Análise do banco de dados de traumas

Felipe Pinto

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## Warning: package 'pastecs' was built under R version 4.1.3

#### *Carregando dados do arquivo “traumas\_centrosul\_total.csv” correspondente a dados do centro-sul do Peru entre os períodos PIP (Período Intermédio Primeiro) HM (Horizonte Médio) e PIT(Período Intermédio Tardio):*

##### *obs1: a partir da linha 48 o banco contémm dados de frequência coletados por trabalhos que não foi possível obter acesso direto.*

##### *obs2:apenas os dados do HM e PIT foram analisados*

dados\_traumas <- read.csv("traumas\_centrosul\_total.csv", na.strings = "NA", sep = ";")   
names(dados\_traumas) #execute este comando para ver os nomes das colunas e variáveis presentes no banco de dados

## [1] "autor\_ano" "referencia"   
## [3] "pais" "regiao"   
## [5] "grupo.regional" "sitio"   
## [7] "status\_mortuario" "contx\_violencia"   
## [9] "lat" "long"   
## [11] "elevação\_m" "cultura"   
## [13] "cronologia" "cronologia.ORD"   
## [15] "data\_absBP\_.inicial" "data\_absBP\_final"   
## [17] "sexo" "fx\_idade"   
## [19] "n\_id" "n\_id\_afetados"   
## [21] "n\_id\_naoafetados" "n\_fr\_afetados"   
## [23] "n\_id\_antimortem" "n\_les\_antimortem"   
## [25] "n\_id\_perimortem" "n\_les\_perimortem"   
## [27] "anti\_peri" "n\_tr\_anterior"   
## [29] "n\_antimortem\_anterior" "n\_perimortem\_anterior"   
## [31] "nasal" "maxilar"   
## [33] "boca\_mandibula" "frontal"   
## [35] "sutura\_frontozigomatica" "n\_tr\_posterior"   
## [37] "n\_antimortem\_posterior" "n\_perimortem\_posterior"   
## [39] "occipital" "n\_tr\_pariental"   
## [41] "parietal\_e" "pariental\_d"   
## [43] "pterion" "n\_tr\_lateral"   
## [45] "n\_antimortem\_lateral" "n\_tr\_perimortem\_lateral"   
## [47] "lateral\_e" "lateral\_d"   
## [49] "zigomatico" "processo\_zigo\_d"   
## [51] "processo\_zigo\_e" "n\_tr\_temporal"   
## [53] "temporal\_e" "temporal\_d"   
## [55] "n\_tr\_superior" "n\_antimortem\_superior"   
## [57] "n\_perimortem\_superior" "n\_cabeca\_.trofeu"   
## [59] "n\_cabeca\_.trofeu\_trauma" "n\_cabeca\_.trofeu\_trauma\_anti"   
## [61] "n\_cabeca\_.trofeu\_trauma\_peri" "n\_postcranio"   
## [63] "n\_postcranio\_afetado" "costela"   
## [65] "vert\_lombares" "vert\_toráxicas"   
## [67] "vert\_cervicais" "torax"   
## [69] "n\_membros\_superior" "glenoid"   
## [71] "humero" "radio"   
## [73] "ulna" "acetabulo"   
## [75] "escapula" "femur"   
## [77] "tibia" "fibula"   
## [79] "frat\_depressiva" "Frat\_Perfurante"   
## [81] "frat\_cortante" "frat\_circular"   
## [83] "flecha\_projetil" "arma\_lamina"   
## [85] "arma\_corpo" "Outro.instrumento"   
## [87] "agressão.interpessoal" "rading\_invasao"   
## [89] "guerra" "canibalismo"   
## [91] "ritual" "acidental\_laboral"   
## [93] "n\_id\_deformacoes" "n\_patologias"   
## [95] "n\_cribia\_orbitaria" "n\_hiperostosis\_porotica"   
## [97] "n\_periostiti" "infec\_osteomielite"   
## [99] "n\_congenitas" "n\_exostose\_ouvido"   
## [101] "n\_caries" "n\_hipoplasia\_linear"   
## [103] "n\_reabsorcao\_aveolar" "n\_poscr\_cribia\_orbitaria"   
## [105] "n\_poscr\_hiperostosis\_porotica" "Infec\_posCr\_periostiti"   
## [107] "n\_poscr\_osteomeliti" "n\_fusao\_vert"   
## [109] "n\_pt\_ambientais" "n\_osteoporose"   
## [111] "n\_exostose" "n\_osteofitose"   
## [113] "n\_espodilose" "n\_osteoartrite"   
## [115] "padr\_funerário" "cultura\_material"   
## [117] "iconografia\_v" "grafismos\_v"   
## [119] "ev\_fort" "estr\_sociopolitica"   
## [121] "pad\_assentamento" "bioma"   
## [123] "clima" "carc\_geografica"   
## [125] "estrg\_subsistencia"

View(dados\_traumas) #execute para visualizar todo o conjunto de dados em uma janela separada  
  
#head(dados\_traumas) #execute para visualizar apenas as primeiras 5 observações dos dados

#### *Aplicação dos modelos de regressão lineares generalizados:*

#library(MASS)  
#plot(data\_hmpit$cronologia.ORD,data\_hmpit$n\_id\_afetados, xlab = "Periodo",  
 # ylab= "individuos com traumas")  
  
#M1 <- glm.nb(n\_id\_afetados b< cronologia.ORD+n\_id\_naoafetados,   
 #link = "log", data = data\_hmpit)  
  
#summary(M1)  
#effects(M1)  
#predict.glm(M1)  
#hist(predict.glm(M1))

## *Testando a semelhança entre traumas antimortem, perimortem, anterior e posterior por meio do teste Exato de Fisher. O teste foi aplicado considerando apenas os dados do banco de dados que foi possível revisar e extrair os dados quantitativos dessas variáveis*

#M x F hm antimortem  
hm.anti <- as.table(rbind(c(6,80),c(54,149)))  
dimnames(hm.anti)<-list(sexo = c("f","m"),  
 amostra = c("antimortem","n total"))  
hm.anti

## amostra  
## sexo antimortem n total  
## f 6 80  
## m 54 149

#chisq.test(hm.anti)  
fisher.test(hm.anti)

##   
## Fisher's Exact Test for Count Data  
##   
## data: hm.anti  
## p-value = 0.0001075  
## alternative hypothesis: true odds ratio is not equal to 1  
## 95 percent confidence interval:  
## 0.06998741 0.51173642  
## sample estimates:  
## odds ratio   
## 0.207849

fr.F <- 6/80  
fr.F

## [1] 0.075

fr.M <- 54/149  
fr.M

## [1] 0.3624161

#M x F hm anterior  
hm.anter <- as.table(rbind(c(2,80),c(93,149)))  
dimnames(hm.anter)<-list(sexo = c("f","m"),  
 amostra = c("anterior","n total"))  
hm.anter

## amostra  
## sexo anterior n total  
## f 2 80  
## m 93 149

#chisq.test(hm.anter)  
fisher.test(hm.anter)

##   
## Fisher's Exact Test for Count Data  
##   
## data: hm.anter  
## p-value = 4.917e-12  
## alternative hypothesis: true odds ratio is not equal to 1  
## 95 percent confidence interval:  
## 0.00470475 0.15692406  
## sample estimates:  
## odds ratio   
## 0.04029247

fr.F <- 2/80  
fr.F

## [1] 0.025

fr.M <- 93/149  
fr.M

## [1] 0.6241611

#M <- as.table(rbind(c(762, 327, 468), c(484, 239, 477)))  
#dimnames(M) <- list(gender = c("F", "M"),  
# party = c("Democrat","Independent", "Republican"))  
#(Xsq <- chisq.test(M)) # Prints test summary  
  
#M x F hm posterior  
hm.post <- as.table(rbind(c(32,149),c(14,80)))  
dimnames(hm.post)<-list(sexo = c("m","f"),  
 amostra = c("posterior","n total"))  
hm.post

## amostra  
## sexo posterior n total  
## m 32 149  
## f 14 80

#chisq.test(hm.post)  
fisher.test(hm.post)

##   
## Fisher's Exact Test for Count Data  
##   
## data: hm.post  
## p-value = 0.6125  
## alternative hypothesis: true odds ratio is not equal to 1  
## 95 percent confidence interval:  
## 0.5948853 2.6390769  
## sample estimates:  
## odds ratio   
## 1.226332

fr.M <- 32/149  
fr.M

## [1] 0.2147651

fr.F<- 14/80   
fr.F

## [1] 0.175

#M x F pit antimortem  
  
pit.anti <- as.table(rbind(c(55,222),c(35,207)))  
dimnames(pit.anti)<-list(sexo = c("m","f"),  
 amostra = c("antimortem","n total"))  
pit.anti

## amostra  
## sexo antimortem n total  
## m 55 222  
## f 35 207

#chisq.test(pit.anti)  
fisher.test(pit.anti)

##   
## Fisher's Exact Test for Count Data  
##   
## data: pit.anti  
## p-value = 0.1306  
## alternative hypothesis: true odds ratio is not equal to 1  
## 95 percent confidence interval:  
## 0.8999559 2.4064972  
## sample estimates:  
## odds ratio   
## 1.464173

fr.M <- 55/222  
fr.M

## [1] 0.2477477

fr.F <- 35/207  
fr.F

## [1] 0.1690821

#M x F pit perimortem  
  
pit.peri <- as.table(rbind(c(20,222),c(17,207)))  
dimnames(pit.peri)<-list(sexo = c("m","f"),  
 amostra = c("perimotem","n total"))  
pit.peri

## amostra  
## sexo perimotem n total  
## m 20 222  
## f 17 207

#chisq.test(pit.peri)  
fisher.test(pit.peri)

##   
## Fisher's Exact Test for Count Data  
##   
## data: pit.peri  
## p-value = 0.8645  
## alternative hypothesis: true odds ratio is not equal to 1  
## 95 percent confidence interval:  
## 0.5293258 2.2964487  
## sample estimates:  
## odds ratio   
## 1.096745

fr.M <- 20/222   
fr.M

## [1] 0.09009009

fr.F <- 17/207  
fr.F

## [1] 0.0821256

#M x F pit anterior  
pit.anter <- as.table(rbind(c(61,222),c(49,207)))  
dimnames(pit.anter)<-list(sexo = c("m","f"),  
 amostra = c("anterior","n total"))  
pit.anter

## amostra  
## sexo anterior n total  
## m 61 222  
## f 49 207

#chisq.test(pit.anter)  
fisher.test(pit.anter)

##   
## Fisher's Exact Test for Count Data  
##   
## data: pit.anter  
## p-value = 0.5216  
## alternative hypothesis: true odds ratio is not equal to 1  
## 95 percent confidence interval:  
## 0.7460929 1.8115928  
## sample estimates:  
## odds ratio   
## 1.160461

fr.M <- 61/222   
fr.M

## [1] 0.2747748

fr.F <- 49/207  
fr.F

## [1] 0.236715

#M x F pit posterior  
  
pit.post <- as.table(rbind(c(30,222),c(30,207)))  
dimnames(pit.post)<-list(sexo = c("m","f"),  
 amostra = c("posterior","n total"))  
pit.post

## amostra  
## sexo posterior n total  
## m 30 222  
## f 30 207

#chisq.test(pit.post)  
fisher.test(pit.post)

##   
## Fisher's Exact Test for Count Data  
##   
## data: pit.post  
## p-value = 0.8905  
## alternative hypothesis: true odds ratio is not equal to 1  
## 95 percent confidence interval:  
## 0.5231033 1.6624739  
## sample estimates:  
## odds ratio   
## 0.9325852

fr.M <- 30/222  
fr.M

## [1] 0.1351351

fr.F <- 30/207  
fr.F

## [1] 0.1449275

Comparando os sexos masculinos entre os perC-odos HM e PIT:

#Mhm x Mpit antimortem  
  
Mhm.pit.anti <- as.table(rbind(c(54,149),c(55,222)))  
dimnames(Mhm.pit.anti)<-list(grupo = c("Mhm","Mpit"),  
 amostra = c("antimortem","n total"))  
Mhm.pit.anti

## amostra  
## grupo antimortem n total  
## Mhm 54 149  
## Mpit 55 222

#chisq.test(Mhm.pit.anti)  
fisher.test(Mhm.pit.anti)

##   
## Fisher's Exact Test for Count Data  
##   
## data: Mhm.pit.anti  
## p-value = 0.0979  
## alternative hypothesis: true odds ratio is not equal to 1  
## 95 percent confidence interval:  
## 0.9299919 2.2980405  
## sample estimates:  
## odds ratio   
## 1.461626

fr.Mhm <- 54/149  
fr.Mhm

## [1] 0.3624161

fr.Mpit <- 55/222  
fr.Mpit

## [1] 0.2477477

Comparando traumas nos indivC-duos masculinos entre os perC-odos

#Mhm x Mpit perimortem  
  
Mhm.pit.peri <- as.table(rbind(c(5,149),c(20,222)))  
dimnames(Mhm.pit.peri)<-list(grupo = c("Mhm","Mpit"),  
 amostra = c("perimortem","n total"))  
Mhm.pit.peri

## amostra  
## grupo perimortem n total  
## Mhm 5 149  
## Mpit 20 222

#chisq.test(Mhm.pit.peri)  
fisher.test(Mhm.pit.peri)

##   
## Fisher's Exact Test for Count Data  
##   
## data: Mhm.pit.peri  
## p-value = 0.05577  
## alternative hypothesis: true odds ratio is not equal to 1  
## 95 percent confidence interval:  
## 0.1070743 1.0547815  
## sample estimates:  
## odds ratio   
## 0.3732951

fr.Mhm <- 5/149  
fr.Mhm

## [1] 0.03355705

fr.Mpit <- 20/222  
fr.Mpit

## [1] 0.09009009

#Mhm x Mpit anterior  
  
  
Mhm.pit.anter <- as.table(rbind(c(93,149),c(61,222)))  
dimnames(Mhm.pit.anter)<-list(grupo = c("Mhm","Mpit"),  
 amostra = c("anterior","n total"))  
Mhm.pit.anter

## amostra  
## grupo anterior n total  
## Mhm 93 149  
## Mpit 61 222

#chisq.test(Mhm.pit.anter)  
fisher.test(Mhm.pit.anter)

##   
## Fisher's Exact Test for Count Data  
##   
## data: Mhm.pit.anter  
## p-value = 3.262e-05  
## alternative hypothesis: true odds ratio is not equal to 1  
## 95 percent confidence interval:  
## 1.520544 3.400550  
## sample estimates:  
## odds ratio   
## 2.267902

fr.Mhm <- 93/149  
fr.Mhm

## [1] 0.6241611

fr.Mpit <- 61/222  
fr.Mpit

## [1] 0.2747748

#Mhm x Mpit posterior  
  
Mhm.pit.post <- as.table(rbind(c(32,149),c(30,222)))  
dimnames(Mhm.pit.post)<-list(grupo = c("Mhm","Mpit"),  
 amostra = c("posterior","n total"))  
Mhm.pit.post

## amostra  
## grupo posterior n total  
## Mhm 32 149  
## Mpit 30 222

#chisq.test(Mhm.pit.post)  
fisher.test(Mhm.pit.post)

##   
## Fisher's Exact Test for Count Data  
##   
## data: Mhm.pit.post  
## p-value = 0.09666  
## alternative hypothesis: true odds ratio is not equal to 1  
## 95 percent confidence interval:  
## 0.8926239 2.8305805  
## sample estimates:  
## odds ratio   
## 1.587474

fr.Mhm <- 32/149  
fr.Mhm

## [1] 0.2147651

fr.Mpit <- 30/222  
fr.Mpit

## [1] 0.1351351

#Fhm x Fpit antimortem  
  
Fhm.pit.anti <- as.table(rbind(c(6,80),c(35,207)))  
dimnames(Fhm.pit.anti)<-list(grupo = c("Fhm","Fpit"),  
 amostra = c("antimortem","n total"))  
Fhm.pit.anti

