In [90]:
```
import pandas as pd
import requests
from zipfile import ZipFile
from io import BytesIO
import numpy as np
pd.set_option('display.max_columns', None)
```

In [105…
```
response = requests.get("https://archive.ics.uci.edu/ml/machine-learning-databases/0
files = ZipFile(BytesIO(response.content))
df = pd.read_csv(files.open("dataset_diabetes/diabetic_data.csv"))
```

In [106…
```
#variavel para pegar as colunas do df em fomra de lista
cols = df.columns

#variavel para selecionar colunas numéricas do df
num_cols = df._get_numeric_data().columns

#variavel que diminui as colunas numéricas das colunas, obtendo-se as colunas categó
cat_col = list(set(cols) - set(num_cols))
```

In [107…
```
#laço for para valores únicos categóricos
for coluna in cat_col:
    print(coluna + str(df[coluna].unique()) + '\n')

#laço for para valores únicos numéricos
for col in num_cols:
    print( str(type(col)) + col + str(df[col].unique()) + '\n')
```

```
readmitted['NO' '>30' '<30']

glipizide-metformin['No' 'Steady']

troglitazone['No' 'Steady']

glyburide['No' 'Steady' 'Up' 'Down']

glimepiride['No' 'Steady' 'Down' 'Up']

chlorpropamide['No' 'Steady' 'Down' 'Up']

tolazamide['No' 'Steady' 'Up']

max_glu_serum['None' '>300' 'Norm' '>200']

payer_code['?' 'MC' 'MD' 'HM' 'UN' 'BC' 'SP' 'CP' 'SI' 'DM' 'CM' 'CH' 'PO' 'WC' 'OT'
 'OG' 'MP' 'FR']

rosiglitazone['No' 'Steady' 'Up' 'Down']

citoglipton['No']

change['No' 'Ch']

metformin-pioglitazone['No' 'Steady']

diag_3['?' '255' 'V27' '403' '250' 'V45' '38' '486' '996' '197' '250.6' '427'
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 '482' '401' '250.41' '585' '781' '278' '998' '568' '682' '618' '250.02'
 '305' '707' '496' '599' '715' '424' '518' '553' '794' '411' 'V42' '531'
 '511' '490' '562' '250.8' '250.7' '250.52' '784' '491' '581' '420' '8'
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 '724' '730' '789' '131' '250.82' '999' '41' '493' '250.03' '753' '786'
 '529' 'E888' '425' '595' '303' '560' '711' '492' '332' '296' '438' '362'
 '250.4' '654' '244' 'V70' '737' '625' '681' '250.51' '404' 'V10' '810'
 '280' '440' '785' '588' '569' '272' '997' '250.43' '918' '584' '54' '788'
 '426' '722' '250.92' '196' '461' '535' '787' '891' '284' '458' '648'
 '780' '182' '285' '593' '413' '664' '564' '201' '356' 'V15' '292' '782'
 '473' '455' 'E932' '357' '348' '294' '250.23' '459' 'E878' '437' '733'
 '507' '525' '250.53' '397' '572' '805' '453' '331' '736' '402' '591'
 '576' '465' '533' '703' '349' '315' '658' '608' '578' '716' '382' '300'
 '282' '571' '536' '596' '287' '644' 'V11' '558' 'E885' '162' '198' '218'
 '412' '396' 'V14' '570' '433' 'E934' '882' '288' '577' '443' '729' '836'
 '295' '799' '281' '304' '153' '410' '616' '250.83' '601' '291' '75' '512'
 '660' '250.5' '598' '337' '574' '653' 'V58' '311' '415' '386' '602' '790'
 '112' '873' '620' '436' '70' '155' '138' '663' '530' '710' '42' '342'
 '250.91' 'E884' '515' '307' '704' '728' '731' '583' '238' '441' '293'
 '573' '532' '290' '594' '319' '250.13' '250.12' '519' '346' '380' '135'
 '642' '698' '924' '905' 'E933' '555' '309' 'E879' '286' '565' '752' '580'
 '446' '444' '344' '252' '35' '813' '394' '301' '575' '258' 'V17' '802'
 '435' '746' 'V12' '709' '881' 'E935' '139' '250.81' '718' '365' '202'
 '334' '185' '398' 'V44' '517' 'E849' '614' '466' '626' '250.9' '368'
 '605' '883' '289' '478' '617' '429' '442' 'V25' '866' '610' '557' '959'
 'E942' '94' '920' '345' '313' '379' '79' '516' '586' '821' '600' '242'
 '373' '592' 'V64' '487' '253' '706' 'E947' '117' '340' 'E950' '656'
 'E949' '590' 'V09' '250.22' '934' '694' '203' '250.93' '995' '726' '923'
 '958' '275' 'E929' '211' 'V18' 'V66' '199' '665' '53' '279' '522' '791'
 '890' '456' 'E938' 'E816' '122' '721' 'V65' '136' '480' '423' 'E920'
 '793' '647' '537' '351' '845' '336' '274' '719' '945' '434' '494' '227'
 '157' '208' '174' 'V57' '812' '734' '150' 'V23' '447' '692' '228' 'V16'
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 '907' '270' '310' '266' '387' 'E931' '783' '245' '607' '355' 'E930' '705'
 '372' '369' '611' '283' 'V46' '110' '867' 'E956' '251' '250.2' '820'
 '712' '695' '567' '343' '723' 'V08' '273' '623' '807' '451' '495' '701'
 '34' 'V53' '314' '472' 'E945' '11' '189' '534' '354' '333' 'V54' '277'
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 '259' 'E870' 'E980' '383' '204' '696' '566' '727' '47' 'E943' '358' '191'
 '965' '921' '432' '27' 'E861' '758' '477' '524' '751' '652' '556' '188'
 '825' '919' '732' '908' '951' '962' '685' 'E850' 'E944' '527' '341' '693'
 '250.1' 'V49' '860' '323' 'V55' '579' '508' '969' '205' '462' 'E880'
 '680' '697' '826' '200' '457' '717' '738' '742' '735' '235' '308' '725'
 '241' '824' '464' '260' '917' '239' '661' '892' '261' 'E883' '943' '744'
 'E936' '796' '318' '967' '350' '854' 'E905' '9' '741' 'E941' '170' '643'
 '317' '759' '909' 'V22' '831' '713' '180' '801' '360' '359' '501' '335'
 '250.11' '306' '811' '690' 'V02' '271' '214' '847' '543' 'V63' '906'
 '842' '686' '445' '808' '861' 'E852' '220' 'E887' 'E858' '915' '970'
 '256' '747' '395' '243' '815' '481' '5' 'E927' '297' '299' '851' '864'
 '922' '384' 'E876' '225' '158' 'E937' '871' '88' '966' 'E917' 'E812'
 'V62' 'E924' '604' '233' 'E916' '377' '797' 'V72' '172' '7' '421' '852'
 'E819' '972' '916' '956' '3' 'E965' '173' '193' '154' '347' '862' '250.3'
 '987' '470' '262' 'E855' '161' '115' '179' '910' '312' '17' '460' '265'
 '66' '163' 'V60' '870' 'E906' '514' '944' '844' '417' '152' '183' '991'
 '216' '385' '164' '935' '510' '814' '485' '850' '250.21' 'E919' '872'
 '195' '431' '597' '933' '171' '884' '156' '868' '483' 'E815' '542' 'V61'
 '853' '374' 'E881' 'E882' 'E822' '192' '754' '327' '523' '500' 'V85'
 '992' '657' '684' '603' 'E826' '550' '913' '376' '755' '361' '186' '720'
 '250.31' '674' '911' 'E813' '226' '365.44' 'E818' '146' '955' 'E894'
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 'V86' 'V03' '338' '989' '388' 'E966' '111' 'E922' '123' '757' 'E901'
 '141' '268' 'E892' '649' '702' '948' '223' '484' 'E886' '838' '928' '236'
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 '217' '877' '391' 'E825' '952' '669' '875' 'E900' '215' '538' '980' '834'
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 '971']

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 '482' '382' 'V65' '572' '283' '78' '250.81' '576' '432' '595' '295' 'V12'
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 '397' '250.23' 'E932' '201' '301' '723' '614' '568' '861' 'V57' '724'
 '189' '297' '453' 'E888' '730' '354' '451' '738' 'E939' '805' 'V43' '155'
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 '404' '681' '470' '279' '281' '531' '443' '799' '337' '311' '719' 'E944'
 '423' 'E870' '465' 'E849' '782' '481' '480' 'V23' '199' '79' '438' '348'
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 '349' '485' '208' '922' '431' '296' 'E934' '753' 'E935' '386' '728' '607'
 'E915' '344' '716' '289' '191' '873' '850' '611' '377' '352' '616' 'V17'
 '136' '455' '933' 'E885' '860' '513' '603' '484' '223' 'V72' '291' '151'
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 '528' '683' '953' '457' '501' 'E900' 'V09' '522' '919' '461' '506' '193'
 '483' 'E936' '717' '802' '335' 'V54' '320' '945' '906' '239' '454' '826'
 '823' 'E941' '226' '795' '684' '844' '250.33' '308' '615' '588' '712'
 '663' '706' '833' '741' '713' '533' 'E884' '586' '555' '755' 'E928' '742'
 '869' '962' 'V11' '543' '373' '870' '913' '152' '810' '965' '907' '908'
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 '521' '917' 'E965' '524' '916' 'E813' '173' '238' '137' '514' '312' '837'
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 '75' 'E927' 'E905' '183' '379' 'E917' '163' 'E868' '495' '747' '989'
 'E854' '240' '832' '605' '602' '644' 'V16' '35' 'V70' '376' '266' 'E918'
 '619' '477' '656' '46' '883' '171' 'V13' '698' '842' 'E850' '800' '269'
 '664' 'E887' '952' '164' 'E881' '527' '685' '366' '836' '27' 'V63' '865'
 '793' '232' '990' '52' '831' '327' '542' '806' '972' '862' 'E829' 'E919'
 '944' 'E916' '963' '316' '645' '347' 'V85' '374' 'V02' '748' '256' '186'
 '866' '975' '96' '395' '262' 'E819' '654' '994' '318' 'E826' '879' '674'
 '641' '822' '145' '797' '353' 'E938' 'E816' '948' '987' '99' '192'
 '250.3' 'E906' '534' '115' 'E818' 'E980' '360' '338' '529' '871' '750'
 '212' '302' '955' '141' '88' 'V25' '215' '350' 'V50' 'V03' 'E853' 'E968'
 'E882' '140' '703' '991' '893' 'E821' '235' 'V69' '670' '195' 'V55' '388'
 '268' '894' '114' '260' '853' '7' '880' 'V86' '180' 'E945' '523' '863'
 '649' '270' '665' '460' '942' '364' '66' 'E883' '123' '884' 'V60' '843'
 '927']

diabetesMed['No' 'Yes']

diag_1['250.83' '276' '648' '8' '197' '414' '428' '398' '434' '250.7' '157'
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 '277' '584' '462' '473' '411' '174' '486' '998' '511' '432' '626' '295'
 '196' '250.6' '618' '182' '845' '423' '808' '250.4' '722' '403' '250.11'
 '784' '707' '440' '151' '715' '997' '198' '564' '812' '38' '590' '556'
```

