities	The Global Organisation for Bioinformatics Learning, Education and Training (GOBLET: <a href="http://mygoblet.org">http://mygoblet.org</a> ) was established to provide a global, sustainable support structure to foster international communities of bioinformatics trainers and trainees. The activities of GOBLET are carried out through committees, which have independent overlapping focus areas. The Learning, Education and Training (LET) Committee primarily focuses on providing resources for bioinformatics trainers. Here we describe some of the recent activities and resources developed by the LET Committee: (i) A set of consensus descriptors for training materials to ensure that materials are consistently described with a minimum, standard amount of information. This brings a strong improvement in discoverability, shareability and traceability of training materials. (ii) The development of core competencies together with the ISCB Education Committee, and how these can be used to elaborate bioinformatics curricula and training materials appropriate for different audiences. (iii) Our e-learning activities in bioinformatics from the perspective of discoverability of existing e-learning materials and the development of new materials. For these activities we partnered up with other networks and organisations with similar goals.	Training poster	Training
<b>P_T007</b>	791	Sarah L Morgan, Richard Grandison, Katrina Costa, Lee Larcombe and Cath Brooksbank	Cath Brooksbank	Providing bioinformatics training for established researchers	The EMBL-EBI training programme provides face-to-face and online learning opportunities focused on accessing public biodata, analysing large data sets and interpreting the results of bioinformatics experiments. Although our major audience is early-stage researchers, we receive frequent requests from experienced researchers needing to enhance their own bioinformatics competency and enable their labs to benefit from data-centric approaches to research. Finding training appropriate to their busy schedules and specific needs has proved challenging, so we have developed two new courses tailored specifically to the needs of (1) bench-based industrial discovery scientists and (2) principal investigators. Bioinformatics for discovery/working with the EMBL-EBI Industry programme and with support from the BBSRC we have developed a blended learning module to enable discovery biologists to incorporate bioinformatics-based approaches into their research projects. A two-day face-to-face workshop is followed by an online, workflow-based component that must be completed within 6 months. During this period trainees continue to interact with each other and their instructors via discussion boards and scheduled online discussions. Bioinformatics for Principal Investigators' more early-stage researchers make bioinformatics a major component of their research projects. PIs of classically bench-based research have been turned to us for guidance on principles and challenges of data acquisition and analysis, and on how best to support their teams. In June 2016 we delivered our first course aimed specifically at PIs. The course covered the fundamentals of bioinformatics and data management combined with discussions on various options for enhancing bioinformatics competency in their teams.	Training poster	Training
<b>P_T008</b>	402	Antonio Fabregat, Konstantinos Sidropoulos, Guilherme Viteri, Florian Korninger, Steven Jupp, Phani Garapati, Peter D'Eustachio, Lincoln Stein and Henning Hermjakob	Antonio Fabregat	Reactome: A curated knowledgebase of biomolecular pathways	Reactome ( <a href="http://www.reactome.org/">http://www.reactome.org/</a> ) is a free, open-source, curated and peer-reviewed knowledgebase of biomolecular pathways. Its aim is to provide intuitive bioinformatics tools for visualisation, interpretation and analysis of pathway knowledge to support basic research, genome analysis, modeling, systems biology and education. Pathways are built from connected "reactions" that encompass many types of biochemical events. Reactions are derived from literature and must cite a publication that experimentally validates them. Pathways are authored by expert biologists and peer reviewed before incorporation into the database. 