In [1]:
```
#Carrega os pacotes
import pandas as pd
import numpy as np
from nltk.corpus import stopwords
import matplotlib.pyplot as plt
import matplotlib as mpl
%matplotlib inline
```

In [2]:
```
#Dados das variaveis de treino
train_variants_df = pd.read_csv("training_variants")
train_variants_df.shape
```

Out[2]:
```
(3321, 4)
```

In [3]:
```
#Dados dos textos de treino
train_text_df = pd.read_csv("training_text", sep="\|\|", engine='python', head
er = None, names=["ID","Text"], skiprows=1)
train_text_df.shape
```

Out[3]:
```
(3321, 2)
```

In [5]:
```
#Juntando os datdasets (subtraíndo 1 das classes para que se iniciem com 0)
df = pd.merge(train_variants_df, train_text_df, how='left', on='ID')
df['Class'] = df['Class'] - 1
df.head()
```

Out[5]:

	ID	Gene	Variation	Class	Text
0	0	FAM58A	Truncating Mutations	0	Cyclin-dependent kinases (CDKs) regulate a var...
1	1	CBL	W802*	1	Abstract Background Non-small cell lung canc...
2	2	CBL	Q249E	1	Abstract Background Non-small cell lung canc...
3	3	CBL	N454D	2	Recent evidence has demonstrated that acquired...
4	4	CBL	L399V	3	Oncogenic mutations in the monomeric Casitas B...

In [6]:
```
df.shape
```

Out[6]:
```
(3321, 5)
```

In [7]:
```
# Valores NA
TextNA = df['Text'].isna()
print('Existem %.0f valores NA' % TextNA[TextNA == True].shape[0])
```

```
Existem 5 valores NA
```

In [8]:
```
# Removendo os valores missing
df = df.drop(TextNA[TextNA == True].index)
df.reset_index(drop=True)
```

Out[8]:

	ID	Gene	Variation	Class	Text
0	0	FAM58A	Truncating Mutations	0	Cyclin-dependent kinases (CDKs) regulate a var...
1	1	CBL	W802*	1	Abstract Background Non-small cell lung canc...
2	2	CBL	Q249E	1	Abstract Background Non-small cell lung canc...
3	3	CBL	N454D	2	Recent evidence has demonstrated that acquired...
4	4	CBL	L399V	3	Oncogenic mutations in the monomeric Casitas B...
5	5	CBL	V391I	3	Oncogenic mutations in the monomeric Casitas B...
6	6	CBL	V430M	4	Oncogenic mutations in the monomeric Casitas B...
7	7	CBL	Deletion	0	CBL is a negative regulator of activated recep...
8	8	CBL	Y371H	3	Abstract Juvenile myelomonocytic leukemia (JM...
9	9	CBL	C384R	3	Abstract Juvenile myelomonocytic leukemia (JM...
10	10	CBL	P395A	3	Oncogenic mutations in the monomeric Casitas B...
11	11	CBL	K382E	3	Noonan syndrome is an autosomal dominant conge...
12	12	CBL	R420Q	3	Noonan syndrome is an autosomal dominant conge...
13	13	CBL	C381A	3	Noonan syndrome is an autosomal dominant conge...
14	14	CBL	P428L	4	Oncogenic mutations in the monomeric Casitas B...
15	15	CBL	D390Y	3	Noonan syndrome is an autosomal dominant conge...
16	16	CBL	Truncating Mutations	0	To determine if residual cylindrical refractiv...
17	17	CBL	Q367P	3	Acquired uniparental disomy (aUPD) is a common...
18	18	CBL	M374V	4	Oncogenic mutations in the monomeric Casitas B...
19	19	CBL	Y371S	3	Acquired uniparental disomy (aUPD) is a common...
20	20	CBL	H94Y	5	Abstract Background Non-small cell lung canc...
21	21	CBL	C396R	3	Oncogenic mutations in the monomeric Casitas B...
22	22	CBL	G375P	3	Oncogenic mutations in the monomeric Casitas B...
23	23	CBL	S376F	3	Recent evidence has demonstrated that acquired...
24	24	CBL	P417A	3	Recent evidence has demonstrated that acquired...
25	25	CBL	H398Y	3	Recent evidence has demonstrated that acquired...

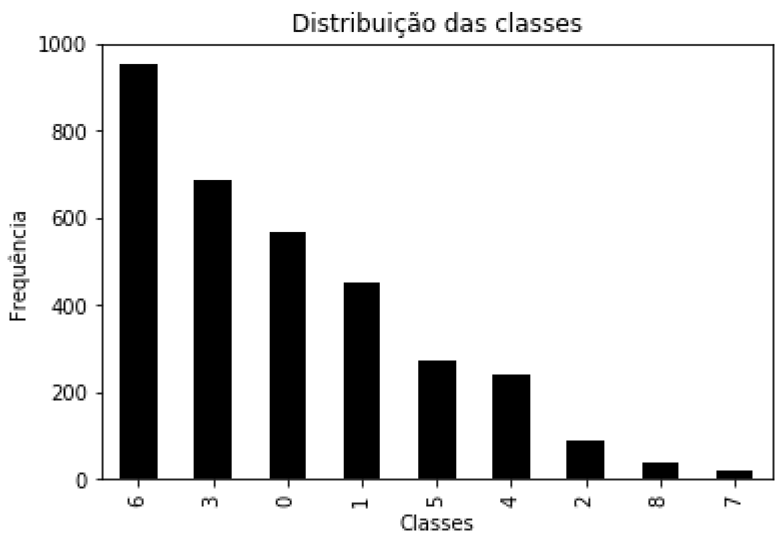
	ID	Gene	Variation	Class	Text
26	26	SHOC2	S2G	3	Abstract N-myristoylation is a common form of...
27	27	TERT	Y846C	3	Heterozygous mutations in the telomerase compo...
28	28	TERT	C228T	6	Sequencing studies have identified many recurr...
29	29	TERT	H412Y	3	Heterozygous mutations in the telomerase compo...
...	...	...	...	...	...
3286	3291	RET	C620R	6	We investigatedthe transformingactivityofthe r...
3287	3292	RET	C634Y	6	We investigatedthe transformingactivityofthe r...
3288	3293	RET	V804G	0	RET is a transmembrane tyrosine kinase partici...
3289	3294	RET	R886W	6	Introduction Inherited germ line activating m...
3290	3295	RET	F893L	3	Many missense mutations in the RET proto-oncog...
3291	3296	RET	Y791F	6	The RET proto-oncogene encodes a receptor tyro...
3292	3297	RUNX1	R177*	3	THE AML1 GENE IS KNOWN as the most frequent ta...
3293	3298	RUNX1	Y113*	3	Introduction Myelodysplastic syndromes (MDS) ...
3294	3299	RUNX1	R139G	3	The BCR-ABL fusion protein generated by t(9;22...
3295	3300	RUNX1	K83N	3	The most frequent mutations associated with le...
3296	3301	RUNX1	R177Q	3	The most frequent mutations associated with le...
3297	3302	RUNX1	R166Q	3	Familial platelet disorder with predisposition...
3298	3303	RUNX1	P173S	3	Introduction Myelodysplastic syndromes (MDS) ...
3299	3304	RUNX1	R201Q	3	Familial platelet disorder with predisposition...
3300	3305	RUNX1	S70fsX93	3	Introduction Myelodysplastic syndromes (MDS) ...
3301	3306	RUNX1	W279*	0	Here we report two new RUNX1 mutations in one ...
3302	3307	RUNX1	Truncating Mutations	0	The RUNX genes have come to prominence recentl...
3303	3308	RUNX1	R174*	6	Familial platelet disorder with propensity to...
3304	3309	RUNX1	D171G	0	The BCR-ABL fusion protein generated by t(9;22...
3305	3310	RUNX1	Amplification	6	RUNX proteins belong to a family of metazoan t...
3306	3311	RUNX1	RUNX1-EVI1 Fusion	3	The AML1/EVI-1 chimeric gene is generated by t...
3307	3312	RUNX1	TEL-RUNX1 Fusion	3	Balanced chromosomal translocations are freque...
3308	3313	RUNX1	H78Q	3	The BCR-ABL fusion protein generated by t(9;22...
3309	3314	RUNX1	G42R	5	Introduction Myelodysplastic syndromes (MDS) ...

