

Proyecto: Analitica de textos

Caso: Elegibilidad de pacientes para ensayos clinicos

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Para este proyecto, se escogio utilizar el modelo regresion logistica para determinar a los pacientes en si son elegibles o si no. Antes de poder entrenar el modelo se debe realizar un preprocesamiento exhaustivo en donde se utilice el modelo de Bag of Words para la vectorización del texto, y despues realizar la lematización del mismo.

0. Importación de librerias

```
import pandas as pd
pd.set_option('display.max_columns', 25)
pd.set_option('display.max_rows', 50)
import numpy as np
np.random.seed(3301)
import pandas as pd

# Preprocesamiento de datos
from sklearn.preprocessing import LabelEncoder
from sklearn.preprocessing import StandardScaler
#para hacer balanceo de los features
from imblearn.over_sampling import SMOTE
# Para realizar la separaciond el conjunto de aprendizaje en entrenamiento y test
from sklearn.model_selection import train_test_split
# Para evaluar el modelo
from sklearn.metrics import confusion_matrix, classification_report, precision_score, recall_score, f1_score, accuracy_score
from sklearn.metrics import plot_confusion_matrix
# Para busqueda de hiperparametros
from sklearn.model_selection import GridSearchCV
# Para la validación cruzada
from sklearn.model_selection import KFold
#Librerias para la visualizacion
import matplotlib.pyplot as plt
#Seaborn
import seaborn as sns

import re

from sklearn.preprocessing import FunctionTransformer

import nltk

nltk.download('stopwords')
from nltk.corpus import stopwords

from nltk.stem.porter import PorterStemmer
from sklearn.feature_extraction.text import TfidfVectorizer

pd.set_option('display.max_colwidth', None) # or 199

from sklearn.feature_extraction.text import CountVectorizer

from sklearn.linear_model import LogisticRegression

from sklearn.pipeline import Pipeline
from sklearn.metrics import mean_squared_error as mse

%matplotlib inline
```

```
[nltk_data] Downloading package stopwords to
[nltk_data] C:\Users\felip\AppData\Roaming\nltk_data...
[nltk_data] Package stopwords is already up-to-date!
```

1. Preprocesamiento

Primero se deben cargar los datos y realizar un perfilamiento de estos, una vez se sabe el estado y pureza de los datos se pueden empezar a limpiar siguiendo lo establecido en el diccionario de datos

```
# Importe
df_eleg = pd.read_csv('../Datos/ElegibilidadEstudiantes/clinical_trials_on_cancer_data_clasificacion.csv', sep=',', encoding='utf-8')
df_eleg.head()
```

	label	study_and_condition
0	__label__0	study interventions are Saracatinib . recurrent verrucous carcinoma of the larynx diagnosis and patients must agree to use adequate birth control for the duration of study participation and for at least eight weeks after discontinuation of study drug
1	__label__1	study interventions are Stem cell transplantation . hodgkin lymphoma diagnosis and history of congenital hematologic immunologic or metabolic disorder which in the estimation of the pi poses prohibitive risk to the recipient
2	__label__0	study interventions are Lenograstim . recurrent adult diffuse mixed cell lymphoma diagnosis and creatinine clearance crcl greater than fifty ml per minute all tests must be performed within twenty-eight days prior to registration
3	__label__0	study interventions are Doxorubicin . stage iii diffuse large cell lymphoma diagnosis and stages ii bulky disease defined as mass size of more than ten cm stage iii or iv ann_arbor staging patients with stage and stage ii non bulky disease are excluded from this study
4	__label__1	study interventions are Poly I-C . prostate cancer diagnosis and unresolved iraes following prior biological therapy except that stable and managed iraes may be acceptable hypothyroidism or hypopituitarism on appropriate replacement

Vemos si existen datos nulos en el dataset:

```
df_eleg.isna().sum()
```

```
label          0
study_and_condition  0
dtype: int64
```

Los datos no tienen nulos pero están presentados de maneras distintas. Algunos comienzan con comillas, otros son espacios. Debemos lograr entradas similares. Adicionalmente la información importante del paciente está ubicada después del primer punto. Adicionalmente vemos que los labels son categóricos y debemos volverlos numéricos. Aunque un label encoder haría esta tarea con facilidad, queremos conservar la categoría implícita que ya traen.

```
def preprocessor(df):
    df = df.replace('""', '')
    df = df.str.strip(' ')
    df = df.str.split('.').str[1]
    return df
print(df_eleg.describe())

def encoder(df):
    df.loc[df['label'] == '__label__0', 'label'] = 0
    df.loc[df['label'] == '__label__1', 'label'] = 1
encoder(df_eleg)
df_eleg
```

	label \	
count	12000	
unique	2	
top	__label__0	
freq	6000	

	study_and_condition	
count	12000	
unique	11987	
top	study interventions are Fludarabine . anaplastic large cell lymphoma diagnosis and donor	
freq	2	

label		study_and_condition
0	0	study interventions are Saracatinib . recurrent verrucous carcinoma of the larynx diagnosis and patients must agree to use adequate birth control for the duration of study participation and for at least eight weeks after discontinuation of study drug
1	1	study interventions are Stem cell transplantation . hodgkin lymphoma diagnosis and history of congenital hematologic immunologic or metabolic disorder which in the estimation of the pi poses prohibitive risk to the recipient
2	0	study interventions are Lenograstim . recurrent adult diffuse mixed cell lymphoma diagnosis and creatinine clearance crcl greater than fifty ml per minute all tests must be performed within twenty-eight days prior to registration
3	0	study interventions are Doxorubicin . stage iii diffuse large cell lymphoma diagnosis and stages ii bulky disease defined as mass size of more than ten cm stage iii or iv ann_arbor staging patients with stage and stage ii non bulky disease are excluded from this study
4	1	study interventions are Poly I-C . prostate cancer diagnosis and unresolved iraes following prior biological therapy except that stable and managed iraes may be acceptable hypothyroidism or hypopituitarism on appropriate replacement
...
11995	0	study interventions are Prednisolone hemisuccinate . recurrent childhood large cell lymphoma diagnosis and no known hypersensitivity to etanercept
11996	0	study interventions are Bevacizumab . recurrent rectal cancer diagnosis and absolute neutrophil count greater_than equal_than one thousand, five hundred ul
11997	1	study interventions are Antibodies, Monoclonal . recurrent lymphoblastic lymphoma diagnosis and and intrathecal intraventricular therapy
11998	0	study interventions are Vorinostat . colorectal cancer diagnosis and patients must have received at least one prior chemotherapy regimen for advanced disease
11999	0	study interventions are Freund's Adjuvant . ovarian cancer diagnosis and more than four weeks since prior participation in any other investigational study

12000 rows × 2 columns

Creamos el pipeline para facilitar el uso del modelo en produccion.

```
pre = [('preproc', FunctionTransformer(preprocessor))]
```

Ahora vamos a preprocesar el texto partiendolo en tokens y lematizandolo. Despues se utilizar un modelo de bag of words y finalmente tf-idf para identificar las palabras importantes. Aprovechamos el corpus de nltk para quitar palabras conectoras que generen ruido.

```

porter = PorterStemmer()
stop = stopwords.words('english')
def tokenizer_porter(sentence):
    tokens = sentence.split()
    stemmed_tokens = [porter.stem(token) for token in tokens if token not in stop]
    return ' '.join(stemmed_tokens)

def transformer_tokenizer(df):
    df = df.apply(tokenizer_porter)
    return df

pre += [('porter', FunctionTransformer(transformer_tokenizer))]

```

```
df_eleg
```

	label	study_and_condition
0	0	study interventions are Saracatinib . recurrent verrucous carcinoma of the larynx diagnosis and patients must agree to use adequate birth control for the duration of study participation and for at least eight weeks after discontinuation of study drug
1	1	study interventions are Stem cell transplantation . hodgkin lymphoma diagnosis and history of congenital hematologic immunologic or metabolic disorder which in the estimation of the pi poses prohibitive risk to the recipient
2	0	study interventions are Lenograstim . recurrent adult diffuse mixed cell lymphoma diagnosis and creatinine clearance crcl greater than fifty ml per minute all tests must be performed within twenty-eight days prior to registration
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...
11995	0	study interventions are Prednisolone hemisuccinate . recurrent childhood large cell lymphoma diagnosis and no known hypersensitivity to etanercept
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12000 rows × 2 columns

Ahora utilizamos el modelo Bag of Words para traducir el texto a un vector numerico que representa las palabras en el mismo. Como la frecuencia de las palabras no importantes tiende a ser elevado entonces utilizamos tfidf para corregirlo.

```

tfidf = TfidfVectorizer(strip_accents=None, lowercase=False, preprocessor=None)

pre += [('tfidf', tfidf)]

```

2. Entrenamiento del modelo de regresión logística.

Para los parametros del modelo tomamos las dos penalidades posibles, y un rango de coeficientes de regularización para que el GridSearch pueda buscar el modelo mas optimo. También se incluye en el grid si se usa o no el IDF para ver esto como varia con el comportamiento frecuencial de los tokens. Se prueban con dos solvers.

```

Y = df_eleg['label'].astype('int')
X = df_eleg['study_and_condition']

X_train, X_test, Y_train, Y_test = train_test_split(X, Y, test_size = 0.15, random_state = 98572398)

model = [('clf', LogisticRegression(random_state=0))]

print(pre+model)

param_grid = {
    'tfidf__ngram_range': [(1,1)],
    'tfidf__use_idf': [False, True],
    'clf__solver': ['newton-cg', 'lbfgs'],
    'clf__penalty': ['none', 'l2'],
    'clf__C': [1.0, 10.0, 100.0]
}

p1 = Pipeline(pre+model)

gs = GridSearchCV(p1, param_grid, scoring='accuracy', cv=5, verbose=1, n_jobs=-1)

gs.fit(X_train, Y_train)
clf = gs.best_estimator_
print(gs.best_params_)

```

```

[('preproc', FunctionTransformer(func=<function preprocessor at 0x000002B3BDB68790>)), ('porter', FunctionTransformer(func=<function
Fitting 5 folds for each of 24 candidates, totalling 120 fits
{'clf__C': 1.0, 'clf__penalty': 'l2', 'clf__solver': 'newton-cg', 'tfidf__ngram_range': (1, 1), 'tfidf__use_idf': True}

```

```
print("Coeficiente de determinación R^2: ", clf.score(X, Y))
```

```
Coeficiente de determinación R^2: 0.8434166666666667
```

El R2 de la regresión es buena, lo que indica que el supuesto de un comportamiento logístico es cierto, y que nuestros resultados tendrán predicciones acorde con el hiperplano establecido por el modelo. Aun así no es una métrica comparable ni utilizable ya que esta orientada a modelos de regresión lineal y en Scikit no existen métricas como Tjur's R squared que si se ajustan mejor a estos comportamientos.

```

y_true = Y
y_predicted = clf.predict(X)

# Note que hay que sacarle la raíz al valor
print("Root-Mean-Square Error (RMSE):", np.sqrt(mse(y_true, y_predicted)))

```

```
Root-Mean-Square Error (RMSE): 0.3957061199088704
```

El RMSE está por debajo de 1, una muy buena métrica. Con estas dos métricas podemos ver que el modelo es correcto y se aproxima a las predicciones esperadas. Desde un punto de vista técnico se recomienda usarlo para el negocio.

```

print('CV Accuracy: %.3f' % gs.best_score_)

print('Test Accuracy: %.3f' % clf.score(X_test, Y_test))

```

```

CV Accuracy: 0.798
Test Accuracy: 0.806

```

Finalmente tenemos métricas para poder compararlo con los otros algoritmos de clasificación ya que estos no tienen R2 ni RMSE. Con métricas cercanas al 80% tienen una accuracy buena y utilizable para el negocio.

```
df_export = df_eleg.copy()['study_and_condition']
df_export = preprocessor(df=df_export)
df_export = transformer_tokenizer(df_export)
tfidf_expo = TfidfVectorizer(strip_accents=None, lowercase=False, preprocessor=None, ngram_range= (1, 1),use_idf= True)
df_export =tfidf_expo.fit_transform(df_export)
```

```
df1 = pd.DataFrame(df_export.toarray(), columns=tfidf_expo.get_feature_names())
print(df1)
```

	0pd	0three_two9	0two_two009	101	15zero	1five	1four	1six	1six0	\
0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
2	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
3	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
4	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
...	
11995	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
11996	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
11997	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
11998	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
11999	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	

	1three	1two	1two0	...	zolmitriptan	zometa	zone	zubrod	μl	\
0	0.0	0.0	0.0	...	0.0	0.0	0.0	0.0	0.0	
1	0.0	0.0	0.0	...	0.0	0.0	0.0	0.0	0.0	
2	0.0	0.0	0.0	...	0.0	0.0	0.0	0.0	0.0	
3	0.0	0.0	0.0	...	0.0	0.0	0.0	0.0	0.0	
4	0.0	0.0	0.0	...	0.0	0.0	0.0	0.0	0.0	
...	
11995	0.0	0.0	0.0	...	0.0	0.0	0.0	0.0	0.0	
11996	0.0	0.0	0.0	...	0.0	0.0	0.0	0.0	0.0	
11997	0.0	0.0	0.0	...	0.0	0.0	0.0	0.0	0.0	
11998	0.0	0.0	0.0	...	0.0	0.0	0.0	0.0	0.0	
11999	0.0	0.0	0.0	...	0.0	0.0	0.0	0.0	0.0	

	μmol	%c	%f	½_tespoon	μl	μmol	ul
0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
1	0.0	0.0	0.0	0.0	0.0	0.0	0.0
2	0.0	0.0	0.0	0.0	0.0	0.0	0.0
3	0.0	0.0	0.0	0.0	0.0	0.0	0.0
4	0.0	0.0	0.0	0.0	0.0	0.0	0.0
...
11995	0.0	0.0	0.0	0.0	0.0	0.0	0.0
11996	0.0	0.0	0.0	0.0	0.0	0.0	0.0
11997	0.0	0.0	0.0	0.0	0.0	0.0	0.0
11998	0.0	0.0	0.0	0.0	0.0	0.0	0.0
11999	0.0	0.0	0.0	0.0	0.0	0.0	0.0

[12000 rows x 5509 columns]

C:\ProgramData\Anaconda3\lib\site-packages\sklearn\utils\deprecation.py:87: FutureWarning: Function get_feature_names is deprecated;
warnings.warn(msg, category=FutureWarning)

```
df1.insert(loc=0, column='%label%', value=Y)
df1.to_csv('datos_finales.csv')
```

```
pd.set_option('display.max_rows', None) # or 1000
df1.sum().sort_values(ascending=False)
```

```
%label%
6000.000000
```

diagnosi	754.466055
cancer	567.779256
lymphoma	440.448009
cell	387.504004
patient	353.119211
stage	352.214177
prior	282.553491
recurr	275.089880
breast	257.388118
carcinoma	246.429865
diseas	235.746845
greater_than	223.430327
one	221.972079
therapi	219.188812
studi	198.252302
adult	192.258823
tumor	187.744355
less_than	186.880418
must	177.631261
two	173.727458
within	173.499092
non	171.470424
doc	162.226231
lung	159.599161
small	155.906632
treatment	155.634566
three	151.486628
iv	149.079369
neoplasm	148.661268
equal_than	148.617795
grade	144.563331
myeloma	139.209984
week	138.031918
histori	135.484496
chemotherapi	134.582166
metastat	134.039287
day	131.800426
multipl	128.848953
iii	122.634861
hundr	122.408351
activ	122.038865
prostat	121.567204
childhood	119.245203
ovarian	118.342069
month	117.328448
malign	113.164310
receiv	110.735515
four	110.668059
system	109.338763
known	108.946015
concurr	107.300677
pregnant	107.009753
larg	106.956268
investig	103.953654
hodgkin	103.332727
requir	103.075312
infect	102.230346
follow	100.635368
brain	100.067831
use	99.836545
colorect	99.093749
medic	98.830166
ii	98.624482
squamou	97.877881
zero	96.214342

year	96.115309
six	96.000233
least	95.760018
donor	95.720892
diffus	94.514722
hepat	93.945828
posit	92.495475
melanoma	91.272003
agent	90.830449
renal	90.050284
pancreat	89.746183
statu	89.700180
perform	89.284427
normal	88.276581
dl	88.132709
solid	88.076784
creatinin	87.865926
adenocarcinoma	87.763315
limit	86.584557
includ	86.273283
surgeri	85.252702
follicular	85.029590
primari	84.179769
drug	83.380010
uncontrol	83.008622
age	82.336050
five	82.166593
uln	81.775441
clinic	81.694861
elig	79.642361
time	78.182393
hiv	78.023240
particip	77.386564
consent	74.850097
characterist	74.191752
radiotherapi	74.135856
mg	73.864388
neg	71.528255
pregnanc	71.149900
dose	70.907781
subject	70.667818
sarcoma	70.435644
inform	69.895955
greater	68.879087
serum	68.461354
signific	68.074531
function	68.063855
protocol	68.049413
metastas	67.878104
condit	67.729182
enrol	67.551993
twenty	67.012888
women	66.958910
test	66.171259
may	66.144504
liver	66.102632
count	64.312430
femal	63.721608
heart	63.703887
margin	63.437285
central	62.485786
measur	61.854676
zone	61.460034
allow	61.451237
refractori	61.208871
... of ...	61.050710

