README.md

This code is for the research paper submitted to Veterinary Microbiology titled “Shifts in the nasal microbiota of swine in response to different routes of oxytetracycline administration”

Several of the functions used in this analysis are from the “funfuns” package which can be found here:

<https://github.com/Jtrachsel/funfuns> or downloaded with devtools:

devtools::install\_github('Jtrachsel/funfuns')  
library(funfuns)

File descriptions

|  |  |
| --- | --- |
| File name | Description |
| FS1b\_FinalDiffAbundNasalGenus\_FCnoRoseburia\_final.csv | Differentially abundant 16S OTUs between in-feed oxytetracycline group and non-medicated feed group in the nasal region as determined by DEseq2, to be used in the 7th section (Differential Abundance of Genera in Nasal Microbiota using DESeq2) |
| FS1b\_FinalDiffAbundNasalGenus\_IC.csv | Differentially abundant 16S OTUs between injected oxytetracycline group and non-medicated feed group in the nasal region as determined by DEseq2, to be used in the 7th section (Differential Abundance of Genera in Nasal Microbiota using DESeq2) |
| FS1babundsingleton2000metadata.csv | 16S metadata file to be used in the 3rd section (Creating phyloseq objects for each tissue), 7th section (Differential Abundance of Genera in Nasal Microbiota using DESeq2), and 8th section (Nasal and Tonsil Microbiota: Genus Abundance) |
| FS1babundsingleton2000OTUtable.csv | 16S OTU table to be used in the 3rd section (Creating phyloseq objects for each tissue) |
| FS1bfinal.outsingletons.abund.opti\_mcc.0.03.cons.taxonomy, FS1bfinal.outsingletons.abund.taxonomy.csv | 16S SILVA taxonomy output by mothur and csv version of the taxonomy output are both to be used in the 2nd section (Creating OTU Table), 7th section (Differential Abundance of Genera in Nasal Microbiota using DESeq2), and 8th section (Nasal and Tonsil Microbiota: Genus Abundance) |
| FS1bfinal.outsingletons.abund.opti\_mcc.0.03.subsample.shared, FS1bfinal.singleton.abund.subsample.shared.csv | 16S OTU table rarefied to 2000 sequences per sample by mothur and csv version of the OTU table are both to be used in the 2nd section (Creating OTU Table) and 8th section (Nasal and Tonsil Microbiota: Genus Abundance) |
| FS1bfinal.outsingletons.abund.opti\_mcc.shared | 16S OTU table output by mothur to be used in the 7th section (Differential Abundance of Genera in Nasal Microbiota using DESeq2) |
| Nasal\_MagnitudeOfChange.csv | PERMANOVA F-statistic values to be used in the 6th section (Magnitude of Change in Nasal Microbiota) |
| Metadata.csv | 16S metadata used specifically for the 9th section (Nasal Oxytetracycline Levels) |
| Nasal\_results.csv | Nasal oxytetracycline level measurements to be used in the 9th section (Nasal Oxytetracycline Levels) |
| phyloseq.nw2 | Nasal 16S phyloseq data file containing OTU table, sample data, and taxonomy table; to be used in 3rd section (Creating phyloseq objects for each tissue), 4th section (Beta diversity), and 5th section (Alpha diversity) |
| phyloseq.tt2 | Tonsil 16S phyloseq data file containing OTU table, sample data, and taxonomy table; to be used in 3rd section (Creating phyloseq objects for each tissue), 4th section (Beta diversity), and 5th section (Alpha diversity) |