Resource Summary Report

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Plasmid Sequence Analysis from Long Reads

DOI:10.17504/protocols.io.bqu3mwyn
Type: Protocol

Proper Citation

David Eccles 2020. Plasmid Sequence Analysis from Long Reads. protocols.io dx.doi.org/10.17504/protocols.io.bqu3mwyn

Protocol Information

URL: https://dx.doi.org/10.17504/protocols.io.bqu3mwyn

Authors: David Eccles

Summary: This protocol demonstrates how to assemble reads from plasmid DNA, and generate a circularised and non-repetitive consensus sequenceAt the moment, this protocol uses Canu to de-novo assemble high-quality single-cut reads.Input(s): demultiplexed fastq files (see protocol Demultiplexing Nanopore reads with LAST). I've noticed that the default demultiplexing carried out by Guppy (at least up to v4.2.2, as used in the first version of this protocol) has issues with chimeric reads, which can affect assembly.Output(s):Consensus sequence per barcode as a fasta fileOutput(s):

Affiliations: Malaghan Institute of Medical Research (NZ)

Version: 4

Publication Date: 2020

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