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 '578' '250.32' '433' 'V58' '569' '185' '536' '255' '250.13' '599' '558'
 '574' '491' '560' '244' '250.03' '577' '730' '188' '824' '250.8' '332'
 '562' '291' '296' '510' '401' '263' '438' '70' '250.02' '493' '642' '625'
 '571' '738' '593' '250.42' '807' '456' '446' '575' '250.41' '820' '515'
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 '426' '388' '607' '337' '82' '531' '596' '288' '656' '573' '492' '220'
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 '404' '823' '532' '416' '346' '535' '453' '250' '595' '211' '303'
 '250.01' '852' '218' '782' '540' '457' '285' '431' '340' '550' '54' '351'
 '601' '723' '555' '153' '443' '380' '204' '424' '241' '358' '694' '331'
 '345' '681' '447' '290' '158' '579' '436' '335' '309' '654' '805' '799'
 '292' '183' '78' '851' '458' '586' '311' '892' '305' '293' '415' '591'
 '794' '803' '79' '655' '429' '278' '658' '598' '729' '585' '444' '604'
 '727' '214' '552' '284' '680' '708' '41' '644' '481' '821' '413' '437'
 '968' '756' '632' '359' '275' '512' '781' '420' '368' '522' '294' '825'
 '135' '304' '320' '250.31' '669' '868' '496' '250.43' '826' '567' '3'
 '203' '53' '251' '565' '161' '495' '49' '250.1' '297' '663' '576' '355'
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 '11' '751' '716' '250.3' '199' '464' '580' '836' '664' '283' '813' '966'
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 '7' '736' '233' '42' '250.5' '397' '395' '201' '421' '253' '250.92' '600'
 '494' '977' '39' '659' '312' '614' '647' '652' '646' '274' '861' '425'
 '527' '451' '485' '217' '250.53' '442' '970' '193' '160' '322' '581'
 '475' '623' '374' '582' '568' '465' '801' '237' '376' '150' '461' '913'
 '226' '617' '987' '641' '298' '790' '336' '362' '228' '513' '383' '746'
 '353' '911' '506' '873' '155' '860' '534' '802' '141' 'V45' '396' '310'
 '341' '242' '719' '239' '533' '616' '519' '301' 'V66' '5' '989' '230'
 '385' '300' '853' '871' '570' '848' '463' '9' '934' '250.21' '236' '361'
 '594' '501' '810' '643' '430' '528' '205' '791' '983' '992' '490' '172'
 '171' '622' '306' '863' '864' '474' '660' '759' '356' '634' '967' '551'
 '695' '187' '732' '747' '323' '308' '370' '252' '152' '846' '164' '365'
 '718' '48' '266' '720' '94' '344' '797' '170' '878' '904' 'V56' '882'
 '843' '709' '973' '454' '686' '939' '487' '229' '991' '483' '357' '692'
 '796' '693' '935' '936' '800' '920' 'V26' '261' '307' '262' '250.9' '831'
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metformin-rosiglitazone['No' 'Steady']

tolbutamide['No' 'Steady']

medical_specialty['Pediatrics-Endocrinology' '?' 'InternalMedicine'
 'Family/GeneralPractice' 'Cardiology' 'Surgery-General' 'Orthopedics'
 'Gastroenterology' 'Surgery-Cardiovascular/Thoracic' 'Nephrology'
 'Orthopedics-Reconstructive' 'Psychiatry' 'Emergency/Trauma'
 'Pulmonology' 'Surgery-Neuro' 'Obsterics&Gynecology-GynecologicOnco'
 'ObstetricsandGynecology' 'Pediatrics' 'Hematology/Oncology'
 'Otolaryngology' 'Surgery-Colon&Rectal' 'Pediatrics-CriticalCare'
 'Endocrinology' 'Urology' 'Psychiatry-Child/Adolescent'
```

```
 'Pediatrics-Pulmonology' 'Neurology' 'Anesthesiology-Pediatric'
 'Radiology' 'Pediatrics-Hematology-Oncology' 'Psychology' 'Podiatry'
 'Gynecology' 'Oncology' 'Pediatrics-Neurology' 'Surgery-Plastic'
 'Surgery-Thoracic' 'Surgery-PlasticwithinHeadandNeck' 'Ophthalmology'
 'Surgery-Pediatric' 'Pediatrics-EmergencyMedicine'
 'PhysicalMedicineandRehabilitation' 'InfectiousDiseases' 'Anesthesiology'
 'Rheumatology' 'AllergyandImmunology' 'Surgery-Maxillofacial'
 'Pediatrics-InfectiousDiseases' 'Pediatrics-AllergyandImmunology'
 'Dentistry' 'Surgeon' 'Surgery-Vascular' 'Osteopath'
 'Psychiatry-Addictive' 'Surgery-Cardiovascular' 'PhysicianNotFound'
 'Hematology' 'Proctology' 'Obstetrics' 'SurgicalSpecialty' 'Radiologist'
 'Pathology' 'Dermatology' 'SportsMedicine' 'Speech' 'Hospitalist'
 'OutreachServices' 'Cardiology-Pediatric' 'Perinatology'
 'Neurophysiology' 'Endocrinology-Metabolism' 'DCPTEAM' 'Resident']

repaglinide['No' 'Up' 'Steady' 'Down']

acetohexamide['No' 'Steady']

weight['?' '[75-100)' '[50-75)' '[0-25)' '[100-125)' '[25-50)' '[125-150)'
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glyburide-metformin['No' 'Steady' 'Down' 'Up']

race['Caucasian' 'AfricanAmerican' '?' 'Other' 'Asian' 'Hispanic']

insulin['No' 'Up' 'Steady' 'Down']

A1Cresult['None' '>7' '>8' 'Norm']

pioglitazone['No' 'Steady' 'Up' 'Down']

glimepiride-pioglitazone['No' 'Steady']

examide['No']

glipizide['No' 'Steady' 'Up' 'Down']

miglitol['No' 'Steady' 'Down' 'Up']

metformin['No' 'Steady' 'Up' 'Down']

acarbose['No' 'Steady' 'Up' 'Down']

age['[0-10)' '[10-20)' '[20-30)' '[30-40)' '[40-50)' '[50-60)' '[60-70)'
 '[70-80)' '[80-90)' '[90-100)']

gender['Female' 'Male' 'Unknown/Invalid']

nateglinide['No' 'Steady' 'Down' 'Up']

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 19 27]

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 75 72 74]

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21 18 19]

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```

In [108…

```python
#valores a serem excluídos
drop_values = ["?","Unknown/Invalid"]
```

In [109…

```python
df
```

Out[109…

	encounter_id	patient_nbr	race	gender	age	weight	admission_type_id	dischar
0	2278392	8222157	Caucasian	Female	[0-10)	?	6	
1	149190	55629189	Caucasian	Female	[10-20)	?	1	
2	64410	86047875	AfricanAmerican	Female	[20-30)	?	1	
3	500364	82442376	Caucasian	Male	[30-40)	?	1	
4	16680	42519267	Caucasian	Male	[40-50)	?	1	
...	...	...	...	...	...	...	...	
101761	443847548	100162476	AfricanAmerican	Male	[70-80)	?	1	
101762	443847782	74694222	AfricanAmerican	Female	[80-90)	?	1	
101763	443854148	41088789	Caucasian	Male	[70-80)	?	1	
101764	443857166	31693671	Caucasian	Female	[80-90)	?	2	

	encounter_id	patient_nbr	race	gender	age	weight	admission_type_id	dischar
101765	443867222	175429310	Caucasian	Male	[70-80)	?	1	

101766 rows × 50 columns

In [110…

```
#lógica para excluir linhas que possuem valores na lista drop_values
df = df[~df.isin(drop_values).any(axis=1)]

cols = df.columns
```

In [111…

```
#variavel para selecionar colunas numéricas do df
num_cols = df._get_numeric_data().columns

#variavel que diminui as colunas numéricas das colunas, obtendo-se as colunas categó
cat_col = list(set(cols) - set(num_cols))

#laço for para valores únicos categóricos
for coluna in cat_col:
    print(coluna + str(df[coluna].unique()) + '\n')

#laço for para valores únicos numéricos
for col in num_cols:
    print( str(type(col)) + col + str(df[col].unique()) + '\n')
```

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troglitazone['No']

glyburide['No' 'Steady' 'Up' 'Down']

glimepiride['No' 'Steady' 'Down' 'Up']

chlorpropamide['No']

tolazamide['No']

max_glu_serum['None']

payer_code['UN' 'CP' 'DM' 'BC' 'MC' 'HM' 'OT' 'MD' 'CM' 'SP' 'WC']

rosiglitazone['No' 'Steady']

citoglipton['No']

change['Ch' 'No']

metformin-pioglitazone['No']

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 '996' '584' '578' '593' '305' '348' '333' '427' '414' '285' '599' '394'
 '682' '250.6' 'E878' '511' '158' '492' 'E812' '402' '591' '455' '530'
 '197' '411' '274' '404' '496' 'E849' '458' '425' '416' 'E942' '790' '491'
 '272' '280' '486' '218' 'E879' '789' '998' '287' '357' '617' '202' '719'
 '515' '397' '571' '787' '574' '721' '250.02' '443' '135' '728' '250.8'
 '707' 'E885' '196' '295' '410' '997' '250.13' 'E935' '518' '517' '412'
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 '426' '867' 'V42' '453' '278' '553' '537' 'E947' '478' '152' '596' '459'
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 'E939' '482' 'V43' 'E917' '585' '250.42' 'V45' '674' 'V27' '568' '311'
 'E931' '211' 'V58' '252' '162' '540' 'V09' 'E944' '738' '289' '714' '256'
 '112' 'E934' '138' '201' '730' '729' '250.43' '153' 'V15' '560' '327'
 '726' '588' '236' 'V85' '611' '296' '456' '799' '533' '457' '535' '433'
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 '438']

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 '233' '585' '277' '453' '136' '590' '154' '250.11' '250.51' '784' '211'
 '459' 'V10' '883' '250.92' '188' '787' '304' '79' '289' '623' '473' '245'
 '70' '196' 'V15' '156' '378' '864' '963' 'E932' 'V58' '153' '442' 'V43'
 '327' '924' 'E917' '625' '785' '456' '620' '718' '723' '412' 'E816' '205'
 'E928' '214' '434' '746' 'E934' '715' 'E881' 'E941' 'E888' '998' '151'
 'E936' '9' '626' '920' '997' '532' '731' '250.13' '719' '850' '816' '455'
 '594' '295' '278' '781' '204' '753' '550' 'V45' '745' '458' '807' '331'
 '756' '296' '812' '348' '435' '193' '250.2' 'V85' '722' '440' '332' '555']

diabetesMed['Yes' 'No']

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 'V55' 'V58' '599' '225' '591' '491' '578' '276' '891' '562' '437' '733'
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metformin-rosiglitazone['No']

tolbutamide['No']

medical_specialty['Surgery-General' 'Family/GeneralPractice' 'Cardiology' 'Psychiatr
y'
 'InternalMedicine' 'ObstetricsandGynecology' 'Dentistry' 'Pediatrics']

repaglinide['No' 'Steady' 'Up']

acetohexamide['No']

weight['[75-100)' '[50-75)' '[100-125)' '[125-150)' '[25-50)' '[150-175)'
 '[175-200)' '[0-25)']

glyburide-metformin['No']

race['Caucasian' 'AfricanAmerican' 'Other' 'Asian']

insulin['Steady' 'No' 'Down' 'Up']
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A1Cresult['None' 'Norm' '>8' '>7']

pioglitazone['No' 'Steady' 'Up' 'Down']

glimepiride-pioglitazone['No']

examide['No']

glipizide['Steady' 'No' 'Up' 'Down']

miglitol['No']

metformin['No' 'Steady' 'Up' 'Down']

acarbose['No' 'Steady']

age['[70-80)' '[80-90)' '[60-70)' '[40-50)' '[50-60)' '[90-100)' '[20-30)'
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gender['Female' 'Male']

nateglinide['No' 'Steady']

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```

```
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  97708986 113392368]

<class 'str'>admission_type_id[3 1 2 5]

<class 'str'>discharge_disposition_id[ 3 11  1  6  5  7 13  4  2 18]

<class 'str'>admission_source_id[ 1  5  7  4  6 17]

<class 'str'>time_in_hospital[10  6  2  3  4  1  5 11  8  7 14  9 12 13]

<class 'str'>num_lab_procedures[ 65  73  58  33   5  63  75  46   1  50  45  41  47
61  52  70  54  59
  71  69   4  66  76  53  23  44  72  32  79  84  62  67  60  49  21  42
  86  36  27  80  10  51  64  68  43  55  12  56  40  77  35  25  22  78
  57  30  82  48  38  24  81   8  29  39  31  34  74  28  87  18  37  16
  85   7  14  20  83   2  93  15  92  19  11 105  13  88  26  17  89]

<class 'str'>num_procedures[1 0 3 4 2 6 5]

<class 'str'>num_medications[28 16 12  7 11 20 15 10 21 23 17  9 18  8 26 25 31 13 1
4  5 22 44  4 27
 24  3  6 19 32 40 33 39 41 29 30 42 43 36 58 34 55  1  2 52 57 46]

<class 'str'>number_outpatient[ 1  0  4  2  3  5  6 14 10  9  8  7 11 13 15]

<class 'str'>number_emergency[ 1  0  3  2  6  4  5 11]

<class 'str'>number_inpatient[ 3  0  6  1  5  2  4  9 10  7]

<class 'str'>number_diagnoses[9 7 6 8 5 3 4]
```

In [112…

```
df.shape
```

Out[112…

```
(1043, 50)
```

In [113…

```
#lista para colunas a serem excluídas
colunas_excluidas = ['payer_code'
,'medical_specialty'
,'admission_type_id'
,'admission_source_id'
,'discharge_disposition_id'
,'patient_nbr']

df = df.drop(colunas_excluidas, axis = 1)
```

In [114…

```
#colunas diagnoticos para o tipo string
df['diag_1'] = df['diag_1'].astype(pd.StringDtype())
df['diag_2'] = df['diag_2'].astype(pd.StringDtype())
df['diag_3'] = df['diag_3'].astype(pd.StringDtype())
```

In [115…

```
#atribuição do diconarioa de valores para equalizar numericamente as variaveis
df['glipizide-metformin'] = df['glipizide-metformin'].map({'No': 0}) #['No']
df['change'] = df['change'].map({'No': 0, 'Ch': 1}) #['Ch' 'No']
df['tolbutamide'] = df['tolbutamide'].map({'No': 0}) #['No']
df['examide'] = df['examide'].map({'No': 0}) #['No']
df['pioglitazone'] = df['pioglitazone'].map({'No': 0, 'Steady': 1,'Up': 2, 'Down': 3
df['diabetesMed'] = df['diabetesMed'].map({'No': 0, 'Yes': 1}) #['Yes' 'No']
df['citoglipton'] = df['citoglipton'].map({'No': 0}) #['No']
df['insulin'] = df['insulin'].map({'Steady': 0, 'No': 1,'Down': 2, 'Up': 3}) #['Stea
df['troglitazone'] = df['troglitazone'].map({'No': 0}) #['No']
df['glimepiride-pioglitazone'] = df['glimepiride-pioglitazone'].map({'No': 0}) #['No
df['glyburide-metformin'] = df['glyburide-metformin'].map({'No': 0}) #['No']
df['metformin-pioglitazone'] = df['metformin-pioglitazone'].map({'No': 0}) #['No']
df['miglitol'] = df['miglitol'].map({'No': 0}) #['No']
df['glyburide'] = df['glyburide'].map({'No': 0, 'Steady': 1,'Up': 2, 'Down':3}) #['N
df['tolazamide'] = df['tolazamide'].map({'No': 0}) #['No']
df['max_glu_serum'] = df['max_glu_serum'].map({'None': 0, 'Norm': 1,'>200': 2, '>300
df['nateglinide'] = df['nateglinide'].map({'No': 0, 'Steady': 1}) #['No' 'Steady']
df['metformin-rosiglitazone'] = df['metformin-rosiglitazone'].map({'No': 0}) #['No']
df['glimepiride'] = df['glimepiride'].map({'No': 0, 'Steady': 1,'Down': 2, 'Up': 3})
df['metformin'] = df['metformin'].map({'No': 0, 'Steady': 1,'Up': 2, 'Down': 3}) #['
df['A1Cresult'] = df['A1Cresult'].map({'None': 0, 'Norm': 1,'>8': 2, '>7': 3}) #['No
df['chlorpropamide'] = df['chlorpropamide'].map({'No': 0}) #['No']
df['acetohexamide'] = df['acetohexamide'].map({'No': 0}) #['No']
df['rosiglitazone'] = df['rosiglitazone'].map({'No': 0, 'Steady': 1})
df['glipizide'] = df['glipizide'].map({'Steady': 0, 'No': 1,'Up': 2, 'Down': 3})
df['acarbose'] = df['acarbose'].map({'No': 0, 'Steady': 1})
df['repaglinide'] = df['repaglinide'].map({'No': 0, 'Steady': 1,'Up': 2})
df['readmitted'] = df['readmitted'].map({'NO': 0, '<30': 1,'>30': 1})
df["gender"] = df['gender'].map({'Male': 0, 'Female': 1})
df["age"] = df['age'].map({'[0-10)': 0, '[10-20)': 1, '[20-30)': 2, '[30-40)': 3, '[
df['race'] = df['race'].map({'Caucasian': 0, 'AfricanAmerican': 1,'Asian': 2, 'Hispa
df["weight"] = df['weight'].map({'[0-25)': 0, '[25-50)': 1, '[50-75)': 2, '[75-100)'
```

In [117…

```
df = df.dropna()
```

In [121…

```
#lista de atribuição das patologias
Circulatory = np.arange(390,460).tolist() + [785]
Circulatory_str = [str(elemento) for elemento in Circulatory]

Respiratory = np.arange(460,520).tolist() + [786]
Respiratory_str = [str(elemento) for elemento in Respiratory]
```

```
Digestive = np.arange(520,580).tolist() + [787]
Digestive_str = [str(elemento) for elemento in Digestive]

Injury = np.arange(800,1000).tolist() + [786]
Injury_str = [str(elemento) for elemento in Injury]

Musculoskeletal = np.arange(710,740).tolist() + [786]
Musculoskeletal_str = [str(elemento) for elemento in Musculoskeletal]

Genitourinary = np.arange(580,630).tolist() +  [788]
Genitourinary_str = [str(elemento) for elemento in Genitourinary]

Neoplasms = np.arange(140,240).tolist()
Neoplasms_str = [str(elemento) for elemento in Neoplasms]

Other = np.arange(240,250).tolist() + np.arange(251,280).tolist() + [780,781,784,790
Other_str = [str(elemento) for elemento in Other]
```

In [122…

```
#atribuição das patologias dentre as colunas de diagnostico
df.loc[df['diag_1'].str.startswith('250'), 'diag_1'] = 'Diabetes'
df.loc[df['diag_2'].str.startswith('250'), 'diag_2'] = 'Diabetes'
df.loc[df['diag_3'].str.startswith('250'), 'diag_3'] = 'Diabetes'

df.loc[df['diag_1'].isin(Circulatory_str), 'diag_1'] = 'Circulatory'
df.loc[df['diag_1'].isin(Respiratory_str), 'diag_1'] = 'Respiratory'
df.loc[df['diag_1'].isin(Digestive_str), 'diag_1'] = 'Digestive'
df.loc[df['diag_1'].isin(Injury_str), 'diag_1'] = 'Injury'
df.loc[df['diag_1'].isin(Musculoskeletal_str), 'diag_1'] = 'Musculoskeletal'
df.loc[df['diag_1'].isin(Genitourinary_str), 'diag_1'] = 'Genitourinary'
df.loc[df['diag_1'].isin(Neoplasms_str), 'diag_1'] = 'Neoplasms'

df.loc[df['diag_2'].isin(Circulatory_str), 'diag_2'] = 'Circulatory'
df.loc[df['diag_2'].isin(Respiratory_str), 'diag_2'] = 'Respiratory'
df.loc[df['diag_2'].isin(Digestive_str), 'diag_2'] = 'Digestive'
df.loc[df['diag_2'].isin(Injury_str), 'diag_2'] = 'Injury'
df.loc[df['diag_2'].isin(Musculoskeletal_str), 'diag_2'] = 'Musculoskeletal'
df.loc[df['diag_2'].isin(Genitourinary_str), 'diag_2'] = 'Genitourinary'
df.loc[df['diag_2'].isin(Neoplasms_str), 'diag_2'] = 'Neoplasms'

df.loc[df['diag_3'].isin(Circulatory_str), 'diag_3'] = 'Circulatory'
df.loc[df['diag_3'].isin(Respiratory_str), 'diag_3'] = 'Respiratory'
df.loc[df['diag_3'].isin(Digestive_str), 'diag_3'] = 'Digestive'
df.loc[df['diag_3'].isin(Injury_str), 'diag_3'] = 'Injury'
df.loc[df['diag_3'].isin(Musculoskeletal_str), 'diag_3'] = 'Musculoskeletal'
df.loc[df['diag_3'].isin(Genitourinary_str), 'diag_3'] = 'Genitourinary'
df.loc[df['diag_3'].isin(Neoplasms_str), 'diag_3'] = 'Neoplasms'

patology = ["Circulatory","Respiratory","Digestive","Injury","Musculoskeletal","Geni

df.loc[~df['diag_1'].isin(patology), 'diag_1'] = 'Other'
df.loc[~df['diag_2'].isin(patology), 'diag_2'] = 'Other'
df.loc[~df['diag_3'].isin(patology), 'diag_3'] = 'Other'
```

In [123…

```
#verificação da atribuiçãode valores
colunas_excluidas_2 = ['encounter_id']
df = df.drop(colunas_excluidas_2, axis = 1)

len(df["diag_1"].unique()) == len(df["diag_2"].unique()) == len(df["diag_3"].unique(

#laço for para atribuição
diags = ['diag_1','diag_2','diag_3']
```

```
for diag in diags:
    df[diag] = df[diag].map({'Circulatory': 0, 'Respiratory': 1,'Digestive': 2, 'Inj
                , 'Musculoskeletal': 4, 'Genitourinary': 5, 'Neoplasms': 6, 'Other':

df['age'] = df['age'].astype(int)
```

In [126…

```
#importação da biblioteca para plotagem e exploração
from collections import Counter
import matplotlib.pyplot as plt

#slice das variaveis
gender = Counter(df["gender"])
gender
```

Out[126…

```
Counter({1: 508, 0: 513})
```

In [127…

```
age = Counter(df["age"])
age
```

Out[127…

```
Counter({7: 305, 8: 171, 6: 255, 4: 68, 5: 177, 2: 18, 3: 25, 0: 1, 1: 1})
```

In [128…

```
weight = Counter(df["weight"])
weight
```

Out[128…

```
Counter({3: 431, 2: 270, 4: 220, 5: 46, 1: 26, 6: 16, 7: 6, 0: 6})
```

In [129…

```
race = Counter(df["race"])
race
```

Out[129…

```
Counter({0: 977, 1: 30, 4: 13, 2: 1})
```

In [130…

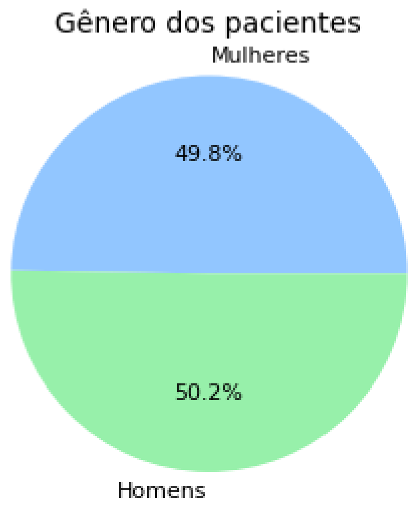
```
race = Counter(df["race"])
race
```

Out[130…

```
Counter({0: 977, 1: 30, 4: 13, 2: 1})
```

In [131…

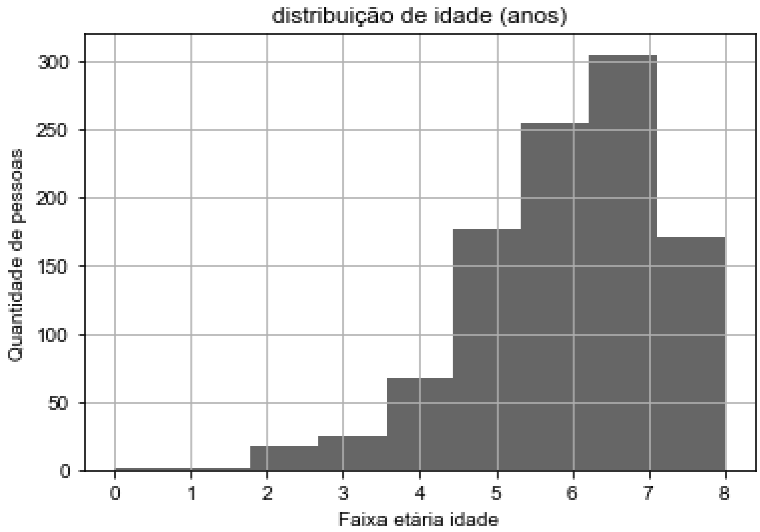
```
plt.style.use('seaborn-pastel')
plt.pie(gender.values(), labels = ["Mulheres","Homens"],
autopct = '%1.1f%%', textprops={'fontsize': 11})
plt.axis("image")
plt.title("Gênero dos pacientes", fontsize=14,pad =12)
plt.show()
```

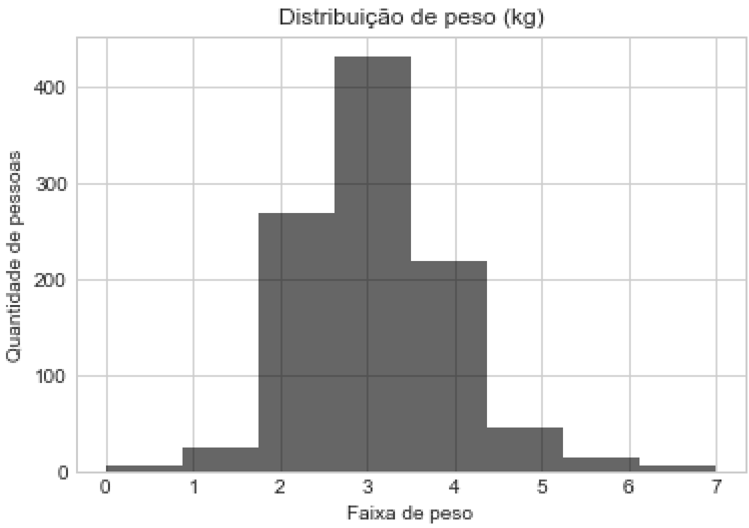


In [132…

```
df.age.hist(bins=9, color = 'black', alpha = 0.6)
plt.style.use('seaborn-whitegrid')
plt.xlabel("Faixa etária idade")
plt.ylabel("Quantidade de pessoas")
plt.title("distribuição de idade (anos)")
plt.show()

df.weight.hist(bins=8, color = 'black', alpha = 0.6)
plt.style.use('seaborn-whitegrid')
plt.xlabel("Faixa de peso")
plt.ylabel("Quantidade de pessoas")
plt.title("Distribuição de peso (kg)")
plt.show()
```





