README

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P.helianthoides SSW 16s microbial analysis

This repository holds script used to analyse the 16s rRNA sequences from tissue samples of healthy, exposed, and actively wasting Pycnopodia helianthoides

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Data Availability   Made public once preprint is posted

Scripts   below is a description of the scrpits used in the analysis

Sequence pre-processing and taxa identification

- `AK_SSW_Qiime2` text file containing annotated code for shell commands for running Qiime2 pipeline for sequence cleaning/trimming, diversity metrics, taxonomic assignment, as well as script for running picrust-2

- `ASV Sequence to Taxa ID` contains code for mapping taxonomic assignment back to ASV sequences

- `ggplot_taxa_bar_plot` plots for taxa relative abundances based on Greenegenes taxonomic assignment

Analysis of Composition of Microbiomes with Bias Correction (ANCOM-BC)

- `ANCOM-BC_lev-7_Species` contains code to compare microbial composition between site-health status: Naive vs Exposed | Exposed vs Wasting. Additional code for ven-diagram for number of enriched and depleted taxa.

Picrust-2 pathway analysis

- `Pathways1_average picrust pathways_KO by site-health` calculating average Metacyc pathway and KO enrichment based on animal site-health status (Naive, Exposed, Wasting)

- `Pathways2_Brite ID for KO terms` mapping KO number to Brite hierarchies for biological function

- `Pathways3_KO_Brite_Plots` plots for Brite hierarchies

Bayesian stochastic blockmodeling