```
rm(list = ls())
time doc1 <- Sys.time()</pre>
library(SuperLearner)
library(expose)
library(ggplot2)
library(expose)
library(ggplot2)
library(knitr)
library(RColorBrewer)
library(repmis)
library(RColorBrewer)
library(devtools)
devtools::install_github("itamuria/expose")
# Download data
source data("https://github.com/itamuria/expose dataset/blob/master/20180818 dtaset.RData?raw=true")
set.seed(22222)
# Define parameters
N <- dim(dtaset)[1]
Outcome="Y4"
seku \leftarrow c(0,0.1,0.2,0.25,0.3,0.4,0.5,0.6,0.7,0.75,0.8,0.9,1)
our.num.sim <- 50
delta=c(0,1)
fecha <- format(Sys.time(), "%Y%m%d%X")
fecha <- gsub(":","",fecha)</pre>
Exposures<- c("Var1","Var2","Var3","Var4","Var5")
Confounders<- c("sex")</pre>
# Crossvalidation
#Choose the library of algorithms to include in the SL
ourlibraries <- c("SL.glm", "SL.glm.interaction", "SL.glmnet", "SL.gam", "SL.nnet",
                "SL.polymars", "SL.svm", "SL.xgboost")
#Performing SL Cross-validation
# Outcome 1
Outcome <- c("Y1")
m1 <- SuperLearner::CV.SuperLearner(Y = dtaset[,Outcome[1]],</pre>
                                X = dtaset[, c(Confounders, Exposures)], V=10, SL.library = ourlibraries,
                                family = "gaussian", method = "method.NNLS",
                                verbose = FALSE)
m1$AllSL[[1]]
# Outcome 2
Outcome <- c("Y2")
m2 <- SuperLearner::CV.SuperLearner(Y = dtaset[,Outcome[1]],</pre>
                                X = dtaset[, c(Confounders, Exposures)], V=10, SL.library = ourlibraries,
                                family = "gaussian", method = "method.NNLS",
                                verbose = FALSE)
m2$AllSL[[1]]
# Outcome 3
Outcome <- c("Y3")
m3 <- SuperLearner::CV.SuperLearner(Y = dtaset[,Outcome[1]],</pre>
                                X = dtaset[, c(Confounders, Exposures)], V=10, SL.library = ourlibraries,
                                family = "gaussian", method = "method.NNLS",
                                verbose = FALSE)
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m3$AllSL[[1]]
# Outcome 4
Outcome <- c("Y4")
m4 <- SuperLearner::CV.SuperLearner(Y = dtaset[,Outcome[1]],</pre>
                            X = dtaset[, c(Confounders, Exposures)], V=10, SL.library = ourlibraries,
                            family = "gaussian", method = "method.NNLS",
                            verbose = FALSE)
m4$AllSL[[1]]
# create basic data frame
Outcome <- c("Y4")
gen <- general_function (dataset = dtaset, exposures = Exposures,</pre>
                   confounders = Confounders,
                   outcomes = Outcome[1], delta=delta, dr = seku)
summary_table_lines <- gen[[2]]</pre>
t1 <- Sys.time()
simu <- run_simulations (dataset = dtaset, exposures = Exposures,</pre>
                   confounders = Confounders, libraries = ourlibraries,
                   outcomes = Outcome[1], num.sim = our.num.sim, delta=delta, dr = seku,
newdata =gen[[1]], show_times = TRUE, verbose = FALSE, save_time = TRUE,
show_num_sim = TRUE, family = "gaussian", method = "method.NNLS")
t2 <- Sys.time()
(t2-t1)
# analysis
ris <- simu[[2]]
len sim <- dim(ris)[2]</pre>
lib <- gsub("SL.","",ris$libraries)</pre>
len_lib <- length(lib)</pre>
df1 <- data.frame(matrix(NA,1,2))</pre>
names(df1) <- c("Library", "Value")</pre>
for(li in 1:len lib)
 \label{eq:df2} \texttt{df2} \, \mathrel{<\!\!\!\!-} \, \texttt{data.frame(rep(lib[li],len\_sim-1),t(ris[li,2:len\_sim]))}
 names(df2) <- c("Library", "Value")
df1 <- rbind(df1,df2)</pre>
df1 <- df1[-1,]
ggplot(df1, aes(x = Library, y = Value, fill = Library)) + geom_boxplot() + theme_bw() +
 coord_flip() + ggtitle("Risk per method (minimize)") + theme(legend.position="none")
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ris_table <- data.frame(lib,apply(ris[,-1],1,mean))</pre>
names(ris_table)<-c("Library", "Performance")</pre>
knitr::kable(ris_table)
coef <- simu[[3]]</pre>
coef_table <- data.frame(lib,apply(coef[,-1],1,mean))</pre>
names(coef_table)<-c("Library", "Estimates")</pre>
knitr::kable(coef table)
df1 <- data.frame(matrix(NA,1,2))</pre>
names(df1) <- c("Library","Value")</pre>
for(li in 1:len lib)
 df2 <- data.frame(rep(lib[li],len_sim-1),t(coef[li,2:len_sim]))</pre>
 names(df2) <- c("Library","Value")</pre>
 df1 <- rbind(df1,df2)
df1 <- df1[-1,]
ggplot(df1, aes(x = Library, y = Value, fill = Library)) + geom_boxplot() + theme_bw() +
 coord_flip() + ggtitle("Coefficient per method (weight)") + theme(legend.position="none")
# Naive ACE: Average causal effect
ace.df.g <- naive ace (allsim = simu[[1]], dataset = dtaset, ic dis = "IC", st = summary table lines,
                    exposures = Exposures, delta = delta)
knitr::kable(ace.df.g)
# Use 95% confidence interval instead of SEM
pd <- position_dodge(0.1)</pre>
ggplot(ace.df.g, aes(x=Group, y=Mean, colour=Group)) +
 geom_errorbar(aes(ymin=ICa, ymax=ICb), width=.1, position=pd) +
 geom_line(position=pd) +
 geom_point(position=pd) + ylab("Estimated (Boostrapped 95% CI") +
 xlab("Library") + geom_hline(yintercept = 0)+ theme_bw() +
 ggtitle("Average Treatment Effect") + theme(legend.position="none")
# Dose Respond
drr.grp <- dose_resp (allsim = simu[[1]], dataset = dtaset, st = summary_table_lines,</pre>
                   dr = seku, exposures = Exposures)
knitr::kable(head(drr.grp))
drr.grp$dose <- as.numeric(gsub("DR_","",drr.grp$Quantile))</pre>
pd <- position dodge(0.1)
ggplot(drr.grp, aes(x=dose, y=Mean)) +
 geom_errorbar(aes(ymin=Mean-SE, ymax=Mean+SE), width=.025, position=pd, size=0.5, color="blue") +
geom hline(yintercept = 0) +
 geom_line(position=pd,col="blue") +
 geom_point(position=pd, size=2, shape=20, fill="black") + facet_grid(Exp ~ ., scales="free") +
ggtitle("Dose response") + theme(legend.position="none") + theme_bw()
ggplot(drr.grp, aes(x=dose, y=Mean)) +
 geom_errorbar(aes(ymin=Mean-SE, ymax=Mean+SE), width=.05, position=pd, size=0.5, color="blue") +
 geom line(position=pd,col="blue") +
 geom_point(position=pd, size=2, shape=20, fill="black") + facet_grid(Exp ~ .) + geom_hline(yintercept = 0)
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ggtitle("Dose response") + theme(legend.position="none") + theme bw()
# ice: individual causal effect
ice res <- ice(allsim = simu[[1]], dataset = dtaset, dr = seku, squem = summary table lines, remove extrem =
FALSE)
# ploting
p=ggplot(ice_res,aes(X, Var1_pred,group=id))
p+geom_line()+theme_bw() +
   scale_x_discrete(breaks=sort(unique(ice_res$X)),
                                labels=as.character(seku))
\# name to save
h <- 1
file_exp_name <- paste0("Invid_",h,".jpg")</pre>
ggsave(file_exp_name)
unlink(file_exp_name)
p=ggplot(ice_res,aes(X, Var2_pred,group=id, color=Var3))
p+geom_line()+ theme_bw() + theme(legend.position="none") + ggtitle("Individual effect") +
   scale_x_discrete(breaks=sort(unique(ice_res$X)),
                                 labels=as.character(seku))
p=ggplot(ice_res,aes(X, Var1_pred,group=id,col=Var3)) + labs(x="Var1 percentiles",y="Predicted Y")
p+geom line()+theme bw()+scale color gradientn(name="Var3",colours=rev(brewer.pal(9,"YlOrRd"))) +
   scale_x_discrete(breaks=sort(unique(ice_res$X)),
                                 labels=as.character(seku)) + ggtitle("Individual effect")
p=ggplot(ice_res,aes(X, Var3_pred,group=id,col=Var5)) + labs(x="Var3 percentiles",y="Predicted Y")
p+geom_line()+theme_bw()+scale_color_gradientn(name="Var5",colours=rev(brewer.pal(9,"YlOrRd"))) +
   scale_x_discrete(breaks=sort(unique(ice_res$X)),
                                 labels=as.character(seku)) + ggtitle("Individual effect")
# discrete variables
 p = ggplot(ice_res, aes(X, Var3\_pred, group=id, col=sex)) + labs(x = "pp-Var3\_percentiles", y = "Predicted Y") \\ p + geom\_line() + theme\_bw() + scale\_color\_gradientn(name = "Sex", colours = c("red", "\#FFFF00")) + labs(x = "pp-Var3\_percentiles", y = "Predicted Y") \\ p + geom\_line() + theme\_bw() + scale\_color\_gradientn(name = "Sex", colours = c("red", "\#FFFF00")) + labs(x = "pp-Var3\_percentiles", y = "Predicted Y") \\ p + geom\_line() + theme\_bw() + scale\_color\_gradientn(name = "Sex", colours = c("red", "\#FFFF00")) + labs(x = "pp-Var3\_percentiles", y = "Predicted Y") \\ p + geom\_line() + theme\_bw() + scale\_color\_gradientn(name = "Sex", colours = c("red", "\#FFFF00")) + labs(x = "pp-Var3\_percentiles", y = pp-Var3\_percentiles = pp-Var3\_percentil
   theme(axis.text.x = element_text(face="bold", size=8, angle=0), legend.position = "none") +
   scale_x_discrete(breaks=sort(unique(ice_res$X)),
                                 labels=as.character(seku)) + ggtitle("Individual effect")
it <- interact (allsim = simu[[1]], dataset = dtaset,exposures = Exposures,</pre>
                           confounders = c("sex"), squem = summary table lines)
knitr::kable(head(it))
pd <- position dodge(0.1)
ggplot(it, aes(x=Interaction, y=Mean, colour=Interaction)) +
   geom_errorbar(aes(ymin=Mean-SD, ymax=Mean+SD), width=.1, position=pd) +
   geom line(position=pd) +
   geom_point(position=pd) + ylab("Estimated (Boostrapped 95% CI") +
   xlab("Interaction") + coord_flip() + geom_hline(yintercept = 0) +
ggtitle("Interaction") + theme_bw() + theme(legend.position="none")
time_doc3 <- Sys.time()</pre>
print(time_doc3 - time_doc1)
```