9,584 reactions in Reactome cover 9,238 human gene products (12,527 including IntAct interactions), supported by 22,338 literature references. Users can search for proteins or compounds and see details of the complexes, reactions and pathways they participate in. Pathway diagrams allow users to examine the molecular events that constitute the steps in pathways and to view details of the proteins, complexes and compounds involved. Different forms of pathways analysis can be performed with the Reactome analysis tools. Users can submit a list of identifiers for overrepresentation analysis or submit quantitative datasets, such as microarray data, for expression analysis. Results of these analyses are overlaid onto the Pathways Overview and Diagram Viewer for easy navigation and interpretation. Interaction data from multiple resources can be used to expand pathways. Interactors from IntAct are included by default in the search feature and can be taken into account in the analysis service. Finally, pathways or all Reactome content can be downloaded in many formats including TSV, CSV, PDF, SBML, BioPax and PSI-MITAB.	Training poster	Training
<b>P_T009</b>	403	Konstantinos Sidropoulos, Antonio Fabregat, Guilherme Viteri, Florian Korninger, Peter D'Eustachio, Lincoln Stein and Henning Hermjakob	Guilherme Viteri	Reactome: New services and widgets to ease third-party integration	Reactome ( <a href="http://www.reactome.org/">http://www.reactome.org/</a> ) is a free, open-source, curated and peer-reviewed knowledge base of biomolecular pathways. It aims to provide intuitive bioinformatics tools for visualisation, interpretation and analysis of pathway knowledge to support basic research, genome analysis, modeling, systems biology and education. Thus, the mainstays of its software development are usability and responsiveness from the user's point of view, likewise modularity and reusability from the developer's side. Reactome offers web services and widgets ( <a href="http://go.gliix.org/vp/">http://go.gliix.org/vp/</a> ) to facilitate integration in third-party software. One service provides database access while the other performs overrepresentation and expression analysis as well as species comparison. Widgets for the Pathways Overview and Pathway Diagrams are provided for JavaScript and GWT. Both widgets overlay the results of the Analysis Service. Protein-protein or protein-chemical interactions can be used to extend pathways beyond Reactome's curated content. IntAct is the default resource but all other PSICQUIC databases can be selected and in addition, users can submit custom interactions. Interaction data from IntAct are also included in the Reactome main search and the Analysis Service, helping users identify pathways of interest. In summary, Reactome has facilitated data integration by providing easy-to-use services and reusable widgets. Several resources such as OpenTargets ( <a href="https://www.targetvalidation.org/">https://www.targetvalidation.org/</a> ), ChEBI ( <a href="https://www.ebi.ac.uk/chebi/">https://www.ebi.ac.uk/chebi/</a> ), BluePrint ( <a href="http://docs.bioprint-epigenome.eu/">http://docs.bioprint-epigenome.eu/</a> ), PRIDE ( <a href="http://www.ebi.ac.uk/pride/archive/">http://www.ebi.ac.uk/pride/archive/</a> ), PINT ( <a href="http://sealion.scripps.edu/pint/">http://sealion.scripps.edu/pint/</a> ) and IP2 ( <a href="http://igoldfish.scripps.edu">http://igoldfish.scripps.edu</a> ) have already integrated these services and widgets.	Training poster	Training
<b>P_T010</b>	416	Thanh Le Van, Matthijs van Leeuwen, Ana Carolina Fierro, Dries De Maeyer, Jimmy Van den Eynden, Lieven Verbeke, Luc De Raedt, Kathleen Marchal and Siegfried Nijssen	Thanh Le Van	Simultaneous discovery of cancer subtypes and subtype features by molecular data integration	Motivations: Subtyping cancer is key to an improved and more personalized prognosis/treatment. The increasing availability of tumor related molecular data provides the opportunity to identify molecular subtypes in a data-driven way. Molecular subtypes are defined as groups of samples that have a similar molecular mechanism at the origin of the carcinogenesis. The molecular mechanisms are reflected by subtype-specific mutational and expression features. Data-driven subtyping is a complex problem as subtyping and identifying the molecular mechanisms that drive carcinogenesis are confounded problems. Many current integrative subtyping methods use global mutational and/or expression tumor profiles to group tumor samples in subtypes but do not explicitly extract the subtype-specific features. We therefore present a method that solves both tasks of subtyping and identification of subtype-specific features simultaneously. Here our method integrates mutational and expression data while taking into account the clonal properties of carcinogenesis. Key to our method is a formalisation of the problem as a rank matrix factorisation of ranked data that the subtyping procedure as a novel integrative procedure to identify subtypes by subtyping features. We formalise the model using rank matrix factorisation, resulting in the SRF algorithm. Experiments on simulated data and the TCGA breast cancer data demonstrate that SRF is able to capture subtle differences that existing methods may miss.	Training poster	Training
