

QIIME 2 Example Moving Pictures tutorial





Moving Pictures

QIIME2 online tutorial

Human microbiome samples

2 individuals

Four body sites

Gut, left palm, right palm, and tongue

Five time points (first immediately before antibiotic usage)

Will look at the difference between the body sites





Questions

1. Is there a difference between the communities of the different body sites?
2. Which body sites are different and which are similar?
3. In what ways are the communities different?
4. Are there any biomarkers for the different body sites?





table.qzv

Table summary

| Metric | Sample |
|--------------------|---------|
| Number of samples | 34 |
| Number of features | 759 |
| Total frequency | 157,298 |





table.qzv

Number of reads per sample

Frequency per sample

| | Frequency |
|-------------------|--------------------|
| Minimum frequency | 917.0 |
| 1st quartile | 1,862.5 |
| Median frequency | 4,139.0 |
| 3rd quartile | 7,057.25 |
| Maximum frequency | 10,095.0 |
| Mean frequency | 4,626.411764705882 |

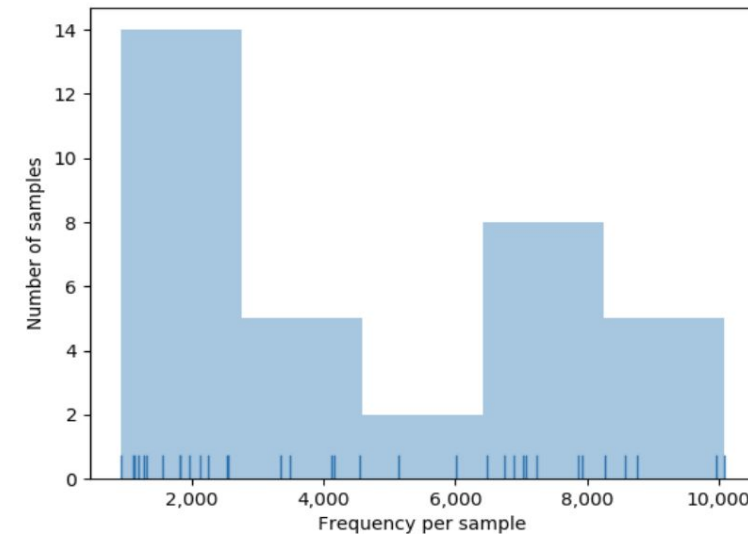


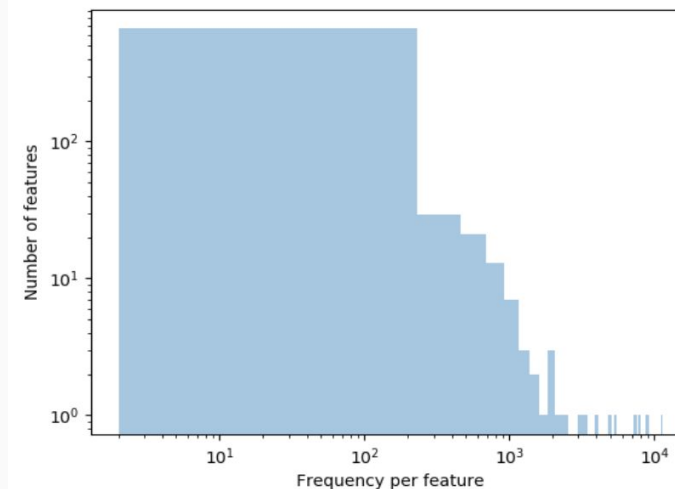


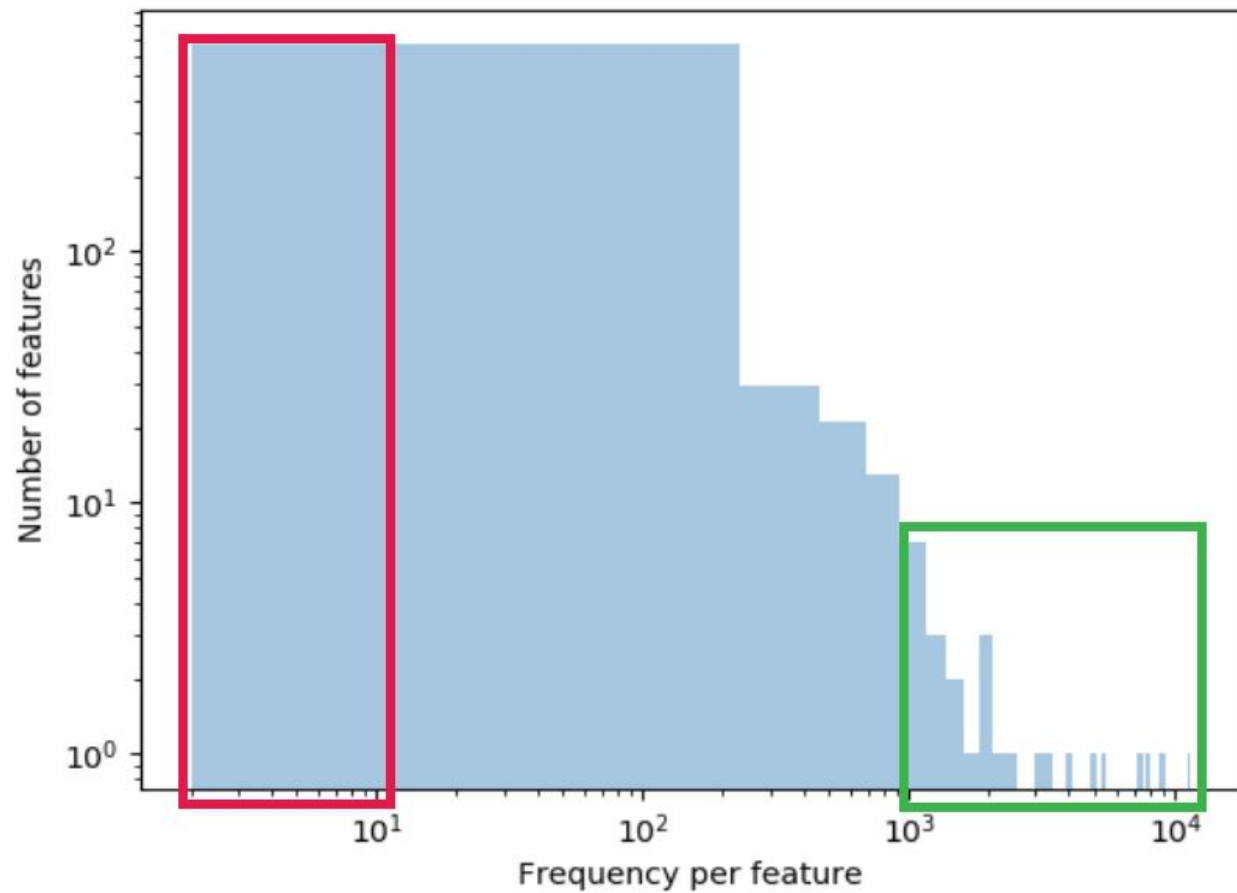
table.qzv

Feature = ASV = Amplicon Sequence Variant
Shows how prevalent different features are

