

Project
Folder

R object “project.folder” is the umbrella folder where all data and outputs will live.

FASTAs

The FASTAs folder will contain FASTA files for your draft genome and queries.

BlastDBs

The BlastDBs folder will be populated with a BLAST database for your draft genome,

Output_FASTAs

The Output_FASTAs folder will be populated with FASTA files contained scaffolds of interest identified via BLAST search.

ORFs_report

The ORFs_report folder will be populated with csv files with data about ORFs identified in scaffolds of interest.

AA_ORFs

The AA_ORFs folder will be populated with FASTA files of all ORFs per scaffold translated to amino acid sequences.

AA_BlastDB

The AA_Blast_DB folder will be populated with BLAST databases for use in annotating ORFs.

AA_FASTA

The AA_FASTA folder will be populated with FASTA files of translated ORFs of interest.