# Microbiome analysis of skin undergoing acne treatments

| Groups | Sample size | Time points |
|---|---|---|
| Healthy, No treatment | 4 | 0 |
| Acne, Receiving Spironolactone | 2 | 0,1 |
| Acne, Receiving Doxycycline | 2 | 0,1 |

| Head Site | Code |
|---|---|
| Forehead | Fh |
| Cheek | Ck |
| Nose | No |
| Chin | Ch |
| Ear | Ra |

Casey Bartow-McKenney

# Treatment effects on all samples
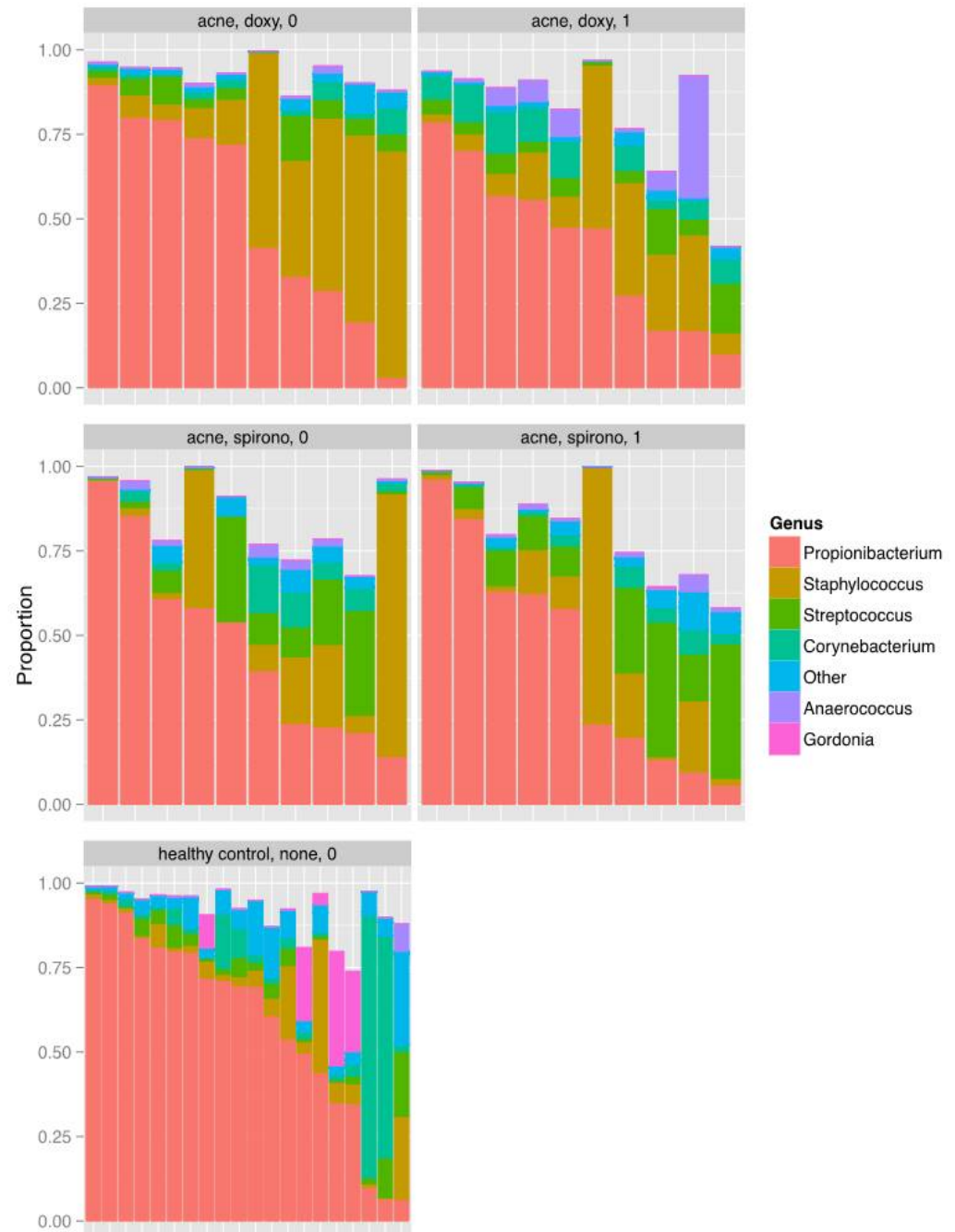


This data shows the relative abundance/proportion of the most prevalent bacterial genera (as represented by different colors) in all sites from all patients. Each