	ID	Gene	Variation	Class	Text
3310	3315	RUNX1	RUNX1-RUNX1T1 Fusion	3	The RUNX gene family includes three evolutiona...
3311	3316	RUNX1	D171N	3	Introduction Myelodysplastic syndromes (MDS) ...
3312	3317	RUNX1	A122*	0	Introduction Myelodysplastic syndromes (MDS) ...
3313	3318	RUNX1	Fusions	0	The Runt-related transcription factor 1 gene (...
3314	3319	RUNX1	R80C	3	The RUNX1/AML1 gene is the most frequent targe...
3315	3320	RUNX1	K83E	3	The most frequent mutations associated with le...

3316 rows × 5 columns

In [9]:
```python
#Verificando a distribuição das classes
ax = df['Class'].value_counts().plot(kind='bar', color='black', title = 'Distr
ibuição das classes')
ax.set_xlabel('Classes')
ax.set_ylabel('Frequência')
```

Out[9]:
```
Text(0,0.5,'Frequência')
```



Temos pouquíssimos casos para as classes 2, 7 e 8, dificultando sua detecção. Teremos que balancear o dataset.

In [10]:
```python
# Vamos verificar as palavras mais frequentes associadas com cada uma das clas
ses

# Agrupando as classes e transformando o texto em uma grande String
palavras = df.groupby('Class').apply(lambda x: x['Text'].str.cat())
```

In [11]:
```python
# Importando funções do sklearn para tratamento do dados
from sklearn.feature_extraction.text import TfidfVectorizer
from sklearn.feature_extraction.text import CountVectorizer
```

In [12]:
```
# Calculando as frequências
stopWords = set(stopwords.words('english'))
vectorizer = CountVectorizer(stop_words=stopWords)
X = vectorizer.fit_transform(palavras)
```

In [13]:
```
# Crianda um dataframe com as paralavras mais frequentes
def PalavrasFrequentesPorClasse(palavras, frequencias):
    dfTopWords = pd.DataFrame()
    for linha in range(len(frequencias)):
        dfTemp = pd.DataFrame({'Classe'+str(linha+1): palavras, 'Freq'+str(lin
ha+1): frequencias[linha]})
        dfTemp = dfTemp.sort_values(by=['Freq'+str(linha+1)], ascending=False)
        dfTopWords = pd.concat([dfTopWords, dfTemp.reset_index(drop=True)], ax
is=1)
    return dfTopWords
```

In [14]:
```
# Crianda um dataframe com as palavras mais frequentes dado a classe
def PalavrasFrequentesTotalClasses(palavras, frequencias, n):
    for linha in range(len(frequencias)):
        dfTemp = pd.DataFrame({'Palavra': palavras, 'Freq'+str(linha+1): frequ
encias[linha]})
        if linha == 0:
            dfTopWordsClasses = dfTemp.sort_values(by=['Freq'+str(linha+1)], a
scending=False)[0:20]
        else:
            dfTemp = dfTemp.sort_values(by=['Freq'+str(linha+1)], ascending=Fa
lse)
            dfTopWordsClasses = pd.merge(dfTopWordsClasses, dfTemp[0:n], how=
'outer', on='Palavra')
    dfTopWordsClasses['TotalClasses'] = dfTopWordsClasses.count(axis='columns'
, numeric_only=True)
    return dfTopWordsClasses.sort_values(by=['TotalClasses'], ascending=False)
```

In [15]:
```
# Top 10 palavras mais frequêntes por classe
dfTopWords = PalavrasFrequentesPorClasse(vectorizer.get_feature_names(), X.toa
rray())
dfTopWords.head(10)
```

Out[15]:

	Classe1	Freq1	Classe2	Freq2	Classe3	Freq3	Classe4	Freq4	Classe5	Freq5	Cl
0	mutations	33719	mutations	34570	mutations	6243	mutations	46483	brca1	14396	
1	cells	28402	cells	23143	brca1	4191	cells	37077	variants	14365	
2	cell	20282	patients	19183	cells	3900	pten	25777	mutations	13049	mut
3	p53	19152	cell	18237	al	3016	protein	23992	cancer	7866	va
4	et	18973	mutation	15148	variants	2936	et	21997	cells	7500	(
5	al	18871	et	14718	et	2843	al	21866	protein	6111	mu
6	fig	18099	al	14653	cancer	2648	activity	21596	mutation	5782	
7	protein	17950	cancer	13217	mutation	2183	fig	21193	functional	5648	
8	cancer	17907	figure	13006	figure	2181	cell	21150	fig	5558	delet
9	mutation	17228	kinase	12615	alk	2075	figure	19398	type	5444	

Algumas palavras são muito comuns, como: mutations, cells, cell, et, al...

In [17]:
```
# Palavras frequentes em todas as classes
dfTopWordsClasses = PalavrasFrequentesTotalClasses(vectorizer.get_feature_name
s(), X.toarray(), 50)
dfTopWordsClasses[dfTopWordsClasses['TotalClasses'] == 9]
```

Out[17]:

	Palavra	Freq1	Freq2	Freq3	Freq4	Freq5	Freq6	Freq7	Freq8	Freq9	Tot
0	mutations	33719.0	34570.0	6243.0	46483.0	13049.0	12135.0	86824.0	1329.0	3590.0	
7	protein	17950.0	7777.0	1611.0	23992.0	6111.0	4766.0	20340.0	367.0	909.0	
17	mutant	12693.0	8294.0	1380.0	14022.0	2974.0	2962.0	27474.0	617.0	2848.0	
14	expression	14532.0	9894.0	1528.0	16113.0	3415.0	2660.0	26844.0	910.0	1728.0	
13	type	15172.0	7304.0	1301.0	16891.0	5444.0	4306.0	19906.0	410.0	1494.0	
10	figure	17109.0	13006.0	2181.0	19398.0	4241.0	4383.0	35016.0	855.0	2215.0	
8	cancer	17907.0	13217.0	2648.0	16655.0	7866.0	7000.0	32058.0	557.0	893.0	
9	mutation	17228.0	15148.0	2183.0	17874.0	5782.0	6819.0	38461.0	572.0	1190.0	
6	fig	18099.0	12555.0	1428.0	21193.0	5558.0	6179.0	37246.0	668.0	1341.0	
5	al	18871.0	14653.0	3016.0	21866.0	3829.0	3887.0	35159.0	1033.0	2030.0	
4	et	18973.0	14718.0	2843.0	21997.0	3827.0	3922.0	35244.0	1026.0	2035.0	
1	cells	28402.0	23143.0	3900.0	37077.0	7500.0	6477.0	73838.0	1374.0	3924.0	
2	cell	20282.0	18237.0	1745.0	21150.0	4321.0	4339.0	52942.0	768.0	2332.0	

In [19]:
```
# Colocando as palavras frequêntes em lista para adicionar no stopWords
palavrasFrequentes = dfTopWordsClasses['Palavra'].values[dfTopWordsClasses['To
talClasses'] == 9]
palavrasFrequentes
```

Out[19]:
```
array(['mutations', 'protein', 'mutant', 'expression', 'type', 'figure',
       'cancer', 'mutation', 'fig', 'al', 'et', 'cells', 'cell'],
      dtype=object)
```

In [20]:
```
#Fazendo a mesma busca para pares de palavras
vectorizer2 = CountVectorizer(stop_words=stopWords, ngram_range=(2, 2))
X2 = vectorizer2.fit_transform(palavras)
```

In [22]:
```
# Palavras frequêntes por classe (ngram = 2)
dfTopWords2 = PalavrasFrequentesPorClasse(vectorizer2.get_feature_names(), X2.
toarray())
dfTopWords2.head(10)
```

Out[22]:

