R Code

***PERMANOVA***

library(vegan)

library(data.table)

library(tidyverse)

*All Sites Unweighted*

metadata = fread("allsites\_metadata.txt", header = T)

unweighted\_bothyears <- read.table("unweighted-both.txt", header = T)

metadata\_both = inner\_join(unweighted\_bothyears, metadata, by = "sampleid")

unweighted\_bothyears <- as.dist(unweighted\_bothyears[,2:59])

adonis(formula = unweighted\_bothyears ~ humaninteraction+group+year+giardiapresence, data = metadata\_both, permutations = 5000)

*All Sites Weighted*

weighted\_bothyears <-read.table("weighted-bothyears-distance-matrix.tsv", header = T)

metadata\_together = inner\_join(weighted\_bothyears, metadata, by="sampleid")

weighted\_bothyears <- as.dist(weighted\_bothyears[,2:59])

adonis(formula = weighted\_bothyears~humaninteraction+group+year+giardiapresence, data=metadata\_together, permutations = 5000)

*Filtered Unweighted Unifrac*

*Rural*

giardiametadata = fread("giardia-metadata.txt", header = T)

unweighted\_rural <- read.table("unweighted-rural-distance-matrix.tsv", header=T)

unweighted\_rural\_metadata = inner\_join(unweighted\_rural, giardiametadata, by = "sampleid")

unweighted\_rural<-as.dist(unweighted\_rural[,2:28])

adonis(formula = unweighted\_rural ~ group+year+giardiapresence, data=unweighted\_rural\_metadata, permutations=5000)

*Village*

unweighted\_village <- read.table("unweighted-village-distance-matrix.tsv", header=T)

unweighted\_village\_metadata = inner\_join(unweighted\_village, giardiametadata, by = "sampleid")

unweighted\_village<-as.dist(unweighted\_village[,2:23])

adonis(formula = unweighted\_village ~ group+year+giardiapresence, data=unweighted\_village\_metadata, permutations = 5000)

*Across habitats*

giardiametadata = fread("giardia-metadata

.txt", header = T)

unweighted\_interaction <- read.table("unweighted-2017-distance-matrix.tsv", header = T)

giardia\_metadata = inner\_join(unweighted\_interaction, giardiametadata, by = "sampleid")

unweighted\_interaction <- as.dist(unweighted\_interaction[,2:49])

adonis(formula = unweighted\_interaction ~ humaninteraction+group+giardiapresence, data = giardia\_metadata, permutations = 5000)

adonis(formula = unweighted\_interaction ~ humaninteraction\*giardiapresence+group, data = giardia\_metadata, permutations = 5000)

*Filtered Weighted Unifrac*

*Rural*

weighted\_rural <- read.table("weighted-rural-distance-matrix.tsv", header=T)

weighted\_rural\_metadata = inner\_join(weighted\_rural, giardiametadata, by = "sampleid")

weighted\_rural<-as.dist(weighted\_rural[,2:28])

adonis(formula = weighted\_rural ~ group+year+giardiapresence, data = weighted\_rural\_metadata, permutations = 5000)

*Village*

weighted\_village <- read.table("weighted-village-distance-matrix.tsv", header=T)

weighted\_village\_metadata = inner\_join(weighted\_village, giardiametadata, by = "sampleid")

weighted\_village<-as.dist(weighted\_village[,2:23])

adonis(formula = weighted\_village ~ group+year+giardiapresence, data = weighted\_village\_metadata, permutations = 5000)

*Across habitats*

weighted\_interaction <- read.table("weighted-2017-distance-matrix.tsv", header = T)

giardia\_metadata = inner\_join(weighted\_interaction, giardiametadata, by = "sampleid")

weighted\_interaction <- as.dist(weighted\_interaction[,2:49])

adonis(formula = weighted\_interaction~humaninteraction+group+giardiapresence, data = giardia\_metadata, permutations = 5000)

adonis(formula = weighted\_interaction ~ humaninteraction\*giardiapresence+group, data = giardia\_metadata, permutations = 5000)

***Pairwise Comparison***

library(pairwiseAdonis)

All Sites Unweighted

pairwise.adonis(unweighted\_bothyears, factors=metadata\_both$humaninteraction, perm = 5000, p.adjust.m = 'holm')

All Sites Weighted

pairwise.adonis(weighted\_bothyears, factors=metadata\_together$humaninteraction, perm = 5000, p.adjust.m = 'holm')

***Linear Mixed Models***

library(nlme)

library(multcomp)

*Alpha diversity*

alpha<-read.csv("alpha-diversity-2017.csv")

faith\_alpha=lme(fixed=faith\_pd~giardiapresence, data=alpha, random=~1|sampleid)

summary(faith\_alpha)

anova(faith\_alpha)

summary(glht(faith\_alpha,linfct=mcp(giardiapresence="Tukey")))

faith\_group=lme(fixed=faith\_pd~group, data=alpha, random=~1|sampleid)

summary(faith\_group)

anova(faith\_group)

summary(glht(faith\_group,linfct=mcp(group="Tukey")))

faith\_interaction\_alpha=lme(fixed=faith\_pd~humaninteraction, data=alpha, random=~1|sampleid)

summary(faith\_interaction\_alpha)

anova(faith\_interaction\_alpha)

summary(glht(faith\_interaction\_alpha,linfct=mcp(humaninteraction="Tukey")))

shannon\_alpha=lme(fixed=shannon~giardiapresence, data=alpha, random=~1|sampleid)

summary(shannon\_alpha)

anova(shannon\_alpha)

summary(glht(shannon\_alpha,linfct=mcp(giardiapresence="Tukey")))

shannon\_group=lme(fixed=shannon~group, data = alpha, random = ~1|sampleid)

summary(shannon\_group)

anova(shannon\_group)

summary(glht(shannon\_group,linfct=mcp(group="Tukey")))

shannon\_interaction\_alpha=lme(fixed=shannon~humaninteraction, data=alpha, random=~1|sampleid)

summary(shannon\_interaction\_alpha)

anova(shannon\_interaction\_alpha)

summary(glht(shannon\_interaction\_alpha,linfct=mcp(humaninteraction="Tukey")))

otu\_alpha=lme(fixed=observed\_otus~giardiapresence, data=alpha, random=~1|sampleid)

summary(otu\_alpha)

anova(otu\_alpha)

summary(glht(otu\_alpha,linfct=mcp(giardiapresence="Tukey")))

otu\_group=lme(fixed=observed\_otus~group, data=alpha, random=~1|sampleid)

summary(otu\_group)

anova(otu\_group)

summary(glht(otu\_group,linfct=mcp(group="Tukey")))

otu\_interaction\_alpha=lme(fixed=observed\_otus~humaninteraction, data=alpha, random=~1|sampleid)

summary(otu\_interaction\_alpha)

anova(otu\_interaction\_alpha)

summary(glht(otu\_interaction\_alpha,linfct=mcp(humaninteraction="Tukey")))

*Taxa*

phyla=read.csv("giardia-2017-phyla.csv", header=TRUE)

family<-read.csv("giardia-2017-family.csv", header=T)

genus<-read.csv("giardia-2017-genus.csv", header=T)

acti=lme(fixed=Actinobacteria~giardiapresence, data=phyla, random=~1|sampleid)

summary(acti)

anova(acti)

summary(glht(acti,linfct=mcp(giardiapresence="Tukey")))

acti\_humaninteraction=lme(fixed=Actinobacteria~humaninteraction, data=phyla, random=~1|sampleid)

summary(acti\_humaninteraction)

anova(acti\_humaninteraction)

summary(glht(acti\_humaninteraction,linfct=mcp(humaninteraction="Tukey")))

bact=lme(fixed=Bacteroidetes~giardiapresence, data=phyla, random=~1|sampleid)

summary(bact)

anova(bact)

summary(glht(bact,linfct=mcp(giardiapresence="Tukey")))

bact\_humaninteraction=lme(fixed=Bacteroidetes~humaninteraction, data=phyla, random=~1|sampleid)

summary(bact\_humaninteraction)

anova(bact\_humaninteraction)

summary(glht(bact\_humaninteraction,linfct=mcp(humaninteraction="Tukey")))

prot=lme(fixed=Proteobacteria~giardiapresence, data=phyla, random=~1|sampleid)

summary(prot)

anova(prot)

summary(glht(prot,linfct=mcp(giardiapresence="Tukey")))

prot\_humaninteraction=lme(fixed = Proteobacteria~humaninteraction, data=phyla, random=~1|sampleid)

summary(prot\_humaninteraction)

anova(prot\_humaninteraction)

summary(glht(prot\_humaninteraction,linfct=mcp(humaninteraction="Tukey")))

firm=lme(fixed=Firmicutes~giardiapresence, data=phyla, random=~1|sampleid)

summary(firm)

anova(firm)

summary(glht(firm,linfct=mcp(giardiapresence="Tukey")))

firm\_humaninteraction=lme(fixed=Firmicutes~humaninteraction, data=phyla, random=~1|sampleid)

summary(firm\_humaninteraction)

anova(firm\_humaninteraction)

summary(glht(firm\_humaninteraction,linfct=mcp(humaninteraction="Tukey")))

prev\_giardia=lme(fixed=Prevotellaceae~giardiapresence, data=family, random=~1|sampleid)

summary(prev\_giardia)

anova(prev\_giardia)

summary(glht(prev\_giardia, linfct=mcp(giardiapresence="Tukey")))

prev\_humaninteraction=lme(fixed=Prevotellaceae~humaninteraction, data=family, random=~1|sampleid)

summary(prev\_humaninteraction)

anova(prev\_humaninteraction)

summary(glht(prev\_humaninteraction,linfct=mcp(humaninteraction="Tukey")))

para\_giardia=lme(fixed=Paraprevotellaceae~giardiapresence, data=family, random=~1|sampleid)

summary(para\_giardia)

anova(para\_giardia)

summary(glht(para\_giardia, linfct=mcp(giardiapresence="Tukey")))

para\_humaninteraction=lme(fixed=Paraprevotellaceae~humaninteraction, data=family, random=~1|sampleid)

summary(para\_humaninteraction)

anova(para\_humaninteraction)

summary(glht(para\_humaninteraction,linfct=mcp(humaninteraction="Tukey")))

lach\_giardia=lme(fixed=Lachnospiraceae~giardiapresence, data=family, random=~1|sampleid)

summary(lach\_giardia)

anova(lach\_giardia)

summary(glht(lach\_giardia, linfct=mcp(giardiapresence="Tukey")))

lach\_humaninteraction=lme(fixed=Lachnospiraceae~humaninteraction, data=family, random=~1|sampleid)

summary(lach\_humaninteraction)

anova(lach\_humaninteraction)

summary(glht(lach\_humaninteraction,linfct=mcp(humaninteraction="Tukey")))

rumi\_giardia=lme(fixed=Ruminococcaceae~giardiapresence, data=family, random=~1|sampleid)

summary(rumi\_giardia)

anova(rumi\_giardia)

summary(glht(rumi\_giardia, linfct=mcp(giardiapresence="Tukey")))

rumi\_humaninteraction=lme(fixed=Ruminococcaceae~humaninteraction, data=family, random=~1|sampleid)

summary(rumi\_humaninteraction)

anova(rumi\_humaninteraction)

summary(glht(rumi\_humaninteraction,linfct=mcp(humaninteraction="Tukey")))

prevo\_giardia=lme(fixed=Prevotella~giardiapresence, data=genus, random=~1|sampleid)

summary(prevo\_giardia)

anova(prevo\_giardia)

summary(glht(prevo\_giardia,linfct=mcp(giardiapresence="Tukey")))

prevo\_humaninteraction=lme(fixed=Prevotella~humaninteraction, data=genus, random=~1|sampleid)

summary(prevo\_humaninteraction)

anova(prevo\_humaninteraction)

summary(glht(prevo\_humaninteraction,linfct=mcp(humaninteraction="Tukey")))