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Metadata File

Figure 1: Metadata file containing sample information such as: sample ID, body site, and antibiotic usage.

Barcode File

Figure 2: This file contains the barcodes used during demultiplexing. Each barcode corresponds to a different sample

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Citations: .qza File

Details of gut-table.qza

name: "gut-table.qza"
uuid: "b7bfebb8-42a0-414d-af55-037160c98fc2"
type: "FeatureTable[Frequency]"
format: "BIOMV210DirFmt"

Citations

Citation Format: BibTex ▽   Download

```
@article{framework|qiime2:2024.10.1|0,
  author = {Bolyen, Evan and Rideout, Jai Ram and Dillon, Matthew R. and Bokulich, Nicholas A. and Abnet, Christian C. and Al-Ghalith, Gabriel A. and Alexa
  doi = {10.1038/s41587-019-0209-9},
  issn = {1546-1696},
  journal = {Nature Biotechnology},
  number = {8},
  pages = {852-857},
  title = {Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2},
  url = {https://doi.org/10.1038/s41587-019-0209-9},
  volume = {37},
  year = {2019}
}

@article{view|types:2024.10.0|BIOMV210DirFmt|0,
  author = {McDonald, Daniel and Clemente, Jose C and Kuczynski, Justin and Rideout, Jai Ram and Stombaugh, Jesse and Wendel, Doug and Wilke, Andreas and H
  doi = {10.1186/2047-217X-1-7},
  journal = {GigaScience},
  number = {1},
```

Figure 3: Screenshot of a .qza file showing gut table information such as citation.

Provenance: .qza File

Figure 4: Screenshot of the provenance of gut-table.qza. It includes steps, commands, and metadata used.

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Rep-seq File

Figure 5: Screenshot of Rep-seq file output representing the sequences as a fasta file. These sequences get denoised by DADA2.

Demux.qvz
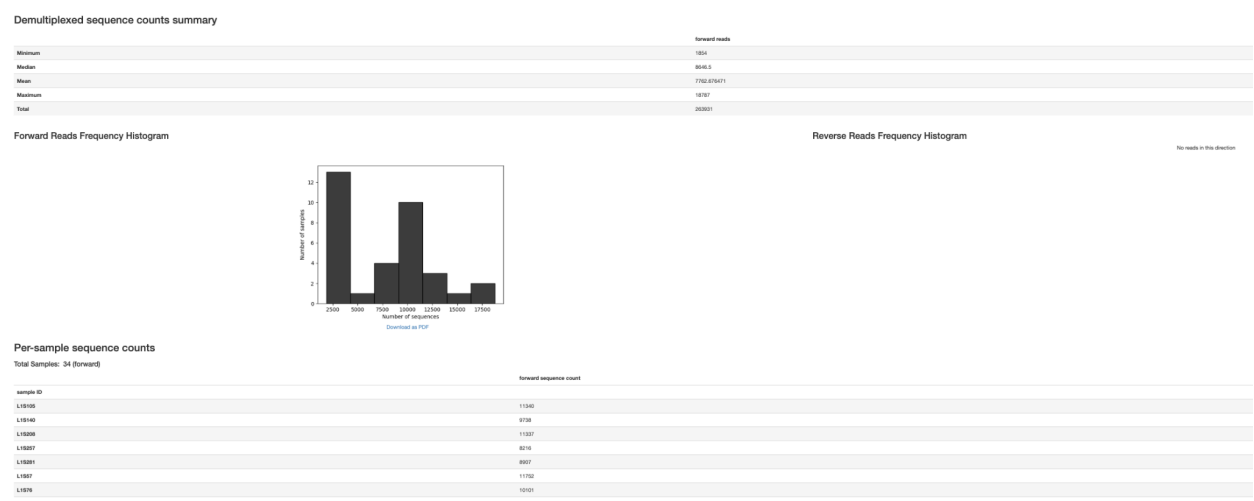
Figure 6: Result summary of the demultiplexed raw sequences. It includes a histogram showing the distribution of forward read counts. No reverse reads, indicating a single-end sequence run.

