EBI Metagenomics: analysing and exploring metagenomics data

Alex Mitchell [1]

- DNA & RNA
- Beginner
- 0.5 hour

EBI metagenomics is a freely available hub for the analysis and exploration of metagenomic, metatranscriptomic, amplicon and assembly datasets. The resource provides rich functional and taxonomic analyses of user-submitted sequences, as well as analysis of publicly available metagenomic datasets held within the European Nucleotide Archive. It is one of the largest metagenomics data repositories in the world, with over 75,000 publicly available datasets analysed using a standardised pipeline, helping to support comparison of results. This webinar will introduce users to the data analysis pipeline, the website and database, and illustrate the use of the search facility for data discovery.

This webinar was recorded on 8 March 2017. It is best viewed in full screen mode using Google Chrome. The slides from this webinar can be downloaded below.

See the EMBL-EBI training pages for a list of upcoming webinars [2].

This webinar is aimed at scientists with an interest in learning more about the EBI Metagenomics database.

Learning objectives:

- Describe what the EBI Metagenomics resource is and why it exists
- Access the EBI Metagenomics resource website
- Describe the EBI Metagenomics data analysis pipeline

Your feedback

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Contributors

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Alex Mitchell is co-ordinator for the InterPro and EBI Metagenomics databases at EMBL-EBI. He obtained his DPhil in pharmacology from the University of Oxford, and was previously employed as a molecular biologist at the Institute of Psychiatry. He moved to the University of Manchester to work on protein sequence analysis and functional classification, before joining EMBL-EBI in 2011.

Source URL: https://www.ebi.ac.uk/training/online/course/ebi-metagenomics-analysing-and-exploring-metagenomics-data

Links
[1] https://www.ebi.ac.uk/training/online/trainers/mitchell