In [133…

```
#slice dataframe pela variavel target
df_readmitted = df.loc[df['readmitted'] == 1 ]
df_not_readmitted = df.loc[df['readmitted'] == 0]

#slice do genero nos dataframes
gender_not_readmitted = Counter(df_not_readmitted["gender"])
gender_not_readmitted
gender_readmitted = Counter(df_readmitted["gender"])
gender_readmitted

plt.style.use('seaborn-pastel')
plt.pie(gender_readmitted.values(), labels = ["Mulheres","Homens"],
autopct = '%1.1f%%', textprops={'fontsize': 11})
plt.axis("image")
plt.title("Gênero dos pacientes readmitidos", fontsize=14,pad =12)
plt.show()

plt.style.use('seaborn-pastel')
plt.pie(gender_not_readmitted.values(), labels = ["Mulheres","Homens"],
autopct = '%1.1f%%', textprops={'fontsize': 11})
plt.axis("image")
plt.title("Gênero dos pacientes não readmitidos", fontsize=14,pad =12)
plt.show()

race_readmitted = Counter(df_readmitted["race"])
race_readmitted
race_not_readmitted = Counter(df_not_readmitted["race"])
race_not_readmitted
weight_readmitted = Counter(df_not_readmitted["weight"])
weight_readmitted
weight_not_readmitted = Counter(df_not_readmitted["weight"])
weight_not_readmitted

plt.style.use('seaborn-whitegrid')
plt.bar(['M','F'], gender_readmitted.values())
plt.ylabel('Número de pacientes')
plt.xlabel('Raça')
plt.title('pacientes por sexo - readmitidos')
plt.show()

plt.style.use('seaborn-whitegrid')
plt.bar(['M','F'], gender_not_readmitted.values())
plt.ylabel('Número de pacientes')
plt.xlabel('Raça')
plt.title('pacientes por sexo - não readmitidos')
```

```
plt.show()

plt.style.use('seaborn-whitegrid')
plt.bar(list(race_readmitted.keys()), race_readmitted.values())
plt.ylabel('Número de pacientes')
plt.xlabel('Raça')
plt.title('pacientes por raça - readmitidos')
plt.show()

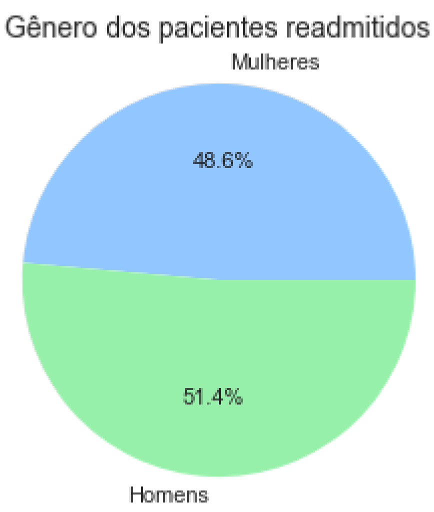
plt.style.use('seaborn-whitegrid')
plt.bar(list(race_not_readmitted.keys()), race_not_readmitted.values())
plt.ylabel('Número de pacientes')
plt.xlabel('Raça')
plt.title('pacientes por raça - não readmitidos')
plt.show()

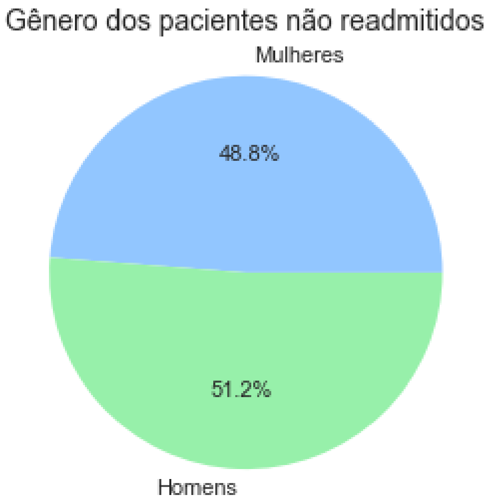
plt.style.use('seaborn-whitegrid')
plt.bar(['M','F'], gender_readmitted.values())
plt.ylabel('Número de pacientes')
plt.xlabel('Raça')
plt.title('pacientes por sexo - readmitidos')
plt.show()

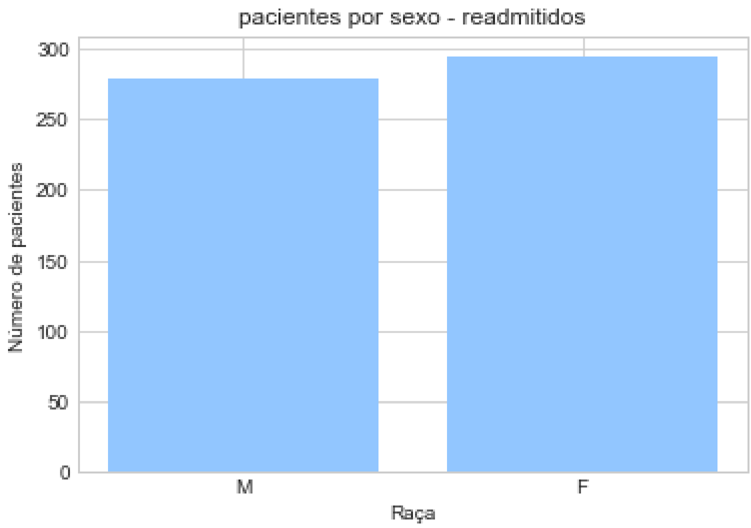
plt.style.use('seaborn-whitegrid')
plt.bar(['M','F'], gender_not_readmitted.values())
plt.ylabel('Número de pacientes')
plt.xlabel('Raça')
plt.title('pacientes por sexo - não readmitidos')
plt.show()

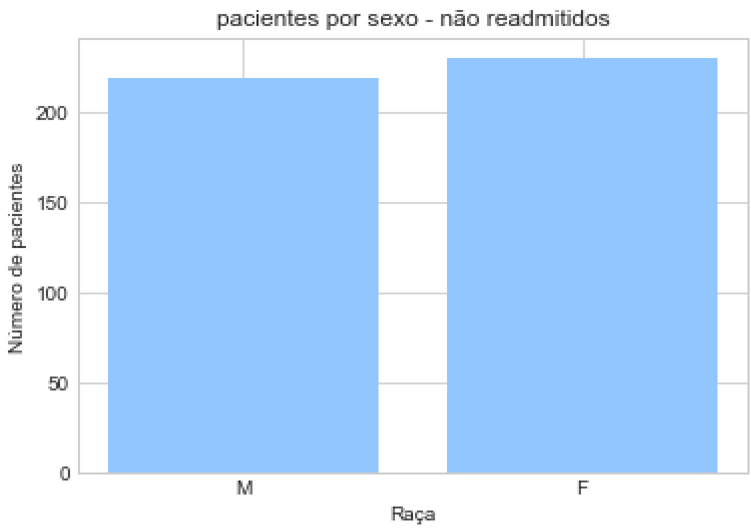
plt.style.use('seaborn-whitegrid')
plt.bar(list(weight_readmitted.keys()), weight_readmitted.values())
plt.ylabel('Número de pacientes')
plt.xlabel('Peso (kg)')
plt.title('Pacientes por peso (kg) - readmitidos')
plt.show()

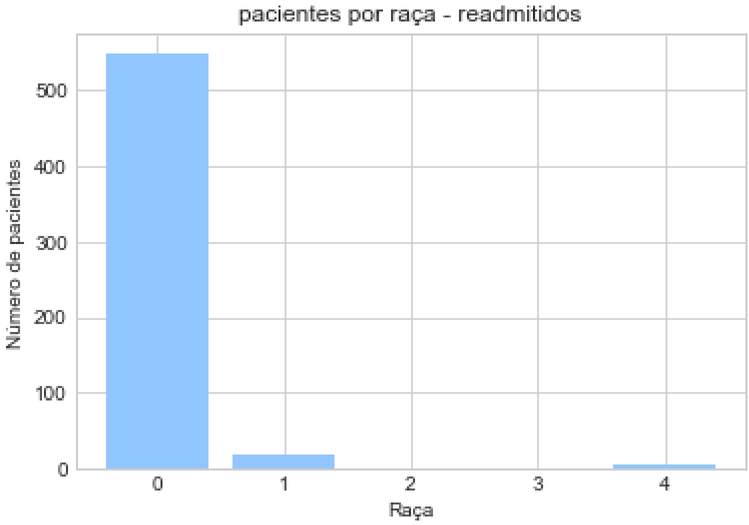
plt.style.use('seaborn-whitegrid')
plt.bar(list(weight_not_readmitted.keys()), weight_not_readmitted.values())
plt.ylabel('Número de pacientes')
plt.xlabel('Peso (kg)')
plt.title('Pacientes por peso (kg) - não readmitidos')
plt.show()
```

