

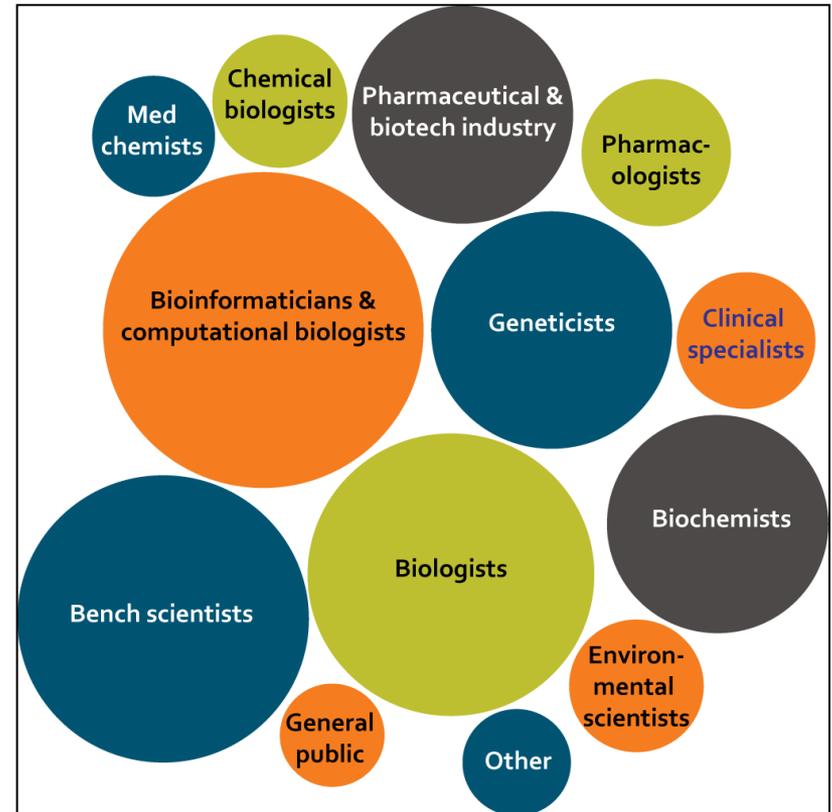
Bioinformatics Training

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Why is bioinformatics training important?

- Data analysis is now the major bottleneck to research in the molecular life sciences
- Many biomedical professionals feel under-qualified to make the most of biological data
- There are an estimated 3 million life scientists in Europe alone; >20 million healthcare professionals
- Potentially all of them are producers or consumers of data managed by Europe's biomedical research infrastructures

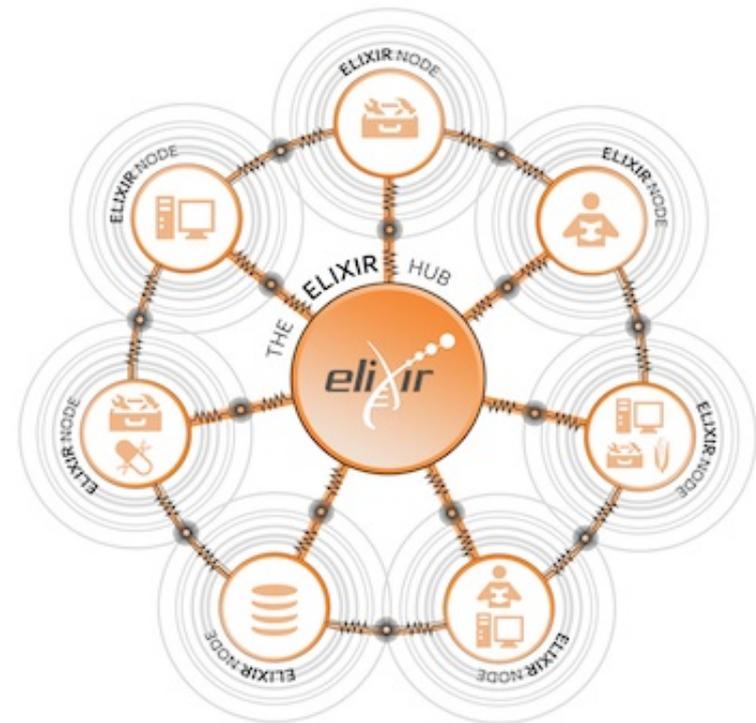


ELIXIR: a distributed infrastructure for life science

Building a **sustainable European infrastructure for biological information**, supporting life science research and its translation to medicine, agriculture, bioindustries and society

ELIXIR unites Europe's leading life science organisations in **managing and safeguarding the massive amounts of data** being generated every day by publicly-funded research

ELIXIR will **provide the facilities necessary for life science researchers to make the most of our rapidly growing store of information** about living systems, which is the foundation on which our understanding of life is built



ELIXIR “platforms” organisation

- **Data**

Sustain core data resources

- **Tools**

Services & connectors to drive access and exploitation

- **Compute**

Access, Exchange & Compute on sensitive data

- **Standards**

Integration and interoperability of data and services.

