Go Wild

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```
rm(list=ls())
require(jsonlite)
require(readtext)
#PDG codes
# pdg.elec <- c(11,-11)
\# pdg.pion \leftarrow c(-211,211)
files <- list.files(path="C:/Users/gerhard/Documents/msc-thesis-data/processed/000265309", pattern="*js
j <- fromJSON(files[1])</pre>
for(i in 2:length(files)){
 f <- fromJSON(files[i])</pre>
  j \leftarrow c(j,f)
1 <- length(j)</pre>
runNumber <- rep(265309,1)</pre>
files <- list.files(path="C:/Users/gerhard/Documents/msc-thesis-data/processed/000265332", pattern="*js
for(i in 1:length(files)){
  f <- fromJSON(files[i])</pre>
  j \leftarrow c(j,f)
prev_1 <- 1
1 <- length(j)</pre>
1 <- l-prev_1
runNumber <- c(runNumber,rep(265332,1))</pre>
files <- list.files(path="C:/Users/gerhard/Documents/msc-thesis-data/processed/000265334", pattern="*js
for(i in 1:length(files)){
  f <- fromJSON(files[i])</pre>
  j \leftarrow c(j,f)
prev_1 <- 1
1 <- length(j)</pre>
```

```
1 <- l-prev_1
runNumber <- c(runNumber,rep(265334,1))</pre>
files <- list.files(path="C:/Users/gerhard/Documents/msc-thesis-data/processed/000265335", pattern="*js
for(i in 1:length(files)){
 f <- fromJSON(files[i])</pre>
  j \leftarrow c(j,f)
prev_1 <- 1
1 <- length(j)</pre>
1 <- l-prev_1
runNumber <- c(runNumber,rep(265335,1))</pre>
files <- list.files(path="C:/Users/gerhard/Documents/msc-thesis-data/processed/000265336", pattern="*js
for(i in 1:length(files)){
 f <- fromJSON(files[i])</pre>
  j \leftarrow c(j,f)
prev_1 <- 1
1 <- length(j)</pre>
1 <- l-prev_1
runNumber <- c(runNumber,rep(265336,1))</pre>
files <- list.files(path="C:/Users/gerhard/Documents/msc-thesis-data/processed/000265338", pattern="*js
for(i in 1:length(files)){
  f <- fromJSON(files[i])</pre>
  j \leftarrow c(j,f)
prev_1 <- 1
1 <- length(j)</pre>
1 <- l-prev_1
runNumber <- c(runNumber,rep(265338,1))</pre>
files <- list.files(path="C:/Users/gerhard/Documents/msc-thesis-data/processed/000265339", pattern="*js
for(i in 1:length(files)){
 f <- fromJSON(files[i])</pre>
  j \leftarrow c(j,f)
```

```
prev_1 <- 1
1 <- length(j)</pre>
1 <- l-prev_1
runNumber <- c(runNumber,rep(265339,1))</pre>
files <- list.files(path="C:/Users/gerhard/Documents/msc-thesis-data/processed/000265342", pattern="*js
for(i in 1:length(files)){
  f <- fromJSON(files[i])</pre>
  j \leftarrow c(j,f)
prev_1 <- 1
1 <- length(j)</pre>
1 <- l-prev_1
runNumber <- c(runNumber,rep(265342,1))</pre>
files <- list.files(path="C:/Users/gerhard/Documents/msc-thesis-data/processed/000265343", pattern="*js
for(i in 1:length(files)){
  f <- fromJSON(files[i])</pre>
 j \leftarrow c(j,f)
prev_1 <- 1
1 <- length(j)</pre>
1 <- l-prev_1
runNumber <- c(runNumber,rep(265343,1))</pre>
files <- list.files(path="C:/Users/gerhard/Documents/msc-thesis-data/processed/000265344", pattern="*js
for(i in 1:length(files)){
  f <- fromJSON(files[i])</pre>
  j \leftarrow c(j,f)
prev_1 <- 1
1 <- length(j)</pre>
1 <- l-prev_1
runNumber <- c(runNumber,rep(265344,1))</pre>
files <- list.files(path="C:/Users/gerhard/Documents/msc-thesis-data/processed/000265377", pattern="*js
for(i in 1:length(files)){
  f <- fromJSON(files[i])</pre>
```

```
j <- c(j,f)
prev_1 <- 1
1 <- length(j)</pre>
1 <- l-prev_1
runNumber <- c(runNumber,rep(265377,1))</pre>
files <- list.files(path="C:/Users/gerhard/Documents/msc-thesis-data/processed/000265378", pattern="*js
for(i in 1:length(files)){
 f <- fromJSON(files[i])</pre>
  j \leftarrow c(j,f)
prev_1 <- 1
1 <- length(j)
1 <- l-prev_1
runNumber <- c(runNumber,rep(265378,1))</pre>
files <- list.files(path="C:/Users/gerhard/Documents/msc-thesis-data/processed/000265381", pattern="*js
for(i in 1:length(files)){
 f <- fromJSON(files[i])</pre>
  j \leftarrow c(j,f)
prev_1 <- 1
1 <- length(j)</pre>
1 <- l-prev_1
runNumber <- c(runNumber,rep(265381,1))</pre>
files <- list.files(path="C:/Users/gerhard/Documents/msc-thesis-data/processed/000265383", pattern="*js
for(i in 1:length(files)){
 f <- fromJSON(files[i])</pre>
  j \leftarrow c(j,f)
prev_1 <- 1
1 <- length(j)
1 <- l-prev_1
runNumber <- c(runNumber,rep(265383,1))</pre>
files <- list.files(path="C:/Users/gerhard/Documents/msc-thesis-data/processed/000265385", pattern="*js
```

```
for(i in 1:length(files)){
 f <- fromJSON(files[i])</pre>
  j \leftarrow c(j,f)
prev_1 <- 1
1 <- length(j)</pre>
1 <- l-prev_1
runNumber <- c(runNumber,rep(265385,1))</pre>
files <- list.files(path="C:/Users/gerhard/Documents/msc-thesis-data/processed/000265388", pattern="*js
for(i in 1:length(files)){
 f <- fromJSON(files[i])</pre>
  j \leftarrow c(j,f)
prev_1 <- 1
1 <- length(j)</pre>
1 <- l-prev_1
runNumber <- c(runNumber,rep(265388,1))</pre>
files <- list.files(path="C:/Users/gerhard/Documents/msc-thesis-data/processed/000265419", pattern="*js
for(i in 1:length(files)){
 f <- fromJSON(files[i])</pre>
  j \leftarrow c(j,f)
prev_1 <- 1
1 <- length(j)</pre>
1 <- l-prev_1
runNumber <- c(runNumber,rep(265419,1))</pre>
files <- list.files(path="C:/Users/gerhard/Documents/msc-thesis-data/processed/000265420", pattern="*js
for(i in 1:length(files)){
  f <- fromJSON(files[i])</pre>
  j \leftarrow c(j,f)
prev_1 <- 1
1 <- length(j)</pre>
1 <- l-prev_1
runNumber <- c(runNumber,rep(265420,1))</pre>
```

```
files <- list.files(path="C:/Users/gerhard/Documents/msc-thesis-data/processed/000265425", pattern="*js
for(i in 1:length(files)){
 f <- fromJSON(files[i])</pre>
  j \leftarrow c(j,f)
prev_1 <- 1
1 <- length(j)</pre>
1 <- l-prev_1
runNumber <- c(runNumber,rep(265425,1))</pre>
files <- list.files(path="C:/Users/gerhard/Documents/msc-thesis-data/processed/000265426", pattern="*js
for(i in 1:length(files)){
 f <- fromJSON(files[i])</pre>
  j \leftarrow c(j,f)
prev_1 <- 1
1 <- length(j)</pre>
1 <- l-prev_1
runNumber <- c(runNumber,rep(265426,1))</pre>
files <- list.files(path="C:/Users/gerhard/Documents/msc-thesis-data/processed/000265499", pattern="*js
for(i in 1:length(files)){
 f <- fromJSON(files[i])</pre>
  j \leftarrow c(j,f)
prev_1 <- 1
1 <- length(j)
1 <- l-prev_1
runNumber <- c(runNumber,rep(265499,1))</pre>
rm(runNumber)
Eta <- sapply(j, `[[`,"Eta")</pre>
P <- sapply(j, `[[`,"P")</pre>
PT <- sapply(j, `[[`,"PT")</pre>
Phi <- sapply(j, `[[`,"Phi")</pre>
Theta <- sapply(j, `[[`,"Theta")</pre>
```

