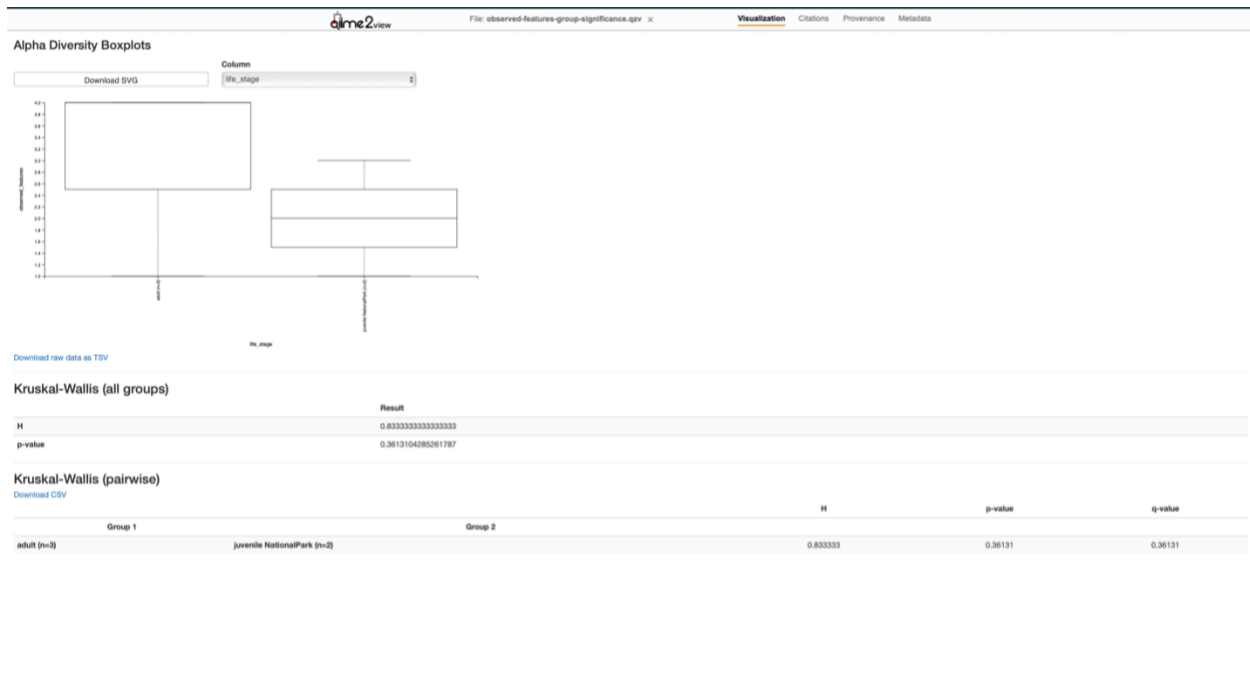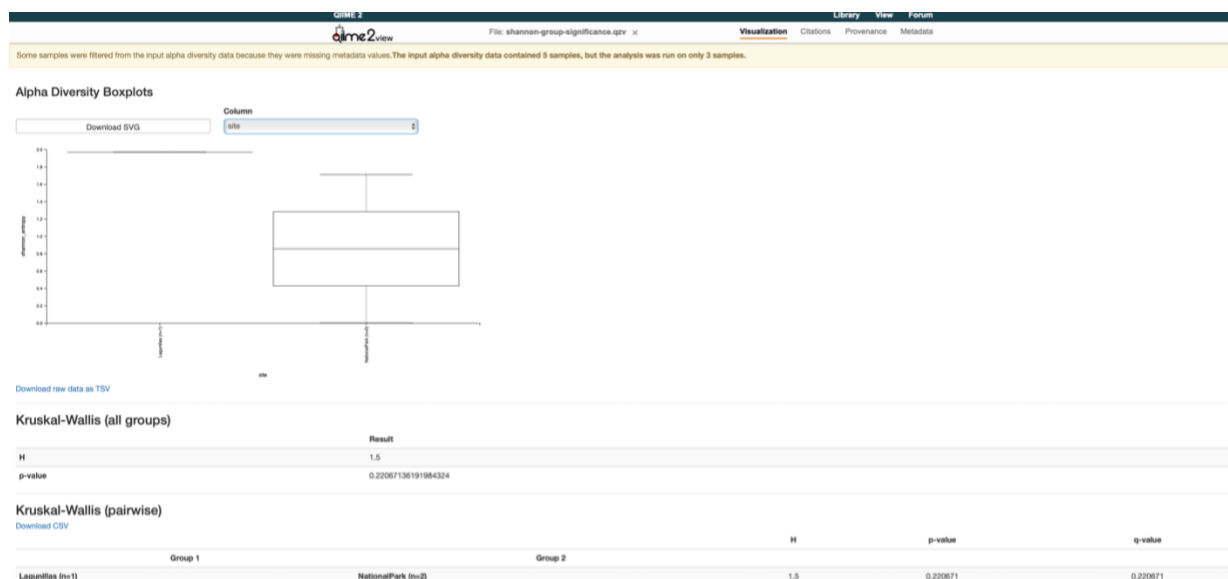1.) All samples had less than 10,000 reads. In total there were 18 samples.
2.) Filing by taxon, majority are from the kingdom bacteria. This file shows us the taxonomic classification results from the sequencing data. The output shows the taxon and confidence values.
3.) The only thing other than bacteria I see is unassigned. Other things that might show up could be mitochondria, chloroplasts, archaea, and unassigned.
4.) When visualizing the taxa bar plot, I notice only the kingdom bacteria was present. Changing level will also include specific classification such as class, order, family...etc. No, there weren't any noticeable changes when sorting to life stage or site of collection.
5.) Shannon diversity measures both richness and evenness of the taxa and their abundance while, observed features only measures richness. They both measure the diversity within a sample.
6.) No, there weren't any significance as all the p-value >0.05. Indicating that there is no correlation between the samples.

