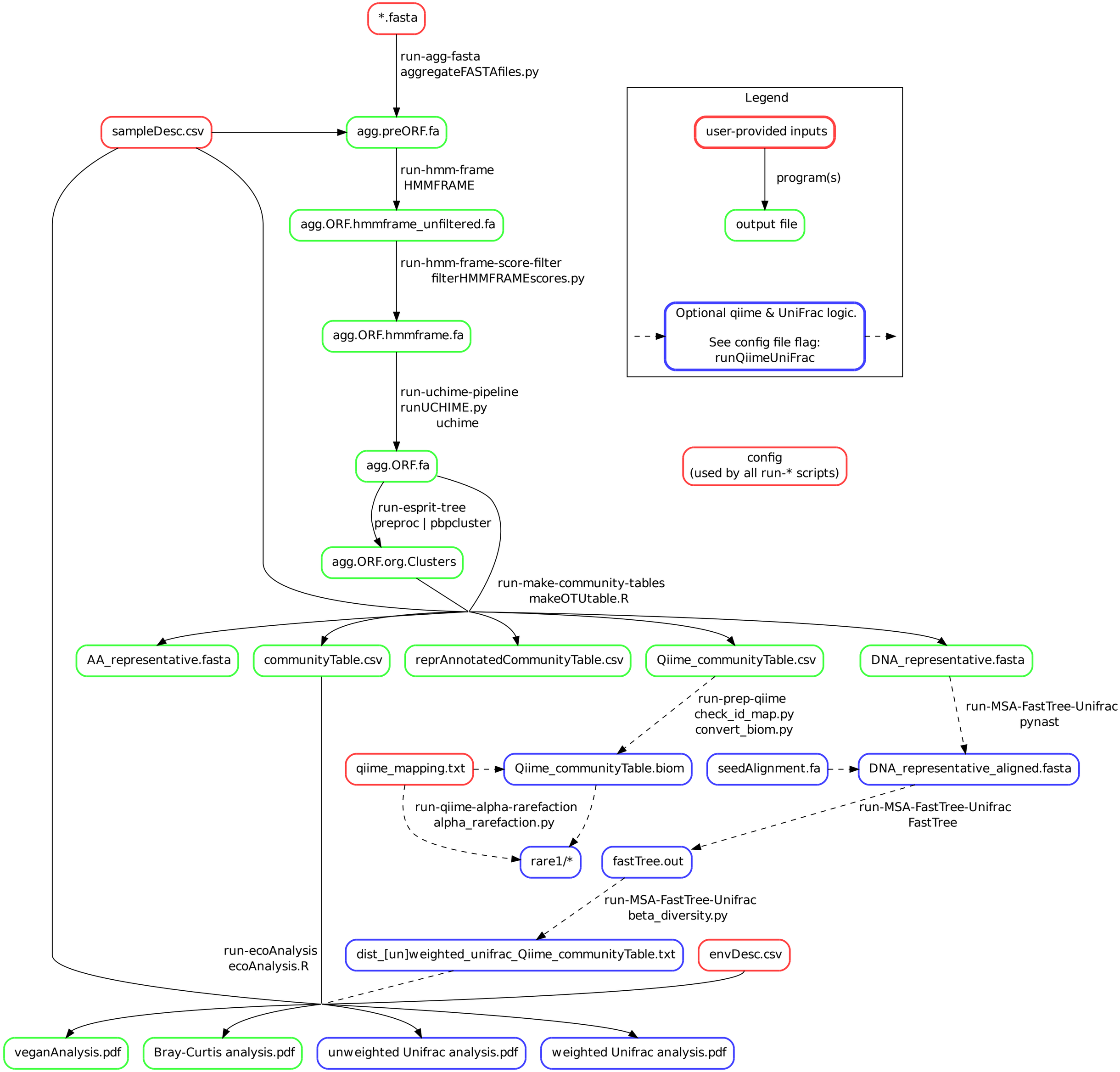
*.fasta
run-agg-fasta
aggregateFASTAfiles.py
sampleDesc.csv
agg.preORF.fa
run-hmm-frame
HMMFRAME
agg.ORF.hmmframe_unfiltered.fa
run-hmm-frame-score-filter
filterHMMFRAMEscores.py
agg.ORF.hmmframe.fa
run-uchime-pipeline
runUCHIME.py
uchime
agg.ORF.fa
run-esprit-tree
preproc | pbpcluster
agg.ORF.org.Clusters
run-make-community-tables
makeOTUtable.R
AA_representative.fasta
communityTable.csv
reprAnnotatedCommunityTable.csv
Qiime_communityTable.csv
DNA_representative.fasta
run-prep-qiime
check_id_map.py
convert_biom.py
run-MSA-FastTree-Unifrac
pynast
qiime_mapping.txt
Qiime_communityTable.biom
seedAlignment.fa
DNA_representative_aligned.fasta
run-qiime-alpha-rarefaction
alpha_rarefaction.py
run-MSA-FastTree-Unifrac
FastTree
rare1/*
fastTree.out
run-MSA-FastTree-Unifrac
beta_diversity.py
run-ecoAnalysis
ecoAnalysis.R
dist_[un]weighted_unifrac_Qiime_communityTable.txt
envDesc.csv
veganAnalysis.pdf
Bray-Curtis analysis.pdf
unweighted Unifrac analysis.pdf
weighted Unifrac analysis.pdf
Legend
user-provided inputs
program(s)
output file
Optional qiime & UniFrac logic.
See config file flag:
runQiimeUniFrac
config
(used by all run-* scripts)