bar represents a site and each chart separates the sites by treatment method (control/doxy/spirono) and time (either 0 or 1).
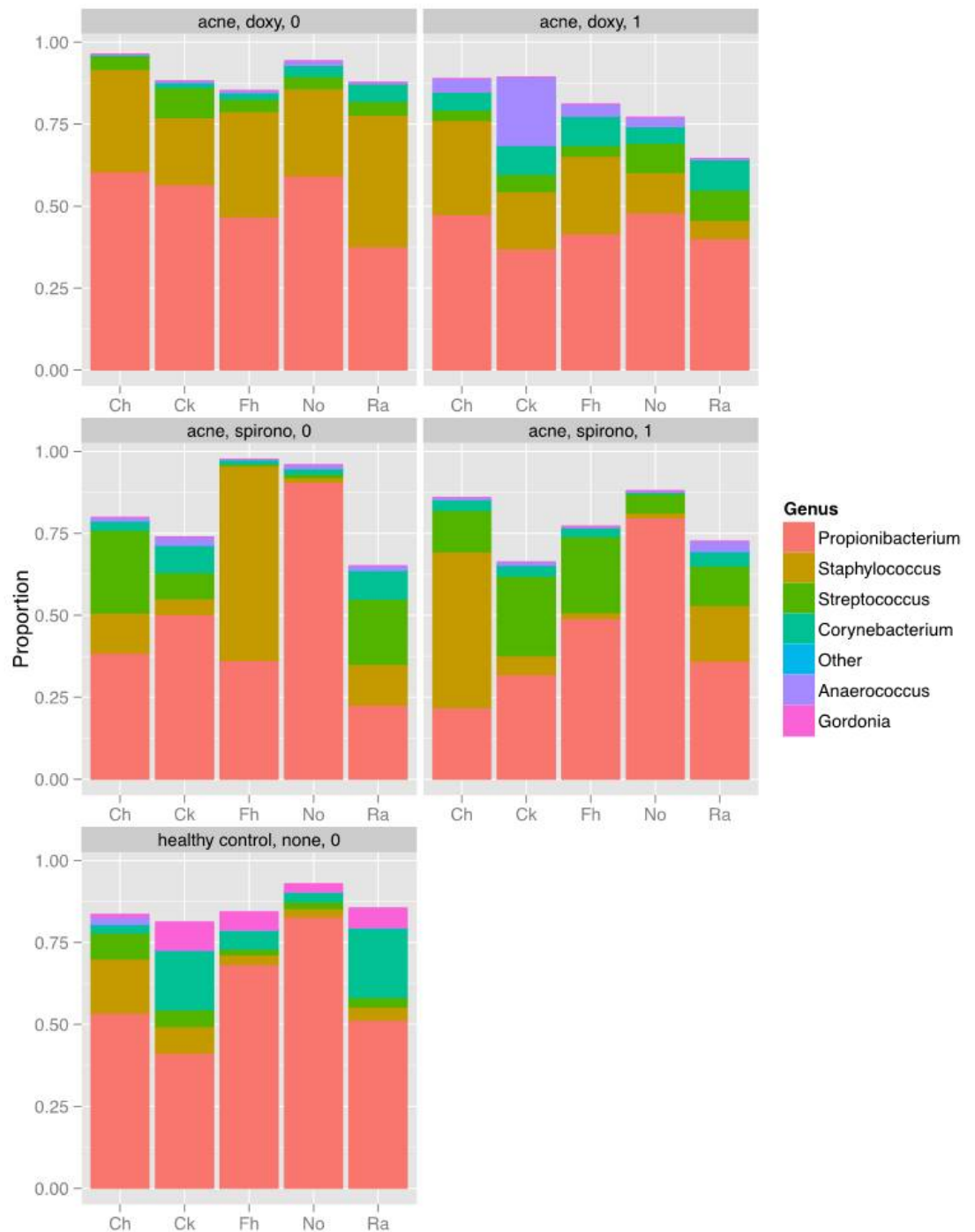
# Treatment effects on individuals



This data shows the relative abundance/proportion of the most prevalent bacterial genera (as represented by different colors) in each patient combining their sites. Each bar represents the average of a patient's sites and each chart separates the patients by treatment method (control/doxy/spirono) and time (either 0 or 1).
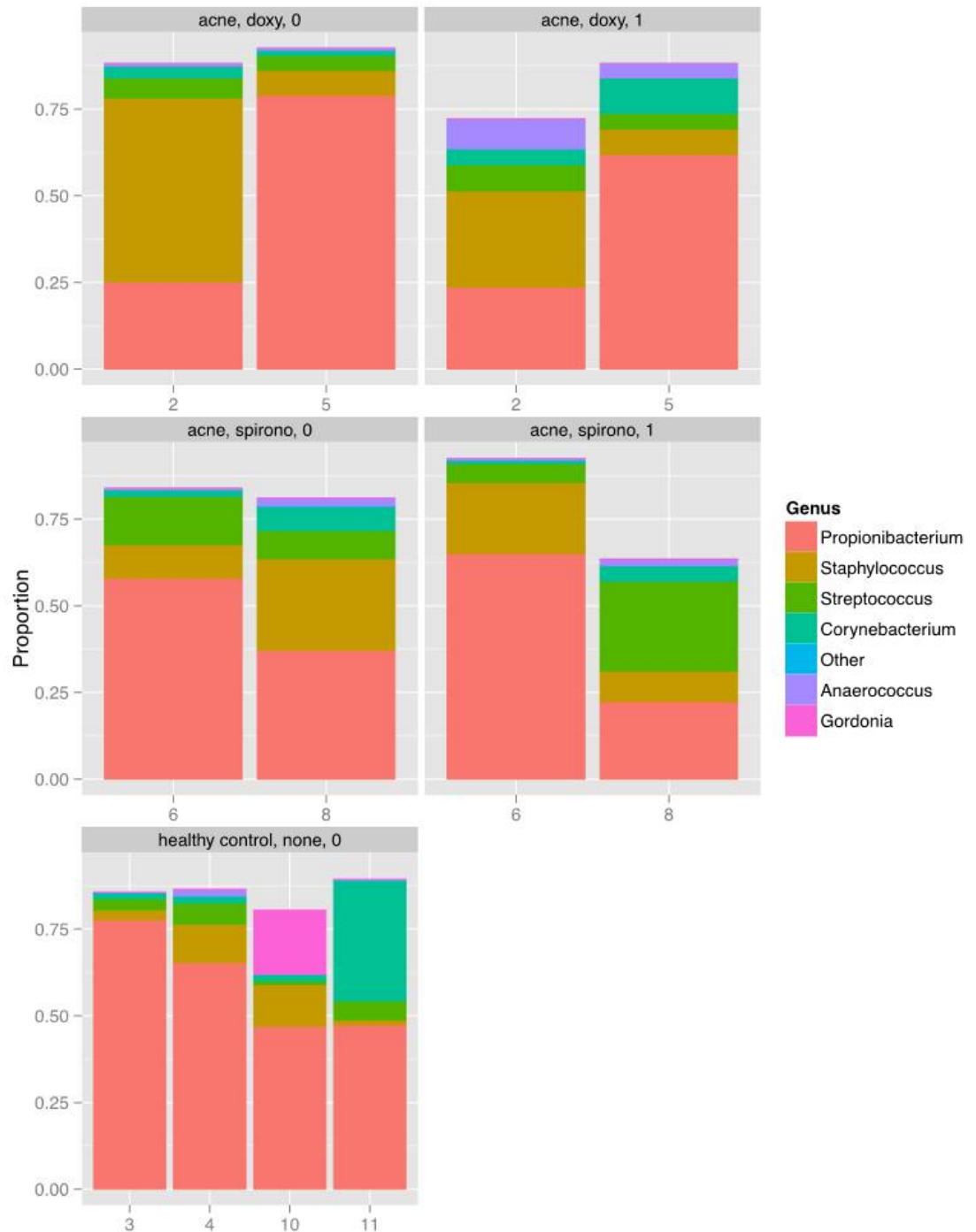
# Treatment effects on sites



