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► In [15]: # Load a pre-trained classifier...
greengenes_classifier = qiime2.Artifact.load(ref_dir / 'gg-13-8-99-nb-classifier.qza')

#... and classify our sequences.
taxonomy, = feature_classifier.classify_sklearn(sequences, greengenes_classifier)
taxonomy.save(str(data_dir / 'taxonomy.qza'))
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Out[15]: 'data-single/taxonomy.qza'
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In [24]: # Compute Biplot
relative_frequency_tbl, = feature_table.relative_frequency(filtered_table)
pcoa_biplot, = diversity.pcoa_biplot(core_metric_results.unweighted_unifrac_pcoa_results, relative_frequency_tbl)
taxonomy_as_md = taxonomy.view(qiime2.Metadata)
emperor_biplot, = emperor.biplot(pcoa_biplot, sample_metadata=sample_metadata, feature_metadata=taxonomy_as_md)
emperor_biplot.save(str(viz_dir / 'uw_unifrac_biplot.qzv'))
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Out[24]: 'data-single/visualizations/uw_unifrac_biplot.qzv'
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