QIIME2 view — File: observed-features-group-significance.qzv — Visualization · Citations · Provenance · Metadata

Alpha Diversity Boxplots

Column: life_stage

Download SVG

Download raw data as TSV

Kruskal-Wallis (all groups)

	Result
H	0.833333333333333
p-value	0.361310428526178

Kruskal-Wallis (pairwise)

Download CSV

Group 1	Group 2	H	p-value	q-value
adult (n=3)	juvenile NationalPark (n=2)	0.833333	0.36131	0.36131

Some samples were filtered from the input alpha diversity data because they were missing metadata values. The input alpha diversity data contained 5 samples, but the analysis was run on only 3 samples.

Alpha Diversity Boxplots

Download raw data as TSV

Kruskal-Wallis (all groups)

	Result
H	1.5
p-value	0.22067136191984324

Kruskal-Wallis (pairwise)
Download CSV

Group 1	Group 2	H	p-value	q-value
Lagunillas (n=1)	NationalPark (n=2)	1.5	0.220671	0.220671

7.) Alpha and beta diversity differ as alpha forces on diversity within a single sample, while beta compares the difference between the samples. Bray-Curtis distance measures how dissimilar two samples are based on the abundance and presence of the species. Weighted UniFrac distance use phylogenetic relationship between the species and the abundance to measure the difference between their evolutionary history.

8.) qiime diversity beta-group-significance \
--i-distance-matrix diversity-metrics-results/weighted_unifrac_distance_matrix.qza \
--m-metadata-file metadata.txt \
--m-metadata-column life_stage \
--o-visualization diversity-metrics-results/weighted-unifrac-life-stage-significance.qzv \
--p-pairwise

qiime diversity beta-group-significance \
--i-distance-matrix diversity-metrics-results/weighted_unifrac_distance_matrix.qza \
--m-metadata-file metadata.txt \
--m-metadata-column site \
--o-visualization diversity-metrics-results/weighted-unifrac-site-significance.qzv \
--p-pairwise

9.) No, there weren't any statistically significant different as the p-value is higher than 0.05 for both metrics. For the site comparison, there weren't any significant differences as the p-value was higher than 0.05 as well.