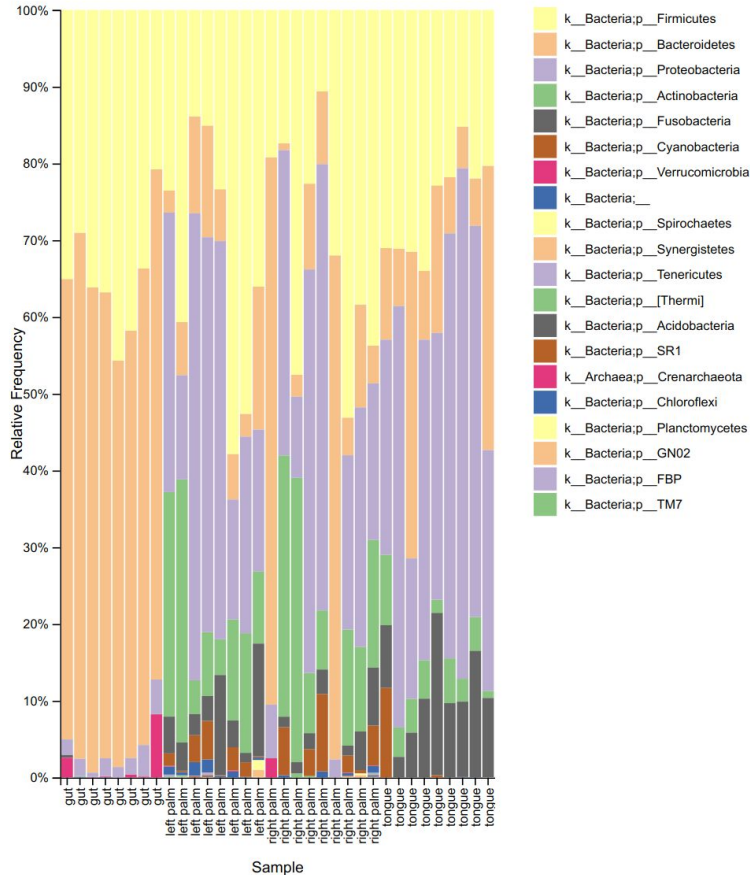
Frequency per feature

| | Frequency |
|-------------------|-------------------|
| Minimum frequency | 2.0 |
| 1st quartile | 9.0 |
| Median frequency | 25.0 |
| 3rd quartile | 83.5 |
| Maximum frequency | 11,497.0 |
| Mean frequency | 207.2437417654809 |





Taxonomy



- QIIME2 plots are interactive
- Can choose different taxa levels to display
- Good for sanity checking
- Does this contain the taxa I expect?
- Any noticeable changes?



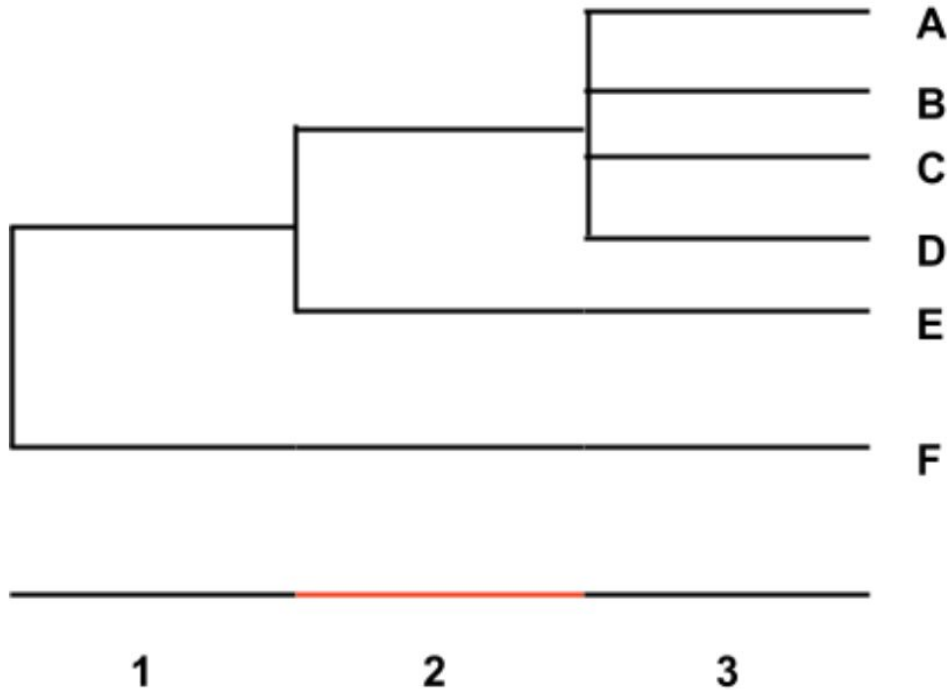


Alpha diversity

- Evenness
 - How even a community is
 - High evenness = all groups have v. similar abundances
 - Low evenness = groups have very dissimilar abundances
- Faith's Phylogenetic Diversity (PD)
 - A qualitative measure of community richness that incorporates phylogenetic relationships between the features
 - In essence a higher PD indicates more diverse ASVs
 - Calculated as the sum of all branch lengths of the ASVs in the group



