

# AUC Confidences

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For table 3 of the figure: \* To report the 95% two-sided confidence intervals of the AUC using the non-parametric method by DeLong. \* For each pathology, we also test whether the AUC of the best approach is significantly better than the AUC of the worst approach using the one-sided DeLong's test for two correlated ROC curves if their difference in AUC is at least 0.01. \* We control for multiple hypothesis testing using the Benjamini-Hochberg procedure

## Setup

requires libraries 'pROC' and 'xtable'

```
library(pROC)
```

```
## Warning: package 'pROC' was built under R version 3.4.4
```

```
## Type 'citation("pROC")' for a citation.
```

```
##
```

```
## Attaching package: 'pROC'
```

```
## The following objects are masked from 'package:stats':
```

```
##
```

```
##      cov, smooth, var
```

```
library(xtable)
```

```
## Warning: package 'xtable' was built under R version 3.4.4
```

## Data Setup

```
pathologies <- c("Atelectasis",  
                 "Cardiomegaly",  
                 "Consolidation",  
                 "Edema",  
                 "Pleural Effusion")
```

```
n_pathologies <- length(pathologies)
```

```
approaches <- c("U.Ignore", "U.Zeros", "U.Ones", "U.Mean", "U.SelfTrained", "U.MultiClass")  
n_approaches <- length(approaches)
```

```
aucs <- matrix(nrow=n_approaches, ncol=n_pathologies, byrow = TRUE)  
aucs_strings <- matrix(nrow=n_approaches, ncol=n_pathologies, byrow = TRUE,  
                      dimnames=list(approaches, pathologies))
```

```
p_values_top <- vector(mode="list", length=n_pathologies)
```

```
names(p_values_top) <- pathologies
```