Overview

	PERMANOVA results
method name	PERMANOVA
test statistic name	pseudo-F
sample size	5
number of groups	2
test statistic	1.847742
p-value	0.403
number of permutations	999
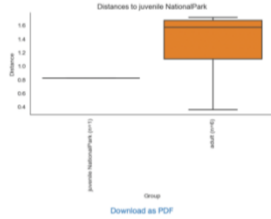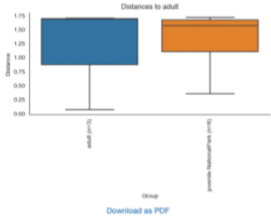
Group significance plots

Download raw data as TSV

Download as PDF

Download as PDF

Pairwise permanova results

Download CSV

Group 1	Group 2	Sample size	Permutations	pseudo-F	p-value	q-value
adult	juvenile NationalPark	5	999	1.847742	0.398	0.398

qiime2view   File: bray-curtis-life-stage-significance.qzv   ×   **Visualization**   Citations   Provenance   Metadata

Overview

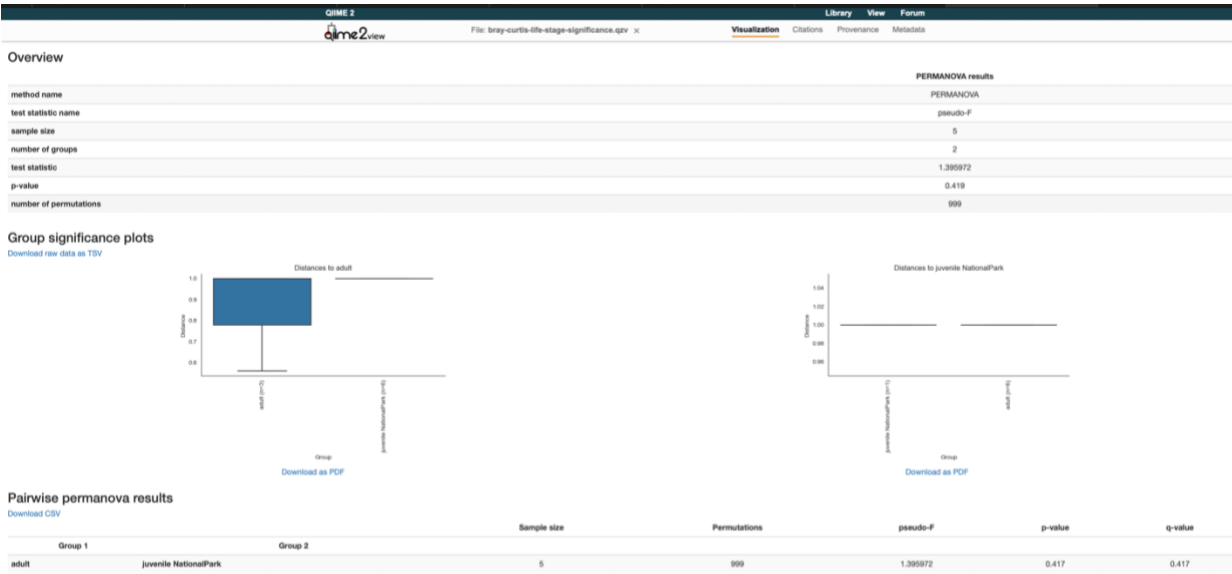|	PERMANOVA results
method name	PERMANOVA
test statistic name	pseudo-F
sample size	5
number of groups	2
test statistic	1.395972
p-value	0.419
number of permutations	999

