```
from tqdm import tqdm
import numpy as np
import pandas as pd
import warnings
warnings.filterwarnings("ignore")
from sklearn.decomposition import PCA
from sklearn.decomposition import NMF
from sklearn.decomposition import FastICA
from sklearn.decomposition import TruncatedSVD
from sklearn.random projection import SparseRandomProjection
from sklearn.feature selection import f regression
from sklearn.feature selection import mutual info regression
from sklearn.metrics import make scorer
from sklearn.metrics import mean squared error
from sklearn.model selection import cross val score
import hypertools as hyp
import seaborn as sns
from seaborn import heatmap
%matplotlib inline
import matplotlib.pyplot as plt
from matplotlib.pyplot import plot
from matplotlib.pyplot import scatter
y train[:5]
train.head()
y_train.describe()
sns.set(style="white", palette="muted", color codes=True)
# Set up the matplotlib figure
f, axes = plt.subplots(figsize=(13, 6), sharex=True)
sns.despine(left=True)
# Plot a simple histogram with binsize determined automatically
sns.distplot(y train, hist=True, color="g", kde kws={"shade": True}, ax
=axes)
plt.ylabel('Frequency')
plt.xlabel('Value')
#plt.setp(axes, yticks=[])
plt.tight layout()
# Plotting Target Variable x = np.array(y train) x.sort()
plt.figure(figsize=(17, 6)) plt.plot(x) plt.title('')
plt.ylabel('Value') plt.xlabel('Data points') plt.legend(['Target'],
loc='upper left') plt.show()
```

```
np.log1p(y_train).describe()
sns.set(style="white", palette="muted", color codes=True)
# Set up the matplotlib figure
f, axes = plt.subplots(figsize=(13, 6), sharex=True)
sns.despine(left=True)
# Plot a simple histogram with binsize determined automatically
sns.distplot(np.log1p(y train), hist=True, color="g", kde kws={"shade":
True } , ax=axes)
plt.ylabel('Frequency')
plt.xlabel('Value')
#plt.setp(axes, yticks=[])
plt.tight_layout()
x = np.array(np.log1p(y train))
x.sort()
plt.figure(figsize=(17, 6))
plt.plot(x)
plt.title('')
plt.ylabel('Value')
plt.xlabel('Data points')
plt.legend(['Target'], loc='upper left')
plt.show()
x = np.array(train[train.columns[0]]) plt.figure(figsize=(17, 6)) plt.plot(x)
plt.title('') plt.ylabel('Value') plt.xlabel('Data points') plt.legend(['Target'],
loc='upper left') plt.show()
sns.set(style="white", palette="muted", color_codes=True) # Set up the
matplotlib figure f, axes = plt.subplots(figsize=(13, 6), sharex=True)
sns.despine(left=True) # Plot a simple histogram with binsize determined
automatically sns.distplot(y_train, hist=True, color="g", kde_kws={"shade":
True}, ax=axes) plt.ylabel('Frequency') plt.xlabel('Value') #plt.setp(axes,
yticks=[]) plt.tight_layout()
x = np.array(train[train.columns[:7]])
plt.figure(figsize=(17, 6))
plt.plot(x)
plt.title('')
plt.ylabel('Value')
plt.xlabel('Data points')
plt.show()
x = np.log1p(np.array(train[train.columns[:7]])) plt.figure(figsize=(17, 6)) plt.plot(x)
plt.title('') plt.ylabel('Value') plt.xlabel('Data points') plt.show()
def check_sparsity(df): non_zeros = (df.ne(0).sum(axis=1)).sum() total =
train.shape[1]*train.shape[0] zeros = total - non zeros sparsity =
round(zeros / total * 100,2) density = round(non zeros / total * 100,2)
print(" Total:",total,"\n Zeros:", zeros, "\n Sparsity [%]: ",
```

```
sparsity, "\n Density [%]: ", density) return density d1 =
check sparsity(train)
non zeros 1 = (train.ne(0).sum(axis=1)) # number of zero elements colum
