

Supplementary File 2

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# TITLE: Create baseline patient and surgical characteristics table, oximetry table, and  
oximetry graphs  
# Author: Clarence Wong  
# Last updated: 2/7/2017  
# RStudio v. 1.0.136  
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library(readr)  
require(lubridate)  
require(TTR)  
require(xts)  
require(zoo)  
require(tableone)  
require(ggplot2)  
library(grid)  
require(gridExtra)  
require(quantreg)  
  
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# 1. Create summary statistics for baseline characteristics  
# 2. Perform statistical analysis on secondary outcomes. e.g post-operative delirium  
# 3. Export tables in csv files  
# Requires baseline characteristic and baseline oximetry data.  
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baseline_db <- read.csv("D:/SS/R_data/baseline/all_baseline.csv", sep="," ,  
stringsAsFactors=TRUE)  
load("other_data.RData")  
  
other_data <- other_data[-c(1,2),]  
  
baseline_db$baseline_L_mu <- other_data$baseline_L_mu  
baseline_db$baseline_L_std <- other_data$baseline_L_std  
baseline_db$baseline_L_N <- other_data$baseline_L_N  
baseline_db$baseline_R_mu <- other_data$baseline_R_mu  
baseline_db$baseline_R_std <- other_data$baseline_R_std  
baseline_db$baseline_R_N <- other_data$baseline_R_N  
  
baseline_db$P_id <- index(baseline_db)
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baseline_db[baseline_db == "#N/A"]<-NA
baseline_db[baseline_db == 9999]<-NA
baseline_db$pCO2_2<-
as.numeric(levels(baseline_db$pCO2_2))[baseline_db$pCO2_2]
baseline_db$BMI<-as.numeric(levels(baseline_db$BMI))[baseline_db$BMI]
vars <-
c("Gender","Age","Weight","BMI","ASA","Diabetes","COPD","Malignancy","Other_C
omorbidities",

"Surgery_type","Duration_Surgery_Minutes","baseline_L_mu","baseline_R_mu")
factorVars <- c("ASA","Diabetes","COPD","Malignancy","Other_Comorbidities")
Tableone <- CreateTableOne(vars,"Group",baseline_db,factorVars)

baseline_db$LOS<-as.numeric(levels(baseline_db$LOS))[baseline_db$LOS]
baseline_db$pH_2<-as.numeric(levels(baseline_db$pH_2))[baseline_db$pH_2]
baseline_db$HCO3_2<-
as.numeric(levels(baseline_db$HCO3_2))[baseline_db$HCO3_2]
baseline_db$Base_excess_2<-
as.numeric(levels(baseline_db$Base_excess_2))[baseline_db$Base_excess_2]
baseline_db$Potassium_2<-
as.numeric(levels(baseline_db$Potassium_2))[baseline_db$Potassium_2]
baseline_db$Total_Hb_2<-
as.numeric(levels(baseline_db$Total_Hb_2))[baseline_db$Total_Hb_2]

baseline_db$pH<-apply(baseline_db[,c("pH_1","pH_2")],1,mean,na.rm=TRUE)
baseline_db$pCO2<-
apply(baseline_db[,c("pCO2_1","pCO2_2")],1,mean,na.rm=TRUE)
baseline_db$HCO3.<-
apply(baseline_db[,c("HCO3_1","HCO3_2")],1,mean,na.rm=TRUE)
baseline_db$Base_excess<-
apply(baseline_db[,c("Base_excess_1","Base_excess_2")],1,mean,na.rm=TRUE)
baseline_db$Potassium<-
apply(baseline_db[,c("Potassium_1","Potassium_2")],1,mean,na.rm=TRUE)
baseline_db$Total_Hb<-
apply(baseline_db[,c("Total_Hb_1","Total_Hb_2")],1,mean,na.rm=TRUE)

vars_2 <-
c("Surgery_type","Duration_Surgery_Minutes","baseline_L_mu","baseline_R_mu","L
OS",

"pH","pCO2","HCO3.","Base_excess","Potassium","Total_Hb","post_op_delirium")
factorVars_2 <- c("post_op_delirium")
Tabletwo <- CreateTableOne(vars_2,"Group",baseline_db,factorVars_2,argsExact =
"post_op_delirium")

print(Tabletwo,exact = "post_op_delirium",nonnormal =
c("Duration_Surgery_Minutes","baseline_L_mu","baseline_R_mu",

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"LOS", "pH", "pCO2", "HCO3.", "Base_excess", "Potassium", "Total_Hb"))

write.csv(print(Tabletwo, exact = "post_op_delirium", nonnormal =
c("Duration_Surgery_Minutes", "baseline_L_mu",
"baseline_R_mu", "LOS", "pH", "pCO2", "HCO3.",
"Base_excess", "Potassium", "Total_Hb")),
"Table_Two.csv")

#-----
# 1. Create summary statistics for percentage change of regional cerebral oxygen
saturation
# 2. Create plots for regional cerebral oxygen saturation over time
# 3. Export oximetry tables in csv files
# Requires baseline characteristic and baseline oximetry data.
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# Normocapnic group

plot_db <- read.csv("D:/SS/R_data/oximetry/MASTER_results_deleted_missing.csv",
sep=",", stringsAsFactors=TRUE)

plot_db[plot_db == "#N/A"] <- NA
plot_db[plot_db == 9999] <- NA

normocapnia <- subset(plot_db, Group %in% 0)
hypercapnia <- subset(plot_db, Group %in% 1)

normo_plot <- ggplot(normocapnia, aes(x=minute_from_baseline, y=L_delta,
group=p_id)) + geom_line() + geom_point()+
  ggtitle("normocapnia: L delta")+ xlab("Time since start of operation (mins)") +
  ylab("% change in oximetry from baseline")

hyper_plot <- ggplot(hypercapnia, aes(x=minute_from_baseline, y=L_delta,
group=p_id)) + geom_line() + geom_point()+
  ggtitle("hypercapnia: L delta")+ xlab("Time since start of operation (mins)") +
  ylab("% change in oximetry from baseline")

means <- tapply(normocapnia$L_delta, normocapnia$time_id, function(x) mean(x, na.rm
= TRUE))
stdevs <- tapply(normocapnia$L_delta, normocapnia$time_id, function(x) sd(x, na.rm =
TRUE))

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N <- tapply(normocapnia$L_delta,normocapnia$time_id,function(x)
length(x[!is.na(x)]))

normo_df_L <- data.frame(means,stdevs)
times<- index(normo_df_L)*5
normo_df_L <- data.frame(means,stdevs,N, times)
total_normo_L <- ggplot(normo_df_L, aes(x=times, y=means)) +
geom_line(colour="blue4") +
  geom_ribbon(normo_df_L,mapping = aes(x=times,
ymax=means+stdevs,ymin=means-stdevs),fill="blue4",alpha=0.1)

means <- tapply(normocapnia$R_delta,normocapnia$time_id,function(x) mean(x,
na.rm = TRUE))
stdevs <- tapply(normocapnia$R_delta,normocapnia$time_id,function(x) sd(x, na.rm =
TRUE))
N <- tapply(normocapnia$R_delta,normocapnia$time_id,function(x)
length(x[!is.na(x)]))

normo_df_R <- data.frame(means,stdevs)
times<- index(normo_df_R)*5
normo_df_R <- data.frame(means,stdevs,N, times)
total_normo_R <- ggplot(normo_df_R, aes(x=times, y=means)) +
geom_line(colour="blue4") +
  geom_ribbon(normo_df_R,mapping = aes(x=times,
ymax=means+stdevs,ymin=means-stdevs),fill="blue4",alpha=0.1)

#-----
# Hypercapnic group

means <- tapply(hypercapnia$L_delta,hypercapnia$time_id,function(x) mean(x, na.rm
= TRUE))
stdevs <- tapply(hypercapnia$L_delta,hypercapnia$time_id,function(x) sd(x, na.rm =
TRUE))
N <- tapply(hypercapnia$L_delta,hypercapnia$time_id,function(x) length(x[!is.na(x)]))

hyper_df_L <- data.frame(means,stdevs)
times<- index(hyper_df_L)*5
hyper_df_L <- data.frame(means,stdevs,N, times)
total_hyper_L <- ggplot(hyper_df_L, aes(x=times, y=means))

means <- tapply(hypercapnia$R_delta,hypercapnia$time_id,function(x) mean(x, na.rm
= TRUE))
stdevs <- tapply(hypercapnia$R_delta,hypercapnia$time_id,function(x) sd(x, na.rm =
TRUE))
N <- tapply(hypercapnia$R_delta,hypercapnia$time_id,function(x) length(x[!is.na(x)]))

hyper_df_R <- data.frame(means,stdevs)
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times<- index(hyper_df_R)*5
hyper_df_R <- data.frame(means,stdevs,N, times)
total_hyper_R <- ggplot(hyper_df_R, aes(x=times, y=means))

total_L <- total_normo_L +
  geom_ribbon(hyper_df_L,mapping = aes(x=times, ymax=means+stdevs,ymin=means-
stdevs),fill="red2",alpha=0.2) +
  geom_line(hyper_df_L,mapping = aes(x=times, y=means),colour="red4") +
  theme_light() +
  xlab("Time since start of surgery (mins)") + ylab("Average % change in cerebral
oximetry on the left") +
  theme(axis.title.y = element_text(size = rel(0.65), angle = 90)) +
  theme(axis.title.x = element_text(size = rel(0.65), angle = 00))

total_R <- total_normo_R +
  geom_ribbon(hyper_df_R,mapping = aes(x=times, ymax=means+stdevs,ymin=means-
stdevs),fill="red2",alpha=0.2) +
  geom_line(hyper_df_R,mapping = aes(x=times, y=means),colour="red4")+
  theme_light() +
  xlab("Time since start of surgery (mins)") + ylab("Average % change in cerebral
oximetry on the right") +
  scale_color_manual(values=c("red4","blue4"))+
  theme(axis.title.y = element_text(size = rel(0.65), angle = 90)) +
  theme(axis.title.x = element_text(size = rel(0.65), angle = 00))

#tiff('oximetry_graph_high_res.tiff', units="in", width=7, height=3.6667, res=600,
compression = 'lzw')

grid.arrange(total_L, total_R, ncol = 2, top=textGrob("Percentage change in cerebral
oximetry from baseline",
              gp=gpar(fontsize=11,fontfamily="Times")),
             vp=viewport(width=0.9, height=0.9))

#insert ggplot code
#dev.off()

temp_hyper_L <- t(paste(round(hyper_df_L$mean,1)," (",
round(hyper_df_L$stdev,1),")", " {" , hyper_df_L$N," }", sep = ""))
temp_normo_L <- t(paste(round(normo_df_L$mean,1)," (",
round(normo_df_L$stdev,1),")", " {" , normo_df_L$N," }", sep = ""))

temp_hyper_R <- t(paste(round(hyper_df_R$mean,1)," (",
round(hyper_df_R$stdev,1),")", " {" , hyper_df_R$N," }", sep = ""))
temp_normo_R <- t(paste(round(normo_df_R$mean,1)," (",
round(normo_df_R$stdev,1),")", " {" , normo_df_R$N," }", sep = ""))

write.csv( temp_normo_L , "normo_df_L.csv")
write.csv( temp_normo_R , "normo_df_R.csv")

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write.csv( temp_hyper_L , "hyper_df_L.csv")  
write.csv( temp_hyper_R , "hyper_df_R.csv")
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