```
col0 <- sapply(j, `[[`,"col0")</pre>
col1 <- sapply(j, `[[`,"col1")</pre>
col2 <- sapply(j, `[[`,"col2")</pre>
col3 <- sapply(j, `[[`,"col3")</pre>
col4 <- sapply(j, `[[`,"col4")</pre>
col5 <- sapply(j, `[[`,"col5")</pre>
dEdX <- sapply(j, `[[`,"dEdX")</pre>
det0 <- sapply(j, `[[`,"det0")</pre>
det1 <- sapply(j, `[[`,"det1")</pre>
det2 <- sapply(j, `[[`,"det2")</pre>
det3 <- sapply(j, `[[`,"det3")</pre>
det4 <- sapply(j, `[[`,"det4")</pre>
det5 <- sapply(j, `[[`,"det5")</pre>
nSigmaElectron <- sapply(j, `[[`,"nSigmaElectron")</pre>
nSigmaPion <- sapply(j, `[[`,"nSigmaPion")</pre>
pdgCode <- sapply(j, `[[`,"pdgCode")</pre>
row0 <- sapply(j, `[[`,"row0")</pre>
row1 <- sapply(j, `[[`,"row1")</pre>
row2 <- sapply(j, `[[`,"row2")</pre>
row3 <- sapply(j, `[[`,"row3")</pre>
row4 <- sapply(j, `[[`,"row4")</pre>
row5 <- sapply(j, `[[`,"row5")</pre>
layer0 <- sapply(j, `[[`,"layer 0")</pre>
layer1 <- sapply(j, `[[`,"layer 1")</pre>
layer2 <- sapply(j, `[[`,"layer 2")</pre>
layer3 <- sapply(j, `[[`,"layer 3")</pre>
layer4 <- sapply(j, `[[`,"layer 4")</pre>
```

```
layer5 <- sapply(j, `[[`,"layer 5")</pre>
rm(f,j)
save.image(file="c:/Users/gerhard/documents/msc-thesis-data/all_data.rdata")
load("c:/Users/gerhard/documents/msc-thesis-data/all_data.rdata")
meta <- data.frame(cbind(col0,col1,col2,col3,col4,col5,det0,det1,det2,det3,det4,det5,</pre>
                          row0,row1,row2,row3,row4,row5,dEdX,Eta,nSigmaElectron,
                          nSigmaPion,P,pdgCode,PT,Theta,Phi))
save(meta,file="c:/Users/gerhard/documents/msc-thesis-data/meta.rdata")
rm(col0,col1,col2,col3,col4,col5,det0,det1,det2,det3,det4,det5,
                          row0,row1,row2,row3,row4,row5,dEdX,Eta,nSigmaElectron,
                          nSigmaPion,P,pdgCode,PT,Theta,Phi,f,j)
rm(files,i,pdg.elec,pdg.pion)
n0 <- unique(c(which(sapply(layer0,typeof)=="list"),which(sapply(layer0, is.null))))
n1 <- unique(c(which(sapply(layer1, typeof)=="list"), which(sapply(layer1, is.null))))
n2 <- unique(c(which(sapply(layer2, typeof)=="list"), which(sapply(layer2, is.null))))
n3 <- unique(c(which(sapply(layer3, typeof)=="list"), which(sapply(layer3, is.null))))
n4 <- unique(c(which(sapply(layer4, typeof)=="list"), which(sapply(layer4, is.null))))
n5 <- unique(c(which(sapply(layer5, typeof)=="list"), which(sapply(layer5, is.null))))
save.image(file="c:/Users/gerhard/documents/msc-thesis-data/all_data.rdata")
load("c:/Users/gerhard/documents/msc-thesis-data/all_data.rdata")
meta1 <- meta
meta2 <- meta
meta3 <- meta
meta4 <- meta
meta5 <- meta
rm(meta)
meta0 <- meta1
meta0 <- meta0[-n0,]
layer0 <- layer0[-n0]</pre>
meta1 <- meta1[-n1,]
layer1 <- layer1[-n1]</pre>
meta2 <- meta2[-n2,]
layer2 <- layer2[-n2]</pre>
meta3 <- meta3[-n3,]
layer3 <- layer3[-n3]</pre>
meta4 \leftarrow meta4[-n4,]
layer4 <- layer4[-n4]</pre>
```

