Section 1: EMR Bots 30-Day Readmission Activity

In [19]:

import required modules

In [15]: #Section Q1) Create your dataframe

encounter_info = pd.read_cav(r'C:\Dera\vitak\Downloada\Rasigment 1 Datasetx\readmissiona\encounter_info.cav')
encounter_labs = pd.read_cav(r'C:\Dera\vitak\Downloada\Rasigment 1 Datasetx\readmissiona\encounter_labs.cav')
readmissions = pd.read_cav(r'C:\Dera\vitak\Downloada\Rasigment 1 Datasetx\readmissiona\encounter_labs.cav')

alldata.head()

Out[15]:

Patier	t_ID Encour	nter_ID	AdmissionStartDate	AdmissionEndDate	PatientGender	PatientRace	PatientEncounterAge	Lab_DTTM	CBCABSOLUTE.LYMPHOCYTE:	CBCABSOLUTE.NEUTROPHILS	CBCRED.BLOOD.CELL.COUNT	CBCWHITE.BLOOD.CELL.COUNT	METABOLICALBUMIN	METABOLICBILLTOTAL	METABOLICBUN	METABOLICCALCIUM	METABOLICCREATININE	METABOLICPOTASSIUM	METABOLICSODIUM	utcome
			996-01-20 14:32:48.440 199			White	36.456455	1996-01-20 17:06:30	25.0	70.0	5.0	7.5	4.2	0.6	17.5	11.5	0.9	4.5	140.0	
1 10000	100000)_2 199	996-01-20 14:32:48.440 199	6-02-06 17:11:05.247	Female	White	36.456455	1996-01-20 17:19:57	25.0	64.6	5.0	7.5	4.2	0.6	17.5	11.5	0.9	4.5	140.0	,
2 10000	100000)_2 199	996-01-20 14:32:48.440 199	6-02-06 17:11:05.247	Female	White	36.456455	1996-01-21 00:22:16	25.0	64.6	5.0	7.5	4.2	0.6	17.5	11.5	0.9	4.5	140.0	/
3 10000	100000)_2 199	996-01-20 14:32:48.440 199	6-02-06 17:11:05.247	Female	White	36.456455	1996-01-21 00:30:20	25.0	64.6	5.0	7.5	4.2	0.6	17.5	11.5	0.9	4.8	140.0	/
4 10000	100000	2 19	996-01-20 14:32:48.440 199	6-02-06 17:11:05.247	Female	White	36.456455	1996-01-21 02:15:42	25.0	64.6	5.2	7.5	4.2	0.6	17.5	11.5	0.9	4.8	140.0	,

Section 1 Question 1

age re ves sd = alldata.loc(alldata('outcome')==1. 'PatientEncounterAge').std()

age_re_no = alldata.loc[alldata['outcome']==0, 'PatientEncounterAge'].mean()

print(age_re_yes)
print(age_re_no)
print(age_re_yes_sd)
print(age_re_no_sd)

In [36]:

There was some ambiguity about the requirements for this section.
So I conducted the analysis on the entire dataset (labs, info, outcomes), and the outcomes data alone

#chi square to compare categorical features

alldata 2 = pd.merge(encounter info.readmissions.on='Encounter ID')

outcome = slldsta_2.loc[:,"outcome"]
sge1 = slldsta_2.loc[:,"PatientEncounterAc
gender1 = slldsta_2.loc[:,"PatientGender"]
race1 = slldsta_2.loc[:,"PatientRace"]

#Age CHI2 Analysis
age_chi2* pd.crosstab(age1, outcome1)
print(age_chi2)
print(stats.chi2_contingency(age_chi2))

#Gender CHI2 Analysis gender_chi2 pd.crosstab(gender1, outcome1) print(gender_chi2) print(stats.chi2_contingency(gender_chi2))

#Race CHI2 Analysis
race_chi2= pd.crosstab(race1, outcome1)
print(race_chi2)
print(stats.chi2_contingency(race_chi2))

[36143 rows x 2 columns]
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(36142,99999999985, 0.49752695298415395, 36142, array([[0.99645851, 0.00354140], [0.99645851, 0.00354149], [0.99645851, 0.00354149],

In [23]:

def symmetry classes, conditions as every parametrizit, if def symmetry classes, conditions; total = insididate(classes) classes = conditions = cond

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Section 1 Question 25

In [25]:

#simplify the "alldata" data set so you analyze only the last-observed lab values for each encounter

drop irrelevant columns
alldata.drop({
 'Patient_ID',
 'AdmissionStartDate',
 'AdmissionEndDate',
},axis=1,inplace=True)

alldata_pruned = alldata.drop_duplicates(keep='last')

display(alldata_pruned)
alldata_pruned.info()
alldata_pruned.describe()

	Encounter_	ID PatientGender	PatientRace	PatientEncounterAge	Lab_DTTM	CBCABSOLUTE.LYMPHOCYTES	CBCABSOLUTE.NEUTROPHILS	CBCBASOPHILS	CBCEOSINOPHILS	CBCHEMATOCRIT	CBCRED.BLOOD.CELL.COUNT	CBCWHITE.BLOOD.CELL.COUNT	METABOLICALBUMIN	METABOLICBILLTOTAL	METABOLICBUN	METABOLICCALCIUM	METABOLICCREATININE	METABOLIC_POTASSIUM	METABOLICSODIUM	outcome
0	100000_2	Female	White	36.456455	1996-01-20 17:06:30	25.0	70.0	0.1	0.3	42.5	5.0	7.5	4.2	0.6	17.5	11.5	0.9	4.5	140.0	0
1	100000_2	Female	White	36.456455	1996-01-20 17:19:57	25.0	64.6	0.1	0.3	42.5	5.0	7.5	4.2	0.6	17.5	11.5	0.9	4.5	140.0	0
2	100000_2	Female	White		1996-01-21 00:22:16		64.6	0.1	0.3	42.8	5.0	7.5	4.2	0.6	17.5	11.5	0.9	4.5	140.0	0
3	100000_2	Female	White	36.456455	1996-01-21 00:30:20	25.0	64.6	0.1	0.3	42.8	5.0	7.5	4.2	0.6	17.5	11.5	0.9	4.8	140.0	0
4	100000_2	Female	White	36.456455	1996-01-21 02:15:42	25.0	64.6	0.1	0.3	42.8	5.2	7.5	4.2	0.6	17.5	11.5	0.9	4.8	140.0	0
490279	9 110000_5	Male	African American		2012-11-07 01:39:35		67.6	0.1	0.5	49.7	6.4	8.3	3.8	0.2	9.0	9.0	0.6	5.0	131.1	0
490280	0 110000_5	Male	African American		2012-11-07 01:58:02		67.6	0.1	0.6	49.7	6.4	8.3	3.8	0.2	9.0	9.0	0.6	5.0	131.1	0
490280	1 110000_5	Male	African American	58.494166	2012-11-07 05:42:19	15.7	67.6	0.1	0.6	49.7	6.4	8.3	3.8	0.2	9.0	9.0	0.6	3.5	131.1	0
490280	110000_5	Male	African American	58.494166	2012-11-07 06:38:10	15.7	67.6	0.1	0.6	49.7	6.4	6.4	3.8	0.2	9.0	9.0	0.6	3.5	131.1	0
490280	3 110000_5	Male	African American	58.494166	2012-11-07 06:57:41	15.7	67.6	0.1	0.6	49.7	6.4	6.4	3.8	0.1	9.0	9.0	0.6	3.5	131.1	0