	Classe1	Freq1	Classe2	Freq2	Classe3	Freq3	Classe4	Freq4	Classe5	Fre
0	et al	18822	et al	14566	et al	2809	et al	21790	wild type	45
1	wild type	11947	wild type	4995	wild type	1157	wild type	13405	et al	38
2	cell lines	4243	cell lines	4141	amino acid	529	missense mutations	4760	vus neutral	19
3	dna binding	3120	kinase domain	2603	breast cancer	490	cell lines	4532	author manuscript	16
4	amino acid	3014	egfr mutations	2562	brca1 variants	479	amino acid	4502	brca1 variants	14
5	breast cancer	2957	tyrosine kinase	2022	vus neutral	416	pten mutations	3682	embryonic stem	14
6	amino acids	2498	cyclin d1	1796	mtor mutations	405	phosphatase activity	3010	brca1 brct	13
7	missense mutations	2416	cell line	1790	cells expressing	391	tumor suppressor	2896	cell lines	12
8	supplementary fig	2345	lung cancer	1790	fâ fâ	372	amino acids	2856	stem cells	11
9	figure figure	2075	amino acid	1751	alk mutations	366	dna binding	2560	pa author	11

In [23]:
```
# Top pares de palavras presentes em pelo menos 7 classes
dfTopWordsClasses2 = PalavrasFrequentesTotalClasses(vectorizer2.get_feature_na
mes(), X2.toarray(), 50)
dfTopWordsClasses2[dfTopWordsClasses2['TotalClasses'] > 6]
```

Out[23]:

	Palavra	Freq1	Freq2	Freq3	Freq4	Freq5	Freq6	Freq7	Freq8	Freq9	Tc
0	et al	18822.0	14566.0	2809.0	21790.0	3822.0	3882.0	34754.0	1026.0	2030.0	
2	cell lines	4243.0	4141.0	331.0	4532.0	1244.0	1058.0	12718.0	182.0	546.0	
1	wild type	11947.0	4995.0	1157.0	13405.0	4532.0	3210.0	15111.0	307.0	1380.0	
11	cell line	1865.0	1790.0	284.0	1877.0	531.0	NaN	5404.0	63.0	219.0	
4	amino acid	3014.0	1751.0	529.0	4502.0	1133.0	1024.0	4139.0	85.0	NaN	
5	breast cancer	2957.0	1266.0	490.0	2023.0	1092.0	1339.0	3169.0	59.0	NaN	
6	amino acids	2498.0	853.0	251.0	2856.0	537.0	764.0	2309.0	52.0	NaN	
30	cells expressing	NaN	1440.0	391.0	1426.0	527.0	477.0	5151.0	92.0	207.0	
8	supplementary fig	2345.0	1595.0	NaN	1724.0	798.0	950.0	2819.0	132.0	258.0	
13	supplementary table	1731.0	1189.0	186.0	1455.0	952.0	NaN	2064.0	136.0	320.0	
9	figure figure	2075.0	1750.0	268.0	2474.0	NaN	NaN	4245.0	90.0	266.0	

In [24]:
```
# Definindo nova lista de stopWords com palavras mais comuns
stopWords = set(stopwords.words('english') + list(palavrasFrequentes))
```

In [ ]:
```
#Montando a matriz Tf-idf final
def MontaTfidf(corpus, stopWords):
    vectorizer = TfidfVectorizer(stop_words=stopWords)
    X = vectorizer.fit_transform(corpus)
    df_Tfindf = pd.DataFrame(X.todense().tolist(), columns=vectorizer.get_feat
ure_names())
    return(df_Tfindf)
```

In [ ]:
```
# Gera matriz Tfidf e salva em hdf
df_Tfindf = MontaTfidf(df['Text'].values, stopWords)
df_Tfindf.to_hdf('TfidfTrain.hdf', 'main', format='fixed')
```

In [25]:
```
# Carrega matriz Tfidf
df_Tfindf = pd.read_hdf('TfidfTrain.hdf')
```

In [26]:
```
df_Tfindf.shape
```

Out[26]:
```
(3316, 164620)
```

In [27]:
```
df_Tfindf.head()
```

Out[27]:

	00	000	0000	0000000000000188	00000001	0000001	000000100	000001	000002	0000
0	0.0	0.017777	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
1	0.0	0.008309	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
2	0.0	0.008309	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
3	0.0	0.000000	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
4	0.0	0.005813	0.0	0.0	0.0	0.0	0.0	0.0	0.0	

5 rows × 164620 columns

In [28]:
```
# Concatena a matriz com as clases
df_Tfindf = pd.concat([df_Tfindf, df['Class']], axis=1, join = 'inner')
```

In [29]:
```
df_Tfindf.head()
```

Out[29]:

	00	000	0000	0000000000000188	00000001	0000001	000000100	000001	000002	0000
0	0.0	0.017777	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
1	0.0	0.008309	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
2	0.0	0.008309	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
3	0.0	0.000000	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
4	0.0	0.005813	0.0	0.0	0.0	0.0	0.0	0.0	0.0	

5 rows × 164621 columns

In [30]:
```
# Agrupa as palavras por classe para realizar feature selection
df_TfindfCount = df_Tfindf.groupby('Class').apply(lambda column: (column != 0)
.sum()).transpose()
df_TfindfCount = df_TfindfCount / df_Tfindf.groupby('Class').count().transpose
()
df_TfindfCount['Media'] = df_TfindfCount[df_TfindfCount.columns[0:9]].mean(1)
df_TfindfCount['Desvio'] = df_TfindfCount[df_TfindfCount.columns[0:9]].std(1)
df_TfindfCount['M_D'] = df_TfindfCount['Desvio'] / df_TfindfCount['Media']
df_TfindfCount['TotalC'] = (df_TfindfCount[df_TfindfCount.columns[0:9]] != 0).
sum(1)
```

```
C:\ProgramData\Anaconda3\lib\site-packages\pandas\core\generic.py:7389: Runti
meWarning: '<' not supported between instances of 'str' and 'float', sort ord
er is undefined for incomparable objects
  other.index, how=join, level=level, return_indexers=True)
```

In [31]:
```
df_TfindfCount[0:5]
```

Out[31]:

Class	0	1	2	3	4	5	6	
00	0.129433	0.119469	0.089888	0.193265	0.140496	0.216117	0.155462	0.1052
000	0.505319	0.519912	0.471910	0.525622	0.557851	0.670330	0.584034	0.6315
0000	0.000000	0.002212	0.000000	0.000000	0.000000	0.000000	0.004202	0.0000
0000000000000188	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.001050	0.0000
00000001	0.000000	0.002212	0.000000	0.001464	0.000000	0.003663	0.001050	0.0000

In [32]:
```
# Filtrando as palavras que aparecem em menos de 5% das classes.
Filtro1 = df_TfindfCount[df_TfindfCount['Media'] < 0.05]
Filtro1
```

Out[32]:

```
           Class         0         1         2         3         4         5         6    7
            0000  0.000000  0.002212  0.000000  0.000000  0.000000  0.000000  0.004202  0.0  0.
0000000000000188  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.001050  0.0  0.
        00000001  0.000000  0.002212  0.000000  0.001464  0.000000  0.003663  0.001050  0.0  0.
         0000001  0.001773  0.002212  0.000000  0.007321  0.000000  0.000000  0.002101  0.0  0.
       000000100  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.001050  0.0  0.
          000001  0.003546  0.000000  0.000000  0.002928  0.008264  0.021978  0.000000  0.0  0.
          000002  0.000000  0.002212  0.000000  0.001464  0.012397  0.000000  0.008403  0.0  0.
        00000397  0.000000  0.000000  0.000000  0.001464  0.000000  0.000000  0.000000  0.0  0.
          000005  0.001773  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.0  0.
          000007  0.003546  0.004425  0.000000  0.000000  0.000000  0.000000  0.005252  0.0  0.
         00000o0  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.001050  0.0  0.
           00001  0.005319  0.011062  0.011236  0.005857  0.000000  0.003663  0.010504  0.0  0.
         0000112  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.003151  0.0  0.
        00001311  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.001050  0.0  0.
      0000149311  0.000000  0.000000  0.000000  0.001464  0.000000  0.000000  0.000000  0.0  0.
         0000208  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.003151  0.0  0.
        00002644  0.001773  0.004425  0.000000  0.000000  0.004132  0.000000  0.004202  0.0  0.
           00003  0.001773  0.002212  0.000000  0.000000  0.000000  0.003663  0.000000  0.0  0.
        00003450  0.000000  0.002212  0.000000  0.000000  0.000000  0.000000  0.001050  0.0  0.
           00004  0.000000  0.002212  0.000000  0.000000  0.000000  0.000000  0.000000  0.0  0.
           00005  0.003546  0.002212  0.000000  0.001464  0.000000  0.000000  0.011555  0.0  0.
           00006  0.003546  0.000000  0.000000  0.000000  0.004132  0.000000  0.001050  0.0  0.
         0000614  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.003151  0.0  0.
         0000645  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.003151  0.0  0.
        00006559  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.003151  0.0  0.
           00008  0.001773  0.002212  0.000000  0.000000  0.000000  0.000000  0.001050  0.0  0.
         0000839  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.003151  0.0  0.
           00009  0.005319  0.002212  0.000000  0.001464  0.000000  0.000000  0.000000  0.0  0.
          000096  0.000000  0.000000  0.000000  0.001464  0.000000  0.000000  0.000000  0.0  0.
         0000965  0.000000  0.000000  0.000000  0.001464  0.000000  0.000000  0.000000  0.0  0.
             ...       ...       ...       ...       ...       ...       ...       ...  ...  .
             ˆ50  0.007092  0.000000  0.000000  0.004392  0.000000  0.007326  0.001050  0.0  0.
            ˆ500  0.000000  0.000000  0.000000  0.002928  0.000000  0.003663  0.000000  0.0  0.
           ˆ500â  0.001773  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.0  0.
            ˆ550  0.001773  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.0  0.
```