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Stats-data2 File

| sample-id #q2:types	input numeric	filtered numeric	percentage of input passed filter numeric	denoised numeric	non-chimeric numeric	percentage of input non-chimeric numeric
_1S105	11340	8571	75.58	8499	7780	68.61
_1S140	9738	7677	78.84	7605	7163	73.56
_1S208	11337	9261	81.69	9152	8152	71.91
_1S257	8216	6705	81.61	6627	6388	77.75
_1S281	8907	7067	79.34	6976	6615	74.27
_1S57	11752	9299	79.13	9260	8702	74.05
_1S76	10101	8395	83.11	8337	7867	77.88
_1S8	12388	7663	61.86	7624	7033	56.77
_2S155	9263	4112	44.39	3932	3932	42.45
_2S175	10692	4546	42.52	4386	4386	41.02
_2S204	7299	3379	46.29	3199	3158	43.27
_2S222	8386	3485	41.56	3187	3187	38
_2S240	11986	5183	43.24	5094	5061	42.22
_2S309	3836	1550	40.41	1419	1419	36.99
_2S357	6254	2526	40.39	2373	2373	37.94
_2S382	9301	4279	46.01	4202	4089	43.96
_3S242	2055	970	47.2	951	897	43.65
_3S294	2318	1313	56.64	1225	1225	52.85
_3S313	1996	1191	59.67	1103	1103	55.26
_3S341	1854	1109	59.82	962	962	51.89

Figure 7: Stats-data2 file containing summary statistics of the DADA2 denoising step. It contains information on read input, filtered, merged, retained.

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Table.qvz
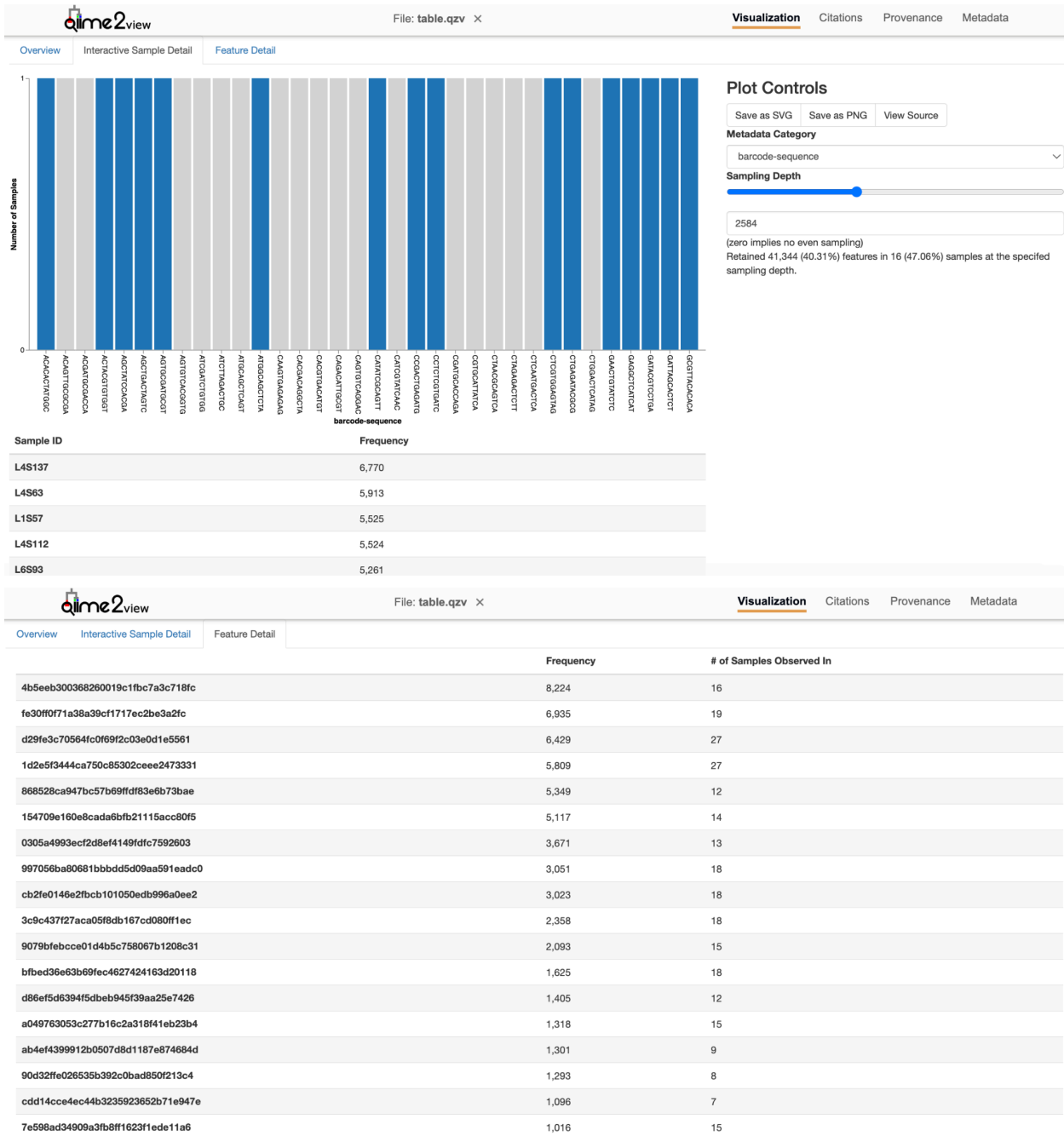
Figure 8: Top figure shows interactive sample detail with adjusted refraction depth. Bottom figure shows figure detail and information of observed representatives per sample.