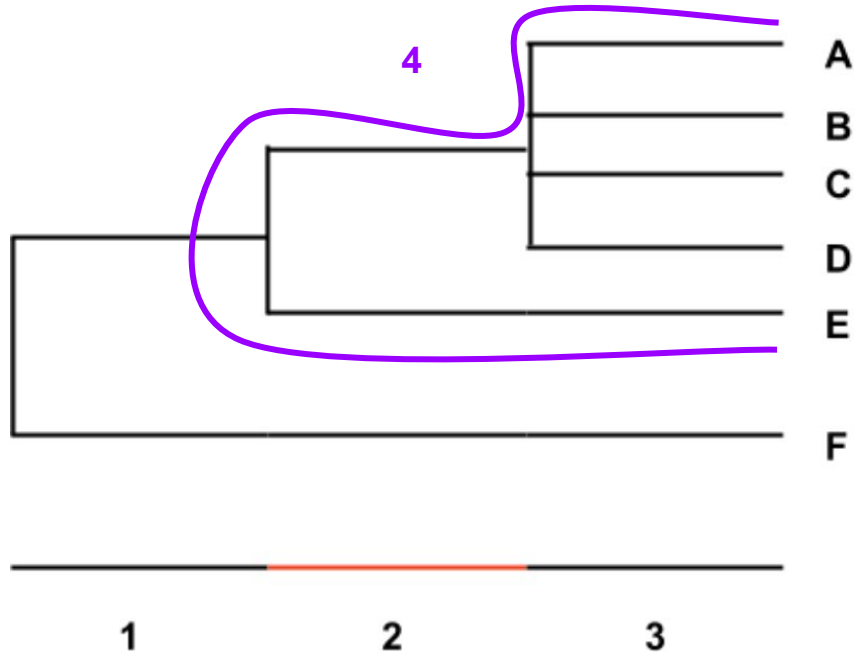
PD example



- Not actual calculation
- Sample 1
 - A & E
 - PD =
- Sample 2
 - A,B,C & D
 - PD =
- Sample 3
 - A, E & F
 - PD =



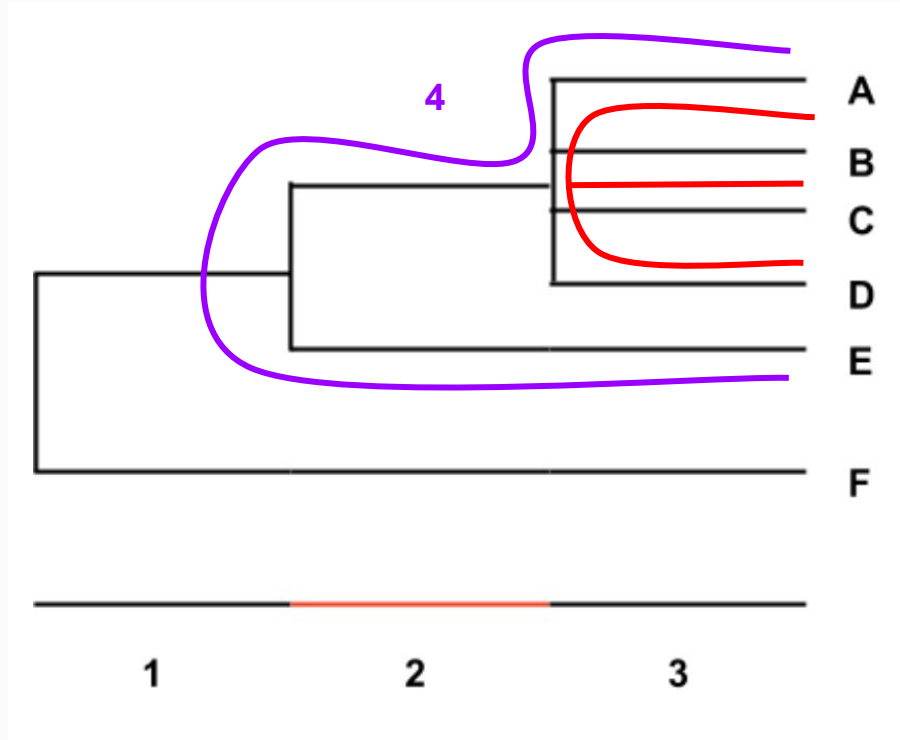
PD example



- Not actual calculation
- Sample 1
 - A & E
 - PD = 4
- Sample 2
 - A,B,C & D
 - PD =
- Sample 3
 - A, E & F
 - PD =



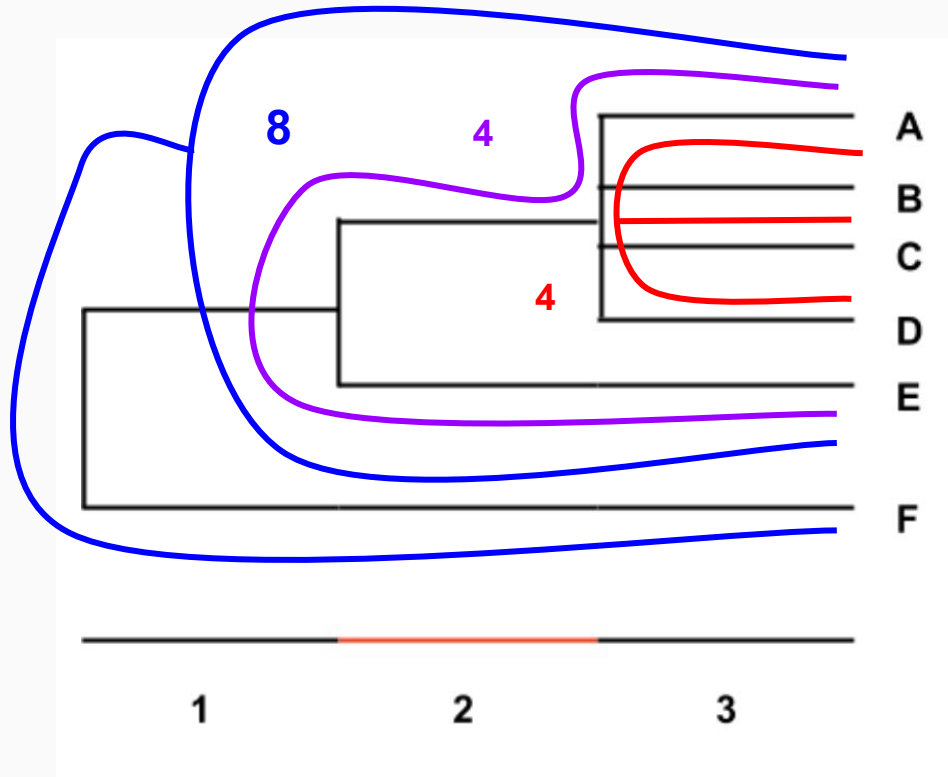
PD example



- Not actual calculation
- Sample 1
 - A & E
 - PD = 4
- 4 • Sample 2
 - A,B,C & D
 - PD = 4
- Sample 3
 - A, E & F
 - PD =



