Analysing target capture data for phylogenomics

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29th November and 6th December OR 6th and 13th December

10:00 – 12:00 [optional]

13:00 – 17:00

1. **Aim**

To train user analysing target capture data, from handling sequencing files to inferring species trees

1. **Target audience**

Everyone dealing with target capture data is welcome

1. **Ideal requirements**
   1. Basic knowledge on command line
   2. Basic knowledge on tree estimation methods
   3. Basic theoretical notion about the recovery process
2. **Structure**

The course is divided in two afternoons, with optional morning sessions for doubts. The afternoons are one week apart to provide time to play with the data on each own pace. Play data will be provided for the training, but attendees are invited to work with their own data afterwards

1. **Programme**
   * Brief review of the pipeline
   * Preparing files (raw reads and target files)
   * Quality check [FASTQC]
   * Quality trimming [Trimmomatic]
   * Sequence assembly [HybPiper]
   * Sequence retrieve [HybPiper]
   * Alignment [MAFFT]
   * Gene tree estimation [RAxML]
   * Species tree estimation [ASTRAL III]
   * Plotting species tree [R]
2. **Schedule**

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| First day | Second day |
| 10:00–12:00 Morning session [opt]  Basic commands  Using cluster  File handling | 10:00–12:00 Morning session [opt]  Doubts and troubleshooting |
| 12:00–13:00 Lunch | 12:00–13:00 Lunch |
| 13:00–17:00 Morning session  Brief review of the pipeline  Preparing files  Quality trimming  Sequence assembly | 13:00–17:00 Morning session  Sequence retrieve and alignment  Gene tree estimation  Species tree estimation  Plotting species tree |