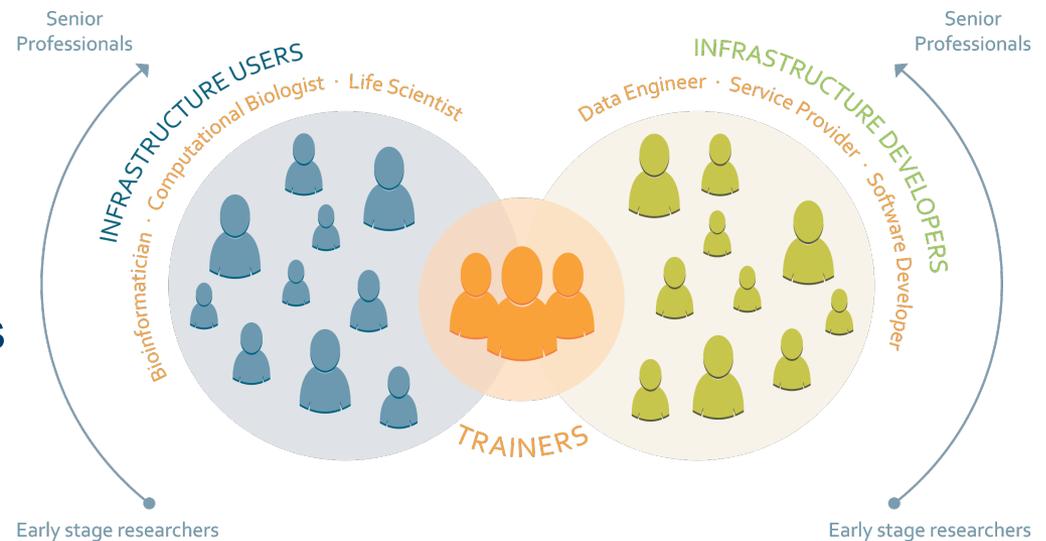
- **Training**

Professional skills for managing and exploiting data



ELIXIR Training Strategy

- Facilitate accessibility to Europe's bioinformatics resources by up-skilling researchers who can more effectively exploit the data, tools, standards and compute services provided by ELIXIR
- Support and train users through e-learning, face-to-face courses and programs held across Europe
- Develop a coordinated pan-European training program of high quality and impact
- Partnership with global efforts such as GOBLET



GOBLET - <http://mygoblet.org/>

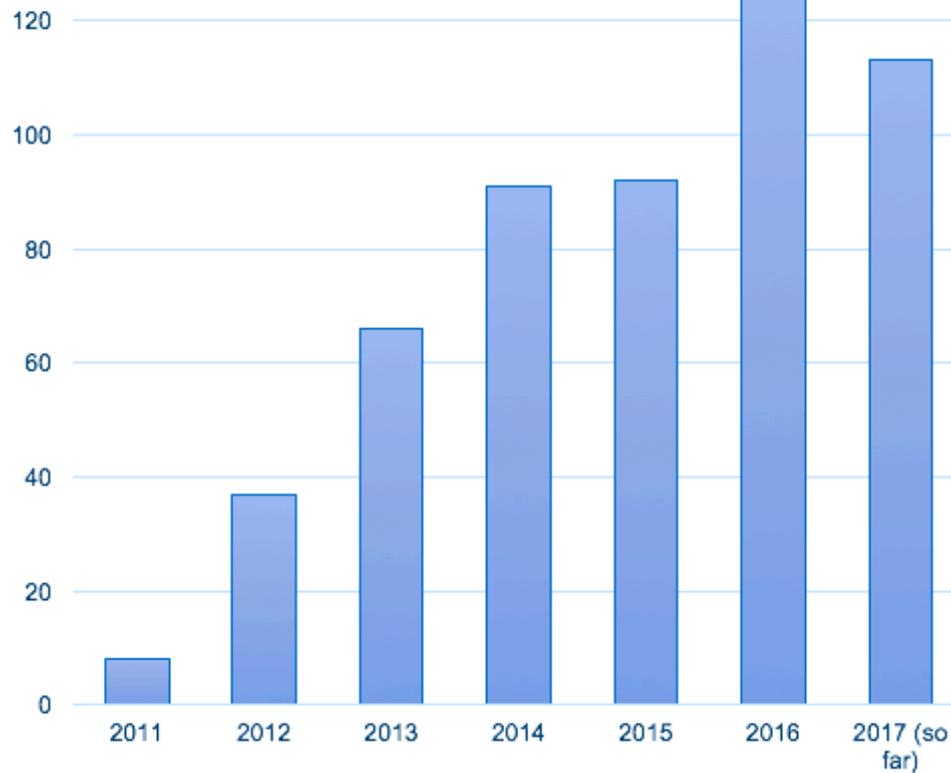
- Global Organisation for Bioinformatics Learning, Education & Training