nwise
non zeros 0 = (train.ne(0).sum(axis=0))
# Set up the matplotlib figure
f, axes = plt.subplots(figsize=(13, 6), sharex=True)
sns.despine(left=True)
# Plot a simple histogram with binsize determined automatically
sns.distplot(non zeros 1, hist=True, color="g", kde kws={"shade": True}
, ax=axes, bins = 100)
plt.ylabel('Frequency')
plt.xlabel('Value')
#plt.setp(axes, yticks=[])
plt.tight layout()
                                                                       17]:
sns.set(style="white", palette="muted", color codes=True)
# Set up the matplotlib figure
f, axes = plt.subplots(figsize=(13, 6), sharex=True)
sns.despine(left=True)
plt.ylabel('Frequency')
plt.xlabel('Value')
# Plot a simple histogram with binsize determined automatically
sns.distplot(non zeros 0, hist=True, color="g", kde kws={"shade": True}, ax
=axes, bins = 100)
plt.tight layout()
# Set up the matplotlib figure
f, axes = plt.subplots(figsize=(18, 18), sharex=True)
# Plot a simple histogram with binsize determined automatically
heatmap(train, vmin=0, vmax=1, cmap="Blues")
plt.tight layout()
pca = PCA(n components=40, copy=True, whiten=False)
train_pca = pca.fit_transform(train)
plt.figure(figsize=(17, 6))
plt.ylabel('Component values')
plt.xlabel('Component values')
scatter(train pca[:,0], train pca[:,1], alpha = 0.1)
pca = PCA(n_components=40, copy=True, whiten=False) train_pca =
pca.fit transform (np.log1p (train)) plt.figure (figsize=(17, 6)) plt.ylabel('Component
values') plt.xlabel('Component values') scatter(train_pca[:,0], train_pca[:,1],
alpha = 0.1
```

```
x = np.array(corr) x.sort() plt.figure(figsize=(18, 6)) plt.plot(x, color = "b")
plt.title('') plt.ylabel('Mutual information') plt.xlabel('Features')
plt.legend(['Mutual information'], loc='upper left') plt.show()
x = np.array(corr[1]) x.sort() plt.figure(figsize=(18, 6)) plt.plot(x, color = "b")
plt.title('') plt.ylabel('p values') plt.xlabel('Features') plt.legend(['p values'],
loc='upper left') plt.show()
#Set up the matplotlib figure f, axes = plt.subplots(figsize=(18, 18),
sharex=True) # Plot a simple histogram with binsize determined automatically
heatmap(data corr, vmin=0, vmax=1, cmap="Blues") plt.ylabel('Features')
plt.xlabel('Features') plt.tight layout()
from sklearn.decomposition import PCA
pca = PCA(n components=None)
x train = pca.fit transform(encoded train)
x test = pca.transform(encoded test)
explained variance = pca.explained variance ratio
explained variance
xgb = xgboost.XGBRegressor(n_estimators=35, learning_rate=0.06, gamma=0,
subsample=0.6, colsample_bytree=0.7, min_child_weight=4, max_depth=3)
xgb.fit (x_train, y_train) predictions = xgb.predict (x_test)
print(metrics.mean_squared_error(y_test, predictions))
rand = RandomForestRegressor(n estimators = 10, random state = 0)
rand.fit(x train, y train)
y pred2 = rand.predict(x test)
print(metrics.mean_squared_error(y_test,y_pred2))
logreg=LinearRegression()
logreg.fit(x_train,y_train)
y pred=logreg.predict(x test)
print(metrics.mean_squared_error(y_test, y_pred))
```

import os import gc import time import pickle import pandas as pd import numpy
as np import lightgbm as lgb from sklearn.metrics import
mean squared error

```
train df = pd.concat([train df statistic, train space reduction], axis=
test df = pd.concat([test df statistic, test space reduction], axis=1)
del train df statistic, test df statistic