```
meta5 <- meta5[-n5,]
layer5 <- layer5[-n5]</pre>
rm(n0,n1,n2,n3,n4,n5)
save.image(file="c:/Users/gerhard/documents/msc-thesis-data/all_data.rdata")
load("c:/Users/gerhard/documents/msc-thesis-data/all_data.rdata")
meta0$layer <- 0</pre>
meta1$layer <- 1
meta2$layer <- 2
meta3$layer <- 3</pre>
meta4$layer <- 4
meta5$layer <- 5</pre>
meta0$col <- meta0$col0</pre>
meta0$det <- meta0$det0
meta0$row <- meta0$row0</pre>
meta1$col <- meta1$col1</pre>
meta1$det <- meta1$det1
meta1$row <- meta1$row1</pre>
meta2$col <- meta2$col2</pre>
meta2$det <- meta2$det2
meta2$row <- meta2$row2</pre>
meta3$col <- meta3$col3</pre>
meta3$det <- meta3$det3
meta3$row <- meta3$row3</pre>
meta4$col <- meta4$col4</pre>
meta4$det <- meta4$det4
meta4$row <- meta4$row4
meta5$col <- meta5$col5</pre>
meta5$det <- meta5$det5</pre>
meta5$row <- meta5$row5</pre>
meta0 <- meta0[,-c(1:18)]
meta1 \leftarrow meta1[,-c(1:18)]
meta2 <- meta2[,-c(1:18)]
meta3 \leftarrow meta3[,-c(1:18)]
meta4 <- meta4[,-c(1:18)]
meta5 <- meta5[,-c(1:18)]
save.image(file="c:/Users/gerhard/documents/msc-thesis-data/all_data.rdata")
load("c:/Users/gerhard/documents/msc-thesis-data/all_data.rdata")
# require(dummies)
meta0 <- as.data.frame(lapply(meta0,unlist))</pre>
meta1 <- as.data.frame(lapply(meta1,unlist))</pre>
```

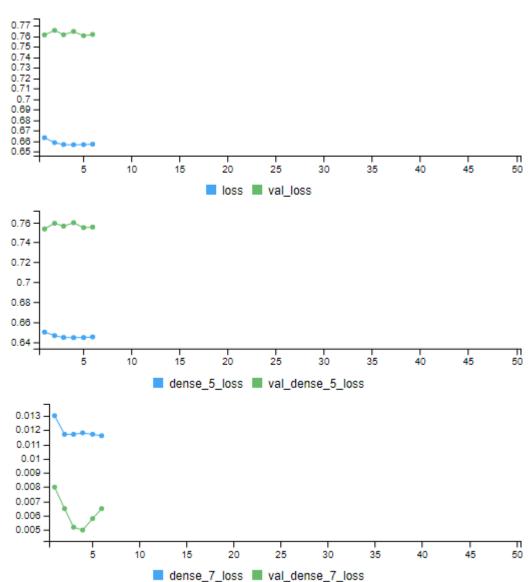
```
meta2 <- as.data.frame(lapply(meta2,unlist))</pre>
meta3 <- as.data.frame(lapply(meta3,unlist))</pre>
meta4 <- as.data.frame(lapply(meta4,unlist))</pre>
meta5 <- as.data.frame(lapply(meta5,unlist))</pre>
meta <- data.frame(rbind(meta0,meta1,meta2,meta3,meta4,meta5))</pre>
# meta <- dummy.data.frame(data=meta,names=list("layer","col","det","row"))</pre>
# names(meta0) == names(meta1)
rm(meta0, meta1, meta2, meta3, meta4, meta5)
cs0 <- lapply(layer0,colSums)</pre>
cs1 <- lapply(layer1,colSums)</pre>
cs2 <- lapply(layer2,colSums)
cs3 <- lapply(layer3,colSums)
cs4 <- lapply(layer4,colSums)
cs5 <- lapply(layer5,colSums)</pre>
rs0 <- lapply(layer0,rowSums)
rs1 <- lapply(layer1,rowSums)
rs2 <- lapply(layer2,rowSums)
rs3 <- lapply(layer3,rowSums)
rs4 <- lapply(layer4,rowSums)
rs5 <- lapply(layer5,rowSums)
cs0 <- do.call(rbind,cs0)
cs1 <- do.call(rbind,cs1)
cs2 <- do.call(rbind,cs2)
cs3 <- do.call(rbind,cs3)
cs4 <- do.call(rbind,cs4)
cs5 <- do.call(rbind,cs5)
rs0 <- do.call(rbind,rs0)
rs1 <- do.call(rbind,rs1)
rs2 <- do.call(rbind,rs2)
rs3 <- do.call(rbind,rs3)
rs4 <- do.call(rbind,rs4)
rs5 <- do.call(rbind,rs5)
rm(layer0,layer1,layer2,layer3,layer4,layer5)
signal <- data.frame(</pre>
  cbind(
    rbind(cs0,cs1,cs2,cs3,cs4,cs5),
    rbind(rs0,rs1,rs2,rs3,rs4,rs5)
  )
)
rm(cs0,cs1,cs2,cs3,cs4,cs5,
   rs0,rs1,rs2,rs3,rs4,rs5)
e <- which(abs(meta$pdgCode)==11)
```

```
p <- which(abs(meta$pdgCode)!=11)</pre>
p <- sample(p,length(e),replace = F)</pre>
meta <- meta[c(e,p),]</pre>
singal <- signal[c(e,p),]</pre>
rm(e,p,l,prev_l,signal)
names (meta)
meta$Phi <- scale(meta$Phi)</pre>
meta$Theta <- scale(meta$Theta)</pre>
meta$PT <- scale(meta$PT)</pre>
meta$P <- scale(meta$P)</pre>
meta$nSigmaPion <- scale(meta$nSigmaPion)</pre>
meta$nSigmaElectron <- scale(meta$nSigmaElectron)</pre>
meta$pdgCode <- ifelse(abs(meta$pdgCode)==11,1,0)</pre>
meta$dEdX <- scale(meta$dEdX)</pre>
meta$Eta <- scale(meta$Eta)</pre>
ys <- data.frame(cbind(meta$pdgCode,meta$nSigmaElectron,meta$nSigmaPion))
meta <- meta[,-c(3,4,6)]
names (meta)
require(dummies)
meta <- dummy.data.frame(meta,names=names(meta)[7:10])</pre>
names (meta)
singal <- cbind(singal,meta$dEdX,meta$Eta,meta$P,meta$PT,meta$Theta,meta$Phi)
meta \leftarrow meta[,-c(1:6)]
load(file="c:/Users/gerhard/documents/msc-thesis-data/all_data.rdata")
singal[,1:41] <- scale(singal[,1:41])</pre>
meta <- as.matrix(meta)</pre>
singal <- as.matrix(singal)</pre>
ys <- as.matrix(ys)</pre>
```

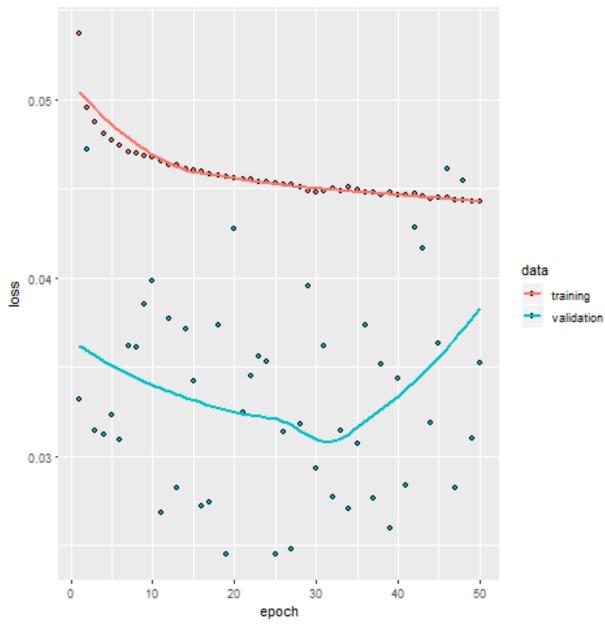
```
test_ind <- sample(1:nrow(meta), size=round(0.15*nrow(meta)), replace = F)</pre>
meta_test <- meta[test_ind,]</pre>
meta <- meta[-test_ind,]</pre>
singal_test <- singal[test_ind,]</pre>
singal <- singal[-test_ind,]</pre>
ys_test <- ys[test_ind,]</pre>
ys <- ys[-test_ind,]
require(keras)
rm(meta,meta_test)
ys <- ys[,1]
ys_test <- ys_test[,1]</pre>
main_input <- layer_input(shape = c(47), name = 'main_input')</pre>
aux_input <- layer_input(shape = c(659), name = 'aux_input')</pre>
embed_out <- aux_input %>%
  layer_dense(256,activation = "relu") %>%
  layer dense(128,activation = "relu") %>%
  layer_reshape(target_shape = c(128))
main_out <- main_input %>%
  layer_dense(256, "relu") %>%
  layer_dense(128,"relu")
merge1 <- layer_concatenate(list(embed_out,main_out)) %>%
  layer_dense(128, "relu") %>%
  layer_dense(2)
merge2 <- layer concatenate(list(embed out, main out)) %>%
  layer_dense(128, "relu") %>%
  layer_dense(1)
model <- keras_model(</pre>
  inputs = c(main_input, aux_input),
  outputs = c(merge1,merge2)
summary(model)
```

