

ASSEMBLY AND CURATION OF REFERENCE GENOMES FOR THE EARTH BIOGENOME PROJECT

The Earth Biogenome Project (EBP) aims to sequence, assemble, catalog and characterize the genome of every eukaryotic species on Earth. This is now possible thanks to the substantial advances that have taken place in the last years both in the field of sequencing technologies and bioinformatic resources and tools. Genome assemblies generated as part of the EBP should meet certain standards of quality to ensure their contiguity, accuracy, completeness and chromosomal representation. The reference-grade genome assemblies obtained through this initiative can be of great use for downstream analysis to help researchers in biodiversity, conservation, evolution and agrigenomics and, well, cool unexpected biological discoveries.

In this 4-day long course we will focus on how to obtain high-quality chromosome level assemblies by showing how to produce genome assemblies with long-reads and Hi-C data. We will cover all the steps needed to produce and evaluate a genome assembly, paying special attention to the manual curation step.

DETAILS:



06/05/2024 to 09/05/2024

10h to 17h

Edifici Antoni Maria Alcover UIB

- Language: English.
- On-site. Theoretical and practical.
- Maximum 21 attendees.

INTENDED FOR:

Anyone working in and/or interested in genome assembly: graduate students, postdocs, faculty.

TEACHING STAFF:

Tyler Alioto (Centro Nacional de Análisis Genómico - CNAG)

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With assistance of Karen Schöninger (Centre Balear de Biodiversitat, CBB - UIB)

<https://centrebaleardebiodiversitat.uib.es/equipo-3/>

REQUIREMENTS:

- Personal laptop computer: Mac, Linux or Windows (with MobaXterm or similar terminal installed)
- Software: PretextView (<https://github.com/wtsi-hpag/PretextView>), IGV (igv.org).
- Installation of specific R packages.

Free course. REGISTRATION required

Organised by <https://centrebaleardebiodiversitat.uib.cat/> Contact: a.diaz@uib.cat



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