Class	0	1	2	3	4	5	6	7	
ˆ557	0.000000	0.002212	0.000000	0.000000	0.000000	0.000000	0.000000	0.0	0.
ˆ6	0.005319	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.0	0.
ˆ60	0.001773	0.000000	0.000000	0.004392	0.000000	0.000000	0.000000	0.0	0.
ˆ602	0.000000	0.002212	0.000000	0.000000	0.000000	0.000000	0.000000	0.0	0.
ˆ624	0.000000	0.002212	0.000000	0.000000	0.000000	0.000000	0.000000	0.0	0.
ˆ669	0.000000	0.002212	0.000000	0.000000	0.000000	0.000000	0.000000	0.0	0.
ˆ675	0.005319	0.000000	0.000000	0.013177	0.000000	0.000000	0.000000	0.0	0.
ˆ7	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.003151	0.0	0.
ˆ70	0.005319	0.002212	0.000000	0.001464	0.000000	0.000000	0.000000	0.0	0.
ˆ730	0.000000	0.002212	0.000000	0.000000	0.000000	0.000000	0.000000	0.0	0.
ˆ75	0.003546	0.000000	0.000000	0.000000	0.000000	0.000000	0.001050	0.0	0.
ˆ77	0.000000	0.002212	0.000000	0.000000	0.000000	0.000000	0.003151	0.0	0.
ˆ791	0.000000	0.002212	0.000000	0.000000	0.000000	0.000000	0.000000	0.0	0.
ˆ8	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.001050	0.0	0.
ˆ80	0.001773	0.000000	0.000000	0.002928	0.000000	0.007326	0.001050	0.0	0.
ˆ85	0.000000	0.002212	0.000000	0.000000	0.000000	0.000000	0.001050	0.0	0.
ˆ9	0.003546	0.000000	0.000000	0.002928	0.000000	0.000000	0.000000	0.0	0.
ˆ90	0.007092	0.000000	0.000000	0.004392	0.000000	0.000000	0.000000	0.0	0.
ˆ90â	0.001773	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.0	0.
ˆ91	0.000000	0.002212	0.000000	0.000000	0.000000	0.000000	0.000000	0.0	0.
ˆ97	0.000000	0.002212	0.000000	0.000000	0.000000	0.000000	0.003151	0.0	0.
ˆarg	0.001773	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.0	0.
ˆequal	0.000000	0.002212	0.000000	0.000000	0.000000	0.000000	0.000000	0.0	0.
ˆi	0.005319	0.000000	0.000000	0.001464	0.004132	0.007326	0.001050	0.0	0.
ˆiã	0.003546	0.000000	0.000000	0.000000	0.000000	0.007326	0.001050	0.0	0.
ˆã	0.001773	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.0	0.

158817 rows × 13 columns

Dessa forma, conseguimos exluir 97% das variáveis, sem perda significativa no modelo

In [33]:
```
# Excluindo as variáveis acima
df_TfindfCount = df_TfindfCount.drop(Filtro1.index.values)
```

In [35]:
```
# Com isso, temos uma matriz Tfindf muito menor, o que facilita na criação de
 modelos
df_TfindfCount.shape
```

Out[35]:
```
(5804, 13)
```

In [36]:
```
from sklearn.model_selection import train_test_split
```

In [37]:
```
variaveis = df_TfindfCount.iloc[:-1,:].index
X_treino, X_test, y_treino, y_test = train_test_split(df_Tfindf[variaveis].val
ues, df_Tfindf['Class'].values, test_size = 0.30)
```

Balanceando o dataset

In [38]:
```
# Removendo dados das clases majoritárias
from imblearn.under_sampling import TomekLinks
```

```
Using TensorFlow backend.
```

In [39]:
```
tl = TomekLinks(sampling_strategy=[0,1,3,4,7,8])
X_tl, y_tl = tl.fit_sample(X_treino, y_treino)
```

In [40]:
```
unique_elements, counts_elements = np.unique(y_treino, return_counts=True)
```

In [41]:
```
unique_elements2, counts_elements2 = np.unique(y_tl, return_counts=True)
```

In [42]:
```
# Aumentando a quantidade de registros das classes com poucas amostras
oversampling = np.where([y_treino == 2, y_treino == 7, y_treino == 8])[1]
valores = np.random.choice(oversampling, size=round(oversampling.shape[0]*0.6
), replace=False)
X_tl = np.append(X_tl, X_treino[valores], axis=0)
y_tl = np.append(y_tl, y_treino[valores], axis=0)
```

In [43]:
```
unique_elements3, counts_elements3 = np.unique(y_tl, return_counts=True)
```

In [44]:
```
# Criando novos dados através de SMOTE
from imblearn.over_sampling import SMOTE
```

In [45]:
```
classes = {2:180, 7:50, 8:100}
smote = SMOTE(sampling_strategy=classes)
X_sm, y_sm = smote.fit_sample(X_tl, y_tl)
```

In [46]:
```
unique_elements4, counts_elements4 = np.unique(y_sm, return_counts=True)
```

In [47]:
```
# Diminuindo a classe 6 que ainda está maior que as outras
indice = np.where(y_sm == 6)
excluir = indice[0].shape[0] - 550
valores = np.random.choice(indice[0], size=excluir, replace=False)
X_treino = np.delete(X_sm, valores, 0)
y_treino = np.delete(y_sm, valores)
```

In [48]:
```
unique_elements5, counts_elements5 = np.unique(y_treino, return_counts=True)
```

In [49]:
```
print('Classes originais')
counts_elements
```

```
Classes originais
```

Out[49]:
```
array([394, 316,  63, 482, 168, 190, 665,  13,  26], dtype=int64)
```

In [50]:
```
print('Classes após TomekLinks')
counts_elements2
```

```
Classes após TomekLinks
```

Out[50]:
```
array([364, 275,  63, 454, 151, 190, 665,  12,  25], dtype=int64)
```

In [51]:
```
print('Classes após Oversample')
counts_elements3
```

```
Classes após Oversample
```

Out[51]:
```
array([364, 275, 103, 454, 151, 190, 665,  20,  38], dtype=int64)
```

In [52]:
```
print('Classes após SMOTE')
counts_elements4
```

```
Classes após SMOTE
```

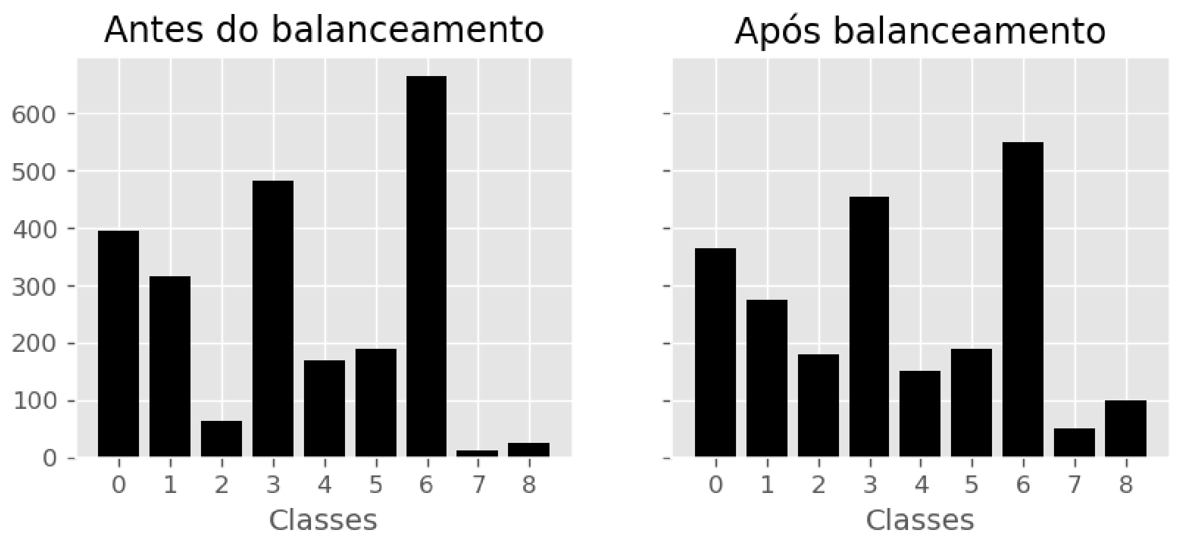
Out[52]:
```
array([364, 275, 180, 454, 151, 190, 665,  50, 100], dtype=int64)
```

In [53]:
```
print('Classes após Undersample')
counts_elements5
```

```
Classes após Undersample
```

Out[53]:
```
array([364, 275, 180, 454, 151, 190, 550,  50, 100], dtype=int64)
```

In [54]:
```
plt.style.use('ggplot')
fig, axes = plt.subplots(1,2, figsize=(8, 3), dpi = 120, squeeze = False, shar
ey='row')
vetor = [counts_elements, counts_elements5]
titulo = ['Antes do balanceamento', 'Após balanceamento']
k=0
for linha in axes:
    for ax in linha:
        ax.bar(np.arange(9), vetor[k], color='black')
        ax.set_xlabel('Classes'); # x label
        ax.set_title(titulo[k])
        #ax.set_xticklabels(['1','2','3','4','5','6','7','8','9'])
        ax.set_xticks(np.arange(9))
        k+=1

plt.show()
```

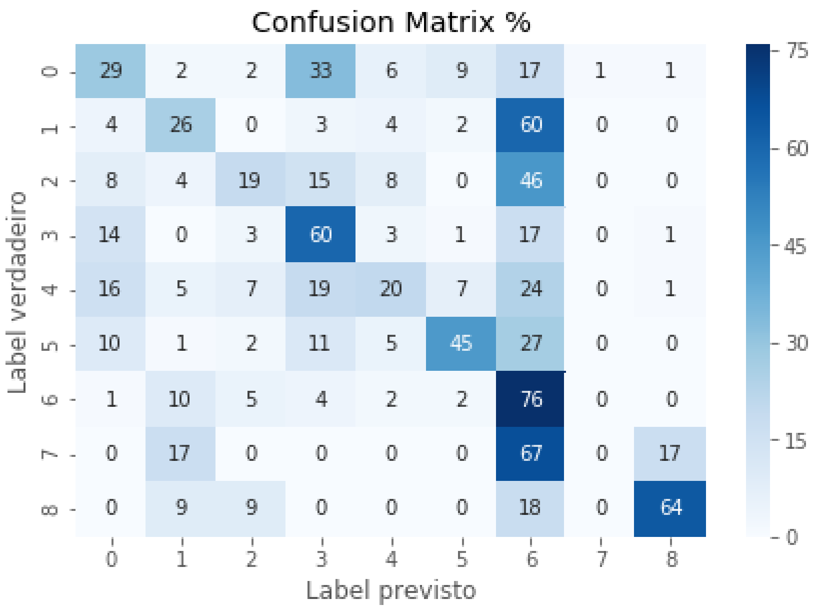


In [55]:
```
# Random Forest
from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import classification_report
from sklearn.metrics import confusion_matrix
from sklearn.model_selection import cross_val_score
import seaborn as sns
```

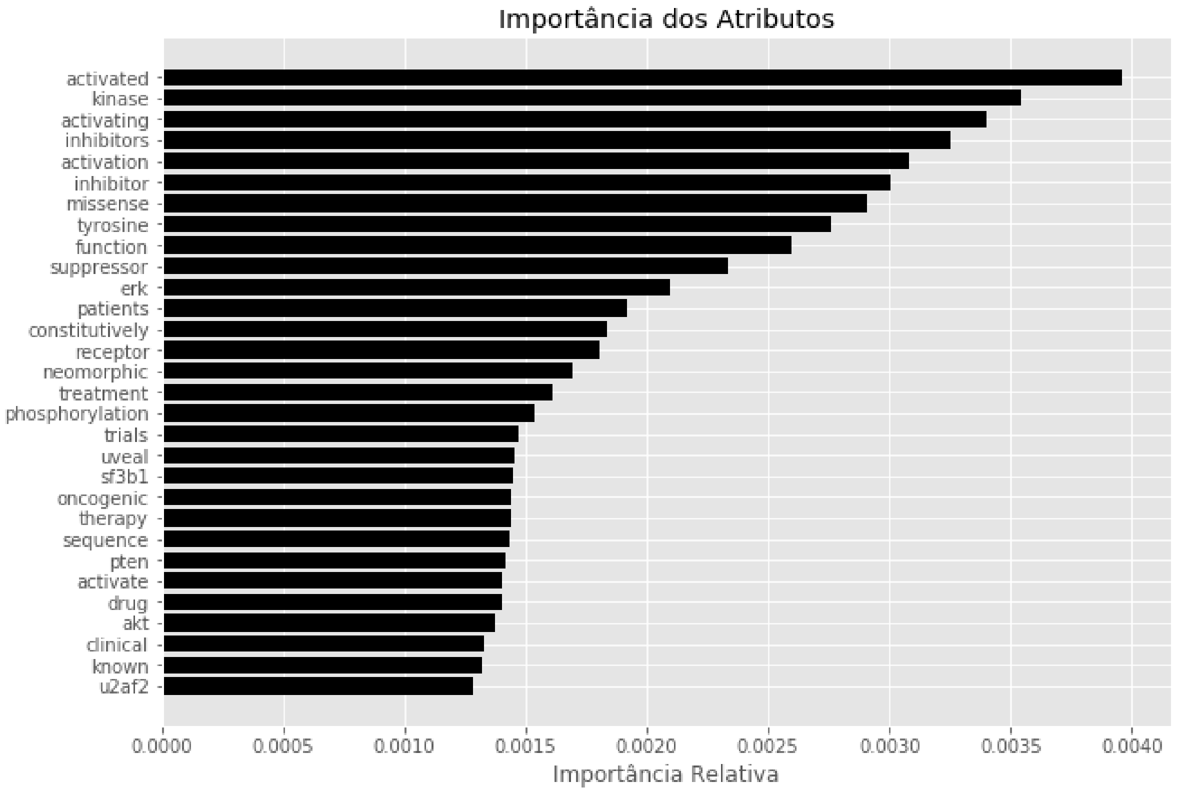
In [56]:
```
# Cria uma função para construir a Confusion Matrix de forma gráfica
def CriaConfusionMatrix(cm):
    #confusionMatrix = confusion_matrix(y_test, predictions)
    ConfusionMatrixNorm = np.around(cm / cm.sum(axis=1)[:, np.newaxis] * 100,
decimals=0)
    sns.heatmap(ConfusionMatrixNorm, annot=True,cmap=plt.cm.Blues)
    plt.tight_layout()
    plt.title('Confusion Matrix %')
    plt.ylabel('Label verdadeiro')
    plt.xlabel('Label previsto')
    return plt.show()
```

In [57]:
```
# Criando um modelo Random Forest para extraírmos as palavras mais relevantes
modeloRF = RandomForestClassifier()
modeloRF.fit(X_treino, y_treino)
# Score
scores = cross_val_score(modeloRF, X_treino, y_treino, cv = 5, scoring = 'accu
racy', n_jobs = -1)
# Imprimindo o resultado
print ("ExtraTreesClassifier -> Acurácia: Média = %0.3f Desvio Padrão = %0.3f"
% (np.mean(scores), np.std(scores)))

# Faz as predições
predictions = modeloRF.predict(X_test)
# Performande do modelo nos dados de teste
print("Avaliação do Modelo nos Dados de Teste")
print(classification_report(y_test, predictions))
# Confusion Matrix do Modelo Final
CriaConfusionMatrix(confusion_matrix(y_test, predictions))
```

```
ExtraTreesClassifier -> Acurácia: Média = 0.535 Desvio Padrão = 0.016
Avaliação do Modelo nos Dados de Teste
              precision    recall  f1-score   support

           0       0.45      0.29      0.36       170
           1       0.46      0.26      0.33       136
           2       0.14      0.19      0.16        26
           3       0.55      0.60      0.57       201
           4       0.31      0.20      0.24        74
           5       0.54      0.45      0.49        83
           6       0.52      0.76      0.61       287
           7       0.00      0.00      0.00         6
           8       0.54      0.64      0.58        11

    accuracy                           0.49       994
   macro avg       0.39      0.38      0.37       994
weighted avg       0.48      0.49      0.47       994
```



In [58]:
```
# Extraindo as importâncias
importances = modeloRF.feature_importances_
indices = np.argsort(importances)

# Obtém os índices
ind=[]
for i in indices:
    ind.append(variaveis[i])

# Plot da Importância dos Atributos
#plt.figure(1)
plt.figure(figsize=(10,7))
plt.title('Importância dos Atributos')
plt.barh(range(len(indices[-30:])), importances[indices[-30:]], color = 'blac
k', align = 'center')
plt.yticks(range(len(indices[-30:])),ind[-30:])
#plt.xlim([0,0.005])
plt.xlabel('Importância Relativa')
plt.show()
```



Como o projeto sugeria, vamos criar alguns modelos no keras

In [59]:
```
from keras.models import Sequential
from keras.layers import Dense, Dropout
from keras.optimizers import SGD
from keras.utils import to_categorical
from keras.wrappers.scikit_learn import KerasClassifier
```

In [60]:
```
# Transforma as variáveis em HotEncode
y_treinoHotEncode = to_categorical(y_treino)
y_testHotEncode = to_categorical(y_test)
```

In [61]:
```
# Dimensao de entrada
dimensao = X_treino.shape[1]
```

Vamos testar alguns modelos de redes, variando a otimização e topologia.

- Otimização:
  - Adam
  - SGD
  - RMSprop
- Topologia:
  - 2 e 3 camadas ocultas
  - Com e sem dropout para regularização

In [62]:
```
# Função que define a rede para fazermos o Grid Search
def CriaModeloKeras(numCamadas, numNeuronios, numDropout, otimizador):
    # Cria o modelo
    model = Sequential()
    # Camda de entrada
    model.add(Dense(numNeuronios, input_dim=dimensao, activation='relu'))
    if numDropout != 0: model.add(Dropout(numDropout))
    # Camada 2
    model.add(Dense(numNeuronios, activation='relu'))
    if numDropout != 0: model.add(Dropout(numDropout))
    # Camada 3
    if numCamadas == 3: model.add(Dense(numNeuronios, activation='relu'))
    if numDropout != 0 and numCamadas == 3: model.add(Dropout(numDropout))
    # Camada de saída
    model.add(Dense(9, activation='softmax'))

    # Compila o modelo
    model.compile(loss='categorical_crossentropy', optimizer=otimizador, metri
cs=['accuracy'])
    return model
```

In [66]:
```
# Função para o Grid Search
def GriSearchKeras(otimizador, numCamadas, numNeuronios, numDropout, batch_siz
e, epochs):
    acuracias = []
    parametros = []
    for camada in numCamadas:
        for neuronio in numNeuronios:
            for dropout in numDropout:
                for batch in batch_size:
                    for epoch in epochs:
                        modeloKeras = CriaModeloKeras(camada,neuronio,dropout,
otimizador)
                        modeloKeras.fit(X_treino, y_treinoHotEncode, epochs =
epoch, batch_size = batch, verbose=0)
                        scores = modeloKeras.evaluate(X_test, y_testHotEncode,
verbose=0)
                        acuracias.append(scores[1])
                        parametros.append(dict(Camadas=camada, Neuronios=neuro
nio, Dropout=dropout, Batch=batch, Epoch=epoch))
                        print("%s: %.1f%% (Camadas: %.0f | Neuronios: %.0f | D
ropout: %.1f | Batch: %.0f | Epoch: %.0f |)" % (modeloKeras.metrics_names[1],
scores[1]*100, camada, neuronio, dropout, batch, epoch))
    return acuracias, parametros
```

In [64]:
```
# Definindo os hyperparametros
optimizers = [SGD(lr = 0.01, momentum = 0.9, nesterov = True), 'adam','rmspro
p']

numCamadas = [2,3]
numNeuronios = [50,150]
numDropout = [0,0.5]
batch_size = [10, 20]
epochs = [50, 150]
```

In [65]:
```
# Testando o otimizador Stochastic gradient descent
acuraciasSGD, parametrosSGD = GriSearchKeras(optimizers[0], numCamadas, numNeu
ronios, numDropout, batch_size, epochs)
```

```
accuracy: 44.3% (Camadas: 2 | Neuronios: 50 | Dropout: 0.0 | Batch: 10 | Epoc
h: 50 |)
accuracy: 44.8% (Camadas: 2 | Neuronios: 50 | Dropout: 0.0 | Batch: 10 | Epoc
h: 150 |)
accuracy: 43.9% (Camadas: 2 | Neuronios: 50 | Dropout: 0.0| Batch: 20 | Epoc
h: 50 |)
accuracy: 46.1% (Camadas: 2 | Neuronios: 50 | Dropout: 0.0 | Batch: 20 | Epoc
h: 150 |)
accuracy: 45.5% (Camadas: 2 | Neuronios: 50 | Dropout: 0.5 | Batch: 10 | Epoc
h: 50 |)
accuracy: 48.0% (Camadas: 2 | Neuronios: 50 | Dropout: 0.5 | Batch: 10 | Epoc
h: 150 |)
accuracy: 49.0% (Camadas: 2 | Neuronios: 50 | Dropout: 0.5 | Batch: 20 | Epoc
h: 50 |)
accuracy: 47.8% (Camadas: 2 | Neuronios: 50 | Dropout: 0.5 | Batch: 20 | Epoc
h: 150 |)
accuracy: 46.8% (Camadas: 2 | Neuronios: 150 | Dropout: 0.0 | Batch: 10 | Epo
ch: 50 |)
accuracy: 46.4% (Camadas: 2 | Neuronios: 150 | Dropout: 0.0 | Batch: 10 | Epo
ch: 150 |)
accuracy: 46.9% (Camadas: 2 | Neuronios: 150 | Dropout: 0.0 | Batch: 20 | Epo
ch: 50 |)
accuracy: 48.0% (Camadas: 2 | Neuronios: 150 | Dropout: 0.0 | Batch: 20 | Epo
ch: 150 |)
accuracy: 49.5% (Camadas: 2 | Neuronios: 150 | Dropout: 0.5 | Batch: 10 | Epo
ch: 50 |)
accuracy: 50.6% (Camadas: 2 | Neuronios: 150 | Dropout: 0.5 | Batch: 10 | Epo
ch: 150 |)
accuracy: 51.4% (Camadas: 2 | Neuronios: 150 | Dropout: 0.5 | Batch: 20 | Epo
ch: 50 |)
accuracy: 49.5% (Camadas: 2 | Neuronios: 150 | Dropout: 0.5 | Batch: 20 | Epo
ch: 150 |)
accuracy: 44.4% (Camadas: 3 | Neuronios: 50 | Dropout: 0.0 | Batch: 10 | Epoc
h: 50 |)
accuracy: 46.8% (Camadas: 3 | Neuronios: 50 | Dropout: 0.0 | Batch: 10 | Epoc
h: 150 |)
accuracy: 47.2% (Camadas: 3 | Neuronios: 50 | Dropout: 0.0 | Batch: 20 | Epoc
h: 50 |)
accuracy: 44.3% (Camadas: 3 | Neuronios: 50 | Dropout: 0.0 | Batch: 20 | Epoc
h: 150 |)
accuracy: 45.7% (Camadas: 3 | Neuronios: 50 | Dropout: 0.5 | Batch: 10 | Epoc
h: 50 |)
accuracy: 49.4% (Camadas: 3 | Neuronios: 50 | Dropout: 0.5 | Batch: 10 | Epoc
h: 150 |)
accuracy: 47.1% (Camadas: 3 | Neuronios: 50 | Dropout: 0.5 | Batch: 20 | Epoc
h: 50 |)
accuracy: 47.8% (Camadas: 3 | Neuronios: 50 | Dropout: 0.5 | Batch: 20 | Epoc
h: 150 |)
accuracy: 47.5% (Camadas: 3 | Neuronios: 150 | Dropout: 0.0 | Batch: 10 | Epo
ch: 50 |)
accuracy: 48.5% (Camadas: 3 | Neuronios: 150 | Dropout: 0.0 | Batch: 10 | Epo
ch: 150 |)
accuracy: 48.4% (Camadas: 3 | Neuronios: 150 | Dropout: 0.0 | Batch: 20 | Epo
ch: 50 |)
accuracy: 46.9% (Camadas: 3 | Neuronios: 150 | Dropout: 0.0 | Batch: 20 | Epo
ch: 150 |)
accuracy: 48.0% (Camadas: 3 | Neuronios: 150 | Dropout: 0.5 | Batch: 10 | Epo
ch: 50 |)
accuracy: 51.0% (Camadas: 3 | Neuronios: 150 | Dropout: 0.5 | Batch: 10 | Epo
ch: 150 |)
accuracy: 48.7% (Camadas: 3 | Neuronios: 150 | Dropout: 0.5 | Batch: 20 | Epo
ch: 50 |)
accuracy: 48.5% (Camadas: 3 | Neuronios: 150 | Dropout: 0.5 | Batch: 20 | Epo
ch: 150 |)
```

In [67]:
```
# Testando o otimizador Adam
acuraciasAdam, parametrosAdam = GriSearchKeras(optimizers[1], numCamadas, numN
euronios, numDropout, batch_size, epochs)
```

```
accuracy: 46.7% (Camadas: 2 | Neuronios: 50 | Dropout: 0.0 | Batch: 10 | Epoc
h: 50 |)
accuracy: 47.5% (Camadas: 2 | Neuronios: 50 | Dropout: 0.0 | Batch: 10 | Epoc
h: 150 |)
accuracy: 48.4% (Camadas: 2 | Neuronios: 50 | Dropout: 0.0 | Batch: 20 | Epoc
h: 50 |)
accuracy: 46.9% (Camadas: 2 | Neuronios: 50 | Dropout: 0.0 | Batch: 20 | Epoc
h: 150 |)
accuracy: 49.3% (Camadas: 2 | Neuronios: 50 | Dropout: 0.5 | Batch: 10 | Epoc
h: 50 |)
accuracy: 47.0% (Camadas: 2 | Neuronios: 50 | Dropout: 0.5 | Batch: 10 | Epoc
h: 150 |)
accuracy: 49.1% (Camadas: 2 | Neuronios: 50 | Dropout: 0.5 | Batch: 20 | Epoc
h: 50 |)
accuracy: 48.9% (Camadas: 2 | Neuronios: 50 | Dropout: 0.5 | Batch: 20 | Epoc
h: 150 |)
accuracy: 47.0% (Camadas: 2 | Neuronios: 150 | Dropout: 0.0 | Batch: 10 | Epo
ch: 50 |)
accuracy: 46.1% (Camadas: 2 | Neuronios: 150 | Dropout: 0.0 | Batch: 10 | Epo
ch: 150 |)
accuracy: 48.3% (Camadas: 2 | Neuronios: 150 | Dropout: 0.0 | Batch: 20 | Epo
ch: 50 |)
accuracy: 47.7% (Camadas: 2 | Neuronios: 150 | Dropout: 0.0 | Batch: 20 | Epo
ch: 150 |)
accuracy: 47.6% (Camadas: 2 | Neuronios: 150 | Dropout: 0.5 | Batch: 10 | Epo
ch: 50 |)
accuracy: 48.1% (Camadas: 2 | Neuronios: 150 | Dropout: 0.5 | Batch: 10 | Epo
ch: 150 |)
accuracy: 48.5% (Camadas: 2 | Neuronios: 150 | Dropout: 0.5 | Batch: 20 | Epo
ch: 50 |)
accuracy: 48.9% (Camadas: 2 | Neuronios: 150 | Dropout: 0.5 | Batch: 20 | Epo
ch: 150 |)
accuracy: 48.6% (Camadas: 3 | Neuronios: 50 | Dropout: 0.0 | Batch: 10 | Epoc
h: 50 |)
accuracy: 46.1% (Camadas: 3 | Neuronios: 50 | Dropout: 0.0 | Batch: 10 | Epoc
h: 150 |)
accuracy: 47.6% (Camadas: 3 | Neuronios: 50 | Dropout: 0.0 | Batch: 20 | Epoc
h: 50 |)
accuracy: 46.2% (Camadas: 3 | Neuronios: 50 | Dropout: 0.0 | Batch: 20 | Epoc
h: 150 |)
accuracy: 47.7% (Camadas: 3 | Neuronios: 50 | Dropout: 0.5 | Batch: 10 | Epoc
h: 50 |)
accuracy: 47.6% (Camadas: 3 | Neuronios: 50 | Dropout: 0.5 | Batch: 10 | Epoc
h: 150 |)
accuracy: 48.9% (Camadas: 3 | Neuronios: 50 | Dropout: 0.5 | Batch: 20 | Epoc
h: 50 |)
accuracy: 49.7% (Camadas: 3 | Neuronios: 50 | Dropout: 0.5 | Batch: 20 | Epoc
h: 150 |)
accuracy: 47.6% (Camadas: 3 | Neuronios: 150 | Dropout: 0.0 | Batch: 10 | Epo
ch: 50 |)
accuracy: 46.4% (Camadas: 3 | Neuronios: 150 | Dropout: 0.0 | Batch: 10 | Epo
ch: 150 |)
accuracy: 46.8% (Camadas: 3 | Neuronios: 150 | Dropout: 0.0 | Batch: 20 | Epo
ch: 50 |)
accuracy: 46.4% (Camadas: 3 | Neuronios: 150 | Dropout: 0.0 | Batch: 20 | Epo
ch: 150 |)
accuracy: 48.4% (Camadas: 3 | Neuronios: 150 | Dropout: 0.5 | Batch: 10 | Epo
ch: 50 |)
accuracy: 46.9% (Camadas: 3 | Neuronios: 150 | Dropout: 0.5 | Batch: 10 | Epo
ch: 150 |)
accuracy: 49.2% (Camadas: 3 | Neuronios: 150 | Dropout: 0.5 | Batch: 20 | Epo
ch: 50 |)
accuracy: 47.7% (Camadas: 3 | Neuronios: 150 | Dropout: 0.5 | Batch: 20 | Epo
ch: 150 |)
```