specifi	61.052749
bone	61.047108
potenti	60.672689
cardiac	60.527834
skin	60.367252
caviti	60.021352
evid	59.963261
except	59.837287
treat	59.613387
nervou	59.268831
radiat	59.058310
advanc	59.054746
lymphoblast	58.803028
marrow	56.146770
adequ	55.930455
transplant	55.056308
human	54.805524
colon	54.315185
bilirubin	54.287997
fifti	54.150595
current	53.453127
contracept	52.949859
sinc	52.896241
expect	52.743814
note	52.664415
would	52.423214
tube	52.411895
lymphocyt	52.268436
life	52.253336
upper	52.132187
defin	51.617712
platelet	51.431880
mantl	51.389774
effect	50.752002
ecog	50.595148
fallopian	50.527802
chronic	50.454562
neck	50.334157
eight	50.315205
oral	50.186115
sever	49.621786
exclud	49.154477
previou	48.892368
periton	48.856121
plasma	48.811479
less	48.370520
viru	48.367796
peripher	48.104700
seriou	47.815450
rectal	47.561252
ill	47.548486
complet	46.894743
mm	46.821722
criteria	46.589164
cervic	46.449475
anti	46.431689
risk	46.187048
first	46.137410
trial	46.111135
registr	46.030411
major	45.962955
procedur	45.151530
leukemia	45.020070
head	44.842225
glioblastoma	44.755096
failur	44.497830

immunodefici	44.470003
past	43.887610
specif	43.717443
histolog	43.713989
eighteen	43.365028
iiib	43.055022
progress	42.920826
lesion	42.661095
biolog	42.374122
lactat	42.311987
ten	41.948616
confirm	41.810928
start	41.669420
gastric	41.177253
entri	41.041489
cn	40.964655
nurs	40.803821
control	40.787793
seven	40.549486
sign	40.434792
surgic	40.391199
bleed	40.289255
esophag	40.213646
hormon	39.875769
thirti	39.807199
hypersensit	39.634100
tissu	39.574929
associ	39.435761
twelv	39.427624
total	39.068439
iiia	38.995845
institut	38.963168
anaplast	38.944932
burkitt	38.918297
recov	38.793403
hypertens	38.744673
regimen	38.684223
gastrointestin	38.615685
last	38.193765
group	38.038737
sixti	37.688839
unspecifi	37.622484
absolut	37.577532
disord	37.442121
organ	37.402543
relat	37.246962
neuroblastoma	37.214264
hepatocellular	37.107694
pulmonari	36.906740
high	36.894733
syndrom	36.749776
blood	36.595052
neutrophil	36.516384
inhibitor	36.483212
bladder	36.442661
local	35.972269
ml	35.923363
unstabl	35.797272
acut	35.796944
ast	35.344183
biopsi	35.147769
type	35.060246
infarct	34.981671
myocardi	34.819641
feed	34.503147

contigu	34.323742
angina	34.227782
abnorm	34.194933
hemoglobin	34.146814
mix	33.871977
fourteen	33.690472
breastfeed	33.658067
document	33.654819
iiic	33.240564
alt	33.228880
reaction	32.961451
toxic	32.951019
antibodi	32.945811
stem	32.823534
hematopoiet	32.511915
involv	32.477477
clearanc	32.198378
nasal	32.166936
abl	32.118206
congest	31.788500
childbear	31.682936
steroid	31.559991
min	31.522211
glioma	31.267470
written	31.164179
relaps	31.150796
iva	30.957113
karnofski	30.930097
arrhythmia	30.839967
immunoblast	30.762958
provid	30.222211
nine	30.175032
thousand	30.126389
initi	30.088534
equal	29.980473
urin	29.917322
event	29.852008
endometri	29.819781
ivb	29.810508
kidney	29.769162
psychiatr	29.065411
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