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Out[2	15]:																	
	PatientEncounterAge	CBCABSOLUTE.LYMPHOCYTES	CBCABSOLUTE.NEUTROPHILS	CBCBASOPHILS	CBCEOSINOPHILS	CBCHEMATOCRIT	CBCHEMOGLOBIN	CBCPLATELET.COUNT	CBCRED.BLOOD.CELL.COUNT	CBCWHITE.BLOOD.CELL.COUNT	METABOLICALBUMIN	METABOLICBILLTOTAL	METABOLICBUN	METABOLICCALCIUM	METABOLICCREATININE	METABOLICPOTASSIUM	METABOLICSODIUM	outcome
cour	1t 4.902768e+06	4.902768e+06	4.902768e+06	4.902768e+06	4.902768e+06	4.902768e+06	4.902768e+06	4.902768e+06	4.902768e+06	4.902768e+06	4.902768e+06	4.902768e+06	4.902768e+06	4.902768e+06	4.902768e+06	4.902768e+06	4.902768e+06	4.902768e+06
mea	n 4.175990e+01	2.499706e+01	7.000121e+01	1.086038e-01	3.369535e-01	4.249499e+01	1.450186e+01	2.850215e+02	5.003539e+00	7.513503e+00	4.244626e+00	5.999477e-01	1.750029e+01	9.501873e+00	8.541084e-01	4.497314e+00	1.399799e+02	3.533514e-03
std	1.805458e+01	5.568243e+00	5.570806e+00	7.077017e-02	1.498486e-01	6.954853e+00	2.507913e+00	9.203077e+01	1.114242e+00	2.505532e+00	9.766367e=01	3.372594e-01	6.962744e+00	1.392525e+00	1.994363e-01	8.370857e-01	8.356385e+00	5.933826e-02
mir	1.801188e+01	1.500000e+01	6.000000e+01	0.000000e+00	1.000000e-01	3.000000e+01	1.000000e+01	1.200000e+02	3.000000e+00	3.000000e+00	2.500000e+00	0.000000e+00	5.000000e+00	7.000000e+00	5.000000e-01	3.000000e+00	1.250000e+02	0.000000e+00
25%	2.585804e+01	2.030000e+01	6.540000e+01	1.000000e-01	2.000000e-01	3.670000e+01	1.240000e+01	2.084000e+02	4.100000e+00	5.400000e+00	3.400000e+00	3.000000e-01	1.170000e+01	8.300000e+00	7.000000e-01	3.800000e+00	1.330000e+02	0.000000e+00
50%	3.861599e+01	2.500000e+01	7.000000e+01	1.000000e-01	3.000000e-01	4.250000e+01	1.450000e+01	2.851000e+02	5.000000e+00	7.500000e+00	4.200000e+00	6.000000e-01	1.750000e+01	9.500000e+00	9.000000e-01	4.500000e+00	1.400000e+02	0.000000e+00
75%	5.439088e+01	2.960000e+01	7.460000e+01	2.000000e-01	5.000000e-01	4.830000e+01	1.660000e+01	3.616000e+02	5.900000e+00	9.600000e+00	5.100000e+00	9.000000e-01	2.330000e+01	1.070000e+01	1.000000e+00	5.200000e+00	1.469000e+02	0.000000e+00
ma	9.295804e+01	3.500000e+01	8.000000e+01	2.000000e-01	6.000000e-01	5.500000e+01	1.900000e+01	4.500000e+02	7.000000e+00	1.200000e+01	6.000000e+00	1.200000e+00	3.000000e+01	1.200000e+01	1.200000e+00	6.000000e+00	1.550000e+02	1.000000e+00

Section 1 Quesiton 35

In [29]:

#Use the Lab date to create a column for Years

alldata["Year"] = alldata.Lab_DTTM.str[:4]

alldats["Year"] = alldats["Year"].astype(int)

#display(alldata In [18]:

#Train Test Split

train_data = alldata(alldata("Year") <- 2003)

display(train_data)

unspir	syttemani_	Cata)																			
	Encou	inter_ID	PatientGender	PatientRace	PatientEncounterAge	Year	Lab_DTTM 0	CBCABSOLUTE.LYMPHOCYTES	CBCABSOLUTE.NEUTROPHILS	CBCBASOPHILS	CBCEOSINOPHILS	CBCRED.BLOOD.CELL.COUNT	CBCWHITE.BLOOD.CELL.COUNT	METABOLICALBUMIN	METABOLICBILLTOTAL	METABOLICBUN	METABOLICCALCIUM	METABOLICCREATININE	METABOLICPOTASSIUM	METABOLICSODIUM	outcome
0	100000	0_2	Female	White	36.456455	1996 1	1996-01-20 17:06:30	25.0	70.0	0.1	0.3	5.0	7.5	4.2	0.6	17.5	11.5	0.9	4.5	140.0	3
1	100000	0_2	Female	White	36.456455	1996 1	1996-01-20 17:19:57	25.0	64.6	0.1	0.3	5.0	7.5	4.2	0.6	17.5	11.5	0.9	4.5	140.0	J
2	100000	0_2	Female	White	36.456455	1996 1	1996-01-21 00:22:16	25.0	64.6	0.1	0.3	5.0	7.5	4.2	0.6	17.5	11.5	0.9	4.5	140.0	J
3	100000	0_2	Female	White	36.456455	1996 1	1996-01-21 00:30:20	25.0	64.6	0.1	0.3	5.0	7.5	4.2	0.6	17.5	11.5	0.9	4.8	140.0	J
4	100000	0_2	Female	White	36.456455	1996	1996-01-21 02:15:42	25.0	64.6	0.1	0.3	5.2	7.5	4.2	0.6	17.5	11.5	0.9	4.8	140.0)
						J. J.					[[ļ							
49026	110000	0_2	Male	African American	30.322346	1984 1	1984-09-04 19:17:23	19.9	60.1	0.1	0.6	3.9	9.6	3.7	0.5	25.5	11.3	0.6	3.1	132.3)
49026	43 110000	0_2	Male	African American	30.322346	1984 1	1984-09-04 19:49:36	19.9	60.1	0.1	0.6	3.9	9.6	3.7	0.5	25.5	11.3	0.6	3.1	140.8	J
49026	44 110000	0_2	Male	African American	30.322346	1984 1	1984-09-04 19:55:37	19.9	60.1	0.1	0.6	3.9	9.6	3.7	1.1	25.5	11.3	0.6	3.1	140.8	J
49026	45 110000	0_2	Male	African American	30.322346	1984 1	1984-09-04 20:23:38	19.9	60.1	0.1	0.6	3.9	9.6	4.5	1.1	25.5	11.3	0.6	3.1	140.8	J
49026	46 110000	0.2	Male	African American	30 322346	1984 1	1984-09-04 21:06:50	19 9	60.1	0.1	0.6	3.9	9.6	4.5	11	25.5	11.3	0.6	3.1	140.8	0