This data shows the relative abundance/proportion of the most prevalent bacterial genera (as represented by different colors) in each site combining the patients of each treatment group. Each bar represents the average of a site from all patients and each chart separates the sites by treatment method (control/doxy/spirono) and time (either 0 or 1).

This data shows the relative abundance/proportion of the most prevalent bacterial genera (as represented by different colors) of each treatment group. Each bar represents the average of all patients in each treatment/time group and each chart separates the treatment groups by site.
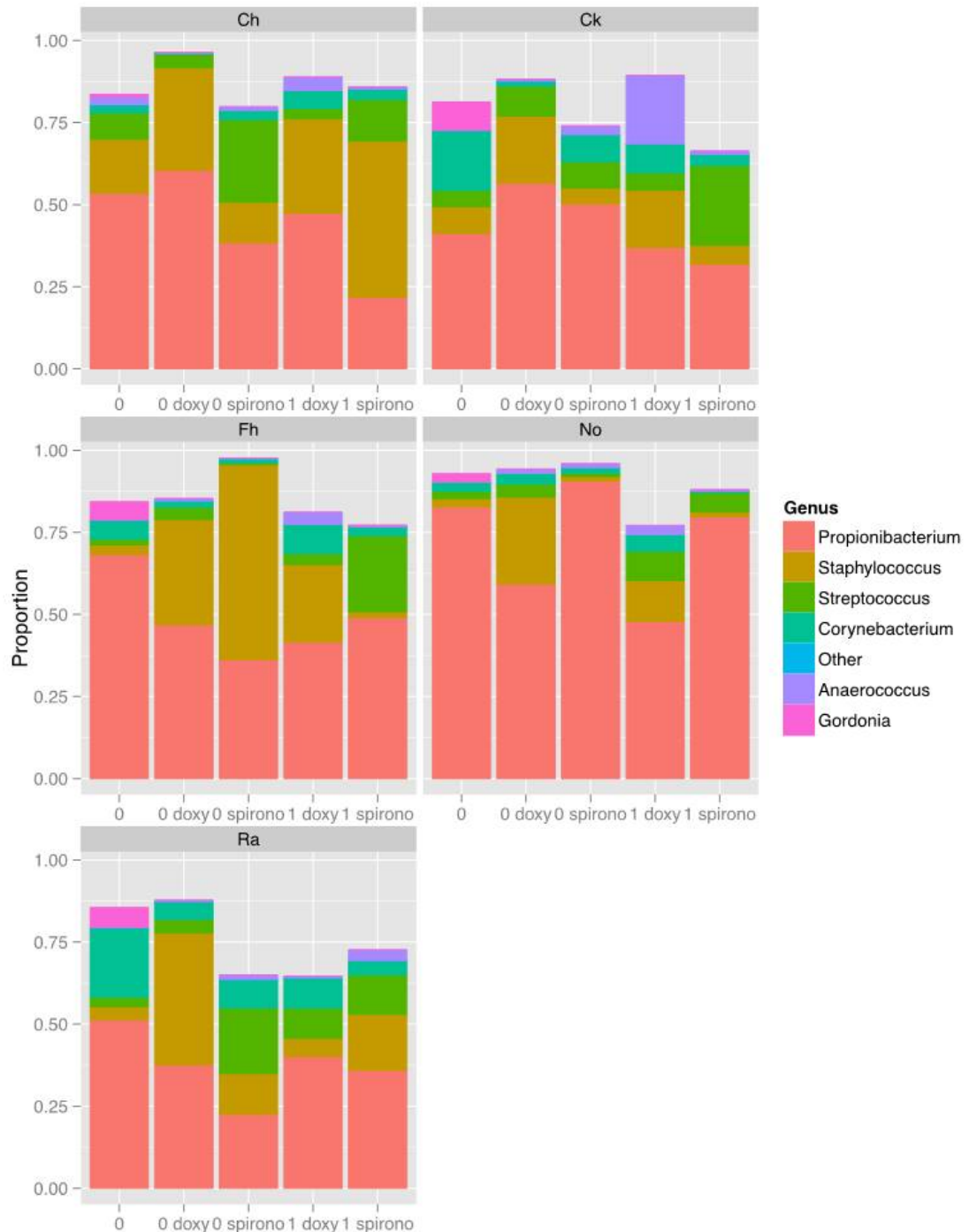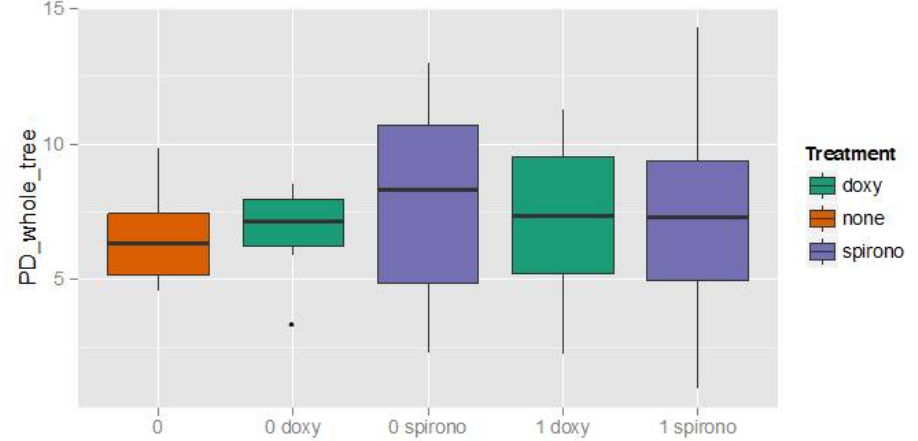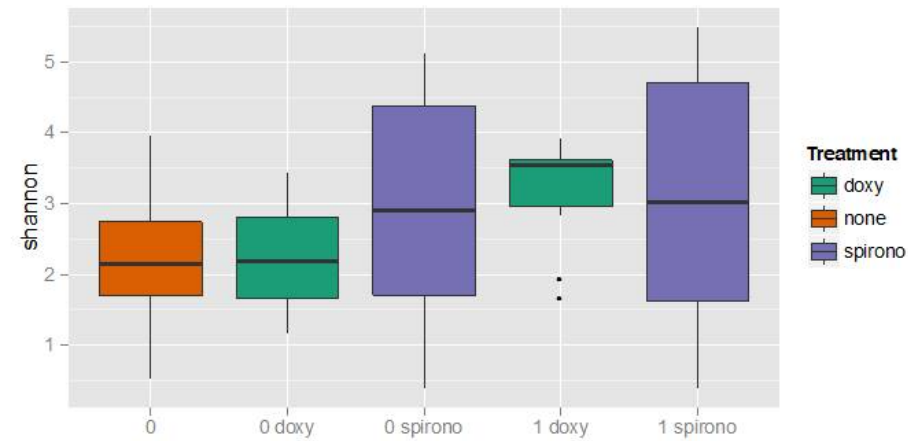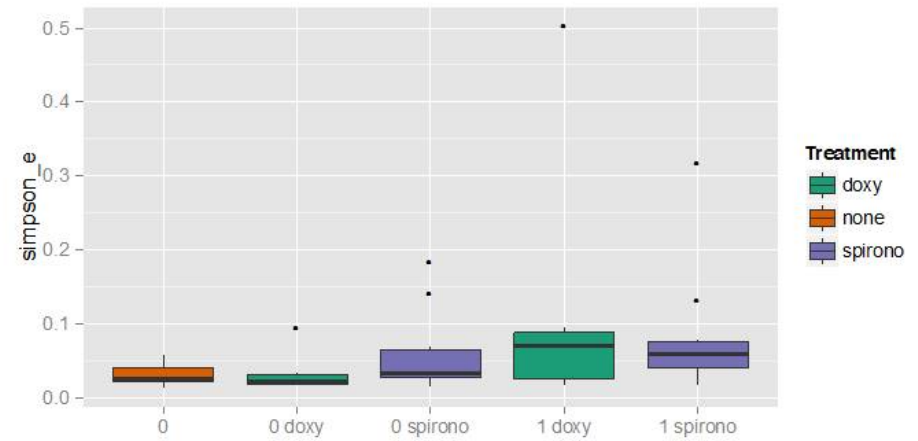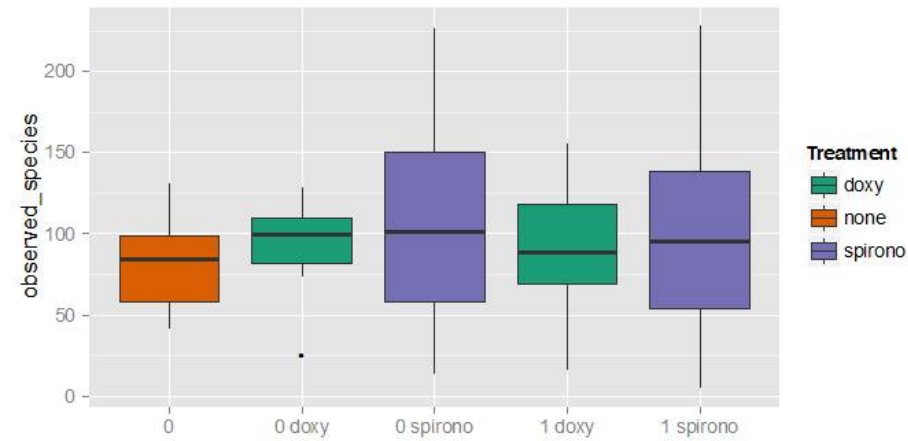
