protocols.io
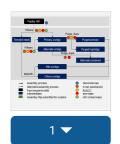
🌐 ToLA Assembly Pipeline 1 V.1

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DToL-ToLA

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Here you find the first assembly pipeline developed by the Tree of Life Assembly Team (ToLA) to assemble the genomes sequenced in the first 2 years of the Darwin Tree of Life Project (DToL), which belongs to the Tree of Life Department of the Wellcome Sanger Institute (https://www.darwintreeoflife.org). DToL aims to generate high-quality genomes for all named eukaryotes occurring in Britain and Ireland. This protocol describes all softwares and bioinformatics steps (assembly, polishing and scaffolding) ran to generate chromosome-level genomes with three data types: (i) PacBio Hifi, (ii) Linked-reads (Chromium 10X) and (iii) Hi-C. First, PacBio HiFi reads are checked and cleaned for adaptors ....

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Reads trimming

1 Pacbio Hifi reads trimming

Input your Pacbio Hifi reads to HiFiAdapterFilt (https://github.com/sheinasim/HiFiAdapterFilt)

HiFiAdapterFilt will convert .bam to .fastq and remove reads with remnant PacBio adapter

sequences.

HiFiAdapterFilt

bash pbadapterfilt.sh [-p file Prefix] [-l minimum Length of adapter match to remove. Default=44] [-m minimum percent Match of adapter to remove. Default=97] [-t Number of threads for blastn. Default=8] [-o outdirectory prefix Default=.]