Assignment 2

January 29, 2017

1 Impact of HbA1c Measurement on Hospital Readmission Rates: Analysis of 70,000 Clinical Database Patient Records

Created by: Paz Bunis (pazbunis@gmail.com) #### based on: Beata Strack, Jonathan P. DeShazo, Chris Gennings, et al., "Impact of HbA1c Measurement on Hospital Readmission Rates: Analysis of 70,000 Clinical Database Patient Records," BioMed Research International, vol. 2014, 11 pages, 2014.

1.1 0. Imports and Initialization

In [422]:
```
from matplotlib import style as style
import matplotlib.pyplot as plt
%matplotlib inline
style.use('ggplot')
import pandas as pd
import numpy as np
import scipy.stats as stats
from kmodes import kmodes
from sklearn.model_selection import KFold
from sklearn.ensemble import RandomForestClassifier
encounters = pd.read_csv('dataset/diabetic_data.csv')
msk = np.random.rand(len(encounters)) < 0.9
encounters_train = encounters[msk]
encounters_test = encounters[~msk]
```

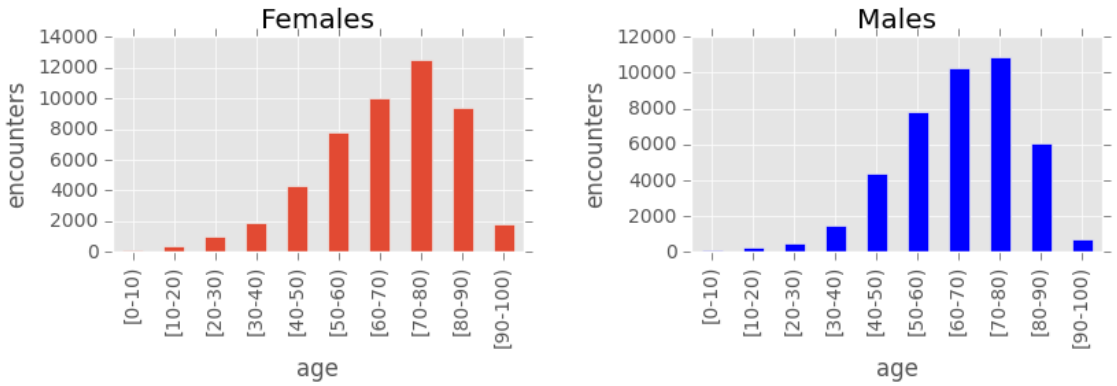
1.2 1. Descriptive Statistics

1.2.1 1.1. Gender vs. other attributes

1.1.1. Gender vs. Age

In [423]:
```
females_age_grouping = encounters_train[encounters_train.gender == 'Female'].groupby('age').s
males_age_grouping = encounters_train[encounters_train.gender == 'Male'].groupby('age').size(
fig, axs = plt.subplots(1,2, figsize=(9,3))
axs[0].set_ylabel("encounters")
axs[1].set_ylabel("encounters")
fig.tight_layout(pad=4)
females_age_grouping.plot.bar(ax = axs[0], title = 'Females')
males_age_grouping.plot.bar(ax = axs[1], title = 'Males', color='b')
```

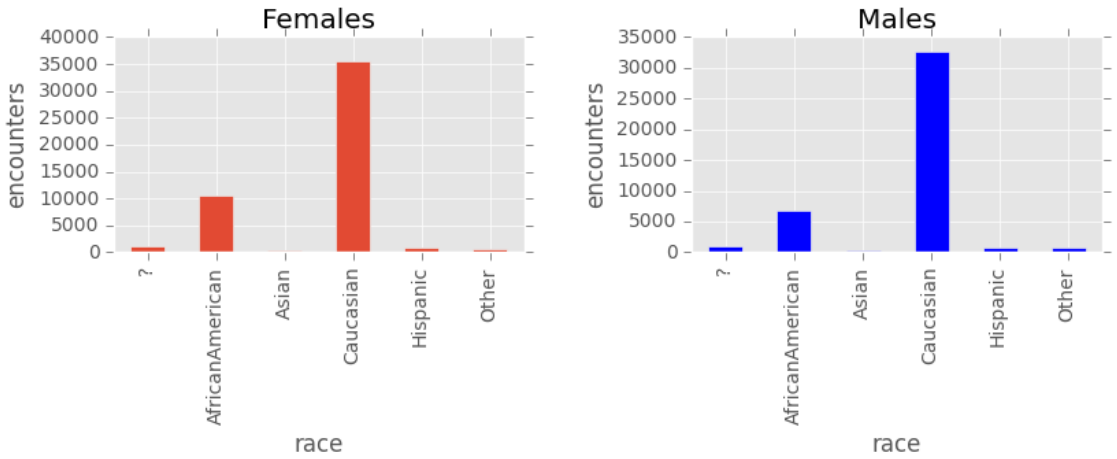
Out[423]:
```
<matplotlib.axes._subplots.AxesSubplot at 0x7fd9cd441908>
```



1.1.2. Gender vs. Race

```
In [424]: females_race_grouping = encounters_train[encounters_train.gender == 'Female'].groupby('race')
          males_race_grouping = encounters_train[encounters_train.gender == 'Male'].groupby('race').size
          fig, axs = plt.subplots(1,2, figsize=(9,3))
          axs[0].set_ylabel("encounters")
          axs[1].set_ylabel("encounters")
          fig.tight_layout(pad=4)
          females_race_grouping.plot.bar(ax = axs[0], title = 'Females')
          males_race_grouping.plot.bar(ax = axs[1], title = 'Males', color='b')
```

```
Out[424]: <matplotlib.axes._subplots.AxesSubplot at 0x7fd9eb82f898>
```