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Beta Diversity - Unweighted Unifrac
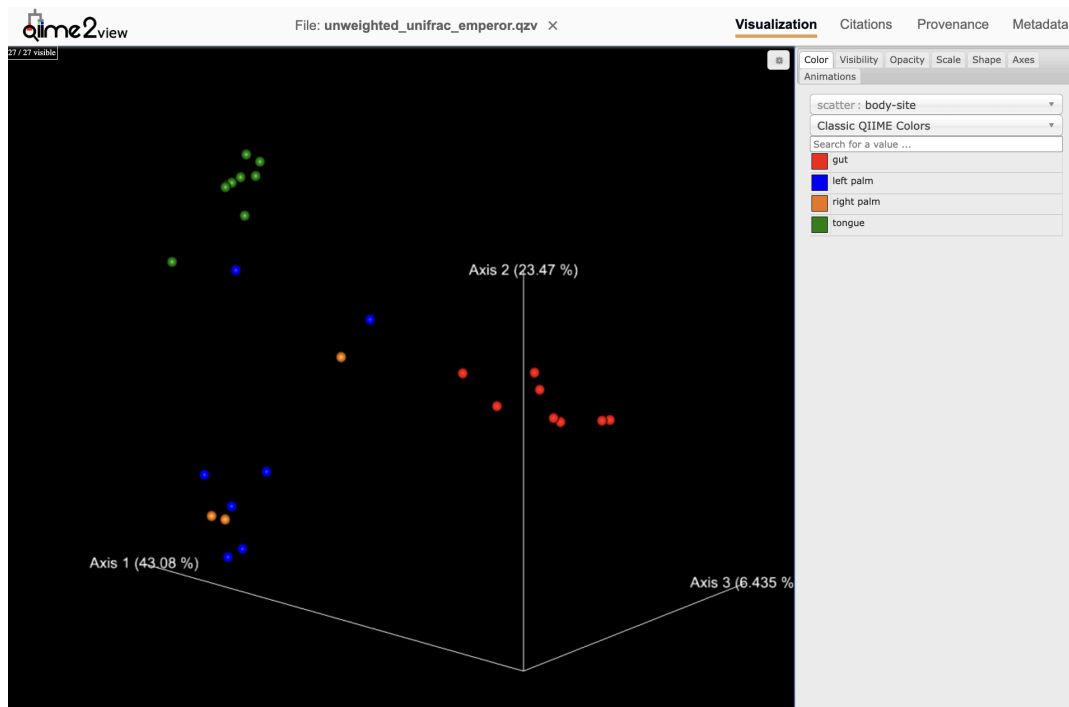
Figure 9: 3D plot of unweighted unifrac (presence or absence) clustered by body-site

Beta Diversity - Weighted Unifrac

Figure 10: 3D plot of weighted unifrac (presence and relative abundance) clustered by body-site

