Introduction to cBioPortal

Welcome!

Course material

Andrew Mason BSc (Hons) PhD AFHEA

Lecturer in Cancer Informatics at The University of York

Run a small bioinformatics-focused research group within the Jack Birch Unit

Work on human urothelial cancers and retroviral cancers in birds

Bioinformatic lead for the bladder cancer group of the 100,000 genomes project

Just started my undergraduate teaching role

Elixir-UK Data Stewardship Training Fellow

Improve data management, not just analysis, in life sciences

Development of data management training resources
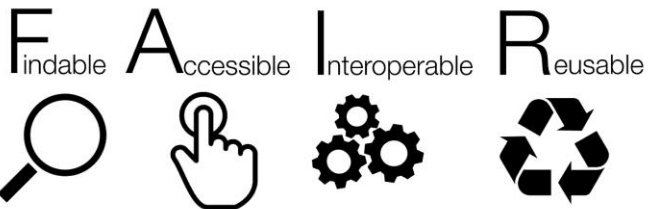
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What is Elixir?

"ELIXIR coordinates and develops life science resources across Europe so that researchers can more easily find, analyse and share data, exchange expertise, and implement best practices."

Improve skills in data management

Improve quality of, and access to, informatics training

Develop and disseminate FAIR data principles in life sciences

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Elixir-UK Data Stewardship Training Fellows

Research Data Management bites ➝ My videos introducing sequencing data

Online training courses, cookbooks and carpentries

Local, in-person training

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Session structure

12.00   Introduction and Learning Objectives

12.10   cBioPortal website demonstration

12.20   Problem-solving tasks

12.45   Recap and Further Resources

12.50   Accessing and using underlying cBioPortal data

13.00   Close

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Learning objectives

1   Recognise the applications and utility of cBioPortal for cancer research

2   Operate and explore the cBioPortal website to identify cancer data of interest

3   Complete two cancer biology problem-solving tasks using cBioPortal

4   Recognise the process for accessing and analysing cBioPortal data

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What is cBioPortal?

cBioPortal
FOR CANCER GENOMICS

cbioportal.org

Public website for exploratory analysis, visualisation and download of large cancer omics datasets, with clinical metadata

Data derived from large consortia, as well as highlighted studies

Data annotated by external reference databases

Depending on the dataset, includes mutations, CNA, gene expression, methylation data *etc.*

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When using cBioPortal, cite the following papers, plus the reference papers for datasets used: Cerami *et al.* 2012, Gao *et al.* 2013

Why use cBioPortal?

cBioPortal
FOR CANCER GENOMICS

Access to the largest, publicly available cancer sequencing studies, all in one place

Explore broader relevance of laboratory/animal studies across cancer types

Hypothesis generation, including student projects

Data visualisation

Exploration of clinical data

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cBioPortal website demo

Introduction to cBioPortal

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