2751795 rows Å 23 columns

In [20]:

#Test Test Split

test_data = alldata[alldata["Year"] > 2003]

display(test_data)

	Encounter_II	PatientGender	PatientRace	PatientEncounterAge	Year	Lab_DTTM	CBCABSOLUTE.LYMPHOCYTES	CBCABSOLUTE.NEUTROPHILS	CBCBASOPHILS	CBCEOSINOPHILS	CBC_RED.BLOOD.CELL.COUNT	CBCWHITE.BLOOD.CELL.COUNT	METABOLICALBUMIN	METABOLICBILLTOTAL	METABOLICBUN	METABOLICCALCIUM	METABOLICCREATININE	METABOLICPOTASSIUM	METABOLICSODIUM	outcon
257	100000_5	Female	White	47.688073	2007 200	07-04-12 03:57:36	25.0	70.0	0.1	0.3	5.0	7.5	4.2	0.6	17.5	9.5	0.9	4.5	140.0	0
258	100000_5	Female	White	47.688073	2007 200	07-04-12 04:36:36	20.4	70.0	0.1	0.3	5.0	7.5	4.2	0.6	17.5	9.5	0.9	4.5	140.0	0
259	100000_5	Female	White			07-04-12 05:06:34		70.0	0.1	0.3	5.0	7.5	4.2	0.1	17.5	9.5	0.9	4.5	140.0	0
260	100000_5	Female	White			07-04-12 11:21:12		70.0	0.1	0.3	5.0	7.5	4.2	0.1	17.5	9.5	0.9	3.3	140.0	0
261	100000_5	Female	White	47.688073	2007 200	07-04-12 11:46:41	20.4	70.0	0.1	0.3	5.0	7.5	4.2	0.1	11.3	9.5	0.9	3.3	140.0	0
			[[[-	[
490279	110000_5	Male	African American	58.494166	2012 201	12-11-07 01:39:35	15.7	67.6	0.1	0.5	6.4	8.3	3.8	0.2	9.0	9.0	0.6	5.0	131.1	0
490280	110000_5	Male	African American	58.494166	2012 201	12-11-07 01:58:02	15.7	67.6	0.1	0.6	6.4	8.3	3.8	0.2	9.0	9.0	0.6	5.0	131.1	0
490280	110000_5	Male	African American	58.494166	2012 201	12-11-07 05:42:19	15.7	67.6	0.1	0.6	6.4	8.3	3.8	0.2	9.0	9.0	0.6	3.5	131.1	0
490280	110000_5	Male	African American			12-11-07 06:38:10		67.6	0.1	0.6	6.4	6.4	3.8	0.2	9.0	9.0	0.6	3.5	131.1	0
490280	110000 5	Male	African American	58 494166	2012 201	12-11-07-06:57:41	15.7	67.6	0.1	0.6	6.4	6.4	3.8	0.1	9.0	9.0	0.6	3.5	131 1	0

```
2151009 rows Å 23 columns
```