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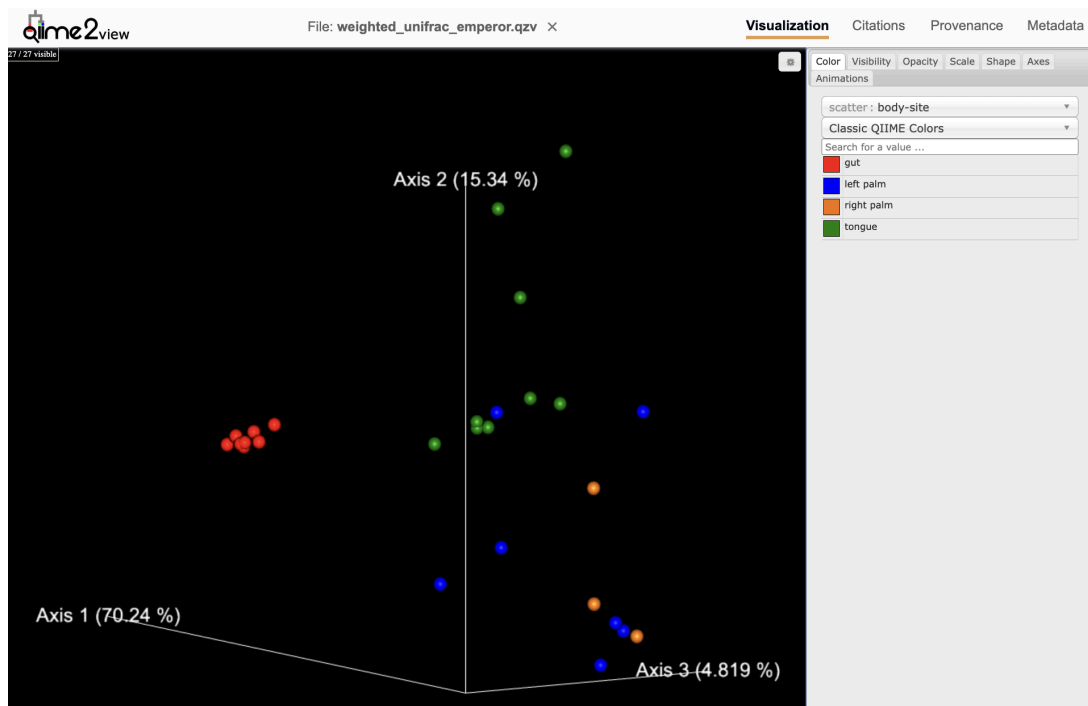## Beta Diversity - Jaccard Distance
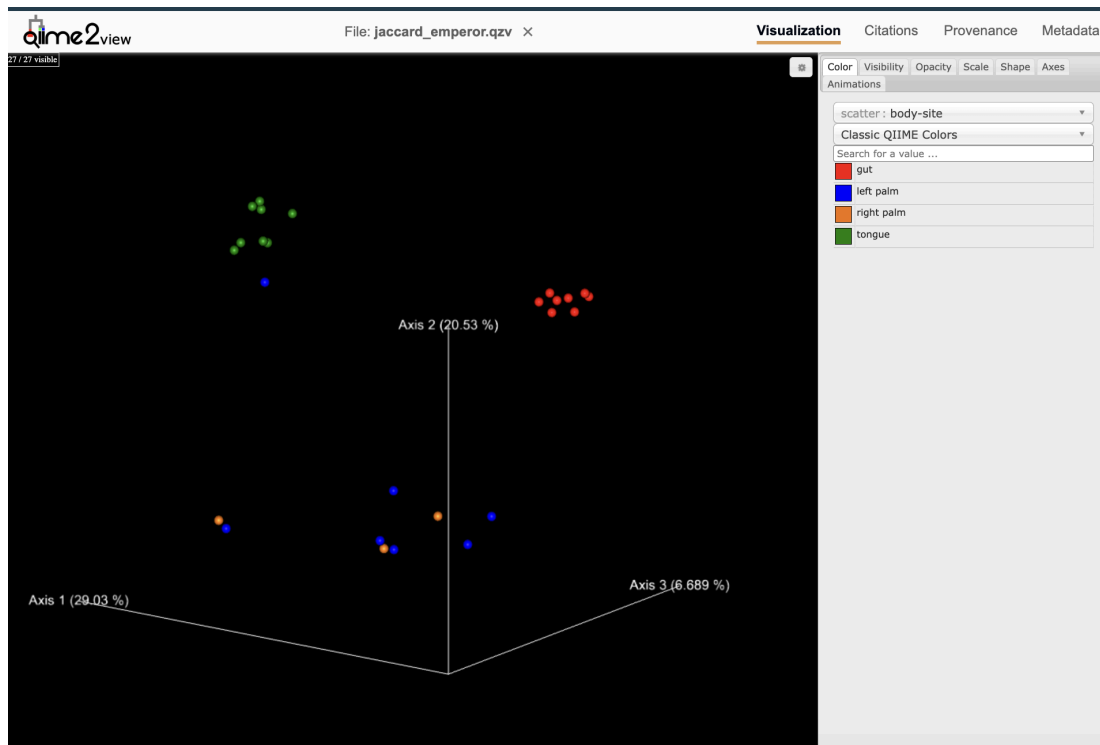
