

Resource Summary Report

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Run Centrifuge using iMicrobe

DOI:10.17504/protocols.io.spuednw

Type: Protocol

Proper Citation

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Protocol Information

URL: <https://dx.doi.org/10.17504/protocols.io.spuednw>

Authors: Alise Ponsero

Group: iMicrobe, Metafunc course 2018

Summary: How to run Centrifuge version 1.0.4-beta (Kim et al. 2016) through the iMicrobe platform. Centrifuge is a microbial classification engine that enables rapid, accurate, and sensitive taxonomic labeling of metagenomic reads and quantification of species. The system uses an indexing scheme based on the Burrows-Wheeler transform (BWT) and the Ferragina-Manzini (FM) index, optimized specifically for the metagenomic classification problem. More information about centrifuge can be found here : <https://ccb.jhu.edu/software/centrifuge/manual.shtml>

Affiliations: University of Arizona

External URL: <https://www.imicrobe.us/#/apps/71>

Version: 1

Publication Date: 2018

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