Functional profiling with Picrust2

Dr. Thomas Keller

Two large questions with 16s

- Who's there
  - Taxonomic profiling (abundance analysis, broadly speaking)
- What are they doing?
  - Functional profiling – extrapolated from marker gene data
    - Main caveat to always keep in mind is that there are several estimations here,
    - Gold standard would be metagenomics to actually assemble metagenomes to more clearly define pathways and abundances

Broad overview of algorithm

- Takes OTUs/ASVs and maps them to a reference 16s with sequenced genomes
- Predict copy number per ASV/OTU
- Predict abundance per sample
- Map gene families to pathways
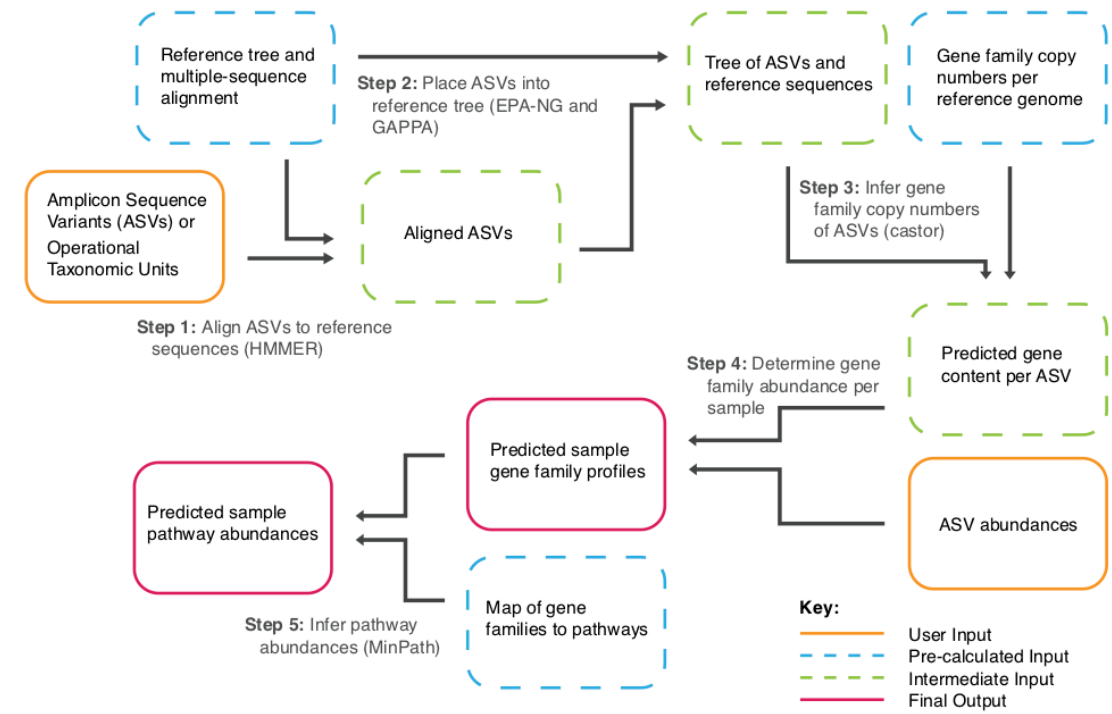
Picrust runs on the commandline/cluster

- We don't have time to delve into linux for this workshop, but I'll show the commands to run Picrust2 for those that want to try this and have a little familiarity with the command line

- The data files provided are the output files from a Picrust2 run

Interpreting Picrust2 data with Aldex2

- The authors of Picrust2 recommend packages like Aldex2 for downstream statistical analysis of the output'

- Gui alternative – STAMP
  - https://beikolab.cs.dal.ca/software/STAMP

- These packages take into account the fact that the data are compositional (relative) based

- Otherwise, the analyses and output very similar to rna-seq differential analyses using DESEQ2 or edgeR