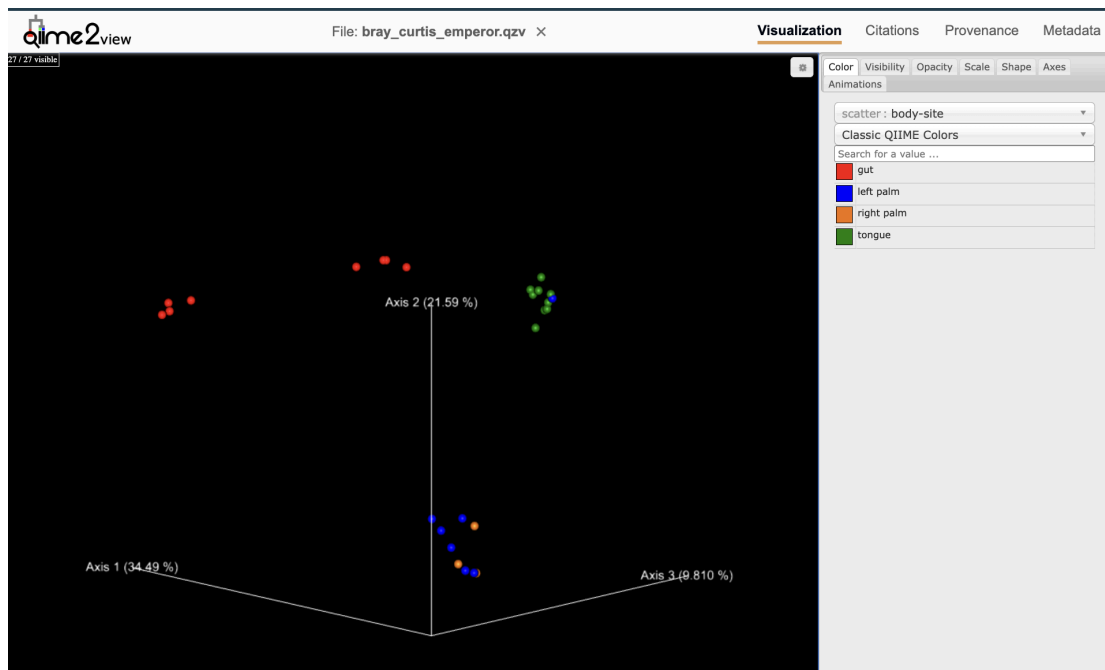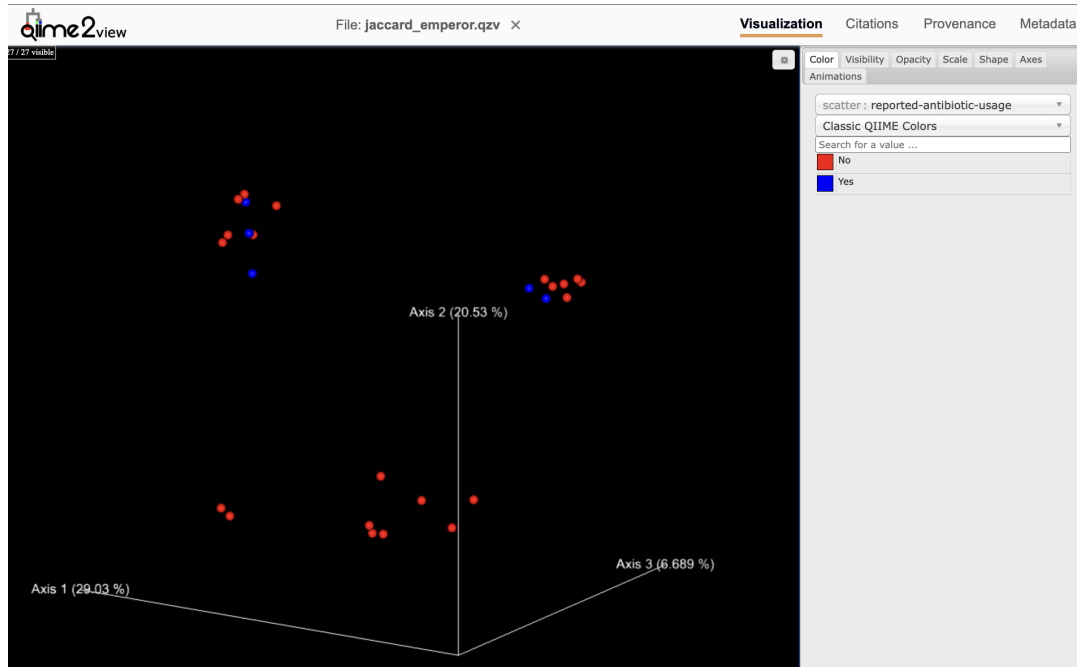**Figure 11:** PCoA plot of jaccard distance (presence or absence) clustered by body-site.

Beta Diversity - Bray-Curtis

Figure 12: 3D plot representing Bray-Curtis distance clustered by body-site. It demonstrates abundant community dissimilarity.
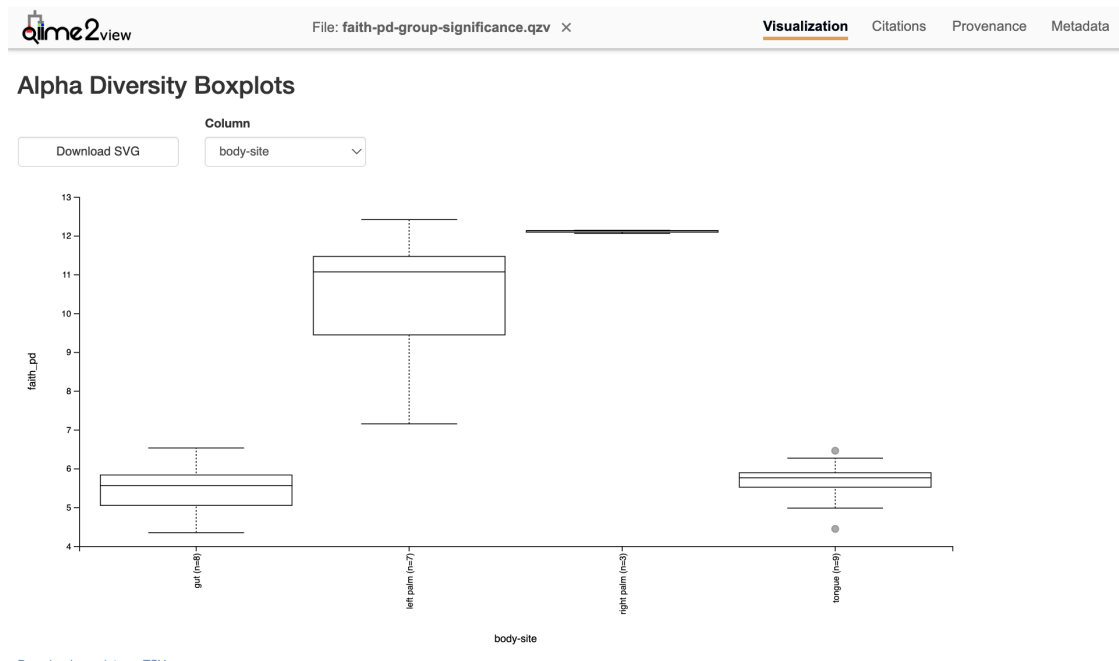
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Beta Diversity - Jaccard Distance