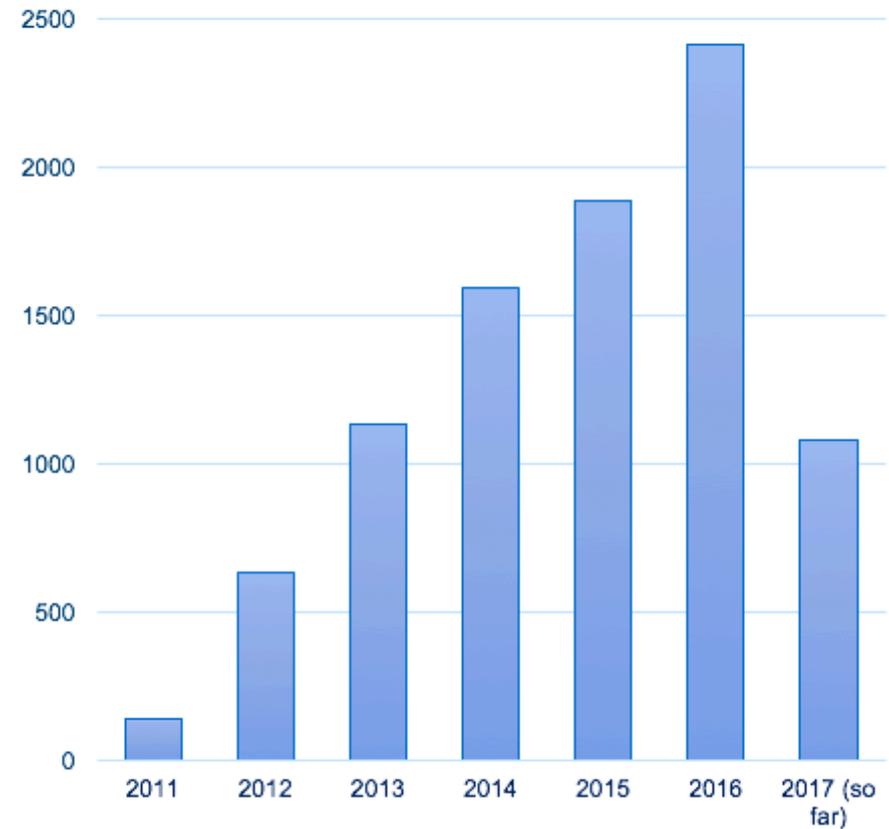
- Provide a global, sustainable support and networking structure for bioinformatics trainers and trainees, including (i) a training portal for sharing materials, tools, tips and techniques; (ii) guidelines and best practice documents; (iii) facilities to help “Train the Trainers”; and (iv) offering different learning pathways for different types of learner