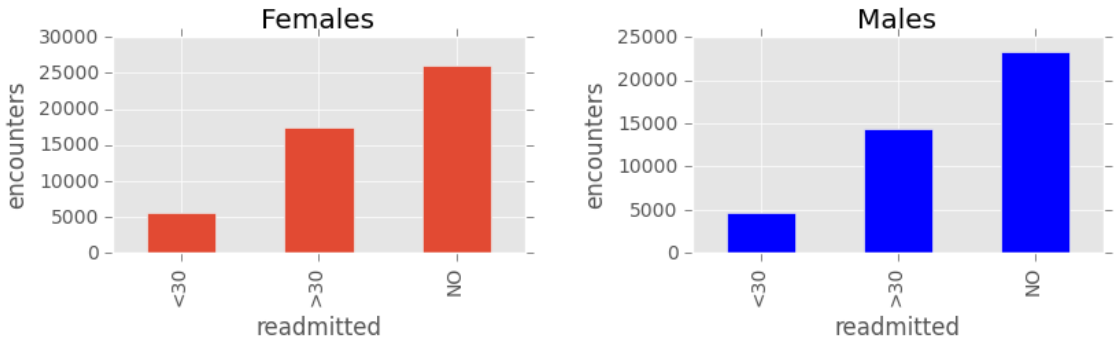


1.1.3. Gender vs. Readmission Value

```
In [425]: females_readmission_grouping = encounters_train[encounters_train.gender == 'Female'].groupby(
          males_readmission_grouping = encounters_train[encounters_train.gender == 'Male'].groupby('rea
          fig, axs = plt.subplots(1,2, figsize=(9,3))
          axs[0].set_ylabel("encounters")
```

```
axs[1].set_ylabel("encounters")
fig.tight_layout(pad=4)
females_readmission_grouping.plot.bar(ax = axs[0], title = 'Females')
males_readmission_grouping.plot.bar(ax = axs[1], title = 'Males', color='b')
```

Out[425]: <matplotlib.axes._subplots.AxesSubplot at 0x7fd9eb9967f0>



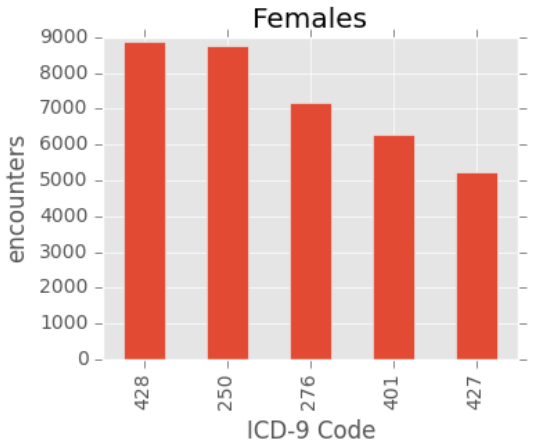
1.1.4. Gender vs. Most Frequently Used ICD-9 Codes (All three diagnosis types are combined to one column)

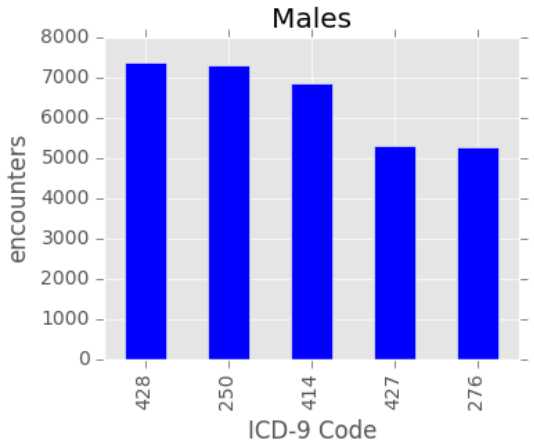
```
In [426]: fem_diags_projection = encounters_train[encounters_train.gender == 'Female'][['diag_1', 'diag
          fem_diags_arr = [fem_diags_projection[['diag_1']],fem_diags_projection[['diag_2']],fem_diags_
          fem_comb_diags = pd.concat(fem_diags_arr, axis=1).stack().reset_index(drop=True)

          male_diags_projection = encounters_train[encounters_train.gender == 'Male'][['diag_1', 'diag_
          male_diags_arr = [male_diags_projection[['diag_1']],male_diags_projection[['diag_2']],male_di
          male_comb_diags = pd.concat(male_diags_arr, axis=1).stack().reset_index(drop=True)

          fig, axs = plt.subplots(1,2, figsize=(9,4))
          axs[0].set_ylabel("encounters")
          axs[0].set_xlabel("ICD-9 Code")
          axs[1].set_ylabel("encounters")
          axs[1].set_xlabel("ICD-9 Code")
          fig.tight_layout(pad=4)
          fem_comb_diags.value_counts().head().plot.bar(ax = axs[0], title = 'Females')
          male_comb_diags.value_counts().head().plot.bar(ax = axs[1], title = 'Males', color='b')
```

Out[426]: <matplotlib.axes._subplots.AxesSubplot at 0x7fd9b604ce10>





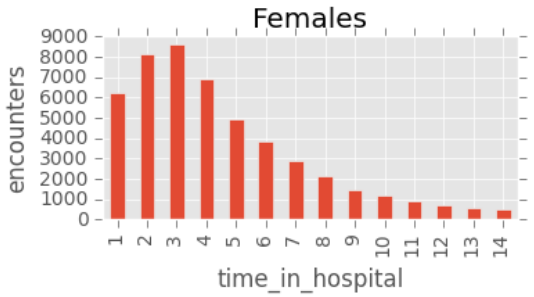
1.2.2 1.2. Days in Hospital and A1c Test Results

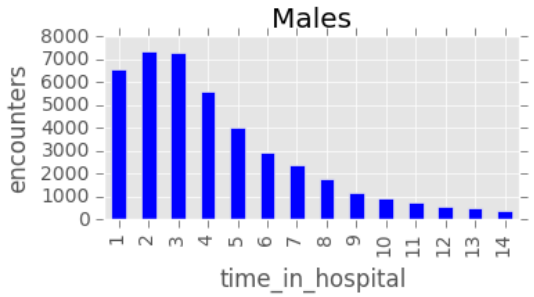
1.2.1. Days in Hospital vs. Gender

```
In [427]: females_hospital_time_grouping = encounters_train[encounters_train.gender == 'Female'].groupby
          males_hospital_time_grouping = encounters_train[encounters_train.gender == 'Male'].groupby('t
          fig, axs = plt.subplots(1,2, figsize=(9,3))
          axs[0].set_ylabel("encounters")
          axs[0].set_xlabel("days")
          axs[1].set_ylabel("encounters")
          axs[1].set_xlabel("days")

          fig.tight_layout(pad=4)
          females_hospital_time_grouping.plot.bar(ax = axs[0], title = 'Females')
          males_hospital_time_grouping.plot.bar(ax = axs[1], title = 'Males', color='b')
```

```
Out[427]: <matplotlib.axes._subplots.AxesSubplot at 0x7fd9cd967a20>
```