These box plots represent the alpha diversity measures of all patients and sites aggregated by time (0 or 1) and treatment method (control/doxy/spirono). The boxes are colored by treatment method, and the x axis separates the groups by time. The Shannon index, number of observed species, and PD whole tree index directly correlate with their measured aspect of diversity (higher index, more diverse). The simpson index indirectly correlates with diversity and measures how dominated a community is by a few members (taxa), thus the higher the index, the less equally distributed abundances are shared between taxa, ~ the less diverse.
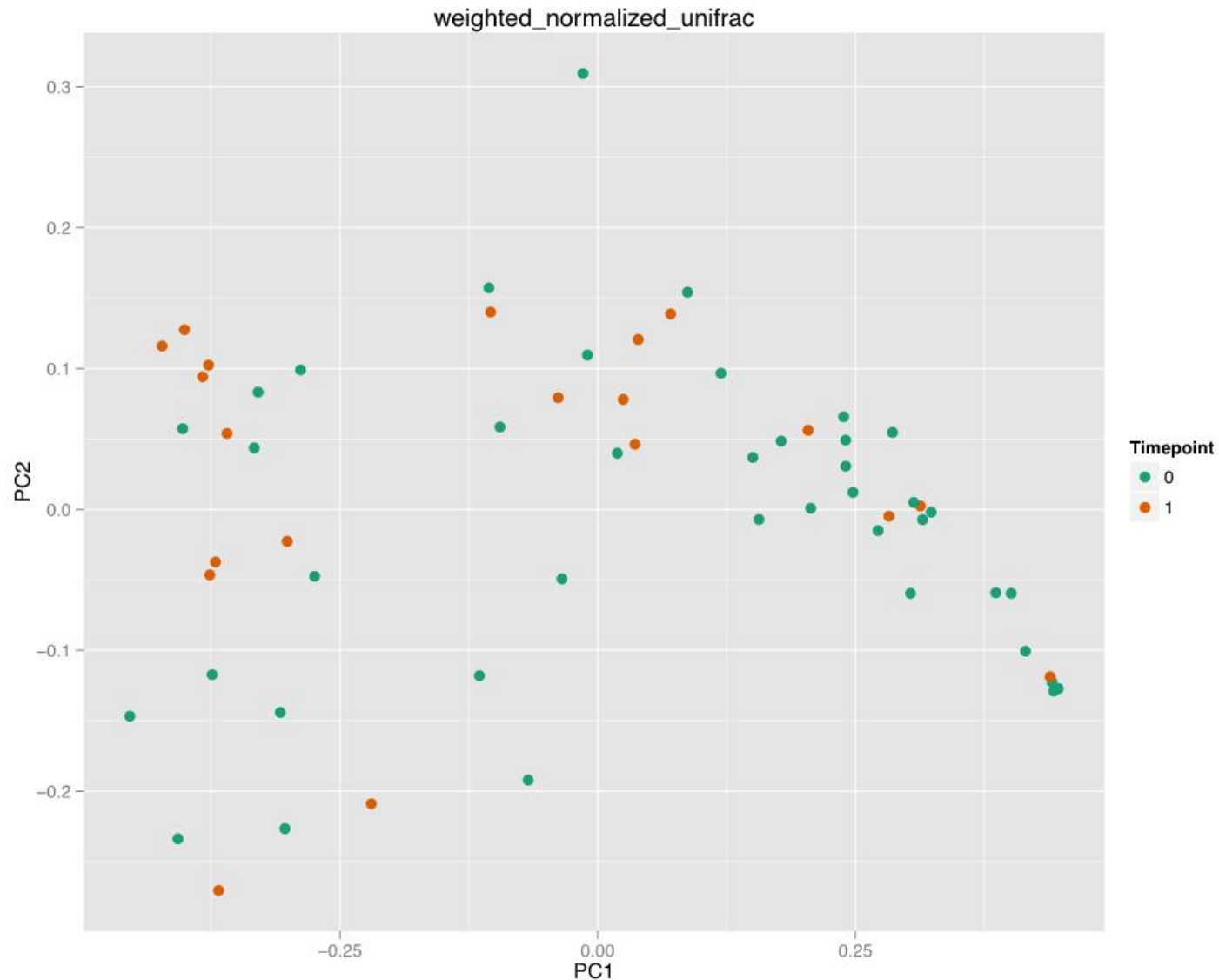
weighted_normalized_unifrac