## amostra  
## grupo antimortem n total  
## Fhm 6 80  
## Fpit 35 207

#chisq.test(Fhm.pit.anti)  
fisher.test(Fhm.pit.anti)

##   
## Fisher's Exact Test for Count Data  
##   
## data: Fhm.pit.anti  
## p-value = 0.08725  
## alternative hypothesis: true odds ratio is not equal to 1  
## 95 percent confidence interval:  
## 0.1471021 1.1236791  
## sample estimates:  
## odds ratio   
## 0.4445072

fr.Fhm <- 6/80  
fr.Fhm

## [1] 0.075

fr.Fpit <- 35/207  
fr.Fpit

## [1] 0.1690821

#Fhm x Fpit posterior  
  
Fhm.pit.post <- as.table(rbind(c(14,80),c(30,207)))  
dimnames(Fhm.pit.post)<-list(grupo = c("Fhm","Fpit"),  
 amostra = c("posterior","n total"))  
Fhm.pit.post

## amostra  
## grupo posterior n total  
## Fhm 14 80  
## Fpit 30 207

#chisq.test(Fhm.pit.post)  
fisher.test(Fhm.pit.post)

##   
## Fisher's Exact Test for Count Data  
##   
## data: Fhm.pit.post  
## p-value = 0.5932  
## alternative hypothesis: true odds ratio is not equal to 1  
## 95 percent confidence interval:  
## 0.5607332 2.4921251  
## sample estimates:  
## odds ratio   
## 1.206762

fr.Fhm <- 14/80  
fr.Fhm

## [1] 0.175

fr.Fpit <- 30/207  
fr.Fpit

## [1] 0.1449275

#Fhm x Fpit anterior  
  
Fhm.pit.anter <- as.table(rbind(c(2,80),c(49,207)))  
dimnames(Fhm.pit.anter)<-list(grupo = c("Fhm","Fpit"),  
 amostra = c("posterior","n total"))  
Fhm.pit.anter

## amostra  
## grupo posterior n total  
## Fhm 2 80  
## Fpit 49 207

#chisq.test(Fhm.pit.anter)  
fisher.test(Fhm.pit.anter)

##   
## Fisher's Exact Test for Count Data  
##   
## data: Fhm.pit.anter  
## p-value = 6.307e-05  
## alternative hypothesis: true odds ratio is not equal to 1  
## 95 percent confidence interval:  
## 0.01220766 0.42099240  
## sample estimates:  
## odds ratio   
## 0.10603

fr.Fhm <- 2/80  
fr.Fhm

## [1] 0.025

fr.Fpit <- 49/207  
fr.Fpit

## [1] 0.236715

hm.pit <- as.table(rbind(c(136,326),c(251,479)))  
dimnames(hm.pit)<-list(grupo = c("hm","pit"),  
 amostra = c("afetados","n total"))  
hm.pit

## amostra  
## grupo afetados n total  
## hm 136 326  
## pit 251 479

#chisq.test(hm.pit)  
fisher.test(hm.pit)

##   
## Fisher's Exact Test for Count Data  
##   
## data: hm.pit  
## p-value = 0.08645  
## alternative hypothesis: true odds ratio is not equal to 1  
## 95 percent confidence interval:  
## 0.6134359 1.0313731  
## sample estimates:  
## odds ratio   
## 0.7962818

set.seed(1234)  
norm <- rnorm(100000,mean=0,sd=1)  
x <-as.data.frame(norm)  
  
plotnorm<-ggplot(x, aes(x=norm)) +   
 geom\_histogram(aes(y=..density..), colour="white", fill="white")+  
 geom\_density(alpha=.6, fill="darkred")  
#ggsave(filename = "curva.jpg",plot = plotnorm,width = 4.5,height = 3)  
#qqplot(norm)