<b>P_T011</b>	747	Sarah Morgan, Teresa K Attwood, Brane Leskosek, Gabriella Rustici and Allegra Via	Brane Leskosek	Surveying training provision, needs and capacity across ELIXIR nodes and EXCELERATE use-cases to map skill transfer routes in Europe	Across Europe, the availability of bioinformatics training opportunities varies greatly. Whilst the need for bioinformatics competencies (and hence training) is well recognised, the ability to provide such training is not yet well developed in all countries. In this context, ELIXIR training is vital for promoting the transfer of skills from nodes where training is more developed to those where specific competencies are needed to develop a bioinformatics based ELIXIR training network. To address this need, EXCELERATE (EXCELerate training network) is a pan-European countries. In 2014, the Society for Experimental Biology, in association with members of GOBLET (Global Organisation for Bioinformatics Learning, Education & Training), surveyed bioinformatics training needs amongst life scientists worldwide. In the context of ELIXIR, we want to gain a node perspective, and a deeper, more detailed view of current bioinformatics training provision, needs and capacity. To this end, the first task of the Training Platform's Train-the-Trainer subtask was to launch a survey across all ELIXIR nodes to determine 1) which nodes have the greatest need to increase their training capacity; 2) the subject areas where capacity needs to be built; 3) which nodes are currently delivering training initiatives; and 4) the course delivery methods employed, including the development/use/need for VM and cloud-based systems and e-learning. The outcome of our analysis will be used to delineate a map of training activities and demands across ELIXIR, and to draft a white paper reporting our recommendations to optimise the transfer of skills between ELIXIR nodes.	Training poster	Training

<b>P_T#012</b>	790	Rafael Hernández-De-Diego, Tomas Klingström, Hadrien Gourié, Elienne P. de Villiers, Ana Conesa and Erik Bogcam-Rudloff	Hadrien Gourié	The eBioKit, a stand-alone educational bioinformatics platform	Bioinformatics skills have become essential for many research areas; however, the availability of qualified researchers is usually lower than the demand, a situation that especially affect developing countries. For many developing countries, bioinformatics has been a strategic area of investment in life science. Initial efforts in developing countries have generated hubs of excellence located in the bigger or more affluent countries. Extensive training is however necessary to provide the research professionals with the necessary skills to analyze the virtual mountains of data generated by modern research. The eBioKit was developed as a response to the lack of reliable internet connections and the short time available to visiting researchers conducting hands-on training at workshops or short courses. The eBioKit is a portable bioinformatics educational platform whose main purpose is to eliminate the dependence on the Internet, by offering locally a wide range of services, tools and databases widely used in genomic research, as well as documentation and training material. The architecture of the eBioKit has demonstrated to be an excellent balance between portability and performance, making the eBioKit a great educational tool but also providing small research groups with a platform to incorporate bioinformatics analysis in their research. The eBioKit has proven itself to be an excellent teaching platform in training activities for the African Bioinformatics Network (H3ABioNet) as part of the initiative H3Africa, the SArBio Initiative, The Biotechnology for Central Africa (BeCA) hub, the International Glossina Genome Initiative, Institute of Biochemistry, Molecular Biology and Biotechnology (IBMBB), and many others.	Training poster	Training