Figure 13: 3D plot of jaccard distance clustered by reported-antibiotic usage.
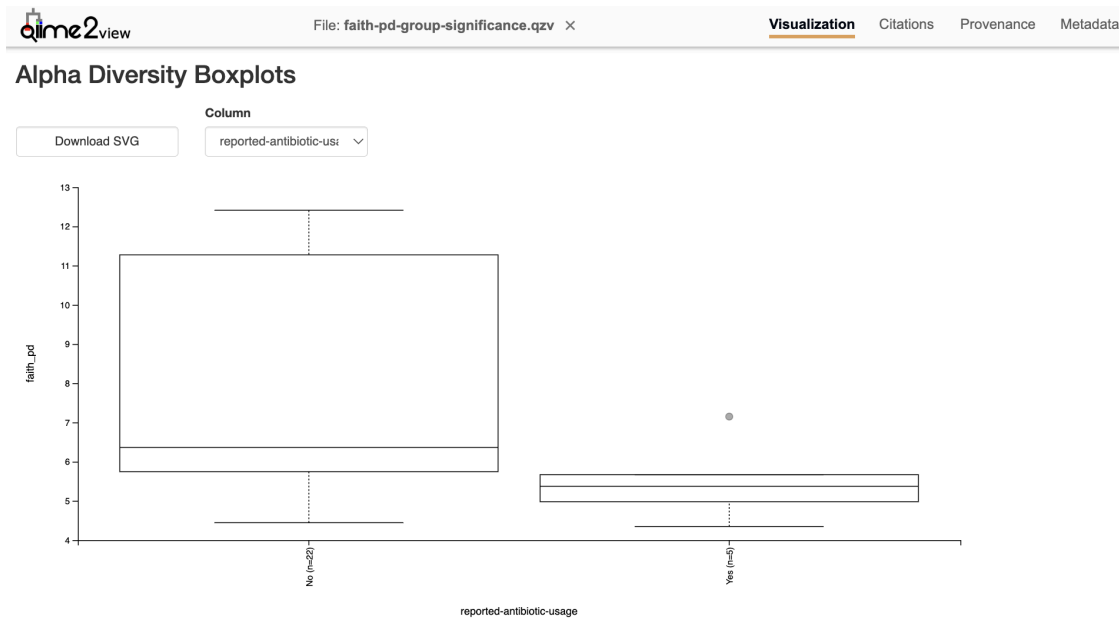
Faith PDs

Figure 14: Boxplot showing significance of Faith PD (phylogenetic diversity) by body site. A Kruskal-Wallis test was performed to test if differences were statistically significant. A p-value of <0.01 was used to show whether diversity differs meaningfully across groups. Left palm had the greatest diversity compared to the other groups.
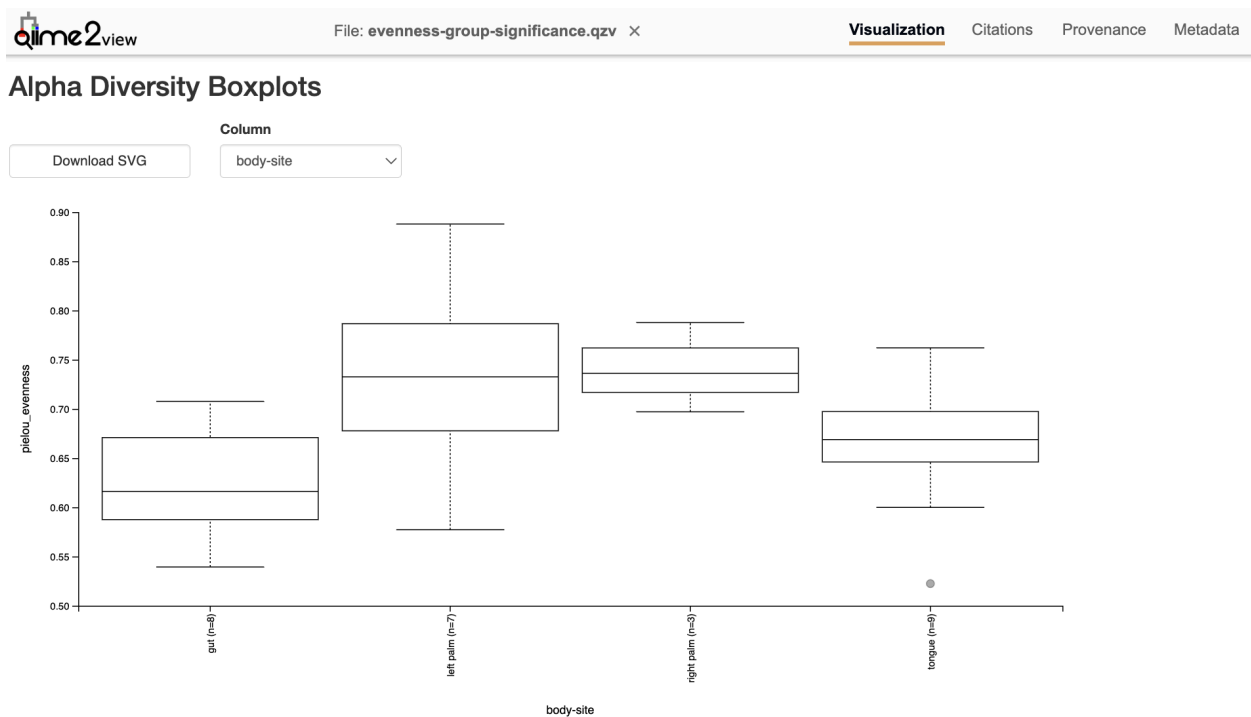
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Alpha Diversity - Faith PDs