In [22]:

#Test Date

test_yes = len(test_data[(test_data[*outcome*]==1)])
perc_test_yes = (test_yes/(len(test_data[*outcome*])))*100
test_no = len(test_data[(test_data[*outcome*])))*100
perc_test_no = (test_no*/(len(test_data[*outcome*])))*100

8776 0.4079945737093615 2142233 99.59200542629064

In [23]:

print(train_yes,perc_train_yes,train_no,perc_train_no)

Section 2: GUSTO 30-Day Mortality Prediction \$\square\$

In [38]:

#Section Q1) Create your dataframe

gusto = pd.read_csv(r*C:\Users\vitak\Downloads\gusto_data.csv*)

Out[38]:

Γ	DAY30	AGE	A65	SEX	KILLIP	SHO	DIA	HYP	HRT	ANT		WEI	SMK	HTN	LIP	PAN	FAM	STE	ST4	TTR	GROUP
0	0	70.313	1	0	1	0	0	0	0	1	Ē	84.0	3	1	1	0	0	1	0	1	west
1	0	59.844	0	0	1	0	1	0	0	1	Ē	115.0	1	ī	0	0	1	6	1	0	west
2	0	59.023	0	0	1	0	0	0	1	0	Ē	76.0	1	1	0	0	1	3	0	0	west
3	1	80.375	1	1	1	0	0	0	1	0		50.0	3	0	0	0	0	3	0	0	west
4	0	64.750	0	0	1	0	0	1	0	0		97.4	1	0	0	1	ī	2	0	1	west

5 rows Å 23 columns

Section 2 Question 15

In [39]:

age_g_yes = gusto.loc[gusto['DAY30']==1, 'AGE'].mean()

age_g_yes_sd = gusto.loc[gusto['DAY30']==1, 'AGE'].std()

age_g_no_sd = gusto.loc[gusto['DAY30']--0, 'AGE'].std() print(age_g_yes)
print(age_g_yes_sd)
print(age_g_no)
print(age_g_no_sd)

In [40]:

#GUSTO Gender and Group Summary

def greenstyfichtens.comition; roll-|rolpystefminens| n_yes - len(gestefminens) = condition) f n_yes - len(gestef(gestef(colesse) = condition) f n_roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-|roll-

gmale = gaunmary('SEX',0)
gfem = gaunmary('SEX',1)
s2 = gaunmary('GEOUP', 'sample2')
s4 = gaunmary('GEOUP', 'sample4')
s5 = gaunmary('GEOUP', 'sample4')
west = gaunmary('GEOUP', 'sample5')

Q2_table = [gmsle,gfem,s2,s4,s5,west]

my_gtable = pd.DataFrame(Q2_table, columns = ["Summary", "Patients who died within 30 days(n)", "%", "Patients who were alive at 30 days(n)", "%"])

Г	Summary	Patients who died within 30 days(n)	%	Patients who were alive at 30 days(n)	%
0		140	3.824092	2581	70.499863
1	1	91	2.485660	849	23.19038
2	sample2	20	0.546299	239	6.528271
3	sample4	52	1.420377	733	20.021852
4	sample5	24	0.655559	405	11.06255
5	west	135	3.687517	2053	56.077574

#chi square to compare categorical features - for P Values

outcome2 = gusto.loc[:,"DAY30"]
age2 = gusto.loc[:,"AGE"]
gender2 = gusto.loc[:,"SEEX"]
race2 = gusto.loc[:,"GROUP"]

#Gusto Age CMI2 Analysis age2_chi2 = pd.crosstab(age2, outcome2) print(age2_chi2) print(stats.chi2_contingency(age2_chi2))

Gusto Gender CMI2 Analysis
gender2_chi2-pd.crosstab(gender2, outcome2)
print(gender2_chi2)
print(stats.chi2_contingency(gender2_chi2))

#Gusto Race CMI2 Analysis
race2_chi2* pd.crosstab(race2, outcome2)
print(race2_chi2)
print(stats.chi2_contingency(race2_chi2))

88.656 0 1 88.828 2 0 88.844 1 0 89.078 0 1 89.484 0 1

Section 2 Question 25

In [42]:

#Split GUSTO Data into Training and Test Sets.

#Train Data (sample 2-5)

gtrain_data = gusto[gusto["GROUP"] != "west"]

display(gtrain_data)

	DAY30	AGE	A65	SEX	KILLIP	SHO	DIA	HYP	HRT	ANT	 WEI	SMK	HTN	LIP	PAN	FAM	STE	ST4	TTR	GROUP
2188	0	59.844	0	0	1	0	1	0	0	1	115.0	1	1	0	0	1	6	1	0	sample2
2189	1	80.375	1	1	1	0	0	0	1	0	50.0	3	0	0	0	0	3	0	0	sample2
2190	1	34.430	0	1	1	0	1	0	1	1	93.0	1	1	1	1	1	5	1	1	sample2
2191		57.977	0	1	2	0	1	0	0	0	59.0	3	1	1	0	1	1	0	0	sample2
2192	0	62.305	0	0	1	0	0	0	0	1	 87.0	2	0	0	1	0	2	0	1	sample2
3656		51.836	0	0	1	0	0	0	0	1	65.0	1	0	0	0	0	7	1	1	sample5
3657		51.836	0	0	1	0	1	0	0	1	72.1	3	0	0	1	0	7	1	1	sample5
3658	0	63.977	0	0	1	0	0	0	0	0	87.2	2	1	0	0	0	2	0	1	sample5
3659	0	59.758	0	1	1	0	0	0	0	0	57.8	3	0	0	0	0	6	1	1	sample5
3660	0	52.195	0	0	1	0	0	0	0	0	75.0	2	1	1	0	1	4	0	1	sample5

1473 rows à 23 columns

In [43]:

#GUSTO Test Data (west)

gtest_data = gusto[gusto["GRCUP"] -- "west"]

	DAY30	AGE	A65	SEX	KILLIP	SHO	DIA	HYP	HRT	ANT		WEI	SMK	HTN	LIP	PAN	FAM	STE	ST4	TTR	GROUP
0	0	70.313	1	0	1	0	0	0	0	1		84.0	3	1	1	0	0	1	0	1	west
1	0	59.844	0	0	1	0	1	0	0	1	[115.0	1	1	0	0	1	6	1	0	west
2	0	59.023	0	0	1	0	0	0	1	0		76.0	1	1	0	0	1	3	0	0	west
3	1	80.375	1	1	1	0	0	0	1	0		50.0	3	0	0	0	0	3	0	0	west
4	0	64.750	0	0	1	0	0	1	0	0		97.4	1	0	0	1	1	2	0	1	west
2183	0	64.609	0	0	1	0	0	0	1	1		72.0	3	1	1	0	0	8	1	0	west
2184	0	70.766	1	0	1	0	0	1	0	0		97.0	2	0	1	0	1	6	1	1	west
2185	0	53.047	0	1	1	0	0	0	1	1		91.0	3	1	0	0	0	7	П	0	west
2186	0	73.141		0	1	0	0	0	0	1		79.4	2	1	0	0	0	7		0	west
2187	0	52.195	0	0	1	0	0	0	0	0		75.0	2	1	1	0	1	4	0	1	west

2188 rows à 23 columns

#GUSTO Test/Train Data Summary

gtrain_yes = len(gtrain_data[(gtrain_data['DAY30'|=1]])
gperc_train_yes = (gtrain_yes/(len(gtrain_data['DAY30'])))*100
gtrain_no = len(gtrain_data[(gtrain_data['DAY30'])))*100
gerc_train_no = (gtrain_nof/len(gtrain_data['DAY30'])))*100

print(otrain was.operc train was.otrain no.operc train no)

96 6.517311608961303 1377 93.48268839103869

In [45]:

#GUSTO Test/Train Data Summary

gtest_yes = len(gtest_data[(gtest_data['DAY30']==1)])
gperc_test_yes = (gtest_yes)(len(gtest_data['DAY30'])))*100
gperc_test_no = (gtest_no/(len(gtest_data['DAY30']=))))*100

print(gtest_yes,gperc_test_yes,gtest_no,gperc_test_no)

135 6.170018281535649 2053 93.82998171846435

Section 2 Question 3

In [46]:

gtest_data.info()

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In [22]:

gtrain_data.info()

steat data describe()

Out[47]

Ot	it[47]:																					
		DAY30	AGE	A65	SEX	KILLIP	SHO	DIA	HYP	HRT	ANT		HEI	WEI	SMK	HTN	LIP	PAN	FAM	STE	ST4	TTR
ce	unt	2188.000000	2188.000000	2188.000000	2188.000000	2188.000000	2188.000000	2188.000000	2188.000000	2188.000000	2188.000000		2188.000000	2188.000000	2188.000000	2188.000000	2188.000000	2188.000000	2188.000000	2188.000000	2188.000000	2188.000000
n	ean	0.061700	60.469186	0.383455	0.248629	1.132084	0.014625	0.142596	0.096435	0.333638	0.372486	8	172.129936	82.888940	1.866545	0.403565	0.404936	0.340494	0.475777	3.999543	0.356033	0.608775
	std	0.240665	12.026568	0.486339	0.432317	0.409550	0.120075	0.349740	0.295254	0.471620	0.483577		10.094343	17.692498	0.821252	0.490724	0.490992	0.473984	0.499527	1.878451	0.478935	0.488136
	nin (0.000000	23.910000	0.000000	0.000000	1.000000	0.000000	0.000000	0.000000	0.000000	0.000000		140.900000	36.000000	1.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
2	5%	0.000000	50.932000	0.000000	0.000000	1.000000	0.000000	0.000000	0.000000	0.000000	0.000000	[165.100000	70.900000	1.000000	0.000000	0.000000	0.000000	0.000000	3.000000	0.000000	0.000000
5	0%	0.000000	60.547000	0.000000	0.000000	1.000000	0.000000	0.000000	0.000000	0.000000	0.000000		173.000000	82.000000	2.000000	0.000000	0.000000	0.000000	0.000000	3.000000	0.000000	1.000000
7	5%	0.000000	69.922000	1.000000	0.000000	1.000000	0.000000	0.000000	0.000000	1.000000	1.000000		180.000000	92.050000	3.000000	1.000000	1.000000	1.000000	1.000000	5.000000	1.000000	1.000000
	nax	1.000000	89.484000	1.000000	1.000000	4.000000	1.000000	1.000000	1.000000	1.000000	1.000000		205.700000	180.000000	3.000000	1.000000	1.000000	1.000000	1.000000	11.000000	1.000000	1.000000

8 rows Å 22 columns

In [48]:

strain data.describe

Out[4	8]:																				
	DAY30	AGE	A65	SEX	KILLIP	SHO	DIA	HYP	HRT	ANT		HEI	WEI	SMK	HTN	LIP	PAN	FAM	STE	ST4	TTR
cour	t 1473.000000	1473.000000	1473.000000	1473.000000	1473.000000	1473.000000	1473.000000	1473.000000	1473.000000	1473.000000	=(1473.000000	1473.000000	1473.000000	1473.000000	1473.000000	1473.000000	1473.000000	1473.000000	1473.000000	1473.000000
mea	0.065173	61.415623	0.410726	0.268839	1.194840	0.020367	0.114732	0.073320	0.292600	0.361168		170.338900	78.200068	1.909029	0.385608	0.386286	0.364562	0.428377	4.150034	0.386965	0.560760
std	0.246915	11.448781	0.492133	0.443507	0.462655	0.141299	0.318806	0.260749	0.455111	0.480502		9.779777	16.531963	0.803275	0.486904	0.487063	0.481471	0.495012	1.865345	0.487221	0.496463
mir	0.000000	25.891000	0.000000	0.000000	1.000000	0.000000	0.000000	0.000000	0.000000	0.000000		141.000000	37.000000	1.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
25%	0.000000	52.578000	0.000000	0.000000	1.000000	0.000000	0.000000	0.000000	0.000000	0.000000		163.800000	68.000000	1.000000	0.000000	0.000000	0.000000	0.000000	3.000000	0.000000	0.000000
50%	0.000000	62.242000	0.000000	0.000000	1.000000	0.000000	0.000000	0.000000	0.000000	0.000000		170.200000	77.000000	2.000000	0.000000	0.000000	0.000000	0.000000	4.000000	0.000000	1.000000
75%	0.000000	70.469000	1.000000	1.000000	1.000000	0.000000	0.000000	0.000000	1.000000	1.000000		177.300000	87.000000	3.000000	1.000000	1.000000	1.000000	1.000000	6.000000	1.000000	1.000000
ma	1.000000	88.828000	1.000000	1.000000	4.000000	1.000000	1.000000	1.000000	1.000000	1.000000		199.700000	180.000000	3.000000	1.000000	1.000000	1.000000	1.000000	10.000000	1.000000	1.000000

8 rows à 22 columns