In this Principal Coordinates Analysis plot, all sampled sites are plotted as separated by the predominant separating axes. The distance matrix used in this PCO plot was calculated using the weighted UniFrac method that finds the taxa and their abundances unique to each sample. The samples are colored by the time at which they were collect (time 0 or 1, or beginning/end).
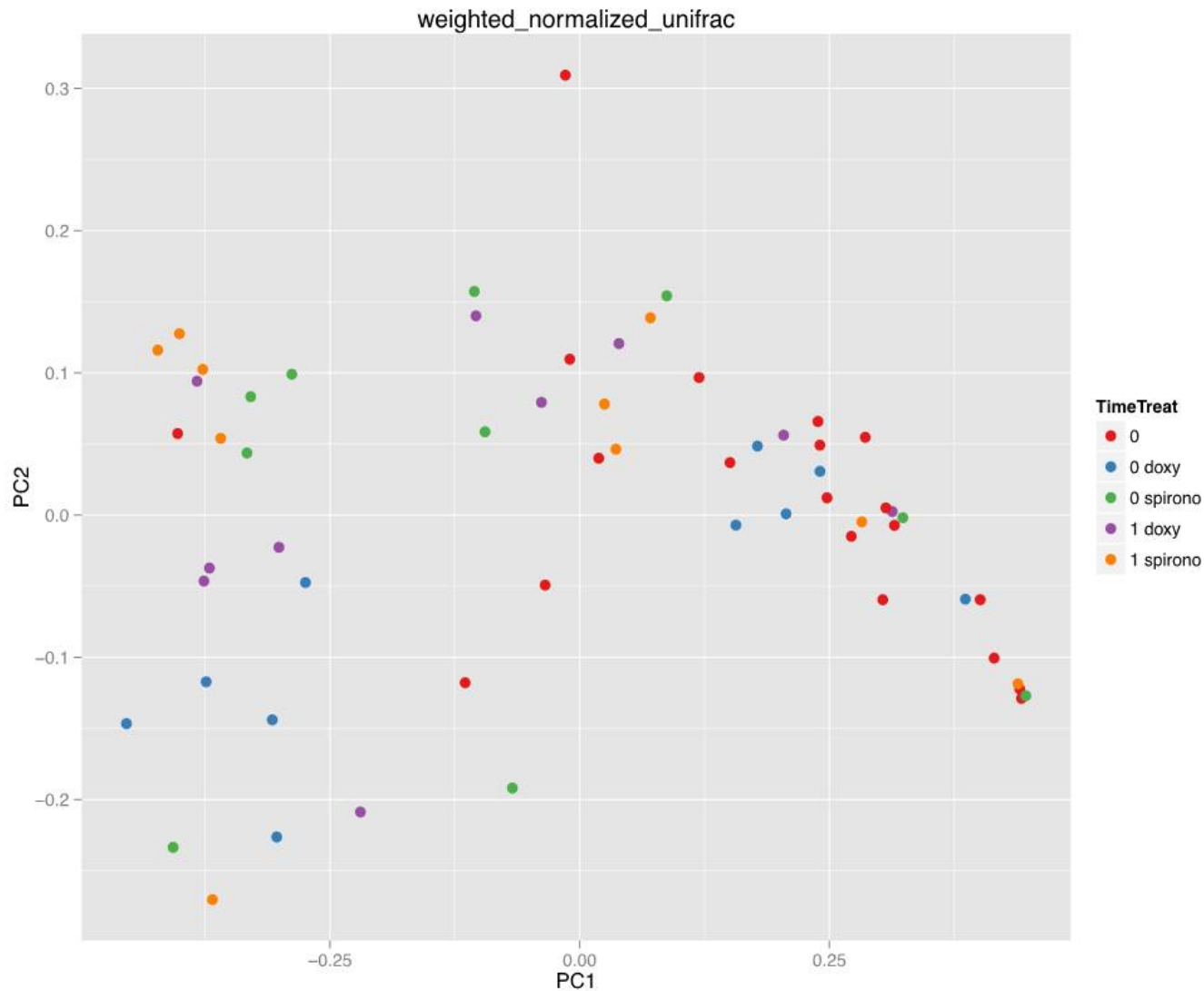
weighted_normalized_unifrac