## Compute AUC

```
indir <- "./data/"
for (path_index in 1:n_pathologies) {
  pathology = pathologies[path_index]
  fn <- paste0(indir,paste0(pathology, ".csv"))
  df <- read.csv(fn)

  rocs <- vector(mode="list", length=n_pathologies)

  for (i in 1:n_approaches) {
    rocs[[i]] <- roc(df$Groundtruth, as.numeric(unlist(df[approaches[i]])))
  }

  for (i in 1:n_approaches) {
    auc <- ci.auc(rocs[[i]])
    aucs[[i, path_index]] <- auc[2] # the mean
    # save format "auc (auc_lower, auc_upper)"
    aucs_strings[[i, path_index]] <- paste0(
      format(round(auc[2], 3), nsmall = 3), " (",
      format(round(auc[1], 3), nsmall = 3), ",",
      format(round(auc[3], 3), nsmall = 3), ")")
  }

  # compute the best and worst auc across approaches
  max_auc = max(aucs[,path_index])
  min_auc = min(aucs[,path_index])

  p_values <- matrix(nrow=n_approaches, ncol=n_approaches, byrow = TRUE)

  # do the paired test only to test that greatest > smallest
  # and when greatest - smallest > 0.01
  for (i in 1:n_approaches) {
    for (j in 1:n_approaches) {
      if (aucs[i, path_index] > (aucs[j, path_index] + 0.01)) {
        if (aucs[i, path_index] == max_auc & aucs[j, path_index] == min_auc) {
          test = roc.test(rocs[[i]], rocs[[j]], alternative='greater', paired=TRUE)
          p_values[[i,j]] <- test$p.value
        }
      } else {
        p_values[[i,j]] <- NA
      }
    }
  }
  p_values_top[[path_index]] <- p_values
}

# print the auc table
print("AUC table")
```

```
## [1] "AUC table"
```

```
print(xtable(aucs_strings))
```

```
## % latex table generated in R 3.4.1 by xtable 1.8-3 package
## % Wed Sep 5 14:20:25 2018
## \begin{table}[ht]
## \centering
## \begin{tabular}{rllllll}
## \hline
## & Atelectasis & Cardiomegaly & Consolidation & Edema & Pleural Effusion & \\
## \hline
## U.Ignore & 0.818 (0.759,0.877) & 0.828 (0.769,0.888) & 0.938 (0.905,0.970) & 0.934 (0.893,0.975) & 0.934 (0.893,0.975) & 0.934 (0.893,0.975) \\
## U.Zeros & 0.811 (0.751,0.872) & 0.840 (0.783,0.897) & 0.932 (0.898,0.966) & 0.929 (0.888,0.970) & 0.929 (0.888,0.970) & 0.929 (0.888,0.970) \\
## U.Ones & 0.858 (0.806,0.910) & 0.832 (0.773,0.890) & 0.899 (0.854,0.944) & 0.941 (0.903,0.980) & 0.941 (0.903,0.980) & 0.941 (0.903,0.980) \\
## U.Mean & 0.821 (0.762,0.879) & 0.832 (0.771,0.892) & 0.937 (0.905,0.969) & 0.939 (0.902,0.975) & 0.939 (0.902,0.975) & 0.939 (0.902,0.975) \\
## U.SelfTrained & 0.833 (0.776,0.890) & 0.831 (0.770,0.891) & 0.939 (0.908,0.971) & 0.935 (0.896,0.971) & 0.935 (0.896,0.971) & 0.935 (0.896,0.971) \\
## U.MultiClass & 0.821 (0.763,0.879) & 0.854 (0.800,0.909) & 0.937 (0.905,0.969) & 0.928 (0.887,0.969) & 0.928 (0.887,0.969) & 0.928 (0.887,0.969) \\
## \hline
## \end{tabular}
## \end{table}
```

```
# Compute p-values per pathology
```

```
print(p_values_top)
```

```
## $Atelectasis
##      [,1]      [,2] [,3] [,4] [,5] [,6]
## [1,]    NA          NA  NA  NA  NA  NA
## [2,]    NA          NA  NA  NA  NA  NA
## [3,]    NA 0.008012165  NA  NA  NA  NA
## [4,]    NA          NA  NA  NA  NA  NA
## [5,]    NA          NA  NA  NA  NA  NA
## [6,]    NA          NA  NA  NA  NA  NA
##
## $Cardiomegaly
##      [,1] [,2] [,3] [,4] [,5] [,6]
## [1,]    NA  NA  NA  NA  NA  NA
## [2,]    NA  NA  NA  NA  NA  NA
## [3,]    NA  NA  NA  NA  NA  NA
## [4,]    NA  NA  NA  NA  NA  NA
## [5,]    NA  NA  NA  NA  NA  NA
## [6,] 0.001655247  NA  NA  NA  NA  NA
##
## $Consolidation
##      [,1] [,2]      [,3] [,4] [,5] [,6]
## [1,]    NA  NA          NA  NA  NA  NA
## [2,]    NA  NA          NA  NA  NA  NA
## [3,]    NA  NA          NA  NA  NA  NA
## [4,]    NA  NA          NA  NA  NA  NA
## [5,]    NA  NA 0.01857262  NA  NA  NA
## [6,]    NA  NA          NA  NA  NA  NA
##
## $Edema
##      [,1] [,2] [,3] [,4] [,5]      [,6]
## [1,]    NA  NA  NA  NA  NA      NA
## [2,]    NA  NA  NA  NA  NA      NA
```

```
## [3,] NA NA NA NA NA 0.0654561
## [4,] NA NA NA NA NA NA
## [5,] NA NA NA NA NA NA
## [6,] NA NA NA NA NA NA
##
## $`Pleural Effusion`
##      [,1] [,2] [,3] [,4] [,5] [,6]
## [1,] NA NA NA NA NA NA
## [2,] NA NA NA NA NA NA
## [3,] NA NA NA NA NA NA
## [4,] NA NA NA NA NA NA
## [5,] NA NA NA NA NA NA
## [6,] NA NA NA NA NA NA
```

## Adjust P Values

```
# the adjusted pvalues
p_values_top_vector <- na.omit(as.vector(unlist(p_values_top)))
p_values_adjusted <- p.adjust(p_values_top_vector, method = "hochberg")
print(p_values_adjusted)
```

```
## [1] 0.02403650 0.00662099 0.03714525 0.06545610
```