del train space reduction, test space reduction
gc.collect()
print('Train:', train df.shape)
print('Test:', test df.shape)
br = BoostARoota (metric='rmse') br.fit (train_df, y)
print('Total features:', train df.shape[1]) print('Number of selected
features:', len(br.keep vars .values))
train df = pd.read csv(os.path.join(PATH TO DATA, 'train boruta stat bi
n_red_thresh098.csv'))
test df = pd.read csv(os.path.join(PATH TO DATA, 'test boruta stat bin
red thresh098.csv'))
def get 20 cv splits(data, in path):
    #stratify classes = y
    train = pd.read csv(os.path.join(PATH TO DATA, 'input/train.csv'),
usecols=['target'])
    stratify classes = train.target.apply(lambda x: int(np.log10(x)))
    splits = {}
    for random state in range(20):
        column = np.zeros(data.shape[0])
        sss = StratifiedShuffleSplit(n splits=5, test size=0.2, random
state=random state)
        for i, ( , test index) in enumerate(sss.split(data, stratify cl
asses)):
            column[test index] = i
        splits["split{}".format(random state)] = column
    pd.DataFrame(splits, index=data.index).to csv(os.path.join(PATH TO
DATA, in path))
def create folds from cv splits (in path, pkl path):
    cv splits = pd.read csv(os.path.join(PATH TO DATA, in path))
    folds list = []
    for ind, i in enumerate(cv splits.columns[1:]):
        folds = list(set(cv splits[i].values))
        folds list.append([])
        for m in folds:
            val idx = list(cv splits[cv splits[i]==m].index)
            train_idx = list(set(list(cv splits.index)) - set(val idx))
            folds list[ind].append((train idx, val idx))
    with open(os.path.join(PATH TO DATA, pkl path), 'wb') as f:
        pickle.dump(folds list, f)
```

```
LOAD CV = True
if LOAD CV:
   with open(os.path.join(PATH TO DATA, 'folds/custom cv boruta thresh
098.pkl'), 'rb') as f:
        cv folds = pickle.load(f)
else:
    get 20 cv splits(train df, in path='folds/cv splits boruta stat bin
red thresh098.csv')
    cv folds = create folds from cv splits(in path='folds/cv splits bor
uta stat bin red thresh098.csv',
                                           pkl path='folds/custom cv bo
ruta thresh098.pkl')
def run_lgb(train_X, train_y, val X, val y, test X):
    params = {
        "objective" : "regression",
        "metric" : "rmse",
```

```
"num_leaves" : 40,
        'max depth': 7,
        "learning rate" : 0.005,
        "bagging fraction" : 0.7,
        "feature fraction" : 0.1,
        "bagging frequency" : 6,
        "bagging seed" : 44,
        "verbosity" : -1,
        'num threads' : 4,
        "seed": 44
    }
    start time = time.time()
    lgtrain = lgb.Dataset(train X, label=train y)
    lgval = lgb.Dataset(val_X, label=val_y)
    model = lgb.train(params, lgtrain, 5000,
                      valid sets=[lgtrain, lgval],
                      early_stopping_rounds=100,
                      verbose eval=150)
   print('Model training done in {} seconds.'.format(time.time() - sta
rt time))
    pred test y = np.expm1(model.predict(test X, num iteration=model.be
st iteration))
   pred oof log = model.predict(val X, num iteration=model.best iterat
ion)
return pred test y, pred oof log, model
```

```
def run_calculations(X, test, big_cv_folds, func_name = None): if not
func_name: return print('The function to run is not defined') else:
y_oof_20_preds = [] fold_errors_20_preds =[] avg_test_pred_20_preds =