```
model %>% compile(
  optimizer = 'rmsprop',
  loss = 'mse'
)

history <- model %>% fit(
  x = list(singal, meta),
  y = list(ys[,2:3],ys[,1]),
  epochs = 50,
  batch_size = 32,
  verbose=2,
  validation_split=0.15,
  metrics=c('mse','acc'),
  shuffle=T
)
```



```
model <- keras_model_sequential() %>%
  layer_dense(256,"tanh") %>%
  layer_dense(128,"tanh") %>%
  layer_dense(1,"sigmoid")
model %>% compile(
  optimizer = 'adam',
 loss = "binary_crossentropy"
history <- model %>% fit(
 x = singal,
  y = ys,
 epochs = 50,
  batch_size = 32,
  verbose=2,
  validation_split=0.15,
  metrics=c('acc'),
  shuffle=T
)
png(filename = "C:/Users/gerhard/documents/Msc-thesis/NEW/ML/m2.png")
plot(history)
dev.off()
```



```
pred <- model %>%
    predict(singal_test)

pred_act <- cbind(pred,ys_test)

pred_act <- data.frame(pred_act)

names(pred_act) <- c("pred","act")

pi <- which(pred_act$act==1)
el <- which(pred_act$act!=1)

while(length(pi)%%6!=0){
    #print(length(pi))</pre>
```

```
pi <- pi[-length(pi)]</pre>
}
while(length(el)%%6!=0){
  #print(length(el))
  el <- el[-length(el)]</pre>
}
pred_act <- pred_act[c(el,pi),]</pre>
six_tracklet_pred <- c()</pre>
for(i in seq(1,nrow(pred_act),6)){
  j=i+5
  this.dat <- prod(pred_act$pred[i:j])/sum(prod(pred_act$pred[i:j]),prod(1-pred_act$pred[i:j]))
  six_tracklet_pred <- c(six_tracklet_pred,this.dat)</pre>
six_tracklet_pred <- data.frame(six_tracklet_pred)</pre>
six_tracklet_pred <- na.omit(six_tracklet_pred)</pre>
six_tracklet_real <- c()</pre>
for(i in seq(1,nrow(pred_act),6)){
  this.dat <- pred_act$act[i]</pre>
  six_tracklet_real <- c(six_tracklet_real,this.dat)</pre>
}
six_tracklet_real <- data.frame(six_tracklet_real)</pre>
which(is.na(six_tracklet_real))
pred_act <- data.frame(cbind(six_tracklet_pred,six_tracklet_real))</pre>
elec_pi_eff_func <- function(model_1.preds,model_1.labels){</pre>
    # model_1.preds <- read.csv(model_1.preds,header=F, sep="")</pre>
    # model_1.labels <- read.csv(model_1.labels,header=F, sep="")</pre>
    model_1 <- data.frame(cbind(model_1.preds,model_1.labels))</pre>