<b>P_T#013</b>	559	Youri Hoogstrate, Saskia Hillemann, Dave Clements, Bjørn Grüning, Andrew Stubbs, Hans-Rudolf Holtz and Galaxy Training Network	Leon Mei	The Galaxy Training Network: centralizing resources for galaxy trainings	The Galaxy Training Network is an international initiative supporting and developing all aspects of training around the Galaxy analysis platform for biomedical research. Scalability is a recurring challenge in all aspects of high-throughput computational biology, including training. There is far more demand for training than can be met by just in-person training by the core Galaxy Team. The Galaxy Training Network supports the project by providing resources and centralizing the training efforts. As member of GOBLET ( <a href="http://www.myglobet.org/">http://www.myglobet.org/</a> ), the Galaxy Training Network takes part in the global coordination of Bioinformatics training. This poster will highlight resources that are available for teaching bioinformatics software in Galaxy and for using and administering Galaxy itself. The Galaxy Training Network unifies core project and community training efforts under one umbrella so that existing training resources become more easily and centrally available, and it makes it easier for new arrivals to get up to speed with training in their locations and communities. We will also highlight directories of tutorial/worked exercises, including up to date sample data, slide sets, videos, the new Galaxy Tours functionality and computational resources such as shared virtual machine images and Amazon Web Service Machine Images.	Training poster	Fundamental Training
<b>P_T#014</b>	682	Gregoire Rossier and Patricia M. Palagi	Gregoire Rossier	The SIB PhD Training Network: an initiative to gather, connect and train PhD students in Bioinformatics	The SIB Swiss Institute of Bioinformatics created in 2007 the SIB PhD Training Network (TN), a community support for PhD students carrying out their research in bioinformatics or computational biology in Switzerland. The TN aims to foster interactions and exchanges among PhD students and to train them in the most up-to-date methods necessary for their doctoral research. Every year, the TN coordinates several training activities, e.g. graduate level courses, where the network members have a registration priority. Furthermore, we organize annual events such as an international seasonal school, usually held in the Swiss Alps, the "Best Practices in Programming" workshop and the TN Retreat. Every two years the "Bioinformatics in the Chalef" workshop offers a unique and challenging experience of building up from scratch a bioinformatics research project. All these are opportunities for students to exchange ideas about their research projects, to seek feedback and help from their peers, and for networking and developing new collaborations. Most of the TN training activities are part of the SIB Training courses' portfolio, which can be found at <a href="http://www.sib.swiss/training">www.sib.swiss/training</a> . The SIB PhD Training Network was a pioneer PhD program in Switzerland and it is still unique in its domain in the country. It has seen near 350 students since the creation of the Network, and counts today close to 230 active members. Students and supervisors recently evaluated the pertinence of the TN and the conclusions of the survey will be presented in this poster.	Training poster	Training
<b>P_T#015</b>	692	Diana Marek, Gregoire Rossier, Geoffrey Fucile, Walid H. Gharib, Frédéric Schütz, Marie-Claude Blatter and Patricia M. Palagi	Diana Marek	The SIB Swiss Institute of Bioinformatics Training Group: Supporting the development and sustainability of effective bioinformatics training	The SIB Swiss Institute of Bioinformatics has an extensive offer of bioinformatics training courses, involving computational biology methods, statistics, machine learning, computing techniques, and the analysis, management, and reproducibility of biological data. The significant increase in the number of SIB groups has expanded SIB's resources and expertise, thus offering an opportunity to broaden the scope, scale, and diversity of SIB's training portfolio. Our courses respond to an increasing demand for bioinformatics training towards ensuring that the Swiss and international scientific community make the best use of bioinformatics and SIB resources. The SIB Training Group teaches, coordinates, and supports courses in close collaboration with SIB members and international partners. In 2015, SIB ran over 50 events, training nearly 1000 participants. These achievements were made possible through a complete planning and organisational framework that fully supports trainers. It includes: an analysis of objectives and requirements, design of course context, content and format, definition of learning objectives and teaching strategies, promotion, an efficient registration system including online payment, a reactive helpdesk for participants, systematic assessment of course quality and learning outcomes, and smooth handling of all logistical/organisational aspects. Our group employs this very efficient training platform to encourage and facilitate participation of SIB members in training activities. Researchers contributing to SIB training can thus increase the visibility and impact of their research activities without the burdens of course logistics and organization. Through this collaborative effort, SIB's training platform stays at the forefront of developments in bioinformatics to offer sustainable and effective training programs.	Training poster	Training