Bioinformatics postgraduate training @ UoC

Total number of courses

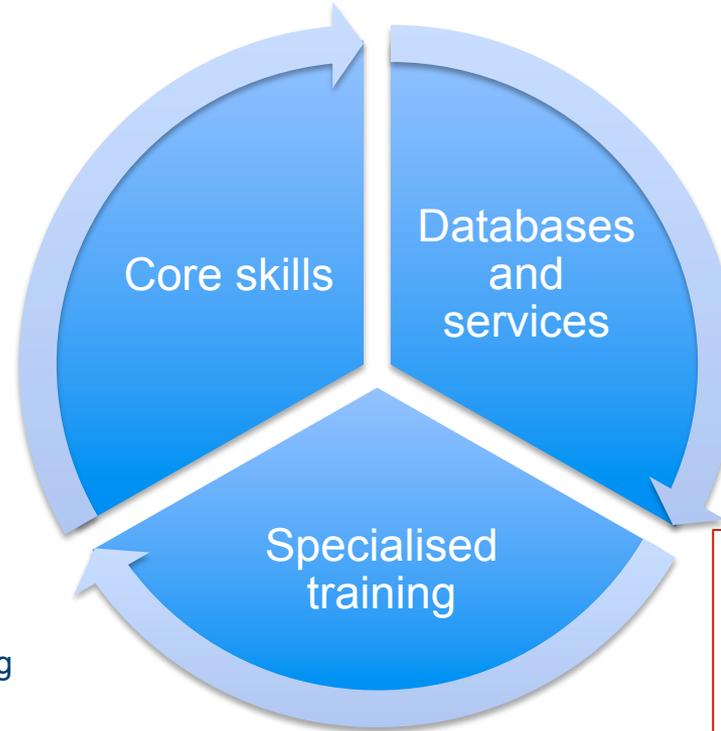


Total number of trainees



Bioinformatics postgraduate training @ UoC

- Introduction to:
 - ✓ MATLAB,
 - ✓ PERL,
 - ✓ Python and
 - ✓ R
- Data Carpentry
- Introductory statistics and experimental design for genomics
- Software Carpentry
- Statistical analysis using R



- Interpreting the clinical genome with Decipher
- Biological data analysis using InterMine
- EMBL-EBI courses:
 - ✓ GWAS catalog
 - ✓ Interactions & pathways – IntAct
 - ✓ Interactions & pathways – Reactome
 - ✓ Network analysis - Cytoscape and PSICQUIC
 - ✓ Ensembl API workshop

- Analysis of DNA methylation using sequencing
- Image analysis for biologists
- Introduction to Galaxy: RNA-seq and ChIP-seq data analysis
- Introduction to RNA-seq and ChIP-seq data analysis
- Molecular phylogenetics

New courses for 2017:

- Analysis of RNA-seq data with Bioconductor
- An introduction to Machine Learning
- Python: Functions and Modules; Best Practices
- Introduction to Machine Learning with R

What do we aim for?

- Course content. Courses consist of a well balance mixture of lectures and hands-on sessions
- Software choice. Focus on the use of open source, stable, actively developed and well-maintained software tools (i.e. Bioconductor, Galaxy,...)
- Objectives. Trainees should learn:
 - ✓ how to interpret biological data;
 - ✓ what a specific data analysis pipeline entails; and
 - ✓ how to critically evaluate the data analysis tools available.
- Objectives. We want to enable you to establish a partnership with your statistician and/or bioinformatician collaborators, based on mutual understanding

Bacterial Genome Assembly & Annotation in Galaxy– June 8

- Cover the basics of *de novo* genome assembly using small genome example
- Focusing on project planning, selecting fragment sizes, initial assembly of reads and then assembling those contigs
- Session includes an introduction to the Galaxy Platform
- Will give participants an understanding of how bacterial genome assembly works, how to run such analysis and be able to annotate a small genome
- Aims:
 1. Introduction to Galaxy
 2. Brief introduction to next generation sequencing data
 3. Genome assembly and its parameters
 4. Automatic genome annotation pipeline

Data Carpentry workshop – Sep 11/12

- Data Carpentry develops and teaches workshops on the fundamental data skills needed to conduct research
- Focus is on the introductory computational skills needed for data management and analysis in all domains of research
- Target audience is learners who have little to no prior computational experience
- Topics:
 1. Data organization in spreadsheets
 2. Data cleaning with OpenRefine
 3. Introduction to R
 4. Data analysis and visualization in R
 5. SQL for data management

Sources of training materials/information

- ELIXIR training portal: <https://tess.elixir-europe.org/>
- GOBLET training portal: <http://mygoblet.org/training-portal>
- Data Carpentry/Software Carpentry:
<http://www.datacarpentry.org/lessons/> and
<http://software-carpentry.org/lessons/>
- See individual course pages on: <http://bioinfotraining.bio.cam.ac.uk/>
- Online resources: EMBL-EBI Train online, EdX (Data for life sciences from Harvard-Irizarry), Coursera, etc.
- Training course catalogue: <https://www.on-course.eu/>
- And many more.....