Prediction of Survival Rate in Titanic Dataset

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Executive Summary

The goal of this analysis was to find out the predictors of whether or not a Titanic passenger would have survived the Titanic accident. The second goal was to evaluate multiple classification algorithms and determine the most accurate and interpretable.

Titanic dataset was provided by AIM ACCESS lab. The dataset was cleaned and run on multiple classification models. The impact of min-max and standard scaling on the dataset to accuracy were also explored. The minimum target accuracy (1.25 X Proportional Chance Criterion) is 66%.

The model that yielded the highest accuracy was gradient boosting machines (GBM) with around 81.2% accuracy using learning rate of 0.1 and maximum depth of 6. However, the downside was it lacked interpretability.

The model that yielded second best accuracy was random forest with accuracy of 80.8%. The highest predictors were ticket number and sex.

The third was nonlinear SVM with RBF kernel and C=0.75 and min-max scaled dataset which yielded 80.8% accuracy. However, the best predictors were not determined for this model.

Fourth, decision tree yielded 80.3% accuracy at maximum depth of 3. The advantage of the decision tree was its interpretability as a tree diagram could be constructed of the step-by-step process in classification process.

Dimensionally reducing the dataset prior to running in GBM and random forest decreased accuracy.

From this analysis, it was found that sex was the highest predictor of whether or not a person would survive the accident. The proportion of females in the survivors were higher than the males, whereas the proportion of females in the non-survivors were much less than the males.

For the models, GBM proved most accurate in classifying and may be used if the goal is merely for prediction. However, for the balance between interpretability and prediction, decision trees classifier is deemed preferrable.

Description of Dataset

AIM provided the dataset for this analysis. The columns in the dataset are:

1. pclass - ticket class (1 - 1st, 2 - 2nd, 3 - 3rd)
2. name - name of passenger
3. sex - sex of passenger
4. age - age of passenger
5. sibsp - no. of siblings or spouses aboard the Titanic
6. parch - no. of parents or children aboard
7. ticket - ticket number
8. fare - passenger fare
9. cabin - cabin number
10. embarked - port of embarkation (C = Cherbourg; Q = Queenstown; S = Southampton)
11. target - whether the passenger survived or not (1 - yes, 0 - no)

Descriptions were sourced from https://github.com/awesomedata/awesome-public-datasets/issues/351 (https://github.com/awesomedata/awesome-public-datasets/issues/351)

Dataset Preparation

We first loaded the `titanic.xls` dataset in a dataframe.

In [1]:
```
import pandas as pd
import numpy as np
df0 = pd.read_excel('titanic.xls')
```

We checked the first 5 rows and last 5 rows below.

```
In [2]: display(df0.head())
        display(df0.tail())
```

	pclass	name	sex	age	sibsp	parch	ticket	fare	cabin	embarked	target
0	1	Allen, Miss. Elisabeth Walton	female	29.0000	0	0	24160	211.3375	B5	S	1
1	1	Allison, Master. Hudson Trevor	male	0.9167	1	2	113781	151.5500	C22 C26	S	1
2	1	Allison, Miss. Helen Loraine	female	2.0000	1	2	113781	151.5500	C22 C26	S	0
3	1	Allison, Mr. Hudson Joshua Creighton	male	30.0000	1	2	113781	151.5500	C22 C26	S	0
4	1	Allison, Mrs. Hudson J C (Bessie Waldo Daniels)	female	25.0000	1	2	113781	151.5500	C22 C26	S	0

	pclass	name	sex	age	sibsp	parch	ticket	fare	cabin	embarked	target
1304	3	Zabour, Miss. Hileni	female	14.5	1	0	2665	14.4542	NaN	C	0
1305	3	Zabour, Miss. Thamine	female	NaN	1	0	2665	14.4542	NaN	C	0
1306	3	Zakarian, Mr. Mapriededer	male	26.5	0	0	2656	7.2250	NaN	C	0
1307	3	Zakarian, Mr. Ortin	male	27.0	0	0	2670	7.2250	NaN	C	0
1308	3	Zimmerman, Mr. Leo	male	29.0	0	0	315082	7.8750	NaN	S	0

The dataset contains 1,309 rows and 11 columns.

```
In [3]: df0.shape

Out[3]: (1309, 11)
```

Among the columns `age`, `cabin`, and `embarked` contain null values.

```
In [4]: df0.info()

<class 'pandas.core.frame.DataFrame'>
RangeIndex: 1309 entries, 0 to 1308
Data columns (total 11 columns):
pclass      1309 non-null int64
name        1309 non-null object
sex         1309 non-null object
age         1046 non-null float64
sibsp       1309 non-null int64
parch       1309 non-null int64
ticket      1309 non-null object
fare        1308 non-null float64
cabin       295 non-null object
embarked    1307 non-null object
target      1309 non-null int64
dtypes: float64(2), int64(4), object(5)
memory usage: 112.6+ KB
```

The original dataset contains 10 features and 1 target column. Among these features, `name` was dropped because it merely identifies each individual and doesn't inform us of information about the individual.

In [5]:
```
df1 = df0.drop('name', axis=1)
df1.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 1309 entries, 0 to 1308
Data columns (total 10 columns):
pclass      1309 non-null int64
sex         1309 non-null object
age         1046 non-null float64
sibsp       1309 non-null int64
parch       1309 non-null int64
ticket      1309 non-null object
fare        1308 non-null float64
cabin       295 non-null object
embarked    1307 non-null object
target      1309 non-null int64
dtypes: float64(2), int64(4), object(4)
memory usage: 102.3+ KB
```

`cabin` column contains too many null values. This too was dropped.

In [6]:
```
df2 = df1.drop('cabin', axis=1)
df2.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 1309 entries, 0 to 1308
Data columns (total 9 columns):
pclass      1309 non-null int64
sex         1309 non-null object
age         1046 non-null float64
sibsp       1309 non-null int64
parch       1309 non-null int64
ticket      1309 non-null object
fare        1308 non-null float64
embarked    1307 non-null object
target      1309 non-null int64
dtypes: float64(2), int64(4), object(3)
memory usage: 92.1+ KB
```

20% of `age` are null values. This was decided to be retained, but missing values were imputed. Similarly, since only 2 of values in `embarked` are missing, these too were imputed.

In [7]:
```
len(df2[df2.age.isnull()])/len(df2)*100
```

Out[7]:
```
20.091673032849503
```

We defined a class to impute or "fill in" missing values with the median per column for numerical data and mode for categorical data.

In [8]:
```
from sklearn.base import TransformerMixin

class DataFrameImputer(TransformerMixin):
    def __init__(self):
        """Impute missing values.
        Columns of dtype object are imputed with the most frequent value
        in column.
        Columns of other types are imputed with median of column.
        """

    def fit(self, X, y=None):
        self.fill = pd.Series([X[c].value_counts().index[0]
                               if X[c].dtype == np.dtype('O') else X[c].median() for c in X],
                              index=X.columns)
        return self

    def transform(self, X, y=None):
        return X.fillna(self.fill)
```

Missing values were imputed and the new dataset was saved in a new dataframe.

In [9]:
```
df3 = DataFrameImputer().fit_transform(df2)
```

```
In [10]: df3.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 1309 entries, 0 to 1308
Data columns (total 9 columns):
pclass      1309 non-null int64
sex         1309 non-null object
age         1309 non-null float64
sibsp       1309 non-null int64
parch       1309 non-null int64
ticket      1309 non-null object
fare        1309 non-null float64
embarked    1309 non-null object
target      1309 non-null int64
dtypes: float64(2), int64(4), object(3)
memory usage: 92.1+ KB
```

```
In [11]: df3.ticket.head(10)
```

```
Out[11]: 0       24160
         1      113781
         2      113781
         3      113781
         4      113781
         5       19952
         6       13502
         7      112050
         8       11769
         9    PC 17609
         Name: ticket, dtype: object
```

`ticket` values contain numerical and mixed letters and numerical values. We split the numerical values from the letter values and saved in separate columns `tick_code` and `tick_num`

```
In [12]: import re

         pat = re.compile('\d.*')
         tick_code = pd.DataFrame(df3.ticket.astype(str).str.replace(pat, '').tolist(), columns =['tick_cod
         e'])
```

```
In [13]: pat = re.compile('[^\d]')
         tick_num = pd.DataFrame(df3.ticket.astype(str).str.replace(pat, '').str.strip(
             '').tolist(), columns=['tick_num'])
```

```
In [14]: df4 = pd.concat([df3, tick_num, tick_code], axis=1).drop('ticket', axis=1)
         display(df4.head())
         display(df4.tail())
```

	pclass	sex	age	sibsp	parch	fare	embarked	target	tick_num	tick_code
0	1	female	29.0000	0	0	211.3375	S	1	24160	
1	1	male	0.9167	1	2	151.5500	S	1	113781	
2	1	female	2.0000	1	2	151.5500	S	0	113781	
3	1	male	30.0000	1	2	151.5500	S	0	113781	
4	1	female	25.0000	1	2	151.5500	S	0	113781	

	pclass	sex	age	sibsp	parch	fare	embarked	target	tick_num	tick_code
1304	3	female	14.5	1	0	14.4542	C	0	2665	
1305	3	female	28.0	1	0	14.4542	C	0	2665	
1306	3	male	26.5	0	0	7.2250	C	0	2656	
1307	3	male	27.0	0	0	7.2250	C	0	2670	
1308	3	male	29.0	0	0	7.8750	S	0	315082	

```
In [15]: df4.tick_num[df4.tick_num == ''] = 0
         df4['tick_num'] = df4.tick_num.astype('int')
```

```
/Users/fernandojavier/anaconda3/lib/python3.6/site-packages/ipykernel_launcher.py:1: SettingWithC
opyWarning:
A value is trying to be set on a copy of a slice from a DataFrame

See the caveats in the documentation: http://pandas.pydata.org/pandas-docs/stable/indexing.html#i
ndexing-view-versus-copy
  """Entry point for launching an IPython kernel.
```

We checked the unique categorical variables in the columns `target`, `pclass`, `sex`, `embarked`, and `tick_code`.

In [16]:
```
from collections import Counter
cols_ = ['target', 'pclass', 'sex', 'embarked', 'tick_code']
for c in cols_:
    counts = Counter(df4[c])

    print("Counts per categorical value in %s" % c)
    display(pd.DataFrame.from_dict(counts, orient='index', columns=['counts']))
```

```
Counts per categorical value in target
```

	counts
1	500
0	809

```
Counts per categorical value in pclass
```

	counts
1	323
2	277
3	709

```
Counts per categorical value in sex
```

	counts
female	466
male	843

```
Counts per categorical value in embarked
```

	counts
S	916
C	270
Q	123

```
Counts per categorical value in tick_code
```

	counts
	957
PC	92
W.E.P.	2
WE/P	2
F.C.	3
P/PP	2
C.A.	46
C.A./SOTON	1
S.O.P.	1
F.C.C.	9
SC/AH	4
W./C.	14
S.O.C.	7
SC/PARIS	11
S.W./PP	1
W/C	1
SCO/W	1
SO/C	1
SC/AH Basle	1
SC/Paris	5
SC	2
S.O./P.P.	7
S.C./PARIS	3
SC/A.	1
SW/PP	1
CA	10
SOTON/O	3
C	8
SOTON/O.Q.	16
A/	31
PP	4
A./	3
SOTON/OQ	8
S.P.	1
SC/A	1
AQ/	2
STON/O	7
A.	1
LINE	4
STON/O	14
A/S	1
A.	3
A	1
Fa	1
S.C./A.	1
LP	1

	counts
CA.	12
STON/OQ.	1

We observed that `tick code` have some variables that are the same but are reported differently. This was cleaned by removing `.` and converting variables to lower case.

```
In [17]: df5 = df4.copy()
         df5['tick_code'] = df4['tick_code'].str.replace('.', '').str.lower().str.strip()
```

```
In [18]: df = df5.copy()
```

Exploratory Data Analysis

```
In [19]: import matplotlib.pyplot as plt
```

We first investigated the counts per categorical data, and the corresponding proportions. Some initial findings are:

1. The proportion of survivors to non-survivors in the dataset is 38:61
2. 24% are first class passengers, 21% are 2nd class, and 54% are 3rd class passengers
3. 35% are female while 64% are male
4. 70% embarked at Southampton, 21% at Cherbourg, and 9% at Queenstown.

In [20]:
```
cols_ = ['target', 'pclass', 'sex', 'embarked', 'tick_code']
for c in cols_:
    counts = Counter(df[c])

    print("Counts per categorical value in %s" % c)

    a = pd.DataFrame.from_dict(counts, orient='index', columns=['counts'])
    a['%'] = a.values/np.sum(a.values)*100

    display(a)
```

```
Counts per categorical value in target
```

	counts	%
1	500	38.197097
0	809	61.802903

```
Counts per categorical value in pclass
```

	counts	%
1	323	24.675325
2	277	21.161192
3	709	54.163484

```
Counts per categorical value in sex
```

	counts	%
female	466	35.599694
male	843	64.400306

```
Counts per categorical value in embarked
```

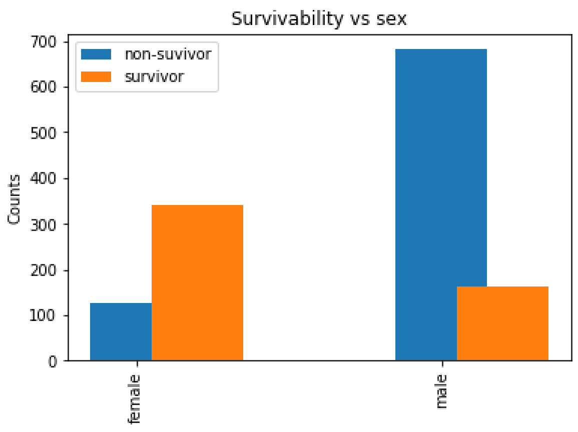
	counts	%
S	916	69.977082
C	270	20.626432
Q	123	9.396486

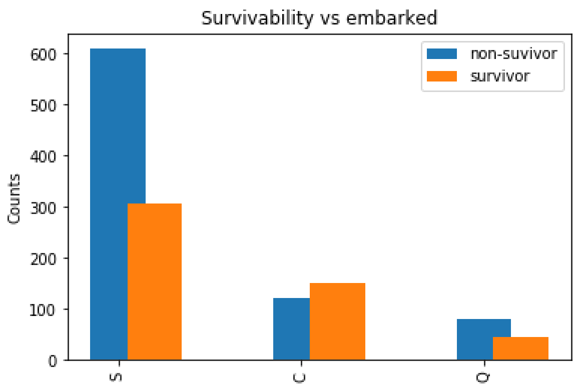
```
Counts per categorical value in tick_code
```

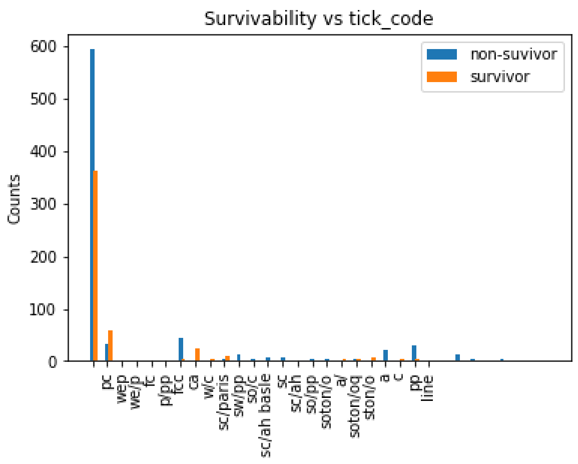
	counts	%
	957	73.109244
pc	92	7.028266
wep	2	0.152788
we/p	2	0.152788
fc	3	0.229183
p/pp	2	0.152788
ca	68	5.194805
ca/soton	1	0.076394
sop	1	0.076394
fcc	9	0.687548
sc/ah	4	0.305577
w/c	15	1.145913
soc	7	0.534759
sc/paris	19	1.451490
sw/pp	2	0.152788
sco/w	1	0.076394
so/c	1	0.076394
sc/ah basle	1	0.076394
sc	2	0.152788
so/pp	7	0.534759
sc/a	3	0.229183
soton/o	3	0.229183
c	8	0.611154
soton/oq	24	1.833461
a/	34	2.597403
pp	4	0.305577
sp	1	0.076394
aq/	2	0.152788
ston/o	21	1.604278
a	5	0.381971
line	4	0.305577
a/s	1	0.076394
fa	1	0.076394
lp	1	0.076394
ston/oq	1	0.076394

From the charts below, we found that **there are far more males than females for non-survivors. And there are more females than males for survivors.**

```
In [21]: labels = ['non-suvivor', 'survivor']
         cols_ = ['sex', 'embarked', 'tick_code']
         for j in range(len(cols_)):
             c = cols_[j]
             for i in range(2):
                 _ = Counter(df[c][df['target'] == i])
                 plt.bar(np.array(range(len(_.keys())))+i/5, _.values(), label=labels[i], width=0.3)
                 plt.xticks(range(len(_.keys())), _.keys(), rotation='vertical')
                 plt.title("Survivability vs %s" % c)
                 plt.ylabel('Counts')
                 plt.legend()
             plt.show()
```







Looking at the summary statistics, we gleaned that:

1. The mean age of passengers was 29.5 years
2. The mean number of siblings/spouses on board per passenger was 0.5
3. The mean number of parents and children on board per passenger was 0.4
4. The average fare was 33.3
5. 75% of passengers have ticket numbers below 347082

```
In [22]: df.describe()
```

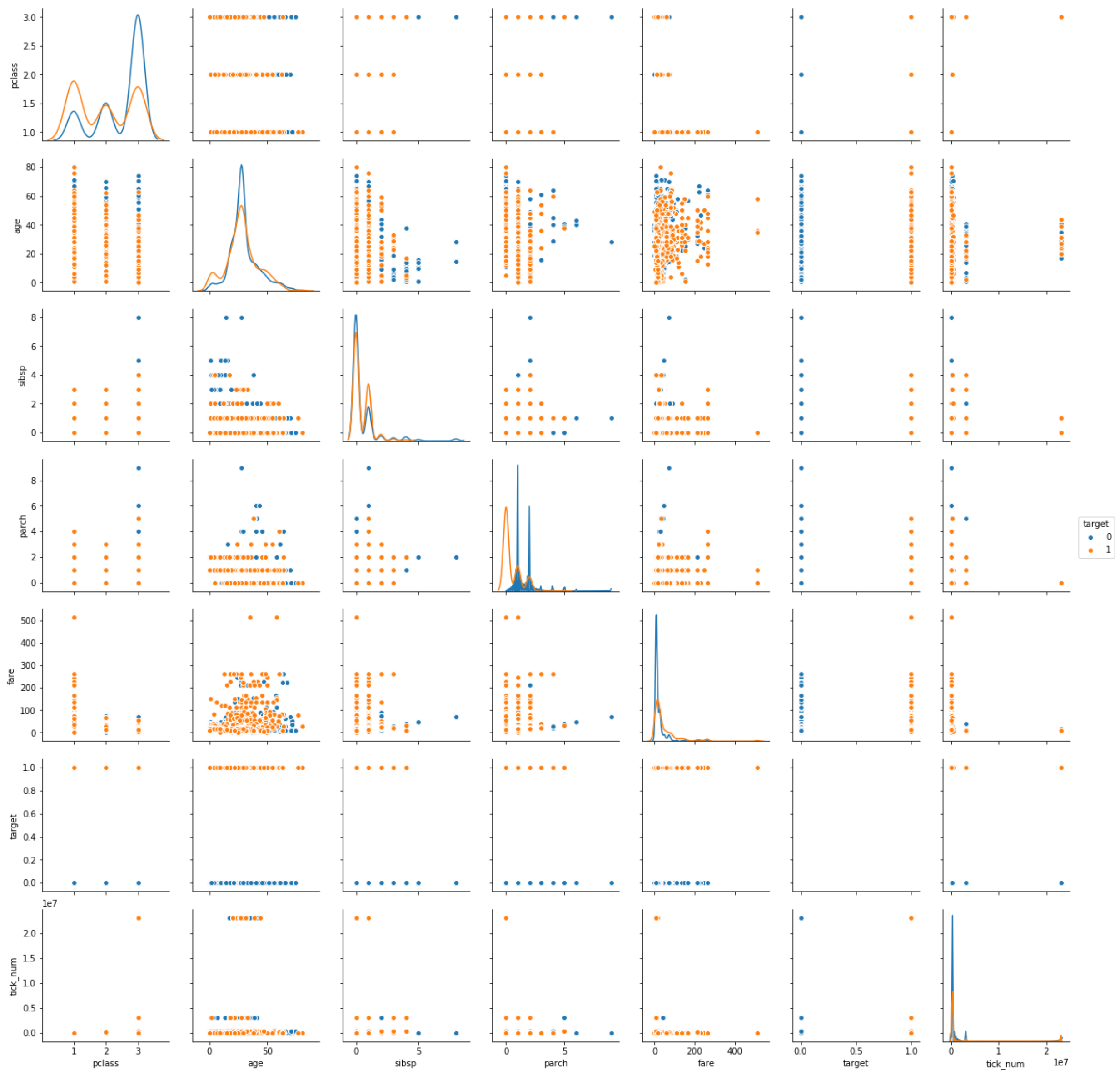
```
Out[22]:
```

	pclass	age	sibsp	parch	fare	target	tick_num
count	1309.000000	1309.000000	1309.000000	1309.000000	1309.000000	1309.000000	1.309000e+03
mean	2.294882	29.503183	0.498854	0.385027	33.281086	0.381971	6.579261e+05
std	0.837836	12.905246	1.041658	0.865560	51.741500	0.486055	3.109678e+06
min	1.000000	0.166700	0.000000	0.000000	0.000000	0.000000	0.000000e+00
25%	2.000000	22.000000	0.000000	0.000000	7.895800	0.000000	1.488800e+04
50%	3.000000	28.000000	0.000000	0.000000	14.454200	0.000000	1.129010e+05
75%	3.000000	35.000000	1.000000	0.000000	31.275000	1.000000	3.470820e+05
max	3.000000	80.000000	8.000000	9.000000	512.329200	1.000000	2.310129e+07

We then plotted the histograms of each variable and scatterplots of two variables. Blue dots indicate non-survivors and orange dots indicate survivors.

In [23]:
```
import seaborn as sns

sns.pairplot(df, hue='target', diag_kind='kde');
```

```
/Users/fernandojavier/anaconda3/lib/python3.6/site-packages/statsmodels/nonparametric/kde.py:488:
RuntimeWarning: invalid value encountered in true_divide
  binned = fast_linbin(X, a, b, gridsize) / (delta * nobs)
/Users/fernandojavier/anaconda3/lib/python3.6/site-packages/statsmodels/nonparametric/kdetools.p
y:34: RuntimeWarning: invalid value encountered in double_scalars
  FAC1 = 2*(np.pi*bw/RANGE)**2
/Users/fernandojavier/anaconda3/lib/python3.6/site-packages/numpy/core/_methods.py:26: RuntimeWar
ning: invalid value encountered in reduce
  return umr_maximum(a, axis, None, out, keepdims)
```



Looking at the histograms and scatterplots, we can see that **no single variable can clearly separate the survivors from the non-survivors, except possibly for the number of children or parents on board, `parch`.**

Dummification of Categorical Data

In order to use the classification models, the values in the dataframe have to be numerical. **The categorical feature values were converted to numerical values using one-hot encoding through `get_dummies` method** which converts all unique values into separate "features" or columns which may take only 0 or 1. 0 if the observation/sample/data point does not possess the feature and 1 if it does. This is appropriate because it's not possible to tell which categorical value is better over the other. The 1s and 0s generated by one-hot encoding merely act like an indicator whether or not the feature applies for a certain data point.

In this case, we we applied one-hot encoding for `sex`, `embarked`, and `tick_code`.

In [24]:
```
df.head()
```

Out[24]:

	pclass	sex	age	sibsp	parch	fare	embarked	target	tick_num	tick_code
0	1	female	29.0000	0	0	211.3375	S	1	24160	
1	1	male	0.9167	1	2	151.5500	S	1	113781	
2	1	female	2.0000	1	2	151.5500	S	0	113781	
3	1	male	30.0000	1	2	151.5500	S	0	113781	
4	1	female	25.0000	1	2	151.5500	S	0	113781	

In [25]:
```
sex_ = pd.get_dummies(df[['sex']], drop_first=True)
embarked_ = pd.get_dummies(df[['embarked']], drop_first=True)
tick_code_ = df.tick_code.str.get_dummies(sep='/')
```

In [26]:
```
dums = pd.concat([sex_, embarked_, tick_code_], axis=1)
dums.head()
```

Out[26]:

	sex_male	embarked_Q	embarked_S	a	ah	ah basle	aq	c	ca	fa	...	so	soc	sop	soton	sp	ston	sw	w	we	wep
0	0	0	1	0	0	0	0	0	0	0	...	0	0	0	0	0	0	0	0	0	0
1	1	0	1	0	0	0	0	0	0	0	...	0	0	0	0	0	0	0	0	0	0
2	0	0	1	0	0	0	0	0	0	0	...	0	0	0	0	0	0	0	0	0	0
3	1	0	1	0	0	0	0	0	0	0	...	0	0	0	0	0	0	0	0	0	0
4	0	0	1	0	0	0	0	0	0	0	...	0	0	0	0	0	0	0	0	0	0

5 rows × 33 columns

The cleaned dataframe after removing `target` and after one-hot encoding was saved in `X_clean`.

In [27]:
```
_ = df.drop(['tick_code', 'embarked', 'sex', 'target'], axis=1)
X_clean = pd.concat([_, dums], axis=1)
X_clean.head()
```

Out[27]:

	pclass	age	sibsp	parch	fare	tick_num	sex_male	embarked_Q	embarked_S	a	...	so	soc	sop	soton	sp
0	1	29.0000	0	0	211.3375	24160	0	0	1	0	...	0	0	0	0	0
1	1	0.9167	1	2	151.5500	113781	1	0	1	0	...	0	0	0	0	0
2	1	2.0000	1	2	151.5500	113781	0	0	1	0	...	0	0	0	0	0
3	1	30.0000	1	2	151.5500	113781	1	0	1	0	...	0	0	0	0	0
4	1	25.0000	1	2	151.5500	113781	0	0	1	0	...	0	0	0	0	0

5 rows × 39 columns

The target values were saved in `y`.

In [28]:
```
y = df.target
y.head()
```

Out[28]:
```
0    1
1    1
2    0
3    0
4    0
Name: target, dtype: int64
```

Classification

Proportional Chance Criterion

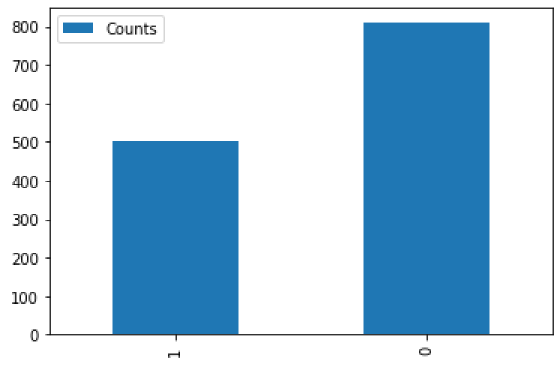
The Proportional Chance Criterion (PCC) measures the chance of correctly classifying a datapoint based on chance alone. As a rule of thumb, to say that our model works, we need to exceed prediction accuracy of 1.25 x PCC. In this case, **the minimum target classification accuracy is 66%.**

In [29]:
```
state_counts = Counter(y)
df_state = pd.DataFrame.from_dict(state_counts, orient='index')
df_state.columns = ['Counts']
df_state.plot(kind='bar')
print("Population per class:")
display(df_state)
num = (df_state['Counts'] / df_state['Counts'].sum())**2
print(
    "1.25 * Proportion Chance Criterion: {0:.2f}%".format(1.25 * 100 * num.sum()))
```

```
Population per class:
```

	Counts
1	500
0	809

```
1.25 * Proportion Chance Criterion: 65.98%
```



We used the following classification functions (We call this code JUDAS 7-in-1 credit to Jude Teves and Prof. Christopher Monterola). We run the each algorithm ten times and get the average accuracies.

Using JUDAS, the following models were run:

1. k Nearest Neighbors - parameter is n neighbors (influence generalizability)
2. Logistic Regression - parameter is alpha is a regularization parameter that affects the influence of each feature on the classifier
3. Linear Support Vector Machines (SVM) - parameter is C which controls how much influence each datapoint has on the datapoints separator (hyperplane)
4. Nonlinear Support Vector Machines (NSVM) - parameters are gamma and C (similar to linear SVM)

```
In [30]: from sklearn.neighbors import KNeighborsClassifier
         from sklearn.linear_model import LogisticRegression
         from sklearn.svm import LinearSVC
         from sklearn.svm import SVC
         from sklearn.model_selection import train_test_split

         Number_trials=50

         def train_knn(X, y):
             score_train = []
             score_test = []

             for seed in range(Number_trials):
                 X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.25, random_state=see
         d)

                 neighbors_settings = range(1,70)
                 acc_train = []
                 acc_test = []

                 for n_neighbors in neighbors_settings:
                     clf = KNeighborsClassifier(n_neighbors=n_neighbors) # build the model
                     clf.fit(X_train, y_train)
                     acc_train.append(clf.score(X_train, y_train))
                     acc_test.append(clf.score(X_test, y_test))

                 score_train.append(acc_train)
                 score_test.append(acc_test)

             score = np.mean(score_test, axis=0)
             #return n_neighbor, accuracy
             return ['kNN', np.amax(score), 'N_Neighbor = {0}'.format(np.argmax(score)+1), 'Not Now']

         def train_logistic(X, y, reg):
             C = [1e-8, 1e-4, 1e-3, 1e-2, 0.1, 0.2,0.4, 0.75, 1, 1.5, 3, 5, 10, 15,  20, 100, 300, 1000, 50
         00]
             #C = [0.01]

             score_train = []
             score_test = []
             weighted_coefs=[]

             for seed in range(Number_trials):
                 training_accuracy = []
                 test_accuracy = []
                 X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.25, random_state=see
         d)
                 for alpha_run in C:
                     lr = LogisticRegression(C=alpha_run, penalty=reg).fit(X_train, y_train)
                     training_accuracy.append(lr.score(X_train, y_train))
                     test_accuracy.append(lr.score(X_test, y_test))
                     if alpha_run == 0.1:
                         coefs=lr.coef_
                         weighted_coefs.append(coefs) #append all the computed coefficients per trial

                 score_train.append(training_accuracy)
                 score_test.append(test_accuracy)

             mean_coefs=np.mean(weighted_coefs, axis=0) #get the mean of the weighted coefficients over all
          the trials
             #print(mean_coefs)
             score = np.mean(score_test, axis=0)
             #return score.shape
             #coefs = lr.coef_
             #return C value, accuracy, column/feature name

             if scaler == 'ON':
                 top_predictor = 'DEBUGGING'
             if scaler == 'OFF':
                 top_predictor=X.columns[np.argmax(np.abs(mean_coefs))]
                 abs_mean_coefs = np.abs(mean_coefs[0,:])
                 coefs_count = len(abs_mean_coefs)
                 fig, ax = plt.subplots(figsize=(3,8))
                 ax.barh(np.arange(coefs_count), sorted(abs_mean_coefs))
                 #ax.barh(np.arange(coefs_count), mean_coefs[0, np.argsort(abs_mean_coefs)])
                 ax.set_yticks(np.arange(coefs_count))
                 ax.set_yticklabels(X.columns[np.argsort(abs_mean_coefs)])
                 ax.set_title('Logistic %s'%reg)

             return ['Logistic ({0})'.format(reg), np.amax(score), \
                     'C = {0}'.format(C[np.argmax(score)]), top_predictor]
```

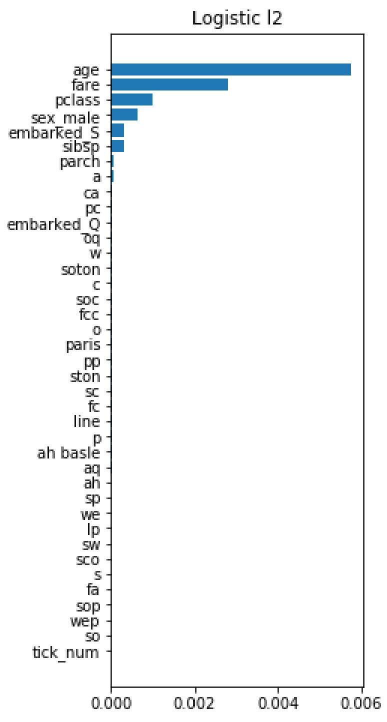
```
def train_svm(X, y, reg):
    C = [1e-8, 1e-4, 1e-3, 1e-2, 0.1, 0.2,0.4, 0.75, 1, 1.5, 3, 5, 10, 15,  20, 100, 300, 1000, 50
00]
    #C = [0.01]

    score_train = []
    score_test = []
    weighted_coefs=[]

    for seed in range(Number_trials):
        training_accuracy = []
        test_accuracy = []
        X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.25, random_state=see
d)
        for alpha_run in C:
            if reg == 'l1':
                svc = LinearSVC(C=alpha_run, penalty=reg, loss='squared_hinge', dual=False).fit(X_
train, y_train)
            if reg == 'l2':
                svc = LinearSVC(C=alpha_run, penalty=reg).fit(X_train, y_train)
            training_accuracy.append(svc.score(X_train, y_train))
            test_accuracy.append(svc.score(X_test, y_test))
            if alpha_run == 0.1:
                coefs = svc.coef_
                weighted_coefs.append(coefs)

        score_train.append(training_accuracy)
        score_test.append(test_accuracy)


    mean_coefs=np.mean(weighted_coefs, axis=0) #get the mean of the weighted coefficients over all
 the trials
    score = np.mean(score_test, axis=0)

    #if scaler == 'ON':
    #    top_predictor = 'DEBUGGING'
    #if scaler == 'OFF':
    top_predictor=X.columns[np.argmax(np.abs(mean_coefs))]
    abs_mean_coefs = np.abs(mean_coefs[0,:])
    coefs_count = len(abs_mean_coefs)
    fig, ax = plt.subplots(figsize=(3,8))
    ax.barh(np.arange(coefs_count), sorted(abs_mean_coefs))
        #ax.barh(np.arange(coefs_count), mean_coefs[0, np.argsort(abs_mean_coefs)])
    ax.set_yticks(np.arange(coefs_count))
    ax.set_yticklabels(X.columns[np.argsort(abs_mean_coefs)])
    ax.set_title('Linear SVM %s'%reg)
        #print(X.columns(np.arg(np.abs(mean_coefs)))
        #print(np.abs(mean_coefs))
    #return score
    #return C value, accuracy, column/feature name
    #y_pred = lsvc_l1.predict(X_test)
    #confmat = confusion_matrix(y_true=y_test, y_pred=y_pred)
    #print(confmat)
    return ['Linear SVM ({0})'.format(reg), np.amax(score), \
            'C = {0}'.format(C[np.argmax(score)]), top_predictor]



def train_Nsvm(X, y, reg):
    #CC = [.1]
    #C = [0.01]
    CC = [1e-8, 1e-4, 1e-3, 1e-2, 0.1, 0.2,0.4, 0.75, 1, 1.5, 3, 5, 10, 15,  20, 100, 300, 1000, 5
000]

    score_train = []
    score_test = []
    weighted_coefs=[]

    for seed in range(Number_trials):
        training_accuracy = []
        test_accuracy = []
        X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.25, random_state=see
d)
        for alpha_run in CC:
            svm = SVC(kernel='rbf', gamma=alpha_run, C=10)
            svc=svm.fit(X_train, y_train)
            training_accuracy.append(svc.score(X_train, y_train))
            test_accuracy.append(svc.score(X_test, y_test))
            #if alpha_run == 0.01:
            #    coefs = svc.coef_
             #   weighted_coefs.append(coefs)
        score_train.append(training_accuracy)
        score_test.append(test_accuracy)


    mean_coefs=np.mean(weighted_coefs, axis=0) #get the mean of the weighted coefficients over all
 the trials
    score = np.mean(score_test, axis=0)
    top_predictor ='Not Now'

    return ['Nonlinear SVM ({0})'.format(reg), np.amax(score), \
            'C = {0}'.format(CC[np.argmax(score)]), top_predictor]


def train_Nsvmpoly(X, y, reg):

    CC = [1e-8, 1e-4, 1e-3, 1e-2, 0.1, 0.2,0.4, 0.75, 1, 1.5, 3, 5, 10, 15,  20, 100, 300, 1000, 5
000]

    score_train = []
    score_test = []
    weighted_coefs=[]

    for seed in range(Number_trials):
        training_accuracy = []
        test_accuracy = []
        X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.25, random_state=see
d)
        for alpha_run in CC:
            svm = SVC(kernel='poly',degree=2,coef0=1, C=alpha_run)
            svc=svm.fit(X_train, y_train)
            training_accuracy.append(svc.score(X_train, y_train))
            test_accuracy.append(svc.score(X_test, y_test))
            #if alpha_run == 0.01:
            #    coefs = svc.coef_
             #   weighted_coefs.append(coefs)

        score_train.append(training_accuracy)
        score_test.append(test_accuracy)


    mean_coefs=np.mean(weighted_coefs, axis=0) #get the mean of the weighted coefficients over all
 the trials
    score = np.mean(score_test, axis=0)

    top_predictor='Not Now'
    return ['Nonlinear SVM ({0})'.format(reg), np.amax(score), \
            'C = {0}'.format(CC[np.argmax(score)]), top_predictor]
```

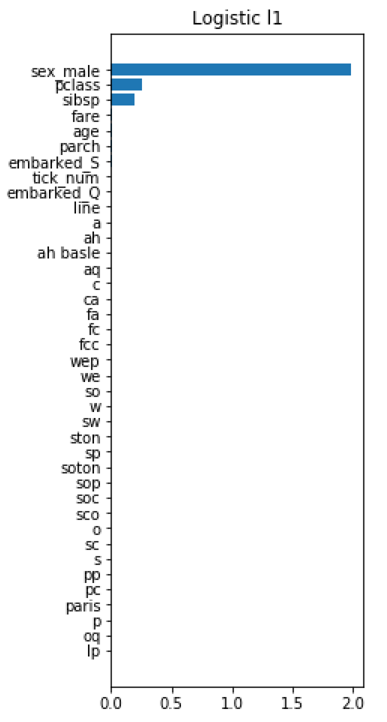
```
In [31]: # %%time
         feature_names = X_clean.columns

         X = X_clean[feature_names]

         scaler='OFF'

         a = train_knn(X,y)
         print(a)
         b = train_logistic(X,y,reg='l2')
         print(b)
         c = train_logistic(X,y,reg='l1')
         print(c)
         d = train_svm(X,y,reg='l2')
         print(d)
         e = train_svm(X,y,reg='l1')
         print(e)
         f = train_Nsvm(X,y,reg='rbf')
         print(f)
         # g = train_Nsvmpoly(X,y,reg='poly')
         # print(g)
```

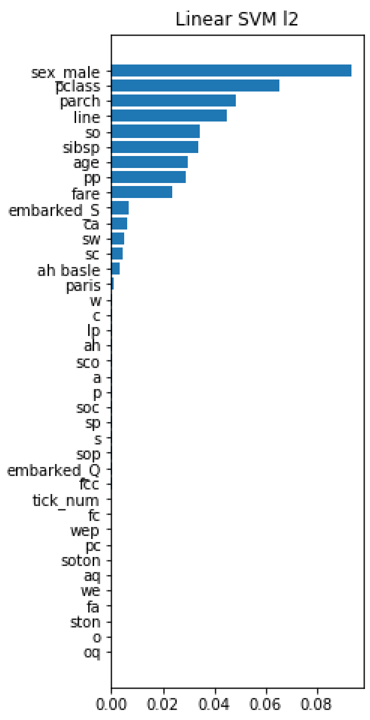
```
['kNN', 0.6775, 'N_Neighbor = 3', 'Not Now']
['Logistic (l2)', 0.6453658536585364, 'C = 0.0001', 'age']
['Logistic (l1)', 0.7886585365853658, 'C = 1.5', 'sex_male']
['Linear SVM (l2)', 0.5841463414634144, 'C = 5', 'sex_male']
['Linear SVM (l1)', 0.7873170731707316, 'C = 0.75', 'sex_male']
```

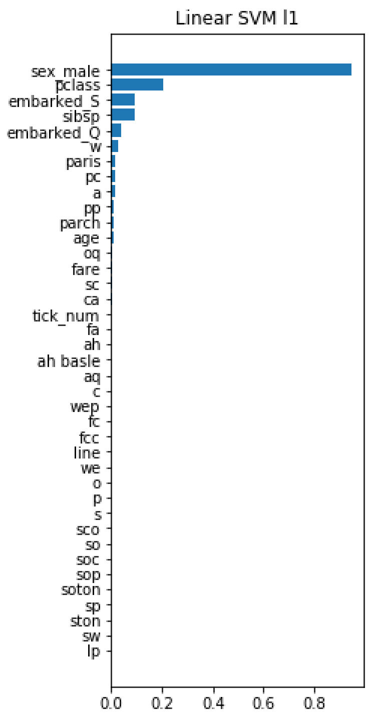
```
/Users/fernandojavier/anaconda3/lib/python3.6/site-packages/numpy/core/fromnumeric.py:2957: Runti
meWarning: Mean of empty slice.
  out=out, **kwargs)
/Users/fernandojavier/anaconda3/lib/python3.6/site-packages/numpy/core/_methods.py:80: RuntimeWar
ning: invalid value encountered in double_scalars
  ret = ret.dtype.type(ret / rcount)
```

```
['Nonlinear SVM (rbf)', 0.6832926829268294, 'C = 0.001', 'Not Now']
```









Without using any scaling, the highest accuracy was obtained from Logistic Regression with L1 penalty. The best predictor is `sex_male`.

```
In [32]: cols = ['Machine Learning Method', 'Test Accuracy', 'Best Parameter', 'Top Predictor Variable']
         df2 = pd.DataFrame(columns=cols)

         df2.loc[0] = a
         df2.loc[1] = b
         df2.loc[2] = c
         df2.loc[3] = d
         df2.loc[4] = e
         df2.loc[5] = f
         # df2.loc[6] = g
         df2
```

Out[32]:

	Machine Learning Method	Test Accuracy	Best Parameter	Top Predictor Variable
0	kNN	0.677500	N_Neighbor = 3	Not Now
1	Logistic (l2)	0.645366	C = 0.0001	age
2	Logistic (l1)	0.788659	C = 1.5	sex_male
3	Linear SVM (l2)	0.584146	C = 5	sex_male
4	Linear SVM (l1)	0.787317	C = 0.75	sex_male
5	Nonlinear SVM (rbf)	0.683293	C = 0.001	Not Now

Scaling

Two scaling methods were used: min-max scaling or standard scaling. Min-max scaling scales the values in a column by the range of values in that column (minimum values to maximum values). Standard scaling scales the values in a column by the mean and standard deviation of the values in that column.

Min-Max Scaling

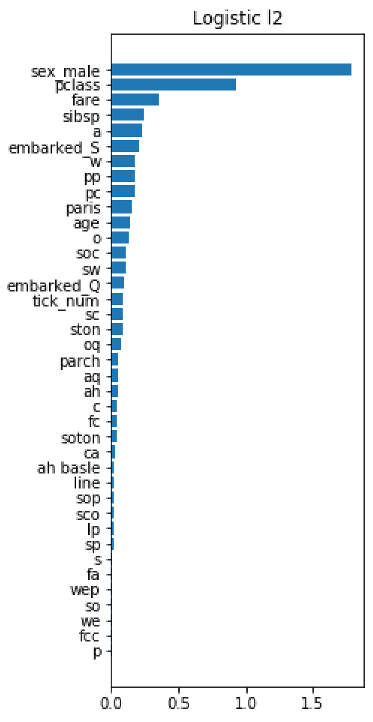
```
In [34]: from sklearn.preprocessing import StandardScaler
         from sklearn.preprocessing import MinMaxScaler
```

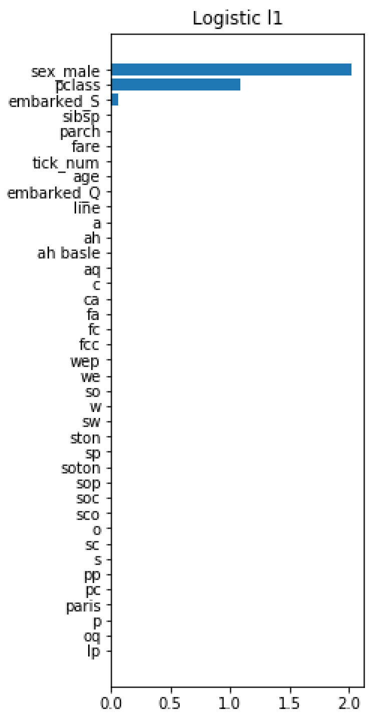
In [35]:
```
# %%time

feature_names = X.columns

X = X_clean[feature_names]

sscaler = MinMaxScaler()
X = sscaler.fit_transform(X)
X = pd.DataFrame(X, columns=feature_names)

a = train_knn(X,y)
print(a)
b = train_logistic(X,y,reg='l2')
print(b)
c = train_logistic(X,y,reg='l1')
print(c)
d = train_svm(X,y,reg='l2')
print(d)
e = train_svm(X,y,reg='l1')
print(e)
f = train_Nsvm(X,y,reg='rbf')
print(f)
# g = train_Nsvmpoly(X,y,reg='poly')
# print(g)
```

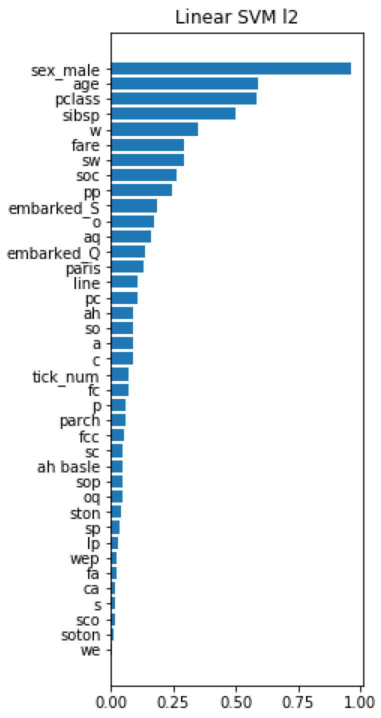
```
['kNN', 0.7979268292682928, 'N_Neighbor = 28', 'Not Now']
['Logistic (l2)', 0.7871341463414632, 'C = 3', 'sex_male']
['Logistic (l1)', 0.7877439024390241, 'C = 1.5', 'sex_male']
['Linear SVM (l2)', 0.7868902439024389, 'C = 0.4', 'sex_male']
['Linear SVM (l1)', 0.7876829268292684, 'C = 0.75', 'sex_male']
```

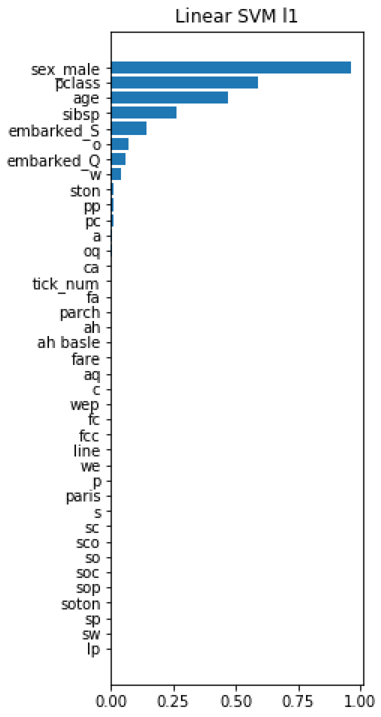
```
/Users/fernandojavier/anaconda3/lib/python3.6/site-packages/numpy/core/fromnumeric.py:2957: Runti
meWarning: Mean of empty slice.
  out=out, **kwargs)
/Users/fernandojavier/anaconda3/lib/python3.6/site-packages/numpy/core/_methods.py:80: RuntimeWar
ning: invalid value encountered in double_scalars
  ret = ret.dtype.type(ret / rcount)
```

```
['Nonlinear SVM (rbf)', 0.8075609756097564, 'C = 0.75', 'Not Now']
```









With min-max scaling, the highest accuracy was obtained from Nonlinear SVM with radial basis function kernel. No top predictor was determined using this model. The best predictor in all other models aside from kNN is still `sex_male`.

```
In [36]: cols = ['Machine Learning Method', 'Test Accuracy', 'Best Parameter', 'Top Predictor Variable']
         df2 = pd.DataFrame(columns=cols)

         df2.loc[0] = a
         df2.loc[1] = b
         df2.loc[2] = c
         df2.loc[3] = d
         df2.loc[4] = e
         df2.loc[5] = f
         # df2.loc[6] = g
         df2
```

Out[36]:

	Machine Learning Method	Test Accuracy	Best Parameter	Top Predictor Variable
0	kNN	0.797927	N_Neighbor = 28	Not Now
1	Logistic (l2)	0.787134	C = 3	sex_male
2	Logistic (l1)	0.787744	C = 1.5	sex_male
3	Linear SVM (l2)	0.786890	C = 0.4	sex_male
4	Linear SVM (l1)	0.787683	C = 0.75	sex_male
5	Nonlinear SVM (rbf)	0.807561	C = 0.75	Not Now

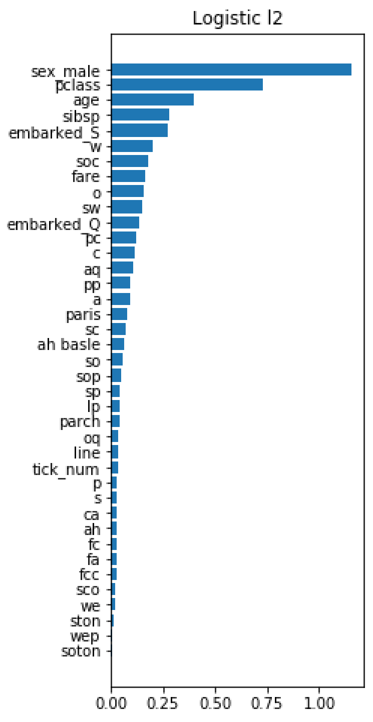
Standard Scaling

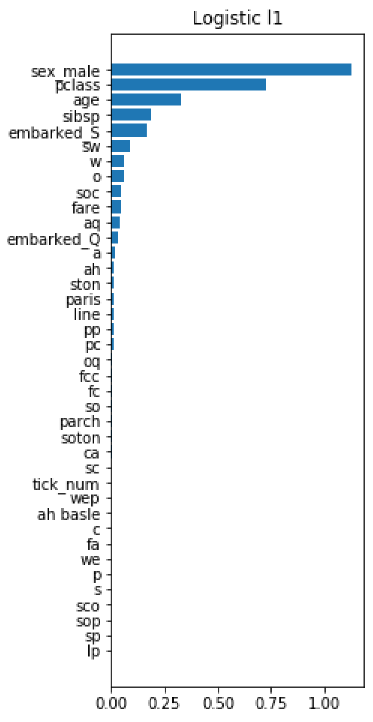
In [37]:
```python
# %%time

feature_names = X.columns

X = X_clean[feature_names]

sscaler = StandardScaler()
X = sscaler.fit_transform(X)
X = pd.DataFrame(X, columns=feature_names)

a = train_knn(X,y)
print(a)
b = train_logistic(X,y,reg='l2')
print(b)
c = train_logistic(X,y,reg='l1')
print(c)
d = train_svm(X,y,reg='l2')
print(d)
e = train_svm(X,y,reg='l1')
print(e)
f = train_Nsvm(X,y,reg='rbf')
print(f)
# g = train_Nsvmpoly(X,y,reg='poly')
# print(g)
```

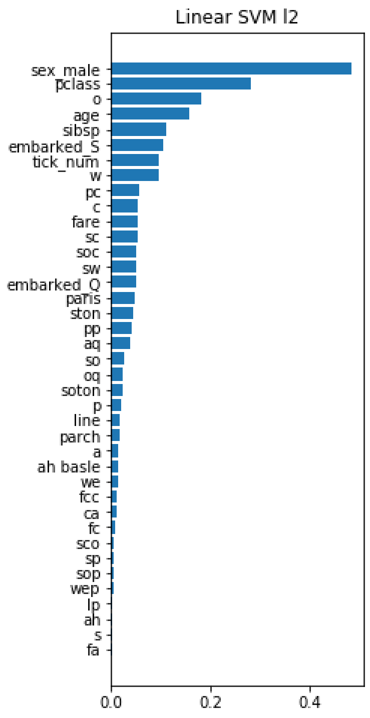
```
['kNN', 0.7897560975609754, 'N_Neighbor = 17', 'Not Now']
['Logistic (l2)', 0.7835975609756096, 'C = 0.2', 'sex_male']
['Logistic (l1)', 0.7866463414634146, 'C = 0.2', 'sex_male']
['Linear SVM (l2)', 0.7848780487804876, 'C = 0.01', 'sex_male']
['Linear SVM (l1)', 0.7871341463414635, 'C = 0.1', 'sex_male']
```

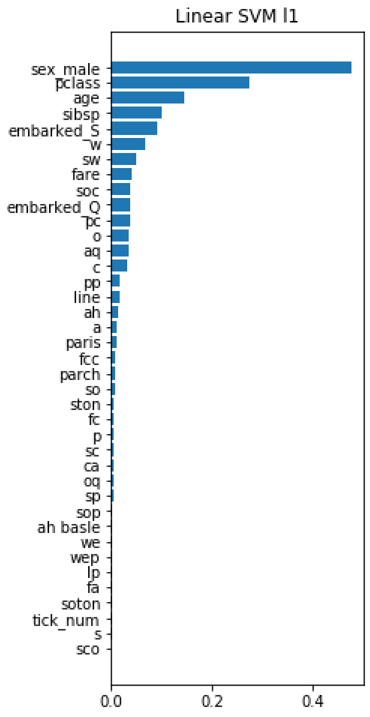
```
/Users/fernandojavier/anaconda3/lib/python3.6/site-packages/numpy/core/fromnumeric.py:2957: Runti
meWarning: Mean of empty slice.
  out=out, **kwargs)
/Users/fernandojavier/anaconda3/lib/python3.6/site-packages/numpy/core/_methods.py:80: RuntimeWar
ning: invalid value encountered in double_scalars
  ret = ret.dtype.type(ret / rcount)
```

```
['Nonlinear SVM (rbf)', 0.790609756097561, 'C = 0.1', 'Not Now']
```









With standard scaling, the highest accuracy was obtained from Nonlinear SVM with radial basis function kernel. No top predictor was determined using this model. The best predictor in all other models aside from kNN is still `sex_male`.

In [38]:
```
cols = ['Machine Learning Method', 'Test Accuracy', 'Best Parameter', 'Top Predictor Variable']
df2 = pd.DataFrame(columns=cols)

df2.loc[0] = a
df2.loc[1] = b
df2.loc[2] = c
df2.loc[3] = d
df2.loc[4] = e
df2.loc[5] = f
# df2.loc[6] = g
df2
```

Out[38]:

	Machine Learning Method	Test Accuracy	Best Parameter	Top Predictor Variable
0	kNN	0.789756	N_Neighbor = 17	Not Now
1	Logistic (l2)	0.783598	C = 0.2	sex_male
2	Logistic (l1)	0.786646	C = 0.2	sex_male
3	Linear SVM (l2)	0.784878	C = 0.01	sex_male
4	Linear SVM (l1)	0.787134	C = 0.1	sex_male
5	Nonlinear SVM (rbf)	0.790610	C = 0.1	Not Now

Decision Trees

Decision trees work like a step-by-step decision-making process. Based on conditions on the value of a feature, you split the dataset into two, and each split will be further split according to new sets of rules. The process continues up to a certain level or depth. **Decision trees are analogous to an inverted tree**, where the trunk braches out into large branches and each branch further branches into smaller and smaller branches.

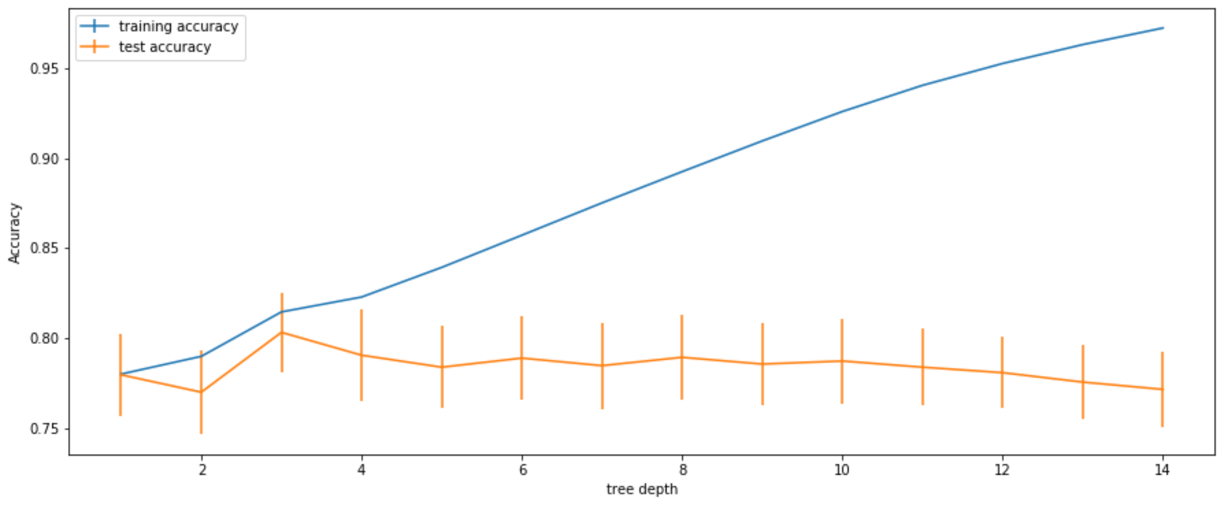
The hyperparameter or "lever" that you tune in a decision tree classifier is the tree's maximum depth. This is the maximum level the tree reach until it stops.

In [39]:
```
X = X_clean.copy()
```

In [40]:
```
from sklearn.tree import DecisionTreeClassifier

lahat_training = pd.DataFrame()
lahat_test = pd.DataFrame()
for seedN in range(1, 50, 1):
    from sklearn.model_selection import train_test_split
    X_train, X_test, y_train, y_test = train_test_split(
        X, y, test_size=0.25, random_state=seedN)

    training_accuracy = []
    test_accuracy = []
    maxdepth_settings = range(1, 15)  # try n_neighbors from 1 to 50

    for depth in maxdepth_settings:
        tree = DecisionTreeClassifier(
            max_depth=depth, random_state=42)  # build the model
        tree.fit(X_train, y_train)

        # record training set accuracy
        training_accuracy.append(tree.score(X_train, y_train))
        # record generalization accuracy
        test_accuracy.append(tree.score(X_test, y_test))

    lahat_training[seedN] = training_accuracy
    lahat_test[seedN] = test_accuracy
```

```
In [41]: fig = plt.figure(figsize=(15, 6))
         plt.errorbar(maxdepth_settings, lahat_training.mean(axis=1),
                      yerr=lahat_training.var(axis=1), label="training accuracy")
         plt.errorbar(maxdepth_settings, lahat_test.mean(axis=1),
                      yerr=lahat_test.std(axis=1), label="test accuracy")
         plt.ylabel("Accuracy")
         plt.xlabel("tree depth")
         plt.legend()
         bestdepth=np.argmax(lahat_test.mean(axis=1))+1
         print("Highest Average Test Set Achieved = %f" % np.amax(lahat_test.mean(axis=1)))
         print("Best Depth Parameter = %d" %bestdepth )
```

```
Highest Average Test Set Achieved = 0.803260
Best Depth Parameter = 3

/Users/fernandojavier/anaconda3/lib/python3.6/site-packages/numpy/core/fromnumeric.py:52: FutureW
arning: 'argmax' is deprecated, use 'idxmax' instead. The behavior of 'argmax'
will be corrected to return the positional maximum in the future.
Use 'series.values.argmax' to get the position of the maximum now.
  return getattr(obj, method)(*args, **kwds)
```

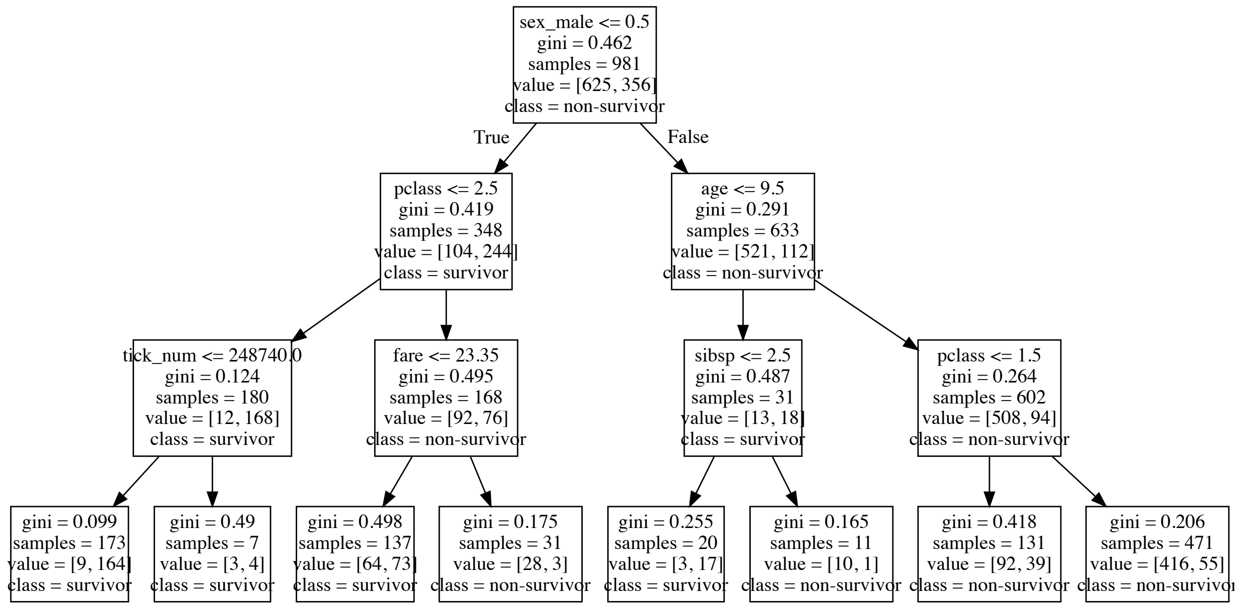


From the accuracy vs tree depth chart above, we found that the ideal depth is tree which results in classification accuracy of 0.803.

Below, we visualize the decision tree, the branches and the conditions per branch that splits the dataset.

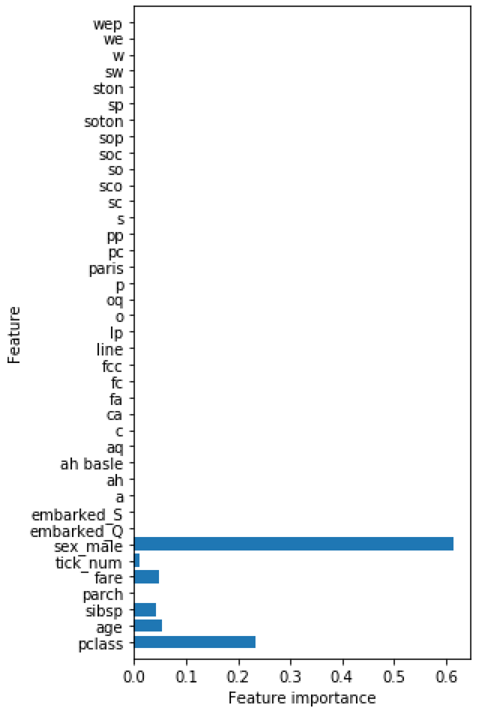
In [42]:
```
X_train, X_test, y_train, y_test = train_test_split(
    X, y, test_size=0.25, random_state=42)

tree = DecisionTreeClassifier(
    max_depth=3, random_state=42)  # build the model
tree.fit(X_train, y_train)

from sklearn.tree import export_graphviz

export_graphviz(tree, out_file="mytree.dot", class_names=["non-survivor", "survivor"],
                feature_names=X_clean.columns)

import graphviz
with open("mytree.dot") as f:
    dot_graph = f.read()
graphviz.Source(dot_graph)
```

Out[42]:



The two highest predictors using a decision tree classifier are `sex` and `pclass`.

In [44]:
```
import numpy as np

def plot_feature_importances(model):
    plt.figure(figsize=(4, 8))
    n_features=len(X.columns)
    plt.barh(range(n_features), model.feature_importances_, align='center')
    plt.yticks(np.arange(n_features), X.columns)
    plt.xlabel("Feature importance")
    plt.ylabel("Feature")
    plt.ylim(-1,n_features)

plot_feature_importances(tree)
```



Random Forest

An aggregate of trees is called a forest. The same analogy goes for decision trees. A random forest is an aggregate of decision trees. The classification from a random forest is the result of many different decision trees.

In [45]:
```
from sklearn.ensemble import RandomForestClassifier
```

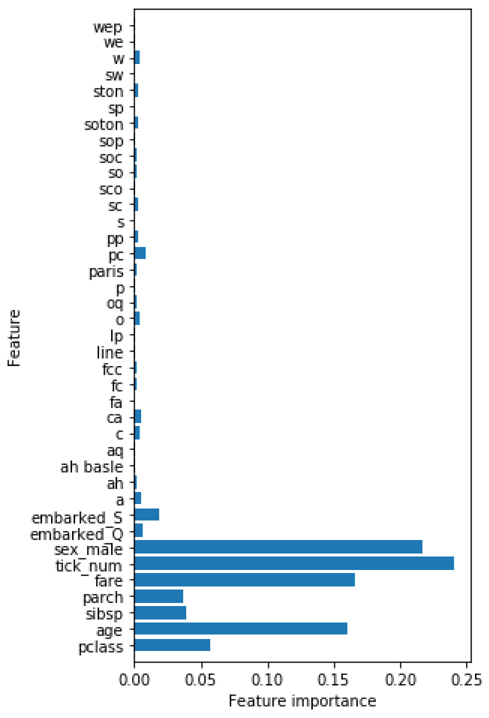
Using a random forest classifier, we got an accuracy of 0.8079 which is higher than a single decision tree but not by much.

In [46]:
```
X = X_clean
X_train, X_test, y_train, y_test = train_test_split(X, y, random_state=42)
forest = RandomForestClassifier(n_estimators=1000, random_state=42)
forest.fit(X_train, y_train)
print("accuracy on training set: %f" % forest.score(X_train, y_train))
print("accuracy on test set: %f" % forest.score(X_test, y_test))
```

```
accuracy on training set: 0.997961
accuracy on test set: 0.807927
```

The best predictors using a random forest classifier are `sex_male`, `tick_num`, `fare`, and `age`.

In [47]:
```
plot_feature_importances(forest)
```



Gradient Boosting Machines

Gradient boosting machines (GBM) or gradient boosted regression trees work similarly to random forests, except that instead of randomizing decision trees, the algorithm starts with one shallow (depth typically around 5) decision tree and keeps adding decision trees that improve classification one after another. It's like a more guided random forest.

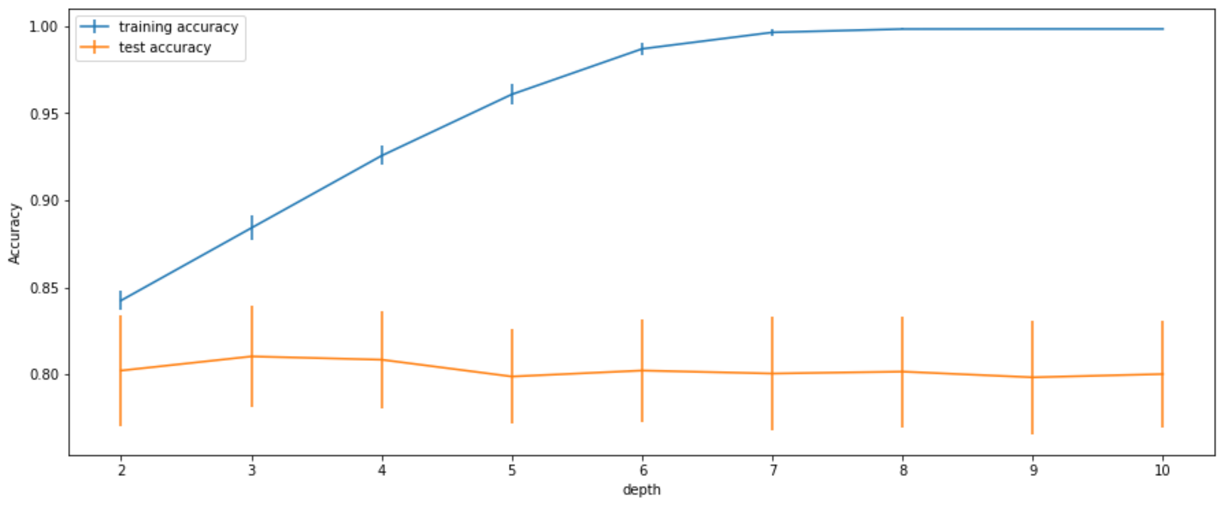
The hyperparameters of GBM are learning rate (higher values are faster but may offshoot optimal accuracy) and maximum tree depth.

In [48]:
```
from sklearn.ensemble import GradientBoostingClassifier

def run_gbm(lr, X):

    lahat_training = pd.DataFrame()
    lahat_test = pd.DataFrame()
    for seedN in range(1,50,1):
        from sklearn.model_selection import train_test_split
        X_train, X_test, y_train, y_test = train_test_split(X,y, stratify=y,
                                                            test_size=0.10, random_state=seedN)

        training_accuracy = []
        test_accuracy = []
        maxdepth_settings = range(2, 8) # try n_neighbors from 1 to 50

        for depth in maxdepth_settings:

            tree = GradientBoostingClassifier(n_estimators=20, learning_rate=lr,
                                              max_depth=depth, random_state=42).fit(X_train, y_train) # b
uild the model

            tree.fit(X_train, y_train)

            training_accuracy.append(tree.score(X_train, y_train)) # record training set accuracy
            test_accuracy.append(tree.score(X_test, y_test))   # record generalization accuracy

        lahat_training[seedN]=training_accuracy
        lahat_test[seedN] = test_accuracy


    fig = plt.figure(figsize=(15, 6))
    plt.errorbar(maxdepth_settings, lahat_training.mean(axis=1),
                 yerr=lahat_training.std(axis=1), label="training accuracy")
    plt.errorbar(maxdepth_settings, lahat_test.mean(axis=1),
                 yerr=lahat_test.std(axis=1), label="test accuracy")
    plt.ylabel("Accuracy")
    plt.xlabel("depth")
    plt.legend()
    bestdepth=np.argmax(lahat_test.mean(axis=1))+1
    print("Highest Average Test Set Achieved = %f" % np.amax(lahat_test.mean(axis=1)))
    print("Best Depth Parameter = %d" %bestdepth )
```

GBM results in the highest accuracy at the expense of interpretability.

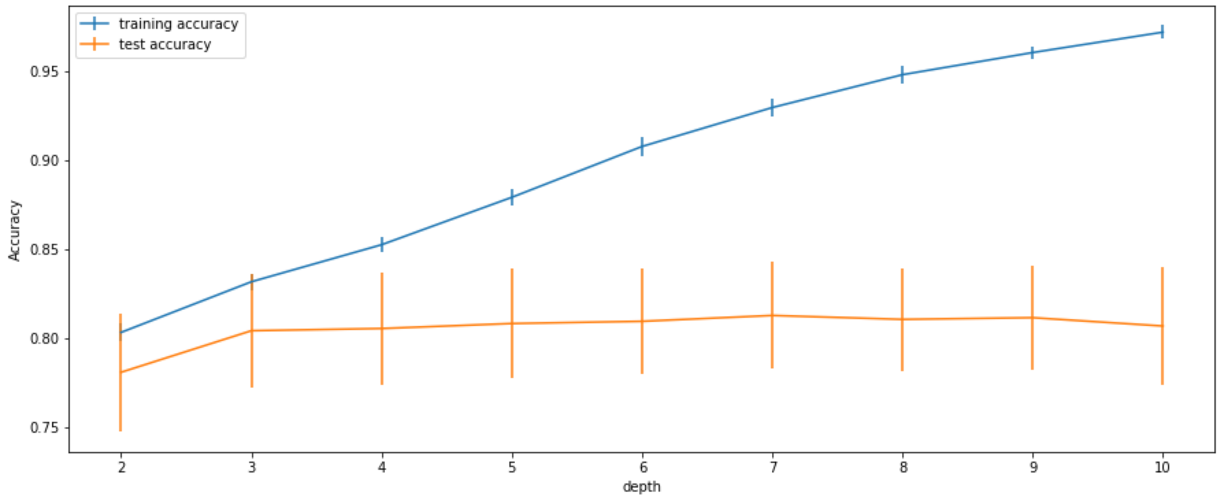
In [50]:
```
run_gbm(0.5, X)
```

```
Highest Average Test Set Achieved = 0.810407
Best Depth Parameter = 2

/Users/fernandojavier/anaconda3/lib/python3.6/site-packages/numpy/core/fromnumeric.py:52: FutureW
arning: 'argmax' is deprecated, use 'idxmax' instead. The behavior of 'argmax'
will be corrected to return the positional maximum in the future.
Use 'series.values.argmax' to get the position of the maximum now.
  return getattr(obj, method)(*args, **kwds)
```



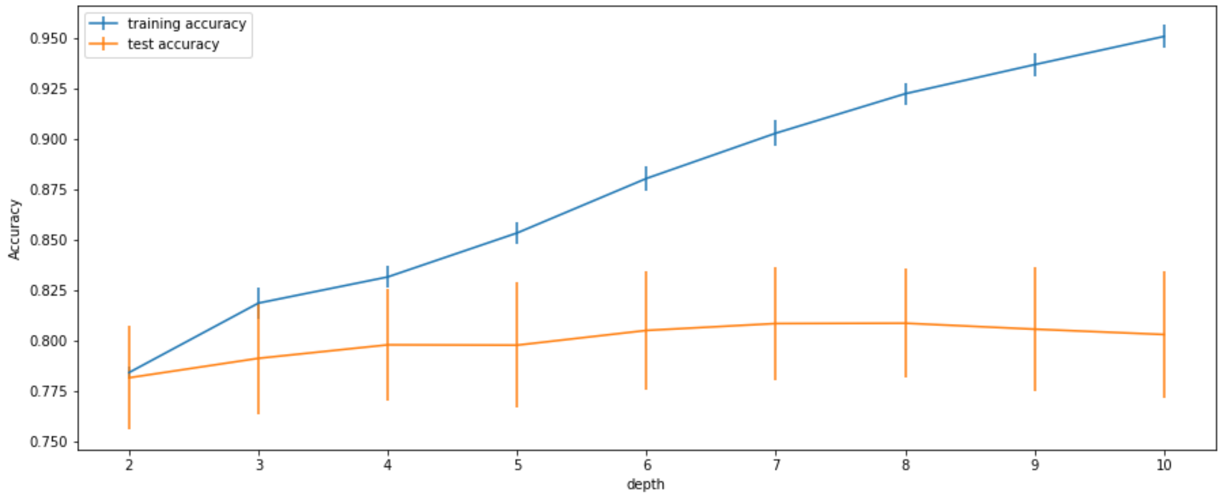
```
In [51]: run_gbm(0.1, X)
```

```
Highest Average Test Set Achieved = 0.812588
Best Depth Parameter = 6

/Users/fernandojavier/anaconda3/lib/python3.6/site-packages/numpy/core/fromnumeric.py:52: FutureW
arning: 'argmax' is deprecated, use 'idxmax' instead. The behavior of 'argmax'
will be corrected to return the positional maximum in the future.
Use 'series.values.argmax' to get the position of the maximum now.
  return getattr(obj, method)(*args, **kwds)
```



```
In [52]: run_gbm(0.05, X)
```

```
/Users/fernandojavier/anaconda3/lib/python3.6/site-packages/numpy/core/fromnumeric.py:52: FutureW
arning: 'argmax' is deprecated, use 'idxmax' instead. The behavior of 'argmax'
will be corrected to return the positional maximum in the future.
Use 'series.values.argmax' to get the position of the maximum now.
  return getattr(obj, method)(*args, **kwds)

Highest Average Test Set Achieved = 0.808537
Best Depth Parameter = 7
```



Rerunning GBM and Random Forests on Dimensionally-Reduced Dataset

We rerun gradient boosting machines and random forest classifiers for dimensionally-reduced matrix. This matrix was obtained by first scaling the original dataset using standard scaler. Afterwhich, singular value decomposition was applied to come up with principal components (new components made up of a combination of features) that explain 95% of the information.

As you will see, **running GBM and random forest classifier on dimensionally-reduced data reduced the accuracy of the classification model.**

Dimensionality Reduction

```
In [53]: sc = StandardScaler()
         Xsc = sc.fit_transform(X_clean)
```

We then performed dimensionality reduction to reduce the number of "features". It might be possible that only few of these features explain 95% of the information. In order to find out, we used a dimensionality reduction method. The method used here is singular value decomposition (SVD). Information about SVD can be found here http://web.mit.edu/be.400/www/SVD/Singular_Value_Decomposition.htm (http://web.mit.edu/be.400/www/SVD/Singular_Value_Decomposition.htm).

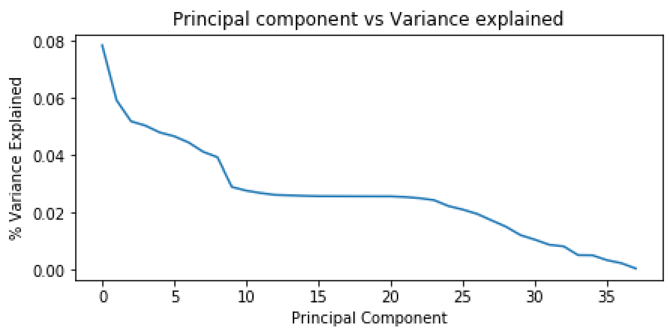
```
In [54]: from sklearