Rarefaction Curve Code

########### Rarefaction curve to justify 300 count sub-sample ##########

# Load Libraries

install.packages("Rarefy")

install.packages("ade4")

installed.packages("adiv")

install.packages("ape")

install.packages("vegan")

install.packages("phyloregion")

install.packages("raster")

library(Rarefy)

library(ade4)

library(adiv)

library(ape)

library(vegan)

library(phyloregion)

library(raster)

# Set Working Directory

setwd("C:/Users/michf/OneDrive/University of Montana/Raw Data/Benthic")

# read in data

benth <- read.csv("benthic\_rarefy.csv",head=T, sep=",")

raremax <- min(rowSums(benth))

rarecurve(benth, step = 5, sample= raremax, col = "blue", cex=0.6)