[] fold_errors_std = [] for ind, cv_folds in enumerate(big_cv_folds):
print('Fitting big fold', ind+1, 'out of', len(big_cv_folds)) y_oof =
np.zeros((y.shape[0])) fold errors =[] pred test list = [] for i,
```

```
(train_index, val_index) in enumerate(cv folds): print('Fitting sub
fold', i+1, 'out of', len(cv folds)) X train, X val =
X.iloc[train index], X.iloc[val index] y train, y val = y[train index],
y[val index] # part to include additional functions if func name ==
'lgb': pred test y, pred oof log, clf = run lgb(X train, y train,
X val, y val, test) elif func name == 'xgb': pred test y, pred oof log,
clf = run xgb(X train, y train, X val, y val, test) else: return
print('The function to run is not correct') y oof[val index] =
pred oof log curr fe = np.sqrt(mean squared error(y val, pred oof log))
print(f'Fold error {curr fe}') fold errors.append(curr fe)
pred test list.append(list(pred test y)) print('Total error',
np.sqrt(mean_squared_error(y, y_oof))) total_fe_std =
round(np.std(fold errors), 5) print(f'Total std {total fe std}')
avg test pred = np.mean(pred test list, axis=0)
avg test pred 20 preds.append(avg test pred)
fold errors 20 preds.append(fold errors) y oof 20 preds.append(y oof)
fold errors std.append(total fe std) return y oof 20 preds,
avg test pred 20 preds, fold errors 20 preds, fold errors std
%%time
y oof lgb, pred test list lgb, fold errors, fold std = run calculations
(train df, test df, cv folds, 'lgb')
# Loading regired libraries
library('ggplot2')
library('scales')
library('grid')
library('gridExtra')
library('RColorBrewer')
library('corrplot')
library(dplyr)
df <- read.csv('train.csv')</pre>
dim(df) # 4459 rows , 4993 columns
str(df)
## Cheking for sparsness
sum(df == 0)/(dim(df)[1]*dim(df)[2])
```

```
p1 <- df %>%
 ggplot(aes(target)) +
 geom_histogram(bins = 100, fill = "red") +
 scale_x_log10() +
 labs(x = "Target") +
 ggtitle("target feature distribution")
p2 <- df %>%
 mutate(tar = as.character(target)) %>%
 group_by(tar) %>%
 count() %>%
 arrange(desc(n)) %>%
 head(10) %>%
 ggplot(aes(reorder(tar, n, FUN = min), n)) +
 geom_col(fill = "blue") +
 coord_flip() +
 labs(x = "Target values", y = "frequency") +
 ggtitle("Most frequent target values")
grid.arrange(p1, p2, layout_matrix = rbind(c(1,2)))
## Analysisnf predictor variables
# Loading reqired libraries
library('data.table')
library('tibble')
```

```
library('tidyr')
library('stringr')
library('forcats')
var_means <- df %>%
 select(-ID, -target) %>%
 summarise_all(funs(mean)) %>%
 gather(everything(), key = "feature", value = "mean")
var_sd <- df %>%
 select(-ID, -target) %>%
 summarise_all(funs(sd)) %>%
 gather(everything(), key = "feature", value = "sd")
stat <- df %>%
 select(-ID, -target) %>%
 summarise_all(funs(sum(.<0.001))) %>%
 gather(everything(), key = "feature", value = "zeros") %>%
 left_join(var_means, by = "feature") %>%
 left_join(var_sd, by = "feature")
# Visualising the above
p1 <- stat %>%
 ggplot(aes(mean+1)) +
 geom_histogram(bins = 30, fill = "red") +
 scale_x_log10() +
 labs(x = "Feature mean + 1") +
 ggtitle("Feature means")
```

```
p2 <- stat %>%
 ggplot(aes(sd+1)) +
 geom_histogram(bins = 30, fill = "blue") +
scale_x_log10() +
labs(x = "Feature std dev + 1") +
 ggtitle("Feature std dev")
p3 <- stat %>%
 mutate(zeros = zeros/nrow(df)*100) %>%
 ggplot(aes(zeros)) +
 geom_histogram(bins = 50, fill = "orange") +