1.2.2. Days in Hospital vs. Age Group

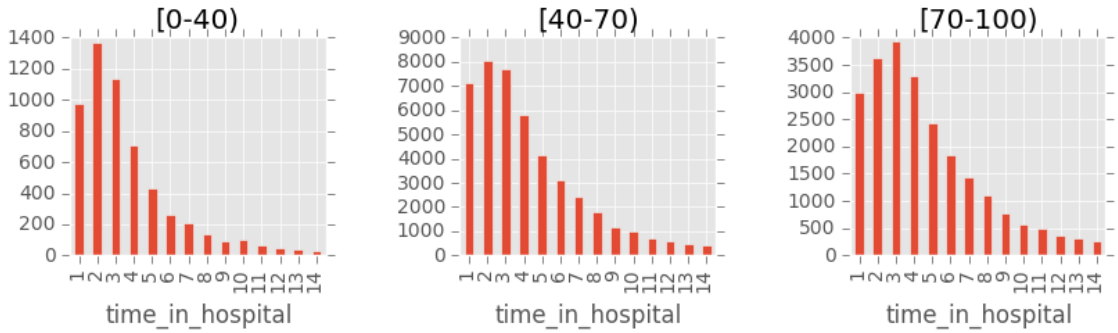
```
In [428]: age_group1= encounters_train[encounters_train.age.isin(['[0-10)','[10-20)', '[20-30)', '[30-4
          age_group2= encounters_train[encounters_train.age.isin(['[40-50)', '[50-60)', '[60-70)'])]
          age_group3= encounters_train[encounters_train.age.isin(['[70-80)', '[80-90), [90-100)'])]
```

```
group1_hospital_time = age_group1.groupby('time_in_hospital').size()
group2_hospital_time = age_group2.groupby('time_in_hospital').size()
group3_hospital_time = age_group3.groupby('time_in_hospital').size()

fig, axs = plt.subplots(1,3, figsize=(9,3))
# axs[0].set_ylabel("encounters")
# axs[0].set_xlabel("days")
# axs[1].set_ylabel("encounters")
# axs[1].set_xlabel("days")

fig.tight_layout(pad=4)
group1_hospital_time.plot.bar(ax = axs[0], title = '[0-40)')
group2_hospital_time.plot.bar(ax = axs[1], title = '[40-70)')
group3_hospital_time.plot.bar(ax = axs[2], title = '[70-100)')
```

Out[428]: <matplotlib.axes._subplots.AxesSubplot at 0x7fd9cd800be0>

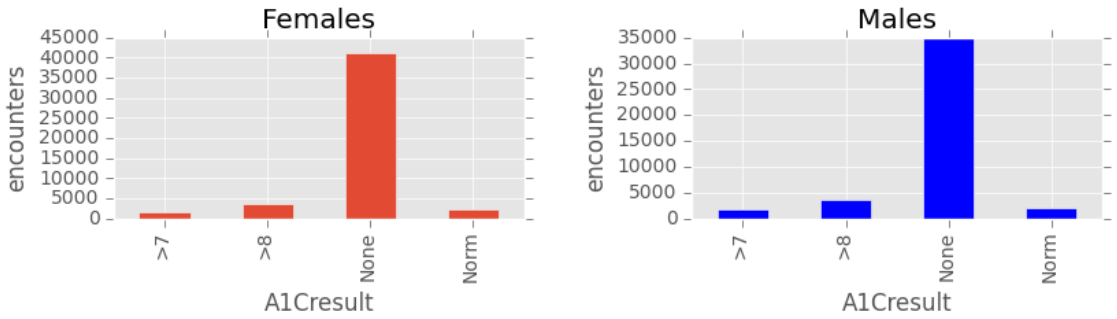


1.2.3. A1c test results vs. Gender

In [429]:
```
females_A1C_grouping = encounters_train[encounters_train.gender == 'Female'].groupby('A1Cresul
males_A1C_grouping = encounters_train[encounters_train.gender == 'Male'].groupby('A1Cresult')
fig, axs = plt.subplots(1,2, figsize=(9,3))
axs[0].set_ylabel("encounters")
axs[0].set_xlabel("days")
axs[1].set_ylabel("encounters")
axs[1].set_xlabel("days")

fig.tight_layout(pad=4)
females_A1C_grouping.plot.bar(ax = axs[0], title = 'Females')
males_A1C_grouping.plot.bar(ax = axs[1], title = 'Males', color='b')
```

Out[429]: <matplotlib.axes._subplots.AxesSubplot at 0x7fd9cd619358>



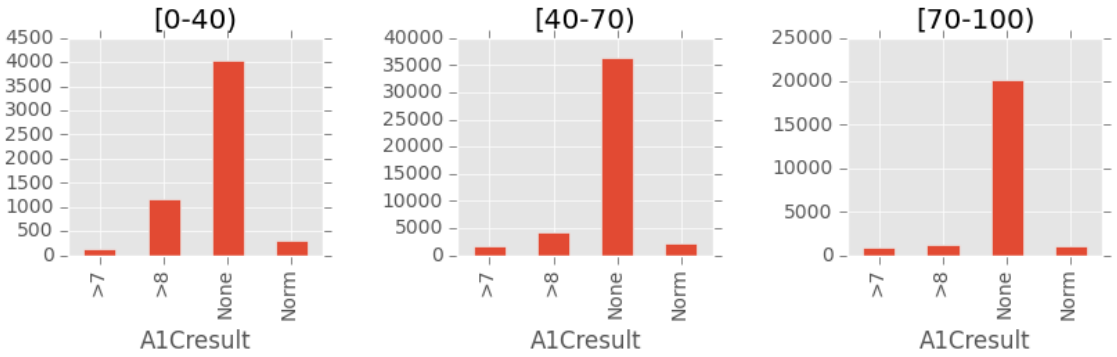
1.2.4. A1c test results vs. Age Group

```
In [430]: age_group1= encounters_train[encounters_train.age.isin(['[0-10)','[10-20)', '[20-30)', '[30-4
          age_group2= encounters_train[encounters_train.age.isin(['[40-50)', '[50-60)', '[60-70)'])]
          age_group3= encounters_train[encounters_train.age.isin(['[70-80)', '[80-90), [90-100)'])]
          group1_hospital_time = age_group1.groupby('A1Cresult').size()
          group2_hospital_time = age_group2.groupby('A1Cresult').size()
          group3_hospital_time = age_group3.groupby('A1Cresult').size()

          fig, axs = plt.subplots(1,3, figsize=(9,3))
          # axs[0].set_ylabel("encounters")
          # axs[0].set_xlabel("days")
          # axs[1].set_ylabel("encounters")
          # axs[1].set_xlabel("days")

          fig.tight_layout(pad=4)
          group1_hospital_time.plot.bar(ax = axs[0], title = '[0-40)')
          group2_hospital_time.plot.bar(ax = axs[1], title = '[40-70)')
          group3_hospital_time.plot.bar(ax = axs[2], title = '[70-100)')

Out[430]: <matplotlib.axes._subplots.AxesSubplot at 0x7fd9cd2d75f8>
```



1.3 2. Hypothesis Testing

1.3.1 2.1. Is Testing HbA1c Associated With a Reduced Rate of Readmission?

Our null hypothesis H_0 is that there is no correlation between the HbA1c test and the rate of readmission. In order to test this, we will use the Fisher exact test and the Chi-square test (which is supposed to be better for larger numbers).

```
In [432]: proj = encounters_train[['A1Cresult', 'readmitted']]
          ct = pd.crosstab(proj.A1Cresult, proj.readmitted, margins=True)
          ct['readmitted'] = ct['<30']
          ct['not_readmitted'] = ct['>30'] + ct['NO']
          ct = ct[['readmitted', 'not_readmitted', 'All']]
          N_readmitted_tested = ct.readmitted.All - ct.readmitted['None']
          N_readmitted_not_tested = ct.readmitted['None']
          N_not_readmitted_tested = ct.not_readmitted.All - ct.not_readmitted['None']
          N_not_readmitted_not_tested = ct.not_readmitted['None']

          print(ct)
```

```
readmitted  readmitted  not_readmitted    All
A1Cresult
>7                 337            3095   3432
>8                 736            6655   7391
None              8713           67442  76155
Norm               435            4045   4480
All              10221           81237  91458
```

Fisher Exact Test

```
In [434]: import scipy
          contingency_table = [[N_readmitted_tested, N_readmitted_not_tested],[N_not_readmitted_tested,
          odds_ratio, p_val = scipy.stats.fisher_exact(contingency_table)
          print('Odds ratio: ' + str(odds_ratio))
          print('P-value: ' + str(p_val))
```

```
Odds ratio: 0.846140267672
P-value: 8.80623124871e-09
```

As we see here, we get $p < 0.001$ and an odds-ratio which is significantly lower than 1, so we should reject the null hypothesis.

Chi-Square Test

```
In [435]: statistic, p_val, _, _ =scipy.stats.chi2_contingency(contingency_table, correction=True)
          print('Statistic value: ' + str(statistic))
          print('P-value: ' + str(p_val))
```

```
Statistic value: 32.1645713459
P-value: 1.41650330152e-08
```

We got a high χ^2 value and $p < 0.001$, so we again conclude that we should reject the null hypothesis.

1.3.2 2.2. Is Drug Prescription or Dosage Change Associated With a Reduced Rate of Readmission?

Our null hypothesis H_0 is that there is no correlation between drug prescription or dosage change and the rate of readmission. As before, we use the Fisher exact test and the Chi-square test for added robustness.

```
In [437]: drug_change_columns = ['metformin', 'repaglinide', 'nateglinide', 'chlorpropamide', 'glimepir
                                 'glipizide', 'glyburide', 'tolbutamide', 'pioglitazone', 'rosiglitazon
                                 'miglitol', 'troglitazone', 'tolazamide', 'examide', 'citoglipton', 'i
                                 'glyburide-metformin', 'glipizide-metformin', 'glimepiride-pioglitazon
                                 'metformin-rosiglitazone', 'metformin-pioglitazone', 'diabetesMed']
          drug_df = encounters_train[drug_change_columns]
          indicators = drug_df.apply(lambda x: ("Up" in x) or (x.diabetesMed == "Yes"), axis=1)
          df = pd.DataFrame(data = {'prescribed_or_upped': indicators, 'readmitted': encounters_train['
          ct = pd.crosstab(df.prescribed_or_upped, df.readmitted, margins=True)
          ct['readmitted'] = ct['<30']
          ct['not_readmitted'] = ct['>30'] + ct['NO']
          ct = ct[['readmitted', 'not_readmitted', 'All']]
          print(ct)
          N_readmitted_prescribed_or_upped = ct.readmitted[True]
          N_readmitted_not_prescribed_or_upped = ct.readmitted[False]
          N_not_readmitted_prescribed_or_upped = ct.not_readmitted[True]
          N_not_readmitted_not_prescribed_or_upped = ct.not_readmitted[False]
```

readmitted	readmitted	not_readmitted	All
prescribed_or_upped			
False	2028	18986	21014
True	8193	62251	70444
All	10221	81237	91458

Fisher Exact Test

```
In [438]: contingency_table = [[N_readmitted_prescribed_or_upped, N_readmitted_not_prescribed_or_upped]
                               [N_not_readmitted_prescribed_or_upped, N_not_readmitted_not_prescribed_o
          odds_ratio, p_val = stats.fisher_exact(contingency_table)
          print('Odds ratio: ' + str(odds_ratio))
          print('P-value: ' + str(p_val))
```

```
Odds ratio: 1.23214593449
P-value: 5.47127442969e-16
```

As we see here, we get $p < 0.001$ and an odds-ratio which is significantly higher than 1, so we should reject the null hypothesis.

Chi-Square Test

```
In [439]: statistic, p_val, _, _ = stats.chi2_contingency(contingency_table, correction=True)
          print('Statistic value: ' + str(statistic))
          print('P-value: ' + str(p_val))
```

```
Statistic value: 63.7112440982
P-value: 1.44059978458e-15
```

We got a high χ^2 value and $p < 0.001$, so we again conclude that we should reject the null hypothesis.

1.4 3.Clustering and Similarity

1.4.1 3.1. Defining a Metric

Since we are clustreting categorical data, one logical option is using the following metric:

Let X, Y be two rows of length k in the data set. Assume that for all $i \in [k]$, $X_i, Y_i \in A_i$ (A_i is a categorical field, for example the 'readmitted' field).

Then: $d(X,Y) = \sum_i \mathbb{1}[X_i \neq Y_i]$

A cluster centroid will be a point $C \in A_1 \times A_2 \times ... \times A_k$.

1.4.2 3.2. Using K-Modes to Cluster Patients

K-modes is a clustering algorithm which uses the metric defined above, and is closely related to K-Means.

It uses the same type of expectation-maximization steps, but updates the centroids at each iteration by the "mode" of the categories, which is the category that has the highest count (within the cluster).

For example, if $\{X^1, X^2, X^3\}$ are one cluster with centroid C, then our update will be:

$$C_i = argmax_{c \in A_i}(\mathbb{1}[X_i^1 = c] + \mathbb{1}[X_i^2 = c] + \mathbb{1}[X_i^3 = c])$$

```
In [440]: # cluster_df = pd.DataFrame({'res': encounters_train[['A1Cresult']]}, dtype="category")
          diag_1 = encounters_train[['diag_1']]['diag_1'].astype("category")
          diag_2 = encounters_train[['diag_2']]['diag_2'].astype("category")
          diag_3 = encounters_train[['diag_3']]['diag_3'].astype("category")
          A1Cres = encounters_train[['A1Cresult']]['A1Cresult'].astype("category")
          readmitted = encounters_train[['readmitted']]['readmitted'].astype("category")

          cols = {'diag_1': diag_1, 'diag_2': diag_2, 'diag_3': diag_3,
                  'A1Cres': A1Cres, 'readmitted': readmitted}
          cluster_df = pd.DataFrame(data = cols, dtype="category")
          c1 = np.array(cluster_df.diag_1.cat.codes)
          c2 = np.array(cluster_df.diag_2.cat.codes)
          c3 = np.array(cluster_df.diag_3.cat.codes)
          c4 = np.array(cluster_df.A1Cres.cat.codes)
          c5 = np.array(cluster_df.readmitted.cat.codes)
          t = np.matrix([c1, c2, c3, c4, c5]).transpose()
          km = kmodes.KModes(n_clusters=4, init='Huang', n_init=5, verbose=1)
          clusters = km.fit_predict(t)
          print(km.cluster_centroids_)
```

```
Init: initializing centroids
Init: initializing clusters
Starting iterations...
Run 1, iteration: 1/100, moves: 7824, cost: 266384.0
Run 1, iteration: 2/100, moves: 0, cost: 266384.0
Init: initializing centroids
Init: initializing clusters
Starting iterations...
Run 2, iteration: 1/100, moves: 10468, cost: 265376.0
Run 2, iteration: 2/100, moves: 0, cost: 265376.0
Init: initializing centroids
Init: initializing clusters
Starting iterations...
Run 3, iteration: 1/100, moves: 9550, cost: 286030.0
Run 3, iteration: 2/100, moves: 0, cost: 286030.0
Init: initializing centroids
Init: initializing clusters
```

```
Starting iterations...
Run 4, iteration: 1/100, moves: 11208, cost: 277867.0
Run 4, iteration: 2/100, moves: 2152, cost: 277867.0
Init: initializing centroids
Init: initializing clusters
Starting iterations...
Run 5, iteration: 1/100, moves: 11448, cost: 285525.0
Run 5, iteration: 2/100, moves: 0, cost: 285525.0
Best run was number 2
[[272 258 83 2 1]
 [259 76 83 2 2]
 [393 76 240 2 1]
 [233 131 386 2 2]]
```

Since we are going to cluster categorical data, a logical choice is to use the K-Modes algorithm. The algorithm uses the following metric: Let

The specifics are at:

```
(1, 2) Huang, Z.: Clustering large data sets with mixed numeric and categorical values, Proceedings of
```

```
In [441]: # get index<->category mappings:
          A1Cres_dict = dict( enumerate(cluster_df.A1Cres.cat.categories) )
          readmitted_dict = dict( enumerate(cluster_df.readmitted.cat.categories) )
```

```
In [442]: centroids = pd.DataFrame(km.cluster_centroids_)
          print('Clusters (rows are clusters, columns are diag_1, diag_2, diag_3, A1Cresult, readmitted
          print(centroids)
          # Cluster info:
          cluster_labels = pd.Series(clusters, dtype="category")
          print('\nCluster sizes:')
          cluster_labels.groupby(cluster_labels).count()
```

```
Clusters (rows are clusters, columns are diag_1, diag_2, diag_3, A1Cresult, readmitted):
     0    1    2  3  4
0  272  258   83  2  1
1  259   76   83  2  2
2  393   76  240  2  1
3  233  131  386  2  2

Cluster sizes:
```

```
Out[442]: 0    41670
          1    41250
          2     3589
          3     4949
          dtype: int64
```

We got 4 pretty big clusters, and their centroids are described above (each row is a centroid).

1.5 4. Prediction

Divide the training data into 10 folds for cross-validation:

```
In [443]: kf = KFold(n_splits=10, shuffle=True)
          fold_idxs = []
          for train_idxs, test_idxs in kf.split(encounters_train):
              fold_idxs.append({'train' : train_idxs, 'test': test_idxs})
```

1.5.1 4.1. Naïve Bayes

4.1.1. Binary Classification

Validation

```
In [444]: from sklearn.naive_bayes import MultinomialNB
          clf = MultinomialNB()
          scores = []
          for fold in fold_idxs:
              train_facts = encounters_train.iloc[fold['train']].copy()
              test_facts = encounters_train.iloc[fold['test']].copy()
              cats_to_factorize = ['race', 'gender', 'age', 'weight', 'change', 'diabetesMed', 'A1Cresul
              train_facts[cats_to_factorize] = train_facts[cats_to_factorize].apply(lambda x: pd.factor
              test_facts[cats_to_factorize] = test_facts[cats_to_factorize].apply(lambda x: pd.factoriz
              features = ['race', 'gender', 'age', 'weight', 'change', 'diabetesMed', 'A1Cresult']
              y_train_bool = train_facts.readmitted == '<30'
              y_train = y_train_bool.values
              X_train = train_facts[features].values
              y_test_bool = test_facts.readmitted == '<30'
              y_test = y_test_bool.values
              X_test = test_facts[features].values
              clf.fit(X_train,y_train)
              scores.append(clf.score(X_test, y_test))
          print('Average: ' + str(np.average(scores)))
          print('Variance: ' + str(np.var(scores)))
```

```
Average: 0.888243821121
Variance: 6.30739300437e-06
```

Test

```
In [445]: clf = MultinomialNB()
          train_facts = encounters_train.copy()
          test_facts = encounters_test.copy()
          cats_to_factorize = ['race', 'gender', 'age', 'weight', 'change', 'diabetesMed', 'A1Cresult']
          train_facts[cats_to_factorize] = train_facts[cats_to_factorize].apply(lambda x: pd.factorize(
          test_facts[cats_to_factorize] = test_facts[cats_to_factorize].apply(lambda x: pd.factorize(x)
          features = ['race', 'gender', 'age', 'weight', 'change', 'diabetesMed', 'A1Cresult']
          y_train_bool = train_facts.readmitted == '<30'
          y_train = y_train_bool.values
          X_train = train_facts[features].values
          y_test_bool = test_facts.readmitted == '<30'
          y_test = y_test_bool.values
          X_test = test_facts[features].values
          clf.fit(X_train,y_train)

          print('Test accuracy: ' + str(clf.score(X_test, y_test)))
```

```
Test accuracy: 0.889794334497
```

We got test accuracy of 0.89.

4.1.2. General Classification

```
In [446]: from sklearn.naive_bayes import MultinomialNB
          from sklearn.metrics import confusion_matrix
          clf = MultinomialNB(class_prior = [0.05,0.6,0.35])
          conf_mat = np.zeros((3,3))

          for fold in fold_idxs:
              train_facts = encounters_train.iloc[fold['train']].copy()
              test_facts = encounters_train.iloc[fold['test']].copy()
              cats_to_factorize = ['A1Cresult', 'diabetesMed', 'readmitted']
              train_facts[cats_to_factorize] = train_facts[cats_to_factorize].apply(lambda x: pd.factor
              test_facts[cats_to_factorize] = test_facts[cats_to_factorize].apply(lambda x: pd.factoriz
              features = ['A1Cresult']
              y_train = train_facts.readmitted.values
              X_train = train_facts[features].values
              y_test = test_facts.readmitted.values
              X_test = test_facts[features].values
              clf.fit(X_train,y_train)
              conf_mat += confusion_matrix(y_test, clf.predict(X_test))
          print(conf_mat)
```

```
[[    0.  36169.      0.]
 [    0.  37358.      0.]
 [    0.  17931.      0.]]
```

After trying many different combinations of features, it seems that naïve bayes isn't the right choice for this task.

```
In [447]: clf = MultinomialNB(class_prior = [0.05,0.6,0.35])
          conf_mat = np.zeros((3,3))

          train_facts = encounters_train.copy()
          test_facts = encounters_test.copy()
          cats_to_factorize = ['A1Cresult', 'diabetesMed', 'readmitted']
          train_facts[cats_to_factorize] = train_facts[cats_to_factorize].apply(lambda x: pd.factorize(
          test_facts[cats_to_factorize] = test_facts[cats_to_factorize].apply(lambda x: pd.factorize(x)
          features = ['A1Cresult']
          y_train = train_facts.readmitted.values
          X_train = train_facts[features].values
          y_test = test_facts.readmitted.values
          X_test = test_facts[features].values
          clf.fit(X_train,y_train)
          conf_mat += confusion_matrix(y_test, clf.predict(X_test))
          print(conf_mat)
```

```
[[    0.  5508.     0.]
 [    0.  3664.     0.]
 [    0.  1136.     0.]]
```

We see that also on the test data our naïve bayes classifier isn't very accurate.

1.5.2 4.2. K-Nearest Neighbors

For this task I am going to convert all the data to numerical data so I can use the Euclidean distance as a metric. This will be accomplished by defining "dummy variables" for the categorial data and leaving the numeric data as is.

In addition, I divide the ICD-9 codes from the table into 20 categories according to: https://en.wikipedia.org/wiki/List_of_ICD-9_codes

```
In [448]: def icd9_to_cat(icd9_code):
              try:
                  num = float(icd9_code)
                  if 1 <= num and num <= 139:
                      return 0
                  if 140 <= num and num <= 239:
                      return 1
                  if 240 <= num and num <= 279:
                      return 2
                  if 280 <= num and num <= 289:
                      return 3
                  if 280 <= num and num <= 289:
                      return 4
                  if 290 <= num and num <= 319:
                      return 5
                  if 320 <= num and num <= 359:
                      return 6
                  if 360 <= num and num <= 389:
                      return 7
                  if 390 <= num and num <= 459:
                      return 8
                  if 460 <= num and num <= 519:
                      return 9
                  if 520 <= num and num <= 579:
                      return 10
                  if 580 <= num and num <= 629:
                      return 11
                  if 630 <= num and num <= 679:
                      return 12
                  if 680 <= num and num <= 709:
                      return 13
                  if 710 <= num and num <= 739:
                      return 14
                  if 740 <= num and num <= 759:
                      return 15
                  if 760 <= num and num <= 779:
                      return 16
                  if 780 <= num and num <= 799:
                      return 17
                  if 800 <= num and num <= 999:
                      return 18
              except ValueError:
                  return 20

          def het_data_to_numerical(sample_data, numer_features, cat_features):
              df = pd.DataFrame()
              cat_dfs = []
              for cat_feat in cat_features:
                  cat_dfs.append(pd.get_dummies(sample_data[cat_feat], prefix=cat_feat))
              raw_cat =  pd.concat([sample_data[numer_features]] + cat_dfs + [sample_data['readmitted']]
              return raw_cat.fillna(-1)
```

4.2.1. Binary Classification

Validation

In [449]:
```
from sklearn.neighbors import KNeighborsClassifier

        cat_features = ['A1Cresult', 'insulin', 'change', 'diabetesMed', 'diag_1', 'diag_2']
        numer_features = ['number_emergency', 'num_procedures']
        all_features = cat_features + numer_features

        accs = []
        for fold in fold_idxs:
            train = encounters_train.iloc[fold['train']].copy()
            test = encounters_train.iloc[fold['test']].copy()
            train['diag_1'] = train['diag_1'].apply(icd9_to_cat)
            train['diag_2'] = train['diag_2'].apply(icd9_to_cat)
            train['diag_3'] = train['diag_3'].apply(icd9_to_cat)
            test['diag_1'] = test['diag_1'].apply(icd9_to_cat)
            test['diag_2'] = test['diag_2'].apply(icd9_to_cat)
            test['diag_3'] = test['diag_3'].apply(icd9_to_cat)
            train_reduced = het_data_to_numerical(train, numer_features, cat_features)
            test_reduced = het_data_to_numerical(test, numer_features, cat_features)
            comb_feat = list(set.intersection(set(train_reduced.columns), set(test_reduced.columns)) -
            X_train = train_reduced[comb_feat]
            y_train = train.readmitted == '<30'
            y_train = y_train

            X_test = test_reduced[comb_feat]
            y_test = test.readmitted == '<30'
            y_test = y_test

            neigh = KNeighborsClassifier(n_neighbors=3)
            print('train fold')
            neigh.fit(X_train, y_train)
            print('test fold')
            accs.append(neigh.score(X_test, y_test))
```

```
train fold
test fold
train fold
test fold
train fold
test fold
train fold
test fold
train fold
test fold
train fold
test fold
train fold
test fold
train fold
test fold
train fold
test fold
train fold
test fold
train fold
test fold
```

```
In [450]: print('Average: ' + str(np.average(accs)))
          print('std: ' + str(np.std(accs)))
```

```
Average: 0.861040093534
std: 0.0045513168534
```

test

```
In [451]: from sklearn.neighbors import KNeighborsClassifier

          cat_features = ['A1Cresult', 'insulin', 'change', 'diabetesMed', 'diag_1', 'diag_2']
          numer_features = ['number_emergency', 'num_procedures']
          all_features = cat_features + numer_features

          train = encounters_train.copy()
          test = encounters_test.copy()
          train['diag_1'] = train['diag_1'].apply(icd9_to_cat)
          train['diag_2'] = train['diag_2'].apply(icd9_to_cat)
          train['diag_3'] = train['diag_3'].apply(icd9_to_cat)
          test['diag_1'] = test['diag_1'].apply(icd9_to_cat)
          test['diag_2'] = test['diag_2'].apply(icd9_to_cat)
          test['diag_3'] = test['diag_3'].apply(icd9_to_cat)
          train_reduced = het_data_to_numerical(train, numer_features, cat_features)
          test_reduced = het_data_to_numerical(test, numer_features, cat_features)
          comb_feat = list(set.intersection(set(train_reduced.columns), set(test_reduced.columns)) - {'
          X_train = train_reduced[comb_feat]
          y_train = train.readmitted == '<30'
          y_train = y_train

          X_test = test_reduced[comb_feat]
          y_test = test.readmitted == '<30'
          y_test = y_test

          neigh = KNeighborsClassifier(n_neighbors=3)
          print('train final')
          neigh.fit(X_train, y_train)
          print('test final')
          print('accuracy: ' + str(neigh.score(X_test, y_test)))
```

```
train final
test final
accuracy: 0.863019014358
```

4.2.2. General Classification

validation

```
In [452]: cat_features = ['A1Cresult', 'insulin', 'change', 'diabetesMed', 'diag_1', 'diag_2']
          numer_features = ['number_emergency', 'num_procedures']
          all_features = cat_features + numer_features

          conf_mat = np.zeros((3,3))
          for fold in fold_idxs:
              train = encounters_train.iloc[fold['train']].copy()
              test = encounters_train.iloc[fold['test']].copy()
```

```
            train['diag_1'] = train['diag_1'].apply(icd9_to_cat)
            train['diag_2'] = train['diag_2'].apply(icd9_to_cat)
            train['diag_3'] = train['diag_3'].apply(icd9_to_cat)
            test['diag_1'] = test['diag_1'].apply(icd9_to_cat)
            test['diag_2'] = test['diag_2'].apply(icd9_to_cat)
            test['diag_3'] = test['diag_3'].apply(icd9_to_cat)
            train_reduced = het_data_to_numerical(train, numer_features, cat_features)
            test_reduced = het_data_to_numerical(test, numer_features, cat_features)
            comb_feat = list(set.intersection(set(train_reduced.columns), set(test_reduced.columns)) -
            X_train = train_reduced[comb_feat]
            y_train = train.readmitted

            X_test = test_reduced[comb_feat]
            y_test = test.readmitted
            neigh = KNeighborsClassifier(n_neighbors=3)
            print('train fold')
            neigh.fit(X_train, y_train)
            print('test fold')
            accs.append(neigh.score(X_test, y_test))
            conf_mat += confusion_matrix(y_test, neigh.predict(X_test))
        print(conf_mat)
```

```
train fold
test fold
train fold
test fold
train fold
test fold
train fold
test fold
train fold
test fold
train fold
test fold
train fold
test fold
train fold
test fold
train fold
test fold
train fold
test fold
[[  1790.   3503.   4928.]
 [  5363.  11032.  15486.]
 [  7521.  14858.  26977.]]
```

test

In [453]:
```
cat_features = ['A1Cresult', 'insulin', 'change', 'diabetesMed', 'diag_1', 'diag_2']
numer_features = ['number_emergency', 'num_procedures']
all_features = cat_features + numer_features

conf_mat = np.zeros((3,3))

train = encounters_train.copy()
```

```
        test = encounters_test.copy()
        train['diag_1'] = train['diag_1'].apply(icd9_to_cat)
        train['diag_2'] = train['diag_2'].apply(icd9_to_cat)
        train['diag_3'] = train['diag_3'].apply(icd9_to_cat)
        test['diag_1'] = test['diag_1'].apply(icd9_to_cat)
        test['diag_2'] = test['diag_2'].apply(icd9_to_cat)
        test['diag_3'] = test['diag_3'].apply(icd9_to_cat)
        train_reduced = het_data_to_numerical(train, numer_features, cat_features)
        test_reduced = het_data_to_numerical(test, numer_features, cat_features)
        comb_feat = list(set.intersection(set(train_reduced.columns), set(test_reduced.columns)) - {'
        X_train = train_reduced[comb_feat]
        y_train = train.readmitted

        X_test = test_reduced[comb_feat]
        y_test = test.readmitted
        neigh = KNeighborsClassifier(n_neighbors=3)
        print('train final')
        neigh.fit(X_train, y_train)
        print('test final')
        accs.append(neigh.score(X_test, y_test))
        conf_mat += confusion_matrix(y_test, neigh.predict(X_test))
        print(conf_mat)
```

```
train final
test final
[[  196.   374.   566.]
 [  609.  1192.  1863.]
 [  842.  1569.  3097.]]
```

1.5.3 4.3. Random Forest

4.3.1. Binary Classification

validation

In [454]:
```
r = RandomForestClassifier(n_estimators=100)
cat_features = ['A1Cresult', 'insulin', 'change', 'diabetesMed', 'diag_1', 'diag_2']
numer_features = ['number_emergency', 'num_procedures']
all_features = cat_features + numer_features

accs = []
for fold in fold_idxs:
    train = encounters_train.iloc[fold['train']].copy()
    test = encounters_train.iloc[fold['test']].copy()
    train['diag_1'] = train['diag_1'].apply(icd9_to_cat)
    train['diag_2'] = train['diag_2'].apply(icd9_to_cat)
    train['diag_3'] = train['diag_3'].apply(icd9_to_cat)
    test['diag_1'] = test['diag_1'].apply(icd9_to_cat)
    test['diag_2'] = test['diag_2'].apply(icd9_to_cat)
    test['diag_3'] = test['diag_3'].apply(icd9_to_cat)
    train_reduced = het_data_to_numerical(train, numer_features, cat_features)
    test_reduced = het_data_to_numerical(test, numer_features, cat_features)
    comb_feat = list(set.intersection(set(train_reduced.columns), set(test_reduced.columns))
    X_train = train_reduced[comb_feat]
    y_train = train.readmitted == '<30'
```

```
            y_train = y_train

            X_test = test_reduced[comb_feat]
            y_test = test.readmitted == '<30'
            y_test = y_test

            print('train fold')
            r.fit(X_train, y_train)
            print('test fold')
            accs.append(r.score(X_test, y_test))
        print('Average: ' + str(np.average(accs)))
        print('std: ' + str(np.std(accs)))
```

```
train fold
test fold
train fold
test fold
train fold
test fold
train fold
test fold
train fold
test fold
train fold
test fold
train fold
test fold
train fold
test fold
train fold
test fold
train fold
test fold
train fold
test fold
Average: 0.878523543173
std: 0.00318218775574
```

test

In [455]:
```
r = RandomForestClassifier(n_estimators=100)
cat_features = ['A1Cresult', 'insulin', 'change', 'diabetesMed', 'diag_1', 'diag_2']
numer_features = ['number_emergency', 'num_procedures']
all_features = cat_features + numer_features

train = encounters_train.copy()
test = encounters_test.copy()
train['diag_1'] = train['diag_1'].apply(icd9_to_cat)
train['diag_2'] = train['diag_2'].apply(icd9_to_cat)
train['diag_3'] = train['diag_3'].apply(icd9_to_cat)
test['diag_1'] = test['diag_1'].apply(icd9_to_cat)
test['diag_2'] = test['diag_2'].apply(icd9_to_cat)
test['diag_3'] = test['diag_3'].apply(icd9_to_cat)
train_reduced = het_data_to_numerical(train, numer_features, cat_features)
test_reduced = het_data_to_numerical(test, numer_features, cat_features)
comb_feat = list(set.intersection(set(train_reduced.columns), set(test_reduced.columns)) - {'
X_train = train_reduced[comb_feat]
```

```
        y_train = train.readmitted == '<30'
        y_train = y_train

        X_test = test_reduced[comb_feat]
        y_test = test.readmitted == '<30'
        y_test = y_test

        print('train final')
        r.fit(X_train, y_train)
        print('test final')
        print('accuracy: ' + str(r.score(X_test, y_test)))
```

```
train final
test final
accuracy: 0.87980209546
```

And our accuracy is 0.88

4.3.2. General Classification

validation

In [456]:
```
from sklearn.metrics import confusion_matrix

        r = RandomForestClassifier(n_estimators=50)
        cat_features = ['A1Cresult', 'insulin', 'change', 'diabetesMed', 'diag_1', 'diag_2']
        numer_features = ['number_emergency', 'num_procedures']
        all_features = cat_features + numer_features

        conf_mat = np.zeros((3,3))
        for fold in fold_idxs:
            train = encounters_train.iloc[fold['train']].copy()
            test = encounters_train.iloc[fold['test']].copy()
            train['diag_1'] = train['diag_1'].apply(icd9_to_cat)
            train['diag_2'] = train['diag_2'].apply(icd9_to_cat)
            train['diag_3'] = train['diag_3'].apply(icd9_to_cat)
            test['diag_1'] = test['diag_1'].apply(icd9_to_cat)
            test['diag_2'] = test['diag_2'].apply(icd9_to_cat)
            test['diag_3'] = test['diag_3'].apply(icd9_to_cat)
            train_reduced = het_data_to_numerical(train, numer_features, cat_features)
            test_reduced = het_data_to_numerical(test, numer_features, cat_features)
            comb_feat = list(set.intersection(set(train_reduced.columns), set(test_reduced.columns)) -
            X_train = train_reduced[comb_feat]
            y_train = train.readmitted

            X_test = test_reduced[comb_feat]
            y_test = test.readmitted

            print('train fold')
            r.fit(X_train, y_train)
            print('test fold')
            conf_mat += confusion_matrix(y_test, r.predict(X_test))
        print('Confusion matrix:')
        print(conf_mat)
```

```
train fold
test fold
train fold
test fold
train fold
test fold
train fold
test fold
train fold
test fold
train fold
test fold
train fold
test fold
train fold
test fold
train fold
test fold
train fold
test fold
Confusion matrix:
[[   349.   2653.   7219.]
 [   855.   8273.  22753.]
 [  1035.   9522.  38799.]]
```

We see that the sum of the confusion matrices isn't ideal.

test

```
In [459]: r = RandomForestClassifier(n_estimators=50)
          cat_features = ['A1Cresult', 'insulin', 'change', 'diabetesMed', 'diag_1', 'diag_2']
          numer_features = ['number_emergency', 'num_procedures']
          all_features = cat_features + numer_features

          conf_mat = np.zeros((3,3))
          train = encounters_train.copy()
          test = encounters_train.copy()
          train['diag_1'] = train['diag_1'].apply(icd9_to_cat)
          train['diag_2'] = train['diag_2'].apply(icd9_to_cat)
          train['diag_3'] = train['diag_3'].apply(icd9_to_cat)
          test['diag_1'] = test['diag_1'].apply(icd9_to_cat)
          test['diag_2'] = test['diag_2'].apply(icd9_to_cat)
          test['diag_3'] = test['diag_3'].apply(icd9_to_cat)
          train_reduced = het_data_to_numerical(train, numer_features, cat_features)
          test_reduced = het_data_to_numerical(test, numer_features, cat_features)
          comb_feat = list(set.intersection(set(train_reduced.columns), set(test_reduced.columns)) - {'
          X_train = train_reduced[comb_feat]
          y_train = train.readmitted

          X_test = test_reduced[comb_feat]
          y_test = test.readmitted

          print('train final')
          r.fit(X_train, y_train)
          print('test final')
```

```
            conf_mat += confusion_matrix(y_test, r.predict(X_test))

            print('Confusion matrix:')
            print(conf_mat)

train final
test final
Confusion matrix:
[[  2008.   1863.   6350.]
 [   312.  12757.  18812.]
 [   338.   5416.  43602.]]
```

This already looks good - the main diagonal has the highest values with a big gap!