

Tutorial 9 – TreeSAPP

13 NOVEMBER 2020

MICB405

Install TreeSAPP
on Orca



Run TreeSAPP on
sample data
provided



`scp` and analyze
output in RStudio
on your laptops

Workflow

Building reference packages with TreeSAPP

Connor Morgan-Lang edited this page on Oct 7 · 10 revisions

Overview

This tutorial is meant for users who would like to analyze a gene family lacking an associated TreeSAPP reference package (refpkg). This tutorial is also useful to people who find a refpkg is completely useless to them and would rather start over than use `treesapp update`.

Supported versions >=0.8.9

Classifying sequences with treesapp assign

Connor Morgan-Lang edited this page on Sep 11 · 4 revisions

Overview

TreeSAPP's gene-centric classification workflow assigns both a gene name and taxonomic label to amino acid sequences. It is capable of classifying either genomic or proteomic sequences in this manner, and they can be derived from genomes (isolate, single-cell amplified or metagenome-assembled) or metagenomes. The TreeSAPP subcommand used for classifying sequences is `treesapp assign`. Nucleotide reference packages are currently not supported.

Supported versions >=0.8.9





CORRECTED PROOF

TreeSAPP: the Tree-based Sensitive and Accurate Phylogenetic Profiler

Connor Morgan-Lang, Ryan McLaughlin, Zachary Armstrong, Grace Zhang, Kevin Chan, Steven J Hallam

Bioinformatics, btaa588, <https://doi-org.ezproxy.library.ubc.ca/10.1093/bioinformatics/btaa588>

Published: 08 July 2020 **Article history**

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