

<pre> 1. library(mlbench) install.packages("dplyr") library(dplyr) library(ggplot2) library(reshape2) data("BostonHousing") housing <- BostonHousing str(housing) housing %>% ggplot(aes(x = medv)) + stat_density(y) + labs(x = "Median Value (\$1000s)", y = "Density", title = "Density Plot of Median Value House Price in Boston") + theme_minimal() summary(housing\$medv) housing %>% select(c(crim, rm, age, rad, tax, lstat, medv)) %>% melt(id.vars = "medv") %>% ggplot(aes(x = value, y = medv, colour = variable)) + geom_point(alpha = 0.7) + stat_smooth(aes(colour = "black")) + facet_wrap(~variable, scales = "free", ncol = 2) + labs(x = "Variable Value", y = "Median House Price (\$1000s)") + theme_minimal() library("caret") set.seed(123) #random number generation to_train <- createDataPartition(y = housing\$medv, p = 0.75, list = FALSE) to_test <- createDataPartition(y=housing\$medv , p=0.25,list=FALSE) train <- housing[to_train,] test <- housing[to_test,] first_lm <- lm(medv ~ crim +rm +tax +lstat, data = train) lm1_rsqu <- summary(first_lm)\$r.squared print(paste("First linear model has an r-squared value of ", round(lm1_rsqu, 3), sep = "")) second_lm <- lm(log(medv) ~ crim +rm + tax +lstat, data = train) lm2_rsqu <- summary(second_lm)\$r.squared print(paste("Our second linear model has an r-squared value of ", round(lm2_rsqu, 3), sep = "")) abs(mean(second_lm\$residuals)) predicted <- predict(second_lm, newdata = test) results <- data.frame(predicted = exp(predicted), original = test\$medv) results %>% ggplot(aes(x = predicted, y = original)) + geom_point() + stat_smooth() + labs(x = "Predicted Values", y = "Original Values", title = "Predicted vs. Original Values") + theme_minimal() </pre>	<pre> 2. library(KernelKnn) data(ionosphere, package = 'KernelKnn') ionosphere = ionosphere[, -2] X = scale(ionosphere[, -c(34)]) y = ionosphere[, c(34)] y = as.numeric(y) train.idx = sample(1:length(y), round(length(y) * 0.75)) test.idx = setdiff(1:length(y), train.idx) train = X[train.idx,] test = X[test.idx,] train.labels = y[train.idx] test.labels = y[test.idx] accuracy = function (y_true, preds) { out = table(y_true, max.col(preds, ties.method = "random")) acc = sum(diag(out))/sum(out) acc } predictions = KernelKnn(train, test, train.labels, k = 5, method = 'euclidean', weights_function = NULL, regression = F, Levels = unique(y)) acc = accuracy(test.labels, predictions) paste('Accuracy is ', acc) predictions = KernelKnn(train, test, train.labels, k = 10, method = 'canberra', weights_function = 'epanechnikov', regression = F, Levels = unique(y)) acc = accuracy(test.labels, predictions) knn = KernelKnnCV(X, y, k = 9, folds = 5, method = 'canberra', weights_function = 'epanechnikov', regression = F, Levels = unique(y), threads = 5) acc_cv = unlist(lapply(1:length(knn\$preds) , function(x) accuracy(y(knn\$folds[[x]]), knn\$preds[x])))) paste('Accuracy is ', mean(acc_cv)) paste('Accuracy is ', acc) </pre>	<pre> 3. install.packages("tm") install.packages("wordcloud") install.packages("e1071") library(tm) library(wordcloud) library(e1071) sms_spam_df <- read.csv(file="E:\\sms_spam.csv",stringsAsFactors=F) View(sms_spam_df) str(sms_spam_df) sms_corpus <- VCorpus(VectorSource(sms_spam_df\$text)) print(sms_corpus) inspect(sms_corpus[1:2]) clean_corpus <- tm_map(sms_corpus, content_transformer(tolower)) clean_corpus <- tm_map(clean_corpus, removeNumbers) clean_corpus <- tm_map(clean_corpus, removePunctuation) stopwords()[1:15] clean_corpus <- tm_map(clean_corpus, removeWords, stopwords()) clean_corpus <- tm_map(clean_corpus, stripWhitespace) inspect(clean_corpus[1:3]) sms_dtm <- DocumentTermMatrix(clean_corpus) str(sms_dtm) spam_indices <- which(sms_spam_df\$type == "spam") ham_indices <- which(sms_spam_df\$type == "ham") wordcloud(clean_corpus[ham_indices], min.freq=40) wordcloud(clean_corpus[spam_indices], min.freq=40) sms_raw_train <- sms_spam_df[1:4169,] sms_raw_test <- sms_spam_df[4170:5559,] sms_dtm_train <- sms_dtm[1:4169,] sms_dtm_test <- sms_dtm[4170:5559,] sms_corpus_train <- clean_corpus[1:4169] sms_corpus_test <- clean_corpus[4170:5559] spam <- subset(sms_raw_train, type == "spam") ham <- subset(sms_raw_train, type == "ham") five_times_words <- findFreqTerms(sms_dtm_train, 5) sms_train <- DocumentTermMatrix(sms_corpus_train, control=list(dictionary = five_times_words)) sms_test <- DocumentTermMatrix(sms_corpus_test, control=list(dictionary = five_times_words)) convert_count <- function(x) { y <- ifelse(x > 0, 1, 0) y <- factor(y, levels=c(0,1), labels=c("No", "Yes")) y } sms_train <- apply(sms_train, 2, convert_count) sms_test <- apply(sms_test, 2, convert_count) sms_classifier <- naiveBayes(sms_train, factor(sms_raw_train\$type)) sms_test_pred <- predict(sms_classifier, newdata=sms_test) k=table(sms_test_pred, sms_raw_test\$type) k accuracy = sum(diag(k))/sum(k)*100 accuracy </pre>	<pre> 4. data(iris) help(iris) iris_dataset<-iris View(iris_dataset) head(iris_dataset,7) colnames(iris_dataset)<- c("Sepal.Length", "Sepal.Width", "Petal.Length", "Petal.Width", "Species") head(iris_dataset,5) library(caret) index <- createDataPartition(iris_dataset\$Species, p=0.80, list=FALSE) testset <- iris_dataset[-index,] trainset <- iris_dataset[index,] dim(trainset) str(trainset) summary(trainset) levels(trainset\$Species) hist(trainset\$Sepal.Width) par(mfrow=c(1,4)) for(i in 1:4) { boxplot(trainset[,i], main=names(trainset)[i]) } library(ggplot2) g <- ggplot(data=trainset, aes(x = Petal.Length, y = Petal.Width)) print(g) g <- g + geom_point(aes(color=Species, shape=Species)) + xlab("Petal Length") + ylab("Petal Width") + ggtitle("Petal Length-Width")+ geom_smooth(method="lm") print(g) box <- ggplot(data=trainset, aes(x=Species, y=Sepal.Length)) + geom_boxplot(aes(fill=Species)) + ylab("Sepal Length") + ggtitle("Iris Boxplot") + stat_summary(fun.y=mean, geom="point", shape=5, size=4) print(box) library(ggthemes) histogram <- ggplot(data=iris, aes(x=Sepal.Width)) + geom_histogram(binwidth=0.2, color="black", aes(fill=Species)) + xlab("Sepal Width") + ylab("Frequency") + ggtitle("Histogram of Sepal Width")+ theme_economist() print(histogram) library(ggthemes) facet <- ggplot(data=trainset, aes(Sepal.Length, y=Sepal.Width, color=Species))+ geom_point(aes(shape=Species), size=1.5) + geom_smooth(method="lm") + xlab("Sepal Length") + ylab("Sepal Width") + ggtitle("Faceting") + theme_fivethirtyeight() + facet_grid(. ~ Species) # Along rows print(facet) 'p:::o' </pre>
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