In [79]:
```
# Testando o otimizador RMSProp
acuraciasRMSProp, parametrosRMSProp = GriSearchKeras(optimizers[2], numCamadas
, numNeuronios, numDropout, batch_size, epochs)
```

```
accuracy: 46.5% (Camadas: 2 | Neuronios: 50 | Dropout: 0.0 | Batch: 10 | Epoc
h: 50 |)
accuracy: 46.2% (Camadas: 2 | Neuronios: 50 | Dropout: 0.0 | Batch: 10 | Epoc
h: 150 |)
accuracy: 47.3% (Camadas: 2 | Neuronios: 50 | Dropout: 0.0 | Batch: 20 | Epoc
h: 50 |)
accuracy: 46.3% (Camadas: 2 | Neuronios: 50 | Dropout: 0.0 | Batch: 20 | Epoc
h: 150 |)
accuracy: 49.0% (Camadas: 2 | Neuronios: 50 | Dropout: 0.5 | Batch: 10 | Epoc
h: 50 |)
accuracy: 47.5% (Camadas: 2 | Neuronios: 50 | Dropout: 0.5 | Batch: 10 | Epoc
h: 150 |)
accuracy: 49.3% (Camadas: 2 | Neuronios: 50 | Dropout: 0.5 | Batch: 20 | Epoc
h: 50 |)
accuracy: 48.1% (Camadas: 2 | Neuronios: 50 | Dropout: 0.5 | Batch: 20 | Epoc
h: 150 |)
accuracy: 45.8% (Camadas: 2 | Neuronios: 150 | Dropout: 0.0 | Batch: 10 | Epo
ch: 50 |)
accuracy: 43.3% (Camadas: 2 | Neuronios: 150 | Dropout: 0.0 | Batch: 10 | Epo
ch: 150 |)
accuracy: 47.2% (Camadas: 2 | Neuronios: 150 | Dropout: 0.0 | Batch: 20 | Epo
ch: 50 |)
accuracy: 47.1% (Camadas: 2 | Neuronios: 150 | Dropout: 0.0 | Batch: 20 | Epo
ch: 150 |)
accuracy: 47.4% (Camadas: 2 | Neuronios: 150 | Dropout: 0.5 | Batch: 10 | Epo
ch: 50 |)
accuracy: 48.0% (Camadas: 2 | Neuronios: 150 | Dropout: 0.5 | Batch: 10 | Epo
ch: 150 |)
accuracy: 49.7% (Camadas: 2 | Neuronios: 150 | Dropout: 0.5 | Batch: 20 | Epo
ch: 50 |)
accuracy: 46.1% (Camadas: 2 | Neuronios: 150 | Dropout: 0.5 | Batch: 20 | Epo
ch: 150 |)
accuracy: 46.9% (Camadas: 3 | Neuronios: 50 | Dropout: 0.0 | Batch: 10 | Epoc
h: 50 |)
accuracy: 45.6% (Camadas: 3 | Neuronios: 50 | Dropout: 0.0 | Batch: 10 | Epoc
h: 150 |)
accuracy: 47.5% (Camadas: 3 | Neuronios: 50 | Dropout: 0.0 | Batch: 20 | Epoc
h: 50 |)
accuracy: 46.5% (Camadas: 3 | Neuronios: 50 | Dropout: 0.0 | Batch: 20 | Epoc
h: 150 |)
accuracy: 48.5% (Camadas: 3 | Neuronios: 50 | Dropout: 0.5 | Batch: 10 | Epoc
h: 50 |)
accuracy: 47.4% (Camadas: 3 | Neuronios: 50 | Dropout: 0.5 | Batch: 10 | Epoc
h: 150 |)
accuracy: 48.1% (Camadas: 3 | Neuronios: 50 | Dropout: 0.5 | Batch: 20 | Epoc
h: 50 |)
accuracy: 46.3% (Camadas: 3 | Neuronios: 50 | Dropout: 0.5 | Batch: 20 | Epoc
h: 150 |)
accuracy: 45.7% (Camadas: 3 | Neuronios: 150 | Dropout: 0.0 | Batch: 10 | Epo
ch: 50 |)
accuracy: 45.9% (Camadas: 3 | Neuronios: 150 | Dropout: 0.0 | Batch: 10 | Epo
ch: 150 |)
accuracy: 46.9% (Camadas: 3 | Neuronios: 150 | Dropout: 0.0 | Batch: 20 | Epo
ch: 50 |)
accuracy: 46.4% (Camadas: 3 | Neuronios: 150 | Dropout: 0.0 | Batch: 20 | Epo
ch: 150 |)
accuracy: 47.8% (Camadas: 3 | Neuronios: 150 | Dropout: 0.5 | Batch: 10 | Epo
ch: 50 |)
accuracy: 46.4% (Camadas: 3 | Neuronios: 150 | Dropout: 0.5 | Batch: 10 | Epo
ch: 150 |)
accuracy: 47.6% (Camadas: 3 | Neuronios: 150 | Dropout: 0.5 | Batch: 20 | Epo
ch: 50 |)
accuracy: 47.9% (Camadas: 3 | Neuronios: 150 | Dropout: 0.5 | Batch: 20 | Epo
ch: 150 |)
```

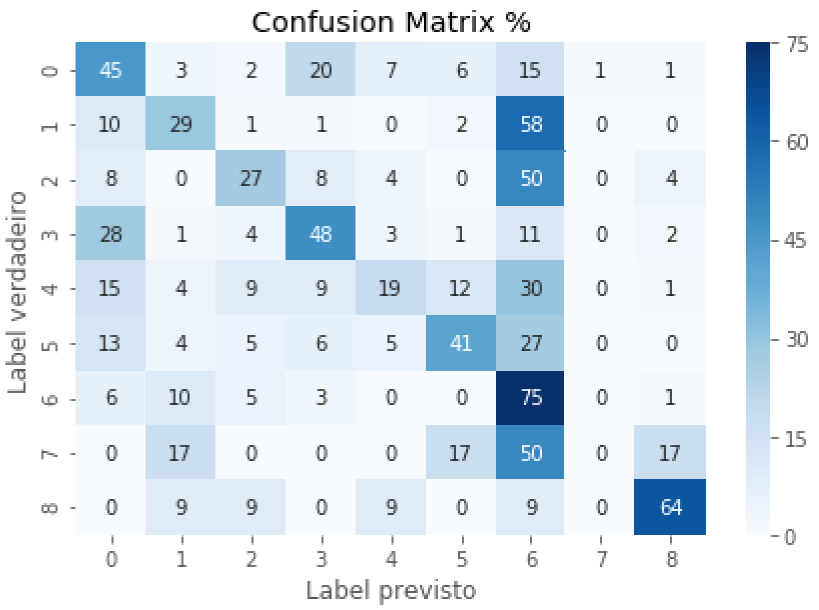
In [84]:
```
BestSGD = max(acuraciasSGD)
BestSGDParameters = parametrosSGD[acuraciasSGD.index(BestSGD)]
print('Modelo SGD: %.2f%%' % (BestSGD*100))
print(BestSGDParameters)
print('\n')

BestAdam = max(acuraciasAdam)
BestAdamParameters = parametrosAdam[acuraciasAdam.index(BestAdam)]
print('Modelo Adam: %.2f%%' % (BestAdam*100))
print(BestAdamParameters)
print('\n')

BestRMSProp = max(acuraciasRMSProp)
BestRMSPropParameters = parametrosRMSProp[acuraciasRMSProp.index(BestRMSProp)]
print('Modelo RMSProp: %.2f%%' % (BestRMSProp*100))
print(BestRMSPropParameters)
```

```
Modelo SGD: 51.41%
{'Camadas': 2, 'Neuronios': 150, 'Dropout': 0.5, 'Batch': 20, 'Epoch': 50}


Modelo Adam: 49.70%
{'Camadas': 3, 'Neuronios': 50, 'Dropout': 0.5, 'Batch': 20, 'Epoch': 150}


Modelo RMSProp: 49.70%
{'Camadas': 2, 'Neuronios': 150, 'Dropout': 0.5, 'Batch': 20, 'Epoch': 50}
```

In [85]:
```
# Recriando o melhor modelo
modeloKeras = CriaModeloKeras(2,150,0.5,optimizers[0])
modeloKeras.fit(X_treino, y_treinoHotEncode, epochs = 50, batch_size = 20, ver
bose=0)
```

Out[85]:
```
<keras.callbacks.callbacks.History at 0x1d59c806648>
```

In [90]:
```
# Confusion matrix
predictions = modeloKeras.predict(X_test)
# Confusion Matrix do Modelo Final
CriaConfusionMatrix(confusion_matrix(y_test, predictions.argmax(axis=1)))
```



	0	1	2	3	4	5	6	7	8
0	45	3	2	20	7	6	15	1	1
1	10	29	1	1	0	2	58	0	0
2	8	0	27	8	4	0	50	0	4
3	28	1	4	48	3	1	11	0	2
4	15	4	9	9	19	12	30	0	1
5	13	4	5	6	5	41	27	0	0
6	6	10	5	3	0	0	75	0	1
7	0	17	0	0	0	17	50	0	17
8	0	9	9	0	9	0	9	0	64

Conclusão:

O modelo conseguiu classificar aproximadamente 50% das classes corretamente. Dado que é um problema multiclasses com 9 classes e a probabilidade de classificação ao acaso é de 11%, o modelo consegue agregar valor. Apesar disso, sua acurácia ainda está longe da ideal. Para aumenta-la, poderíamos aplicar maior tratamento ao texto, utilizar outras técnicas como word2vec e até mesmo tentarmos rede neurais maiores, o que exigiria maior capacidade de treinamento.

In [ ]: