

New bioinformatics methods and measurement technologies call for continuously updated courses and analysis software

Laboratory technologies evolve all the time. New measurement instruments are producing a huge amount of data that needs to be analysed correctly. Being in a continuous state of change and development, biomedicine needs experts who can train researchers in the latest analysis methods.



For several years, ELIXIR Finland's training coordinator, **Eija Korpelainen**, has been teaching researchers to analyse data.

"Life science and medical degrees don't include much data analysis studies. However, the use of modern measurement techniques requires solid data analysis skills, which is why we give courses at CSC. Different types of data require different analysis methods, so a number of courses are

required. ELIXIR also organises courses for trainers."

The content and teaching material of these courses are available via ELIXIR's TeSS training portal. The portal includes bioinformatics courses offered by ELIXIR's member organisations. Courses and course material are also provided by non-ELIXIR organisations.

ELIXIR EXCELERATE scRNA-seq course. The Finnish ELIXIR centre CSC organises an average of 15 bioinformatics courses a year. Ten international experts gave lectures on the scRNA-seq data analysis methods in May 2019. The presentations were recorded on video and have been viewed more than 3,000 times in a period of around six months (June to October 2019).

High-throughput sequencing

Courses must be updated regularly owing to the rapid development of bioinformatics methods. This puts pressure on the development of CSC's Chipster analysis software, because new analysis tools must be added continuously. Korpelainen says that even the name of the software should be updated:

"Chipster refers to the microarrays or "chips" used to analyse the activity of genes. Gene activity is nowadays measured with high-throughput sequencing (HTS). HTS refers to new equipment and techniques that enable faster and more efficient sequencing."

HTS techniques can be used to study a number of topics. By sequencing exomes, i.e. the genomic areas that code proteins, it is possible to learn about gene variants related to illnesses.

The Chipster software consists of more than 400 analysis tools and an extensive collection of reference data. Chipster can be used to analyse, visualise and share data interactively.

"Measurement technology is changing all the time. In addition, because data comes in various types, it must be analysed in different ways," says Eija Korpelainen.

As a platform, Chipster can be used for the full range of scientific disciplines, be-

cause it can be integrated with any analysis tool. For example, CSC has a separate version of Chipster for linguistic analyses.

Single cell sequencing

Nature magazine selected the sequencing of single cells as the method of the year in 2013; this technique has since become available to all researchers as measurement technologies have improved. The RNA-sequencing of a single cell (scRNA-seq) can reveal complex and rare cell populations.

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It measures the expression levels of all the genes in each cell separately, thereby providing a more accurate picture of the differences between cells.

The sequencing of a single cell can be used when analysing changes in a transcriptome (set of messenger RNA molecules in one cell). The first analysis of this kind was

published in 2009, describing cells at the early stages of development.

"Expression profiles can be used, for example, to reveal cancer cells or obtain information about drug resistance or the response to cancer treatment."

Chipster software offers a range of scRNA-seq analysis tools.

Range of courses continuously changing

scRNA-seq and HTS techniques are good examples of how rapidly research is progressing thanks to inventions. In order to make the most of the new techniques, researchers must be able to use the latest methods to analyse the data they produce. This means that a lot of training is needed, as indicated by the courses provided by ELIXIR.

"We must regularly update existing courses and develop new ones," says Eija Korpelainen, who goes on to explain that keeping up with bioinformatics methods is both challenging and interesting.

"It is interesting to talk to various experts and read articles that impartially compare various methods. Data analysis in the life sciences and medicine is now so challenging that it attracts data scientists to the field."

Ari Turunen

MORE INFORMATION:

<http://bit.ly/scRNA-seq>

<https://tess.elixir-europe.org>

<http://chipster.csc.fi>

CSC – IT Center for Science

is a non-profit, state-owned company administered by the Ministry of Education and Culture. CSC maintains and develops the state-owned, centralised IT infrastructure.

<http://www.csc.fi>

<https://research.csc.fi/cloud-computing>

ELIXIR

builds infrastructure in support of the biological sector. It brings together the leading organisations of 21 European countries and the EMBL European Molecular Biology Laboratory to form a common infrastructure for biological information. CSC – IT Center for Science is the Finnish centre within this infrastructure.

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