

# README

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## **P.helianthoides SSW 16s microbial analysis**

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

## **Data Availability**

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Made public once preprint is posted

## **Scripts**

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below is a description of the scripts 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**