Figure 15: Boxplot representing alpha diversity using faith PD to show richness across samples. The group with no antibiotic usage had the greatest richness.

Alpha Diversity - Evenness by Body Site

Figure 16: Boxplot representing alpha diversity by evenness, how even taxa is distributed by body site. Left and right palm had the greatest evenness from the rest of the group which indicates uniform distribution among that specific microbial taxa.
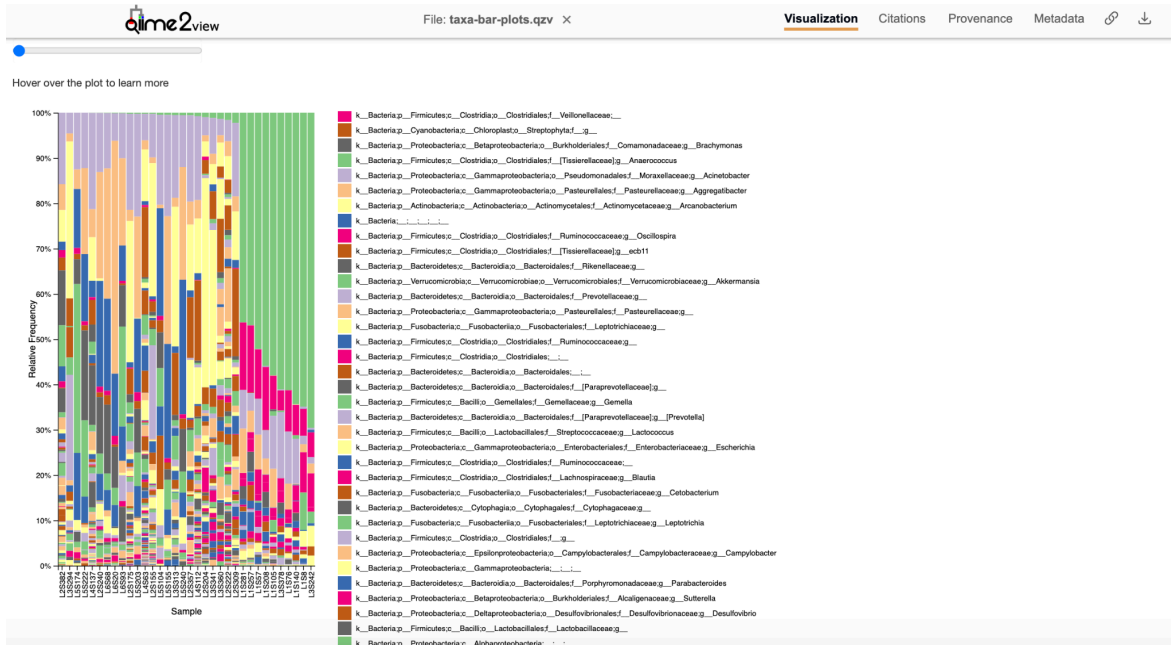
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Alpha Diversity - Evenness by Antibiotic Usage

Figure 17: Alpha diversity microbial evenness by antibiotic usage. The group with no antibiotic usage had a greater microbial evenness distribution, this group dominates.

Taxonomic Analysis

Figure 18: Taxonomic barplot demonstrating microbial composition at genus level. Large green group represents the Bacteroides genus. Commonly found in the human gut microbiome.