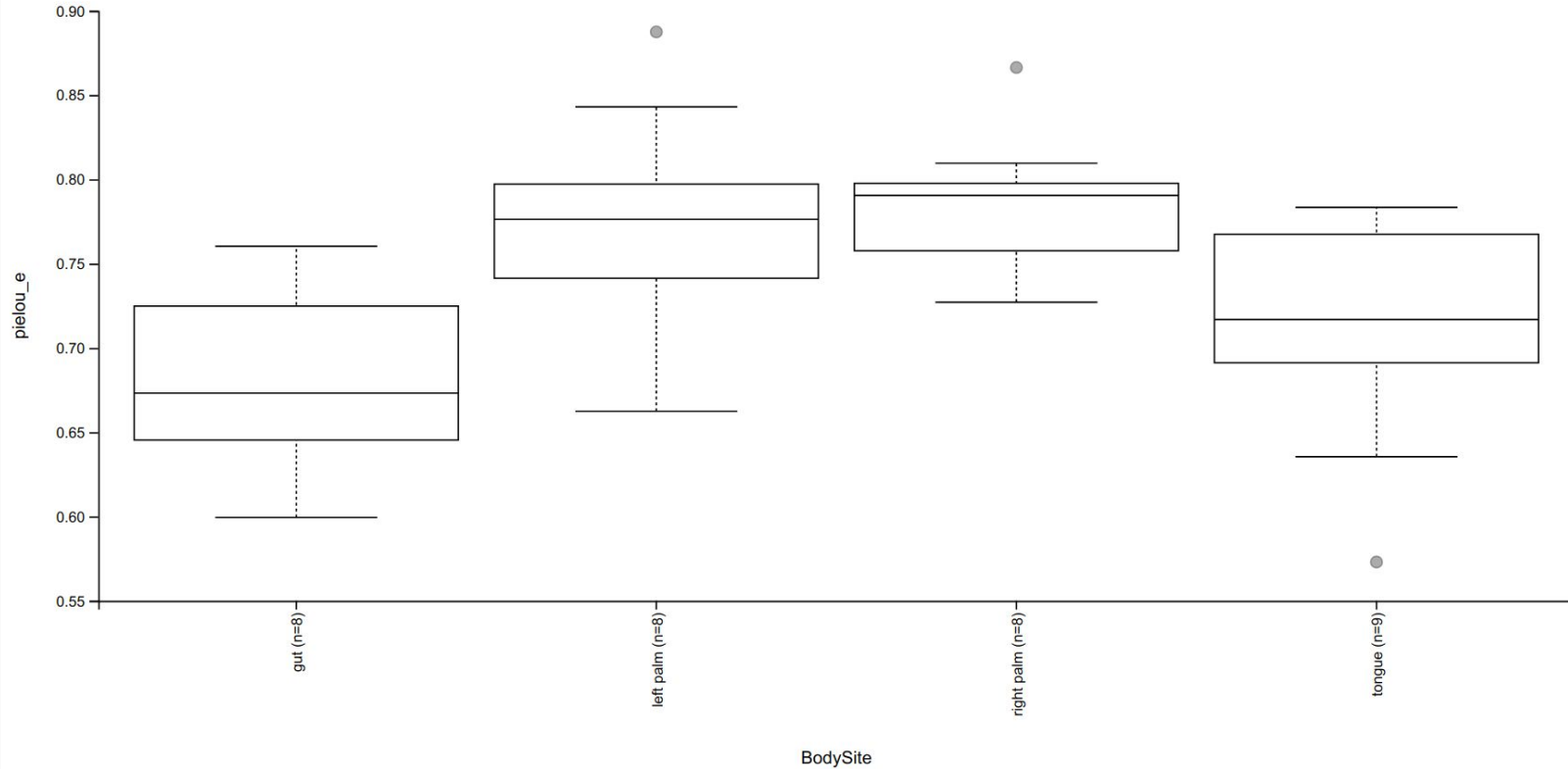
PD example



- Not actual calculation
- Sample 1
 - A & E
 - PD = 4
- Sample 2
 - A, B, C & D
 - PD = 4
- Sample 3
 - A, E & F
 - PD = 8



Body Site Evenness Box plot



Body Site Evenness P & Q values



Kruskal-Wallis (all groups)

| | Result |
|---------|---------------------|
| H | 13.238265002970877 |
| p-value | 0.00414867758580111 |

Kruskal-Wallis (pairwise)

[Download CSV](#)

| | | H | p-value | q-value |
|------------------|------------------|----------|----------|----------|
| Group 1 | Group 2 | | | |
| gut (n=8) | left palm (n=8) | 6.352941 | 0.011719 | 0.024709 |
| | right palm (n=8) | 8.647059 | 0.003276 | 0.019655 |
| | tongue (n=9) | 1.333333 | 0.248213 | 0.297856 |
| left palm (n=8) | right palm (n=8) | 0.397059 | 0.528612 | 0.528612 |
| | tongue (n=9) | 3.000000 | 0.083265 | 0.124897 |
| right palm (n=8) | tongue (n=9) | 6.259259 | 0.012355 | 0.024709 |

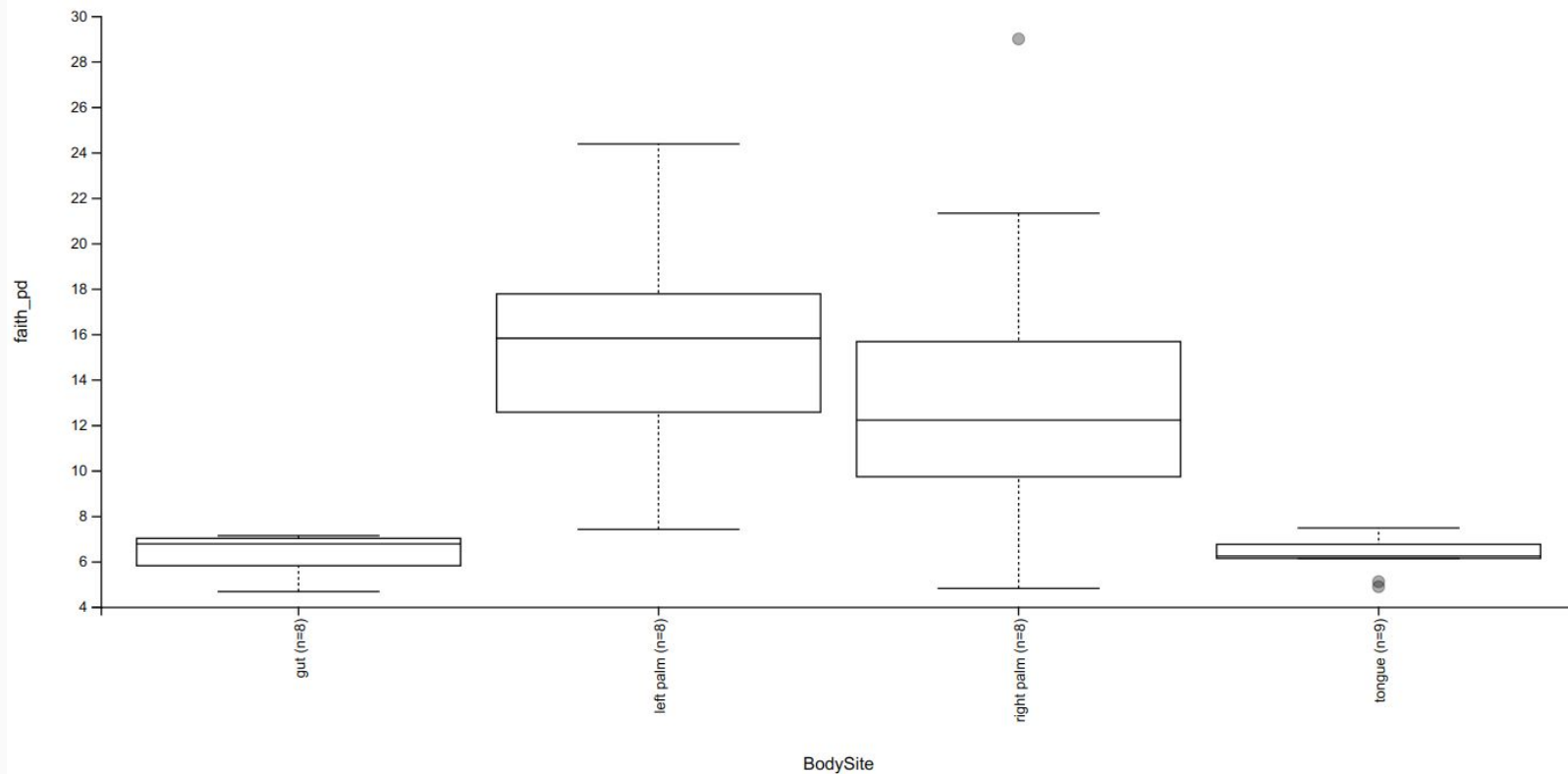


Body site evenness conclusions

- Statistically the evenness of:
 - Gut and tongue are no different
 - Right palm and left palm are no different
 - Gut is different compared to right palm and left palm
 - Tongue is different compared right palm but not left palm
- Two main groupings by evenness
 - Left and right palm - higher evenness
 - Gut and tongue - lower evenness



Body Site PD box plot



Body Site PD P & Q values



Kruskal-Wallis (all groups)

| | Result |
|---------|-----------------------|
| H | 18.87240047534165 |
| p-value | 0.0002905198262917197 |

Kruskal-Wallis (pairwise)

[Download CSV](#)

| | | H | p-value | q-value |
|------------------|------------------|-----------|----------|----------|
| Group 1 | Group 2 | | | |
| gut (n=8) | left palm (n=8) | 11.294118 | 0.000778 | 0.002333 |
| | right palm (n=8) | 6.893382 | 0.008652 | 0.014062 |
| | tongue (n=9) | 0.083333 | 0.772830 | 0.772830 |
| left palm (n=8) | right palm (n=8) | 0.397059 | 0.528612 | 0.634335 |
| | tongue (n=9) | 11.342593 | 0.000757 | 0.002333 |
| right palm (n=8) | tongue (n=9) | 6.750000 | 0.009375 | 0.014062 |





Body site PD conclusions

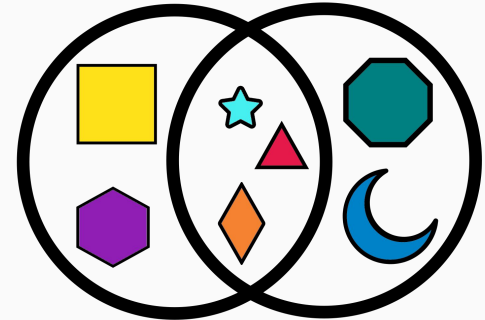
- Statistically the PD of:
 - Gut and tongue are no different
 - Right palm and left palm are no different
 - PD of gut is lower than right palm and left palm
 - PD of tongue is lower than right palm and left palm
- Two groupings by PD
 - Left and right palm - higher diversity
 - Gut and tongue - lower diversity



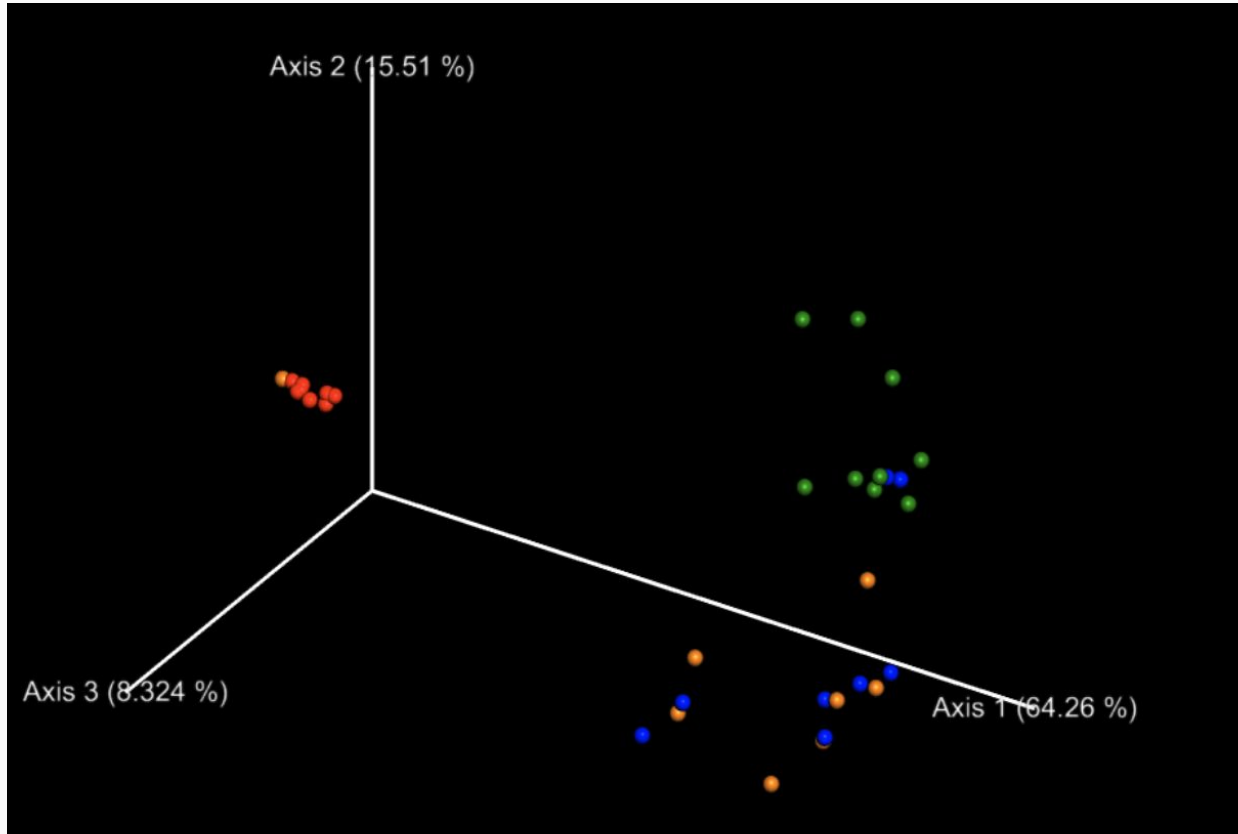
Beta diversity measures



- Jaccard distance
 - measure of community richness dissimilarity (presence/absence)
- Bray-Curtis distance
 - measure of community diversity dissimilarity (abundance)
- unweighted UniFrac distance
 - measure of community richness dissimilarity that incorporates phylogenetic relationships between the features
- weighted UniFrac distance
 - measure of community diversity dissimilarity that incorporates phylogenetic relationships between the features



Weighted Unifrac plot





Weighted Unifrac PERMANOVA

Pairwise permanova results

[Download CSV](#)

| | | Sample size | Permutations | pseudo-F | p-value | q-value |
|------------|------------|-------------|--------------|------------|---------|---------|
| Group 1 | Group 2 | | | | | |
| gut | left palm | 16 | 999 | 78.500534 | 0.001 | 0.0015 |
| | right palm | 16 | 999 | 28.100258 | 0.002 | 0.0024 |
| | tongue | 17 | 999 | 104.356036 | 0.001 | 0.0015 |
| left palm | right palm | 16 | 999 | 0.633407 | 0.883 | 0.8830 |
| | tongue | 17 | 999 | 6.658468 | 0.001 | 0.0015 |
| right palm | tongue | 17 | 999 | 5.231644 | 0.001 | 0.0015 |



Weighted unifrac conclusions

- All the different body sites form statistically distinct clusters (bar the palms)
- This is based on Weighted unifrac which uses:
 - Shared abundance of the different ASVs
 - Phylogenetic information of ASVs
- Left palm and right palm are not statistically different
- 3 Groups: gut, tongue and palm
- Higher community similarity within these groups than between
- Gut communities over time and between patients are very similar compared to tongue and palm communities
- I.e. Gut communities are maintained more consistently



Differential abundance analysis

- Discover biomarkers
- a specific organism/taxa by which a particular type of community can be identified
- Disease example:
 - *Helicobacter pylori* is a biomarker of stomach communities with Ulcers compared to healthy stomachs
 - *H. pylori* causes the disease
- Environmental example:
 - Thermophilic bacteria are biomarkers of hot springs compared to cold springs
 - The temperature of the springs causes this difference
- Note: A biomarker does not mean the organisms/taxa is present in only one type of sample. Biomarkers are determined by difference in abundance.



Differential abundance analysis - ancom



Percentile abundances of features by group

[Download complete table as CSV](#)

| Percentile Group | 0.0 gut | 25.0 gut | 50.0 gut | 75.0 gut | 100.0 gut | 0.0 left palm | 25.0 left palm | 50.0 left palm | 75.0 left palm | 100.0 left palm | 0.0 right palm | 25.0 right palm | 50.0 right palm | 75.0 right palm | 100.0 right palm | 0.0 tongue | 25.0 tongue | 50.0 tongue | 75.0 tongue | 100.0 tongue |
|--|------------|-------------|-------------|-------------|--------------|------------------|-------------------|-------------------|-------------------|--------------------|-------------------|--------------------|--------------------|--------------------|---------------------|---------------|----------------|----------------|----------------|-----------------|
| k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Corynebacteriaceae;g_Corynebacterium | 1.0 | 1.00 | 1.0 | 1.00 | 8.0 | 36.0 | 144.50 | 229.0 | 549.75 | 1443.0 | 1.0 | 56.0 | 409.0 | 944.0 | 1111.0 | 1.0 | 1.0 | 1.0 | 1.0 | 5.0 |
| k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Micrococcaceae;g_Rothia | 1.0 | 1.00 | 1.0 | 1.00 | 1.0 | 8.0 | 14.50 | 21.0 | 44.25 | 179.0 | 1.0 | 1.0 | 10.0 | 49.0 | 85.0 | 32.0 | 46.0 | 83.0 | 109.0 | 225.0 |
| k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_Bacteroides | 3044.0 | 4206.75 | 4577.5 | 4637.25 | 4838.0 | 1.0 | 9.25 | 14.5 | 33.50 | 67.0 | 1.0 | 7.0 | 14.0 | 65.0 | 783.0 | 1.0 | 6.0 | 9.0 | 10.0 | 11.0 |
| k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Prevotellaceae;g_Prevotella | 1.0 | 1.00 | 1.0 | 15.25 | 86.0 | 1.0 | 15.25 | 24.0 | 170.00 | 442.0 | 1.0 | 5.0 | 14.0 | 47.0 | 349.0 | 109.0 | 173.0 | 280.0 | 483.0 | 1964.0 |
| k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Staphylococcaceae;g_Staphylococcus | 1.0 | 1.00 | 1.0 | 1.00 | 10.0 | 1.0 | 74.75 | 106.5 | 253.00 | 352.0 | 1.0 | 30.0 | 76.0 | 492.0 | 1579.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Carnobacteriaceae;g_Granulicatella | 1.0 | 1.00 | 1.0 | 1.00 | 1.0 | 1.0 | 1.00 | 10.5 | 14.50 | 54.0 | 1.0 | 1.0 | 7.0 | 54.0 | 86.0 | 24.0 | 29.0 | 36.0 | 42.0 | 133.0 |
| k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Streptococcus | 1.0 | 1.00 | 2.0 | 7.75 | 31.0 | 134.0 | 210.50 | 477.0 | 662.75 | 934.0 | 4.0 | 40.0 | 81.0 | 568.0 | 2125.0 | 206.0 | 309.0 | 421.0 | 480.0 | 728.0 |
| k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_ | 4.0 | 6.25 | 12.0 | 20.50 | 23.0 | 1.0 | 1.00 | 1.0 | 1.00 | 4.0 | 1.0 | 1.0 | 1.0 | 3.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_ | 1.0 | 14.50 | 34.5 | 37.50 | 39.0 | 1.0 | 1.00 | 1.0 | 3.50 | 9.0 | 1.0 | 1.0 | 1.0 | 1.0 | 3.0 | 1.0 | 1.0 | 3.0 | 4.0 | 13.0 |
| k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_ | 118.0 | 130.00 | 136.5 | 489.50 | 749.0 | 1.0 | 3.75 | 7.5 | 23.50 | 43.0 | 1.0 | 1.0 | 1.0 | 26.0 | 37.0 | 1.0 | 1.0 | 6.0 | 50.0 | 81.0 |
| k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_ | 20.0 | 62.00 | 74.0 | 133.75 | 371.0 | 1.0 | 1.00 | 1.0 | 1.00 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 15.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Blautia | 32.0 | 62.25 | 75.0 | 147.50 | 291.0 | 1.0 | 1.00 | 1.0 | 9.25 | 20.0 | 1.0 | 1.0 | 1.0 | 24.0 | 55.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Coprococcus | 1.0 | 21.75 | 51.0 | 106.00 | 228.0 | 1.0 | 1.00 | 1.0 | 1.00 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 9.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Lachnospira | 14.0 | 250.50 | 379.5 | 656.25 | 669.0 | 1.0 | 1.00 | 1.0 | 1.00 | 5.0 | 1.0 | 1.0 | 1.0 | 1.0 | 22.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Roseburia | 128.0 | 178.50 | 233.5 | 319.25 | 408.0 | 1.0 | 1.00 | 1.0 | 1.00 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 32.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Ruminococcus | 12.0 | 12.75 | 17.0 | 21.75 | 64.0 | 1.0 | 1.00 | 1.0 | 1.00 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_ | 1.0 | 38.25 | 62.5 | 94.25 | 248.0 | 1.0 | 1.00 | 1.0 | 1.00 | 1.0 | 1.0 | 1.0 | 1.0 | 6.0 | 15.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Faecalibacterium | 131.0 | 455.75 | 645.5 | 769.00 | 915.0 | 1.0 | 1.00 | 9.5 | 14.50 | 20.0 | 1.0 | 1.0 | 6.0 | 15.0 | 185.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Oscillospira | 85.0 | 102.50 | 168.5 | 223.75 | 286.0 | 1.0 | 1.00 | 1.0 | 1.50 | 11.0 | 1.0 | 1.0 | 1.0 | 57.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Ruminococcus | 1.0 | 21.75 | 58.5 | 183.75 | 267.0 | 1.0 | 1.00 | 1.0 | 1.50 | 6.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae;g_Phascloarctobacterium | 87.0 | 132.00 | 151.0 | 303.75 | 537.0 | 1.0 | 1.00 | 1.0 | 1.75 | 6.0 | 1.0 | 1.0 | 1.0 | 7.0 | 68.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae;g_Veillonella | 1.0 | 1.00 | 1.0 | 1.00 | 8.0 | 1.0 | 13.75 | 30.5 | 91.25 | 298.0 | 1.0 | 1.0 | 9.0 | 25.0 | 249.0 | 99.0 | 146.0 | 148.0 | 281.0 | 511.0 |
| k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Tissierellaceae;g_Anaerococcus | 1.0 | 1.00 | 1.0 | 1.00 | 1.0 | 8.0 | 40.00 | 52.0 | 122.75 | 173.0 | 1.0 | 11.0 | 48.0 | 135.0 | 425.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Tissierellaceae;g_Peptoniphilus | 1.0 | 1.00 | 1.0 | 1.00 | 11.0 | 5.0 | 27.50 | 41.5 | 65.25 | 106.0 | 1.0 | 1.0 | 25.0 | 81.0 | 520.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| k_Bacteria;p_Firmicutes;c_Erysipelotrichi;o_Erysipelotrichales;f_Erysipelotrichaceae;g_ | 1.0 | 7.00 | 23.5 | 43.50 | 69.0 | 1.0 | 1.00 | 1.0 | 1.00 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| k_Bacteria;p_Fusobacteria;c_Fusobacteriia;o_Fusobacteriales;f_Fusobacteriaceae;g_Fusobacterium | 1.0 | 1.00 | 1.0 | 1.75 | 32.0 | 1.0 | 20.25 | 28.0 | 188.50 | 633.0 | 1.0 | 1.0 | 14.0 | 38.0 | 391.0 | 45.0 | 170.0 | 204.0 | 626.0 | 920.0 |
| k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Neisseriales;f_Neisseriaceae;g_Neisseria | 1.0 | 1.00 | 1.0 | 1.00 | 6.0 | 25.0 | 50.25 | 80.0 | 149.75 | 1232.0 | 1.0 | 23.0 | 24.0 | 165.0 | 617.0 | 20.0 | 449.0 | 490.0 | 1368.0 | 3540.0 |
| k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Desulfobibrionales;f_Desulfobibrionaceae;g_Desulfobivrio | 22.0 | 27.25 | 33.0 | 47.75 | 80.0 | 1.0 | 1.00 | 1.0 | 1.00 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 19.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| k_Bacteria;p_Proteobacteria;c_Epsilonproteobacteria;o_Campylobacterales;f_Campylobacteraceae;g_Campylobacter | 1.0 | 1.00 | 1.0 | 1.00 | 1.0 | 1.0 | 5.00 | 6.5 | 15.50 | 69.0 | 1.0 | 1.0 | 1.0 | 10.0 | 35.0 | 8.0 | 11.0 | 22.0 | 39.0 | 108.0 |
| k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pasteurellales;f_Pasteurellaceae;g_Haemophilus | 1.0 | 1.00 | 1.0 | 2.25 | 6.0 | 21.0 | 38.50 | 71.0 | 102.75 | 1210.0 | 1.0 | 6.0 | 21.0 | 124.0 | 677.0 | 256.0 | 390.0 | 550.0 | 728.0 | 1293.0 |
| k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Pseudomonadaceae;g_Pseudomonas | 1.0 | 1.00 | 1.0 | 1.00 | 1.0 | 1.0 | 34.00 | 64.5 | 174.25 | 1612.0 | 1.0 | 17.0 | 26.0 | 237.0 | 727.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |

Greengenes Level 6



Differential abundance analysis - ancom



Percentile abundances of features by group

[Download complete table as CSV](#)

| Percentile | 0.0 | 25.0 | 50.0 | 75.0 | 100.0 | 0.0 | 25.0 | 50.0 | 75.0 | 100.0 |
|---|--------|---------|--------|---------|--------|-----------|-----------|-----------|-----------|-----------|
| Group | gut | gut | gut | gut | gut | left palm | left palm | left palm | left palm | left palm |
| k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Corynebacteriaceae;g_Corynebacterium | 1.0 | 1.00 | 1.0 | 1.00 | 8.0 | 36.0 | 144.50 | 229.0 | 549.75 | 1443.0 |
| k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Micrococcaceae;g_Rothia | 1.0 | 1.00 | 1.0 | 1.00 | 1.0 | 8.0 | 14.50 | 21.0 | 44.25 | 179.0 |
| k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_Bacteroides | 3044.0 | 4206.75 | 4577.5 | 4637.25 | 4838.0 | 1.0 | 9.25 | 14.5 | 33.50 | 67.0 |
| k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Prevotellaceae;g_Prevotella | 1.0 | 1.00 | 1.0 | 15.25 | 86.0 | 1.0 | 15.25 | 24.0 | 170.00 | 442.0 |
| k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Staphylococcaceae;g_Staphylococcus | 1.0 | 1.00 | 1.0 | 1.00 | 10.0 | 1.0 | 74.75 | 106.5 | 253.00 | 352.0 |
| k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Carnobacteriaceae;g_Granulicatella | 1.0 | 1.00 | 1.0 | 1.00 | 1.0 | 1.0 | 1.00 | 10.5 | 14.50 | 54.0 |
| k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Streptococcus | 1.0 | 1.00 | 2.0 | 7.75 | 31.0 | 134.0 | 210.50 | 477.0 | 662.75 | 934.0 |
| k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_ | 4.0 | 6.25 | 12.0 | 20.50 | 23.0 | 1.0 | 1.00 | 1.0 | 1.00 | 4.0 |
| k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_ | 1.0 | 14.50 | 34.5 | 37.50 | 39.0 | 1.0 | 1.00 | 1.0 | 3.50 | 9.0 |
| k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_ | 118.0 | 130.00 | 136.5 | 489.50 | 749.0 | 1.0 | 3.75 | 7.5 | 23.50 | 43.0 |
| k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_ | 20.0 | 62.00 | 74.0 | 133.75 | 371.0 | 1.0 | 1.00 | 1.0 | 1.00 | 1.0 |
| k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Blautia | 32.0 | 62.25 | 75.0 | 147.50 | 291.0 | 1.0 | 1.00 | 1.0 | 9.25 | 20.0 |
| k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Coprococcus | 1.0 | 21.75 | 51.0 | 106.00 | 228.0 | 1.0 | 1.00 | 1.0 | 1.00 | 1.0 |
| k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Lachnospira | 14.0 | 250.50 | 379.5 | 656.25 | 669.0 | 1.0 | 1.00 | 1.0 | 1.00 | 5.0 |
| k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Roseburia | 128.0 | 178.50 | 233.5 | 319.25 | 408.0 | 1.0 | 1.00 | 1.0 | 1.00 | 1.0 |
| k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Ruminococcus | 12.0 | 12.75 | 17.0 | 21.75 | 64.0 | 1.0 | 1.00 | 1.0 | 1.00 | 1.0 |
| k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_ | 1.0 | 38.25 | 62.5 | 94.25 | 248.0 | 1.0 | 1.00 | 1.0 | 1.00 | 1.0 |
| k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Faecalibacterium | 131.0 | 455.75 | 645.5 | 769.00 | 915.0 | 1.0 | 1.00 | 9.5 | 14.50 | 20.0 |
| k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Oscillospira | 85.0 | 102.50 | 168.5 | 223.75 | 286.0 | 1.0 | 1.00 | 1.0 | 1.50 | 11.0 |

Pseudocounts are added as ANCOM can't handle zeroes,
Therefore minus 1 from all values to get real value





Conclusions

- Alpha diversity
 - The PD of Palms are significantly higher than Gut and Tongue
- Beta diversity
 - The communities of Palms, Gut and Tongue are significantly different
 - There appears to be no significant difference between right and left palms
 - Gut communities are more similar between individuals and time than palms or tongues
- Biomarker detection
 - Most biomarkers between the 4 body sites are genus that are in either high or low abundance in gut and low in the others
 - This matches the clustering seen in the Weighted Unifrac plot