    model_1.electrons <- which(model_1[,2]==1)</pre>
    electrons <- model_1[model_1.electrons,]</pre>
    pions <- model_1[-as.numeric(model_1.electrons),]</pre>
```

```
electrons <- data.frame(electrons)</pre>
    names(electrons) <- c("prediction","label")</pre>
    pions <- data.frame(pions)</pre>
    names(pions) <- c("prediction","label")</pre>
    electron_efficiency <- function(electrons.,par){</pre>
    electrons <- electrons.
    electrons$electron_pred <- ifelse(electrons$prediction>=par[1],1,0)
    correct <- ifelse(electrons$electron_pred==electrons$label,1,0)</pre>
    error_metric <- sum(correct)/nrow(electrons)</pre>
    error_metric <- (error_metric-0.9)^2
    return(error metric)
}
  res <- optim(par=c(0),fn=electron_efficiency,lower = 0,upper = 1,electrons.=electrons,method="Brent")
  require(ggplot2)
  g <- ggplot(pred_act,aes(pred_act[,1],colour=factor(pred_act[,2])))+geom_histogram(bins = 1000)+facet
  print(g)
  hist(pred_act[,1],breaks=1000)
  abline(v=res$par,col="red")
  electrons$predicted_label <- ifelse(electrons$prediction>=res$par,1,0)
  print(paste0("Electron Efficiency: ",sum(electrons$predicted_label)/nrow(electrons)))
  pions$predicted_label <- ifelse(pions$prediction>=res$par,1,0)
  pions$misclassified_as_electron <- ifelse(pions$predicted_label==1,1,0)</pre>
  print(paste0("Pion Efficiency: ",(sum(pions$misclassified_as_electron)/nrow(pions))^6))
  pred_act$final_pred <- ifelse(pred_act[,1]>=res$par,1,0)
  require(caret)
  print(caret::confusionMatrix(data=factor(pred_act$final_pred),reference = factor(pred_act[,2])))
}
```

```
[1] "Electron Efficiency: 1"
[1] "Pion Efficiency: 0"
Confusion Matrix and Statistics

Reference
Prediction 0 1
0 20563 0
1 0 20496

Accuracy: 1
95% CI: (0.9999, 1)
No Information Rate: 0.5008
P-Value [Acc > NIR]: < 2.2e-16

Kappa: 1

Mcnemar's Test P-Value: NA

Sensitivity: 1.0000
Specificity: 1.0000
Pos Pred Value: 1.0000
Neg Pred Value: 1.0000
Prevalence: 0.5008
Detection Rate: 0.5008
Detection Prevalence: 0.5008
Balanced Accuracy: 1.0000
```