<b>P_T#016</b>	672	Patricia M. Palagi, Erik Bogcam-Rudloff, Pedro Fernandes, Elja Korpelainen, Fran Lewitter, Gabriella Rustici, Maria Victoria Schneider, Celia W.G. van Gelder and Teresa K. Athwood	Patricia M. Palagi	Train-the-Trainer: GOBLET's initiative to increase the provision of bioinformatics training in NGS	GOBLET is a global organisation that coordinates, shares and supports bioinformatics training activities worldwide, aiming to plug critical skills gaps, ultimately to facilitate the advancement of health- and life-science research. The focus of GOBLET's Train-the-Trainer initiative is on setting up effective training courses to help plug known skills gaps, especially in the area of NGS data analysis. This initiative will help to share bioinformatics training expertise, experience and resources; train bioinformatics and life-science specialists; support life-science research; promote collaborations among scientists worldwide; build capacity in developing and developed countries. The programme will consist of workshops, which will take place on different continents (e.g., South America, Africa, Asia) and are expected to co-locate as satellite events to major conferences. Each workshop is organised around two main topics: 1) how to exploit NGS data, and 2) how to set up and deliver excellent training courses. Trainers (members of GOBLET, expert in the field) will teach on a volunteer basis. Workshop participants will commit to replicate the workshops at least once, driving an exponential effect. To deliver this ambitious project, GOBLET is seeking partners and sponsors interested in increasing the provision of bioinformatics training in the area of NGS, either as GOBLET collaborators to customise the programme to specific communities or to fund workshops at given locations. To learn more about this project, see <a href="http://www.myglobet.org/content/fund-raising">http://www.myglobet.org/content/fund-raising</a> , contact <a href="mailto:fric@myglobet.org">fric@myglobet.org</a> , talk to us in GOBLET's booth and visit this poster!	Training poster	Training
<b>P_T#017</b>	776	Celia van Gelder, Sanne Abeln, Rita Azevedo, Luiz Otavio Bonino Da Silva Santos, Jeroen Engelberts, Rob W. W. Hooft, Mateusz Kuzak, Leon Mei, Marco Roos, Merlijn van Rijswijk, Andrew Stubbs and Jaap Heringa	Celia van Gelder	Training efforts in the Netherlands: combining forces to provide data – related training for the life science research community	In this era of big data, new skills and competences are needed for life scientists, technologists and data experts. Many people with heterogeneous backgrounds have to be trained. By combining the education expertise present in the Netherlands we work towards establishing a comprehensive, internationally acclaimed and sustainable training and education course portfolio for Life Sciences Research & Technology with a focus on training in new technologies and data integration and stewardship. Our efforts cross bridges between disciplines, application domains, European research infrastructures (ESFRIs and e-infrastructure). Examples of our activities include trainings and training collaborations in Bioinformatics and Systems Biology (BioSB Research School), Software and Data Carpentry (DTL, Netherlands eScience Center, SURFSara), Metabolomics (DTL and Netherlands Metabolomics Centre), Proteomics (DTL, Netherlands Proteomics Community), NGS (DTL, NGS Interest Group, Metagenomics Platform), Galaxy (DTL, ELIXIR-NL, VU Amsterdam, LUMC, ErasmusMC, BMMRI, TraIT), Bring Your Own Data (BYOD) workshops (DTL, ELIXIR-NL), Data Stewardship, Data Management, FAIR Data training (DTL, ELIXIR-NL, LERU, Elsevier), Defining competences and skill sets (DTL, ELIXIR-NL, EDISON), HPC and Cloud (DTL, ELIXIR-NL, SURFSara), Genetic data science (ELIXIR-NL, RDA-CODATA, EDISON) for all this training areas, we are not only collaborating in the Netherlands, but are also actively engaging and aligning efforts with collaborators in Europe (e.g. VIB in Belgium and SIB in Switzerland) and abroad (e.g. GOBLET and RDA-CODATA). Furthermore, ELIXIR-NL is co-leading the ELIXIR Training Platform. All our training activities are open to all and we welcome new collaborations.	Training poster	Training