 labs(x = "Percentage of zero values") +
 ggtitle("Zero values in feature")
p4 <- stat %>%
 ggplot(aes(mean+1, sd + 1)) +
geom_point(col = "darkgreen") +
scale_x_log10() +
scale_y_log10() +
labs(x = "Feature mean + 1", y = "Feature std dev + 1")
grid.arrange(p1, p2, p3, p4, layout_matrix = rbind(c(1,2),c(3,4)))
# Correlation with target variables
#spearman
spearman_correlations <- df %>%
select(-ID, -target) %>%
cor(df$target, method = "spearman") %>%
 as.tibble() %>%
```

```
rename(cor = V1)
ggplot(spearman_correlations, aes(x=cor)) + geom_histogram() + labs(x = "Spearman Correlation")
coefficient") + ggtitle("Spearman Correlation of anonymous vs target")
# Pearson
pearson_correlations <- df %>%
select(-ID, -target) %>%
cor(df$target, method = "pearson") %>%
 as.tibble() %>%
 rename(cor_p = V1)
ggplot(pearson_correlations, aes(x=cor_p)) + geom_histogram() + labs(x = "Pearson Correlation
coefficient") + ggtitle("Pearson Correlation of anonymous vs target")
### Building models
# removing ID column as is of no use
df$ID <- NULL
# Loading reqired libraries
install.packages('tidyverse')
install.packages('caret')
install.packages('glmnet')
library(tidyverse)
library(caret)
library(glmnet)
library(dplyr)
install.packages('psych')
library(psych)
```

```
attach(df)
y <- df %>% select(target) %>% scale(center = TRUE, scale = FALSE) %>% as.matrix()
x <- df %>% select(-target) %>% as.matrix()
dim(x)
dim(y)
### RIDGE Regression
# Perform 10-fold cross-validation to select lambda ------
lambdas_to_try <- 10^seq(-3, 5, length.out = 100)</pre>
# Setting alpha = 0 implements ridge regression
ridge_cv <- cv.glmnet(x, y, alpha = 0, lambda = lambdas_to_try,</pre>
            standardize = TRUE, nfolds = 10)
# Plot cross-validation results
plot(ridge_cv)
# Best cross-validated lambda
lambda_cv <- ridge_cv$lambda.min</pre>
# Fit final model, get its sum of squared residuals and multiple R-squared
model_cv <- glmnet(x, y, alpha = 0, lambda = lambda_cv, standardize = TRUE)
y_hat_cv <- predict(model_cv, x)</pre>
ssr_cv <- t(y - y_hat_cv) %*% (y - y_hat_cv)
rsq_ridge_cv <- cor(y, y_hat_cv)^2
rsq_ridge_cv # 0.86
### LASSO Regression
# Perform 10-fold cross-validation to select lambda ------
lambdas_to_try <- 10^seq(-3, 5, length.out = 100)
# Setting alpha = 1 implements lasso regression
```

```
lasso_cv <- cv.glmnet(x, y, alpha = 1, lambda = lambdas_to_try,</pre>
            standardize = TRUE, nfolds = 10)
# Plot cross-validation results
plot(lasso_cv)
# Best cross-validated lambda
lambda_cv <- lasso_cv$lambda.min</pre>
# Fit final model, get its sum of squared residuals and multiple R-squared
model_cv <- glmnet(x, y, alpha = 1, lambda = lambda_cv, standardize = TRUE)
y_hat_cv <- predict(model_cv, x)</pre>
ssr_cv <- t(y - y_hat_cv) %*% (y - y_hat_cv)
rsq_lasso_cv <- cor(y, y_hat_cv)^2 # 0.4968
#### Elastic Net Regression
library(caret)
# Set training control
train_control <- trainControl(method = "repeatedcv",</pre>
                 number = 5,
                 repeats = 5,
                 search = "random",
                 verboseIter = TRUE)
# Train the model
elastic_net_model <- train(target ~ .,
               data = cbind(y, x),
               method = "glmnet",
```

```
preProcess = c("center", "scale"),
tuneLength = 25,
trControl = train_control)
```

Check multiple R-squared
y_hat_enet <- predict(elastic_net_model, x)
rsq_enet <- cor(y, y_hat_enet)^2 # 0.7119</pre>