Group significance plots

Download raw data as TSV

Distances to adult

Distances to juvenile NationalPark
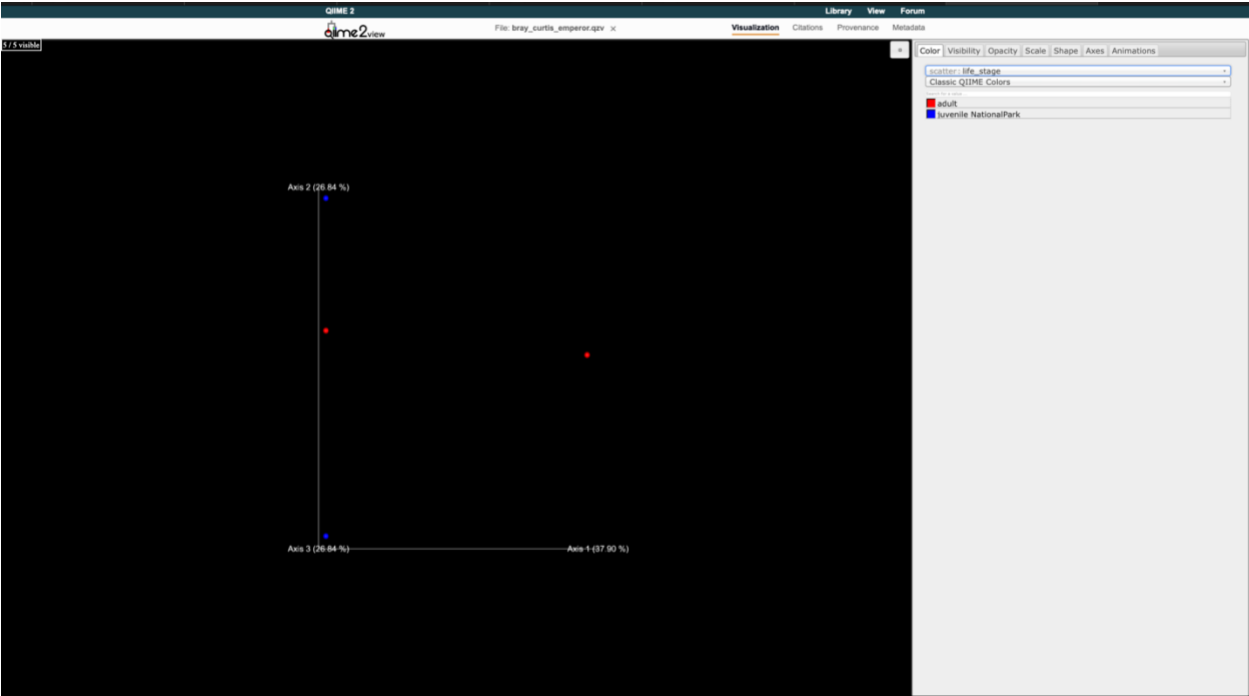
Group

Group

Download as PDF

Download as PDF

Pairwise permanova results

Download CSV

Group 1	Group 2	Sample size	Permutations	pseudo-F	p-value	q-value
adult	juvenile NationalPark	5	999	1.395972	0.417	0.417

10.) As there weren't any differences, the plot showcases that each life stage are randomly placed and show no correlation to one another.

QIIME 2   Library   View   Forum

qiime2view   File: bray_curtis_emperor.qzv   ×   **Visualization**   Citations   Provenance   Metadata

5 / 5 visible

Color | Visibility | Opacity | Scale | Shape | Axes | Animations

scatter life_stage

Classic QIIME Colors

■ adult
■ juvenile NationalPark

Axis 2 (26.84 %)

Axis 3 (26.84 %)   Axis 1 (37.90 %)

11.) No, bar plot could be generate for the life stage. For the site, the only one that was differentially expressed was featureid 133101da24445e40ef32d134c9296a9f under the kingdom bacteria (no species was shown).