TimeTreat
- 0
- 0 doxy
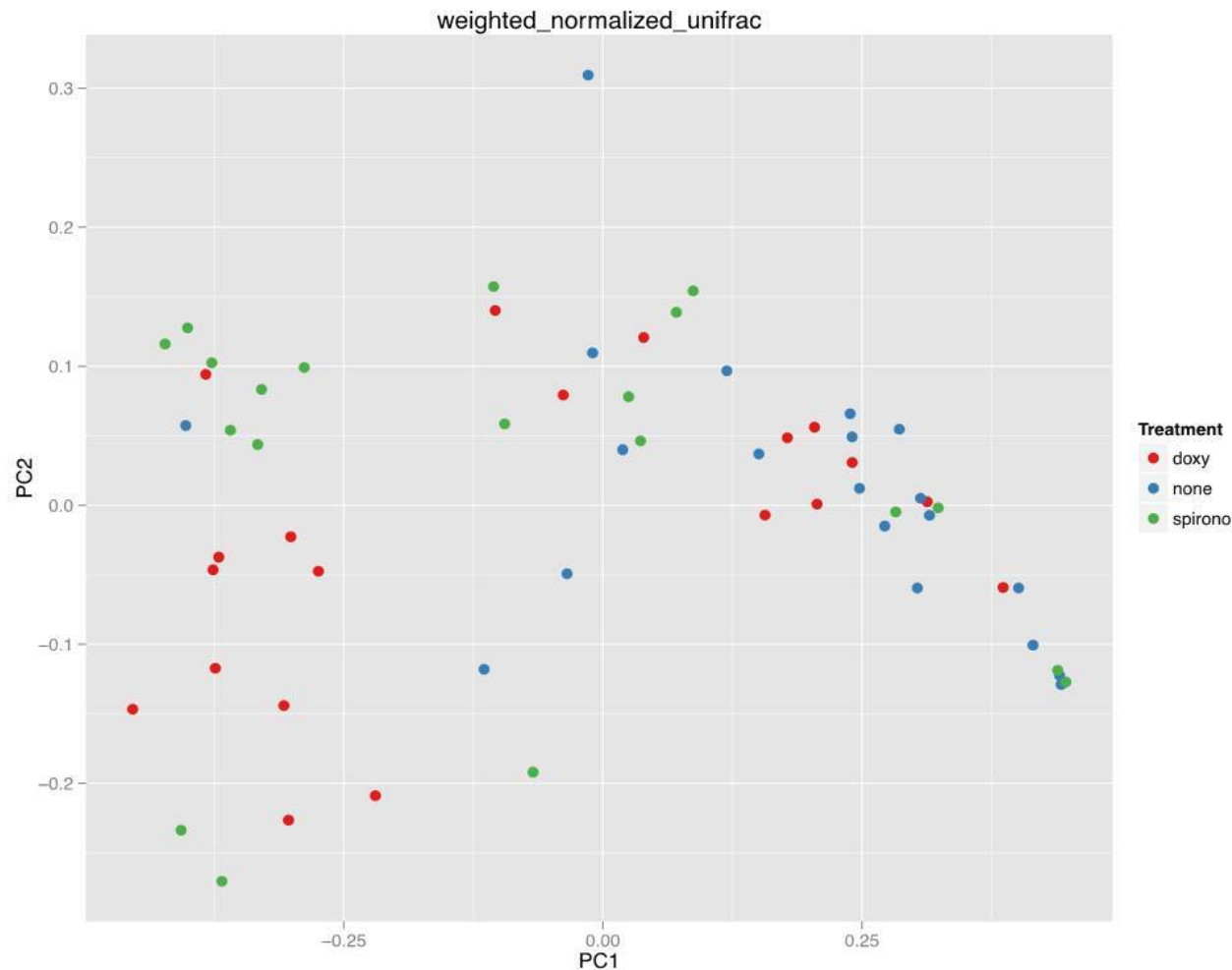- 0 spirono
- 1 doxy
- 1 spirono

In this Principal Coordinates Analysis plot, all sampled sites are plotted as separated by the predominant separating axes. The distance matrix used in this PCO plot was calculated using the weighted UniFrac method that finds the taxa and their abundances unique to each sample. The samples are colored by the treatment (doxy/spirono/control) and time at which they were collected (time 0 or 1, or beginning/end).
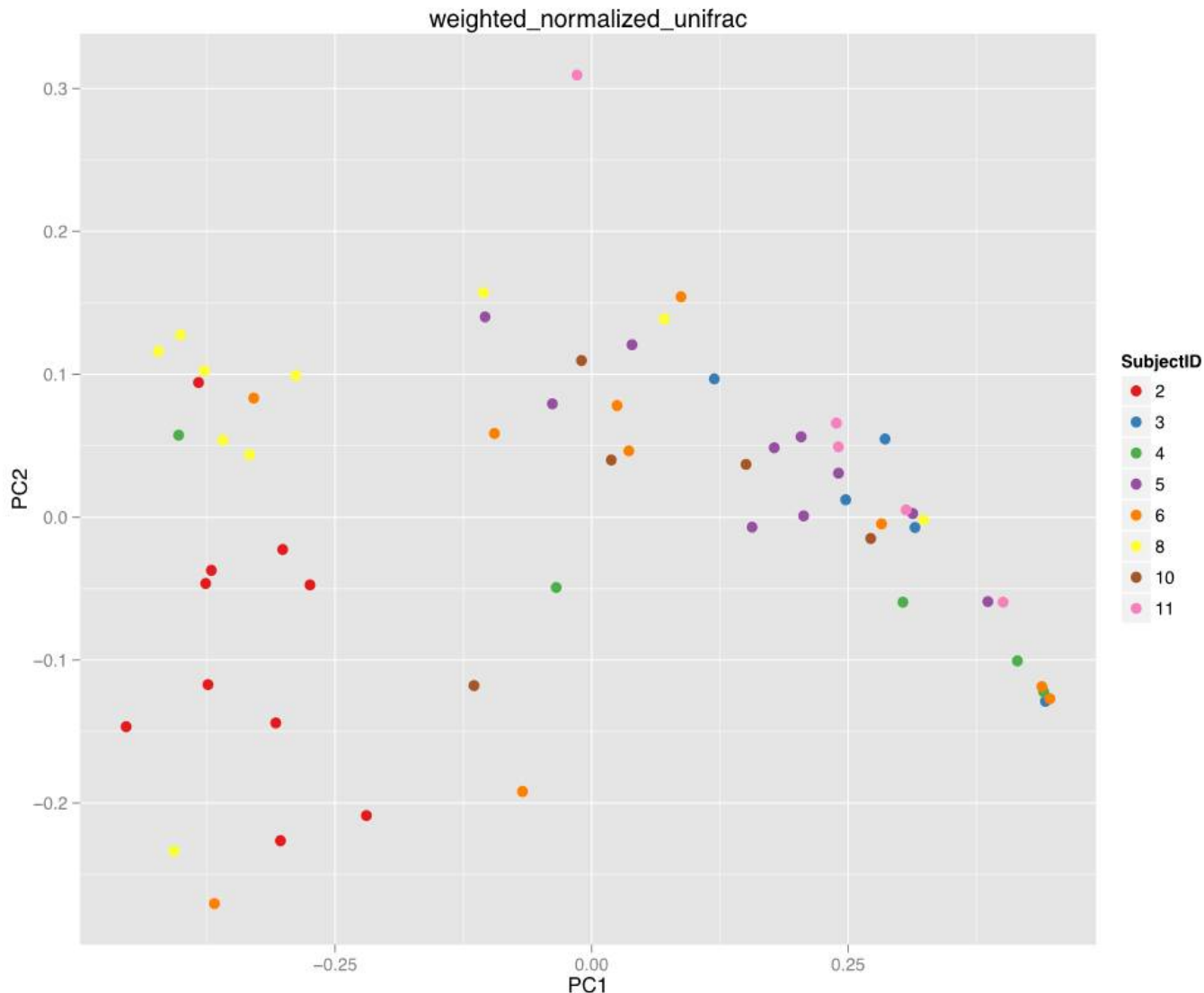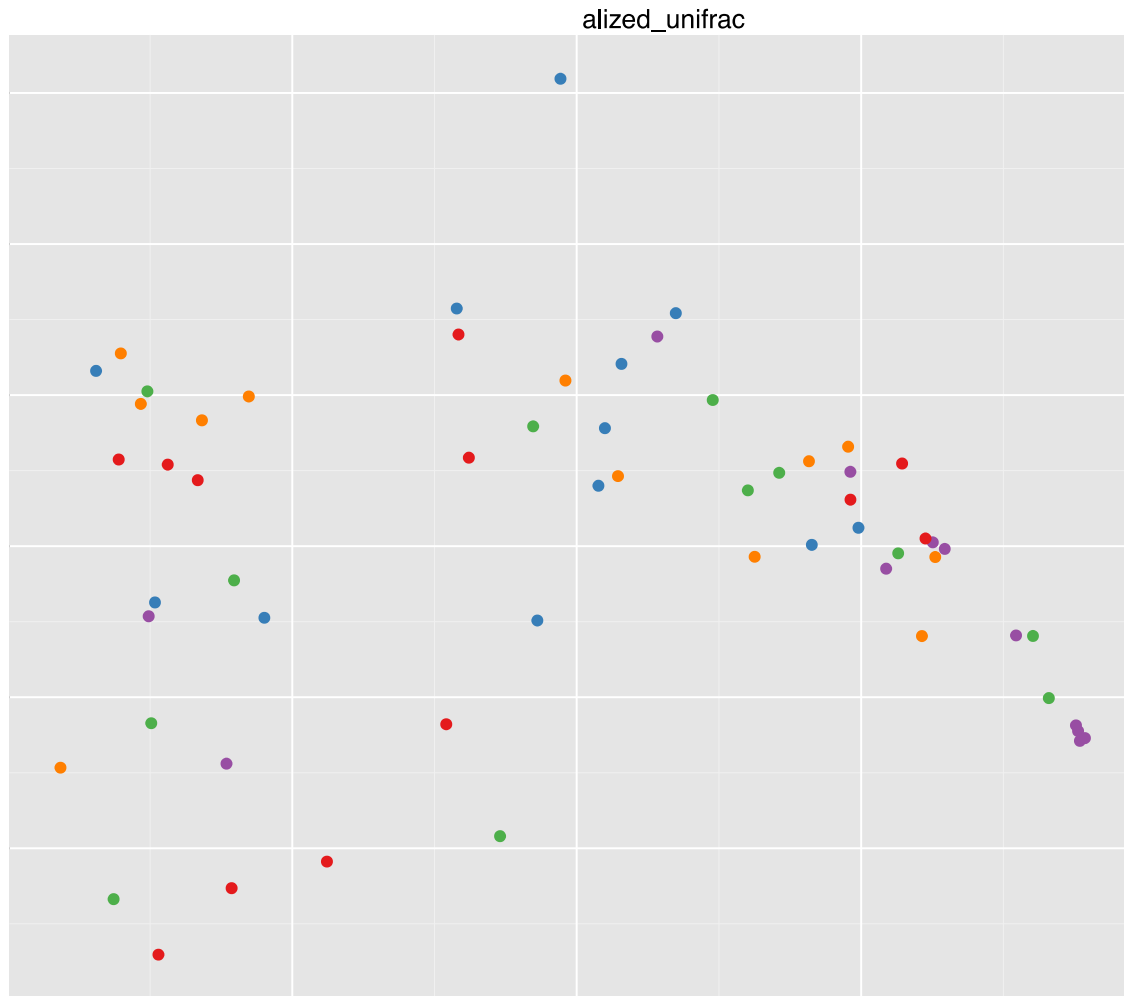
weighted_normalized_unifrac

In this Principal Coordinates Analysis plot, all sampled sites are plotted as separated by the predominant separating axes. The distance matrix used in this PCO plot was calculated using the weighted UniFrac method that finds the taxa and their abundances unique to each sample. The samples are colored by the patient's ID from which the samples were collected. In this plot, we see noticeable clustering, thus identifying the patient as a determining feature of microbiome composition.

weighted_normalized_unifrac

In this Principal Coordinates Analysis plot, all sampled sites are plotted as separated by the predominant separating axes. The distance matrix used in this PCO plot was calculated using the weighted UniFrac method that finds the taxa and their abundances unique to each sample. The samples are colored by the treatment method (doxy/spirono/control). Although we see clusters, the previous plot shows us that the clustering may be an artifact of multiple sites in a treatment originating from the same patient.

alized_unifrac

In this Principal Coordinates Analysis plot, all sampled sites are plotted as separated by the predominant separating axes. The distance matrix used in this PCO plot was calculated using the weighted UniFrac method that finds the taxa and their abundances unique to each sample. The samples are colored by the site from which they were collected (chin, cheek, forehead, nose, ear). We see a few small clusters that shows site as a weak determining factor of microbiome composition in this study.