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##
## Script name: Process_Library_Survey_Data
##
## Purpose of script: fits a binomial logistic regression model to the
library survey data.
##
## Author: Nicholas Macfarlane, PhD
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## Date Created: 2020-04-10
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## Notes:
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## set working directory for PC

setwd("D:/Home/Desktop/IUCN/Library Survey/working")

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## load packages:

require(multcomp)

## -----
## read in cleaned and arranged library survey data file
dat<- read.csv("libraryfrequencyworking_for_analysis.csv", header=T) #1970
x 15 data table of survey responses

#head(dat)
# RespondentID AccessEase Language Gender Region InstitutionalAccess
IUCNCECmember IUCNCEESpmember
# 1 4861786455 1 EN M 2 0
1 0
# 2 4862370473 1 EN F 5 0
0 0
# 3 4862499333 1 EN M 5 0
0 0
# 4 4862762458 1 EN F 5 0
0 0
# 5 4863451450 1 EN M 2 1
0 0
# 6 4866173330 1 EN M 5 0
0 0
# IUCNCEMmember IUCNSSCmember IUCNWCELmember IUCNWCPAmember
IUCNSecretariatstaff Sector Discipline
# 1 0 0 0 0
0 NatNGO CEC
# 2 0 0 0 1
0 GovAgency WCPA

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# 3      0      0      0      1
0  NatNGO  WCPA
# 4      0      0      0      1
0  NatNGO  WCPA
# 5      0      1      0      0
0  NatNGO  SSC
# 6      0      0      0      1
0  IntNGO  WCPA

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## input data processing

# create binary vector for insitutional access ease where 1 is easy or very
easy and 0 is hard or very hard
dat$binary <- rep(0, length(dat$AccessEase))
for (i in 1:length(dat$AccessEase)){
  if(dat$AccessEase[i]>= 3)
    dat$binary[i] <- 1
  else dat$binary[i] <-0
}

# process data as factors
dat$AccessEase <-as.factor(dat$AccessEase)
dat$Language <-as.factor(dat$Language)
dat$Gender <-as.factor(dat$Gender)
dat$Region <-as.factor(dat$Region)
dat$InstitutionalAccess <-as.factor(dat$InstitutionalAccess)

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## model selection and analysis.

## binomial logistic regression model fitting using AIC scores
m1 =glm(binary~ InstitutionalAccess+ Language+ Gender+ Sector+ Region+
Discipline, family="binomial", data = dat)
m2 =glm(binary~ InstitutionalAccess+ Language+ Gender+ Sector+ Region+
IUCNCECmember+ IUCNCEESPmember+ IUCNCEMmember + IUCNSSCmember +
IUCNWCELmember + IUCNWCPAmember, family="binomial", data = dat)
m3 =glm(binary~ InstitutionalAccess+ Language+ Gender+ Region+
IUCNCECmember+ IUCNCEESPmember+ IUCNCEMmember + IUCNSSCmember +
IUCNWCELmember + IUCNWCPAmember, family="binomial", data = dat)

m4 =glm(binary~ InstitutionalAccess+ Gender+ Region+ IUCNCECmember+
IUCNCEESPmember+ IUCNCEMmember + IUCNSSCmember + IUCNWCELmember +
IUCNWCPAmember, family="binomial", data = dat)
m5 =glm(binary~ InstitutionalAccess+ Gender+ Region, family="binomial",
data = dat)

## kruskal wallis comparisons
kruskal.test(binary~Language, data=dat)
kruskal.test(binary~Discipline, data=dat)
kruskal.test(binary~Region, data=dat)

#interactions

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m5a =glm(binary~ InstitutionalAccess*Gender+ Region, family="binomial",
data = dat)
m5b =glm(binary~ InstitutionalAccess+Gender*Region, family="binomial", data
= dat)
m5c =glm(binary~ InstitutionalAccess*Region + Gender, family="binomial",
data = dat)

# tukey post hoc contrasts
t5<-glht(m5, linfct = mcp(Region = "Tukey"))
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