L & D Database practice

N. Brandon Barba

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This Code is to change directory and upload the CSV File

#setwd("/Users/brandon/Library/Mobile  
#Documents/com~apple~CloudDocs/Samus/1|Projects/OB\_GYN Research/L&D/Programs")  
data <- read.csv('../Data/Practice\_Import.csv', header = T)

This chunk is to clean the csv columns

#Clean Weeks  
data$ega <- substr(data$ega,1,2)  
  
#Split Delivery Type  
data$delivery\_type\_1 <- NA  
data$delivery\_type\_2 <- NA  
  
split\_values <- strsplit(as.character(data$delivery\_type),";")  
data$delivery\_type\_1 <- sapply(split\_values, function(x) x[1])  
data$delivery\_type\_2 <- sapply(split\_values, function(x) x[2])  
  
#Fix Estimated Blood loess  
data$ebl<- gsub("mL", "", data$ebl)  
  
#Split Augmentation Method  
data$aug\_method\_1 <- NA  
data$aug\_method\_2 <- NA  
  
split\_values <- strsplit(as.character(data$aug\_method),";")  
data$aug\_method\_1 <- sapply(split\_values, function(x) x[1])  
data$aug\_method\_2 <- sapply(split\_values, function(x) x[2])  
  
#Split C-Section Indications  
data$cs\_ind\_1 <- NA  
data$cs\_ind\_2 <- NA  
data$cs\_ind\_3 <- NA  
data$cs\_ind\_4 <- NA  
data$cs\_ind\_5 <- NA  
  
split\_values <- strsplit(as.character(data$cs\_ind),";")  
data$cs\_ind\_1 <- sapply(split\_values, function(x) x[1])  
data$cs\_ind\_2 <- sapply(split\_values, function(x) x[2])  
data$cs\_ind\_3 <- sapply(split\_values, function(x) x[3])  
data$cs\_ind\_4 <- sapply(split\_values, function(x) x[4])  
data$cs\_ind\_5 <- sapply(split\_values, function(x) x[5])  
  
#Split Fetal Monitor  
data$fhr\_mon\_1 <- NA  
data$fhr\_mon\_2 <- NA  
  
split\_values <- strsplit(as.character(data$fhr\_mon),";")  
data$fhr\_mon\_1 <- sapply(split\_values, function(x) x[1])  
data$fhr\_mon\_2 <- sapply(split\_values, function(x) x[2])  
  
#Split Maternal Complications  
data$mat\_comp\_1 <- NA  
data$mat\_comp\_2 <- NA  
data$mat\_comp\_3 <- NA  
data$mat\_comp\_4 <- NA  
data$mat\_comp\_5 <- NA  
  
split\_values <- strsplit(as.character(data$mat\_comp),";")  
data$mat\_comp\_1 <- sapply(split\_values, function(x) x[1])  
data$mat\_comp\_2 <- sapply(split\_values, function(x) x[2])  
data$mat\_comp\_3 <- sapply(split\_values, function(x) x[3])  
data$mat\_comp\_4 <- sapply(split\_values, function(x) x[4])  
data$mat\_comp\_5 <- sapply(split\_values, function(x) x[5])  
  
#Split Neontal Complications  
data$neonatal\_comp\_1 <- NA  
data$neonatal\_comp\_2 <- NA  
data$neonatal\_comp\_3 <- NA  
data$neonatal\_comp\_4 <- NA  
data$neonatal\_comp\_5 <- NA  
  
split\_values <- strsplit(as.character(data$neonatal\_comp),";")  
data$neonatal\_comp\_1 <- sapply(split\_values, function(x) x[1])  
data$neonatal\_comp\_2 <- sapply(split\_values, function(x) x[2])  
data$neonatal\_comp\_3 <- sapply(split\_values, function(x) x[3])  
data$neonatal\_comp\_4 <- sapply(split\_values, function(x) x[4])  
data$neonatal\_comp\_5 <- sapply(split\_values, function(x) x[5])  
  
#Split Risk Factors  
data$risk\_factors\_1 <- NA  
data$risk\_factors\_2 <- NA  
data$risk\_factors\_3 <- NA  
data$risk\_factors\_4 <- NA  
data$risk\_factors\_5 <- NA  
  
split\_values <- strsplit(as.character(data$risk\_factors),";")  
data$risk\_factors\_1 <- sapply(split\_values, function(x) x[1])  
data$risk\_factors\_2 <- sapply(split\_values, function(x) x[2])  
data$risk\_factors\_3 <- sapply(split\_values, function(x) x[3])  
data$risk\_factors\_4 <- sapply(split\_values, function(x) x[4])  
data$risk\_factors\_5 <- sapply(split\_values, function(x) x[5])  
  
  
#Split Diagnosis  
data$diagnosis\_1 <- NA  
data$diagnosis\_2 <- NA  
data$diagnosis\_3 <- NA  
data$diagnosis\_4 <- NA  
data$diagnosis\_5 <- NA  
  
split\_values <- strsplit(as.character(data$diagnosis),";")  
data$diagnosis\_1 <- sapply(split\_values, function(x) x[1])  
data$diagnosis\_2 <- sapply(split\_values, function(x) x[2])  
data$diagnosis\_3 <- sapply(split\_values, function(x) x[3])  
data$diagnosis\_4 <- sapply(split\_values, function(x) x[4])  
data$diagnosis\_5 <- sapply(split\_values, function(x) x[5])  
  
#Split Risk Pregnancy  
data$risk\_pregancy\_1<- NA  
data$risk\_pregancy\_2<- NA  
data$risk\_pregancy\_3<- NA  
data$risk\_pregancy\_4<- NA  
data$risk\_pregancy\_5 <- NA  
  
split\_values <- strsplit(as.character(data$risk\_pregancy),";")  
data$risk\_pregancy\_1 <- sapply(split\_values, function(x) x[1])  
data$risk\_pregancy\_2 <- sapply(split\_values, function(x) x[2])  
data$risk\_pregancy\_3 <- sapply(split\_values, function(x) x[3])  
data$risk\_pregancy\_4 <- sapply(split\_values, function(x) x[4])  
data$risk\_pregancy\_5 <- sapply(split\_values, function(x) x[5])

Number of Weeks 36-41+ & % Age of Term Deliveries

sum(data$ega == 36, na.rm=TRUE)

## [1] 40

sum(data$ega == 37, na.rm=TRUE)

## [1] 67

sum(data$ega == 38, na.rm=TRUE)

## [1] 91

sum(data$ega == 39, na.rm=TRUE)

## [1] 197

sum(data$ega == 40, na.rm=TRUE)

## [1] 116

sum(data$ega >= 41, na.rm=TRUE)

## [1] 44

Number of C-Sections

## Plots

Note that the echo = FALSE parameter was added to the code chunk to prevent printing of the R code that generated the plot.