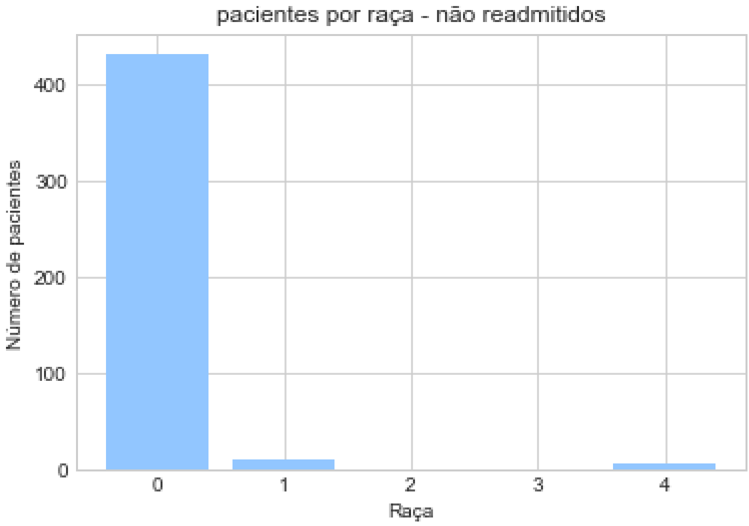


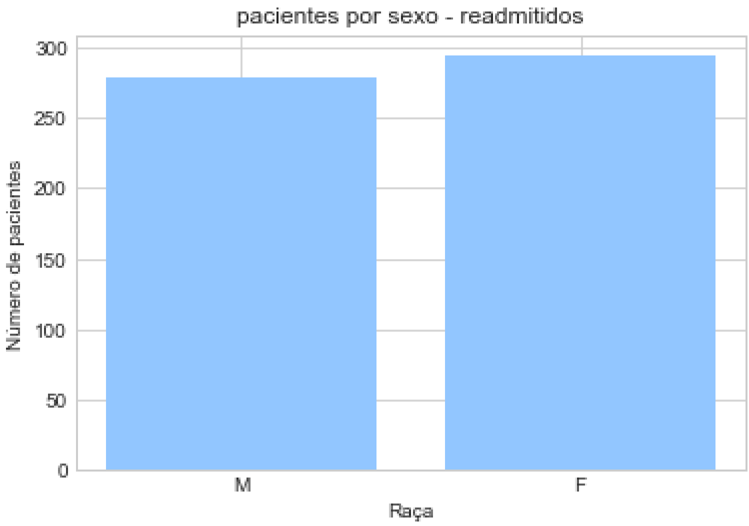

Gênero dos pacientes não readmitidos
Mulheres
48.8%
51.2%
Homens

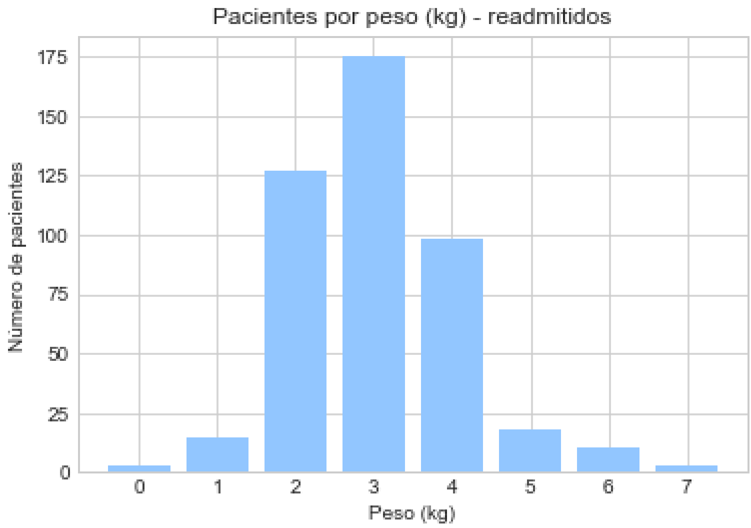

pacientes por sexo - readmitidos
Número de pacientes
300
250
200
150
100
50
0
M
F
Raça

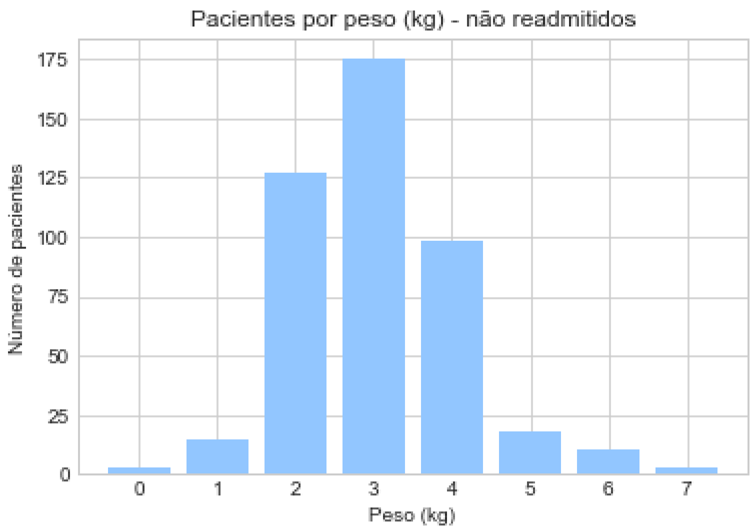

pacientes por sexo - não readmitidos
Número de pacientes
200
150
100
50
0
M
F
Raça


pacientes por raça - readmitidos
Número de pacientes
0
100
200
300
400
500
0
1
2
3
4
Raça


pacientes por raça - não readmitidos
Número de pacientes
0
100
200
300
400
0
1
2
3
4
Raça


pacientes por sexo - readmitidos
Número de pacientes
0
50
100
150
200
250
300
M
F
Raça





In [134…

```
from sklearn.model_selection import train_test_split
from sklearn.metrics import classification_report, accuracy_score

#separação dados de treinno e teste
X = df.drop('readmitted',axis=1).values
y = df['readmitted'].values
X_train,X_test,y_train,y_test = train_test_split(X,y,test_size=0.3,random_state=0)
```

In [135…

```
#aplicação algoritmo KNN
from sklearn.neighbors import KNeighborsClassifier
```

```
knn = KNeighborsClassifier()
knn = knn.fit(X_train, y_train)
print("Acurácia: ", knn.score(X_train, y_train))
tp_knn = knn.predict(X_test)
print("Acurácia de previsão: ", accuracy_score(y_test, tp_knn))
print(classification_report(y_test, tp_knn))
from sklearn.metrics import precision_score, accuracy_score, recall_score, f1_score
print(f"Accuracy: {round(accuracy_score(y_test, tp_knn), 2)}")
print(f"Precision: {round(precision_score(y_test, tp_knn), 2)}")
print(f"Recall: {round(recall_score(y_test, tp_knn), 2)}")
print(f"F1_score: {round(f1_score(y_test, tp_knn), 2)}")
```

```
Acurácia:  0.7058823529411765
Acurácia de previsão:  0.46579804560260585
              precision    recall  f1-score   support

           0       0.41      0.44      0.42       136
           1       0.52      0.49      0.50       171

    accuracy                           0.47       307
   macro avg       0.46      0.46      0.46       307
weighted avg       0.47      0.47      0.47       307

Accuracy: 0.47
Precision: 0.52
Recall: 0.49
F1_score: 0.5
```

In [136…

```
#aplicação algoritmo Naive Bayes
from sklearn.naive_bayes import GaussianNB
from sklearn.metrics import accuracy_score, classification_report
nb = GaussianNB()
nb = nb.fit(X_train, y_train)
print("Acurácia: ", nb.score(X_train, y_train))
tp_nb = nb.predict(X_test)
print(classification_report(y_test, tp_nb))
from sklearn.metrics import precision_score, accuracy_score, recall_score, f1_score
print(f"Accuracy: {round(accuracy_score(y_test, tp_nb), 2)}")
print(f"Precision: {round(precision_score(y_test, tp_nb), 2)}")
print(f"Recall: {round(recall_score(y_test, tp_nb), 2)}")
print(f"F1_score: {round(f1_score(y_test, tp_nb), 2)}")
```

```
Acurácia:  0.6386554621848739
              precision    recall  f1-score   support

           0       0.48      0.63      0.55       136
           1       0.61      0.46      0.53       171

    accuracy                           0.54       307
   macro avg       0.55      0.55      0.54       307
weighted avg       0.56      0.54      0.54       307

Accuracy: 0.54
Precision: 0.61
Recall: 0.46
F1_score: 0.53
```

In [137…

```
#aplicação algoritmo gradiente descendente
from sklearn.linear_model import SGDClassifier
sgd = SGDClassifier()
sgd = sgd.fit(X_train, y_train)
print("Acurácia: ", sgd.score(X_train, y_train))
tp_sgd = sgd.predict(X_test)
print(classification_report(y_test, tp_sgd))
from sklearn.metrics import precision_score, accuracy_score, recall_score, f1_score
```

```
print(f"Accuracy: {round(accuracy_score(y_test, tp_sgd), 2)}")
print(f"Precision: {round(precision_score(y_test, tp_sgd), 2)}")
print(f"Recall: {round(recall_score(y_test, tp_sgd), 2)}")
print(f"F1_score: {round(f1_score(y_test, tp_sgd), 2)}")
```

```
Acurácia:  0.5700280112044818
              precision    recall  f1-score   support

           0       0.57      0.03      0.06       136
           1       0.56      0.98      0.71       171

    accuracy                           0.56       307
   macro avg       0.57      0.51      0.38       307
weighted avg       0.57      0.56      0.42       307

Accuracy: 0.56
Precision: 0.56
Recall: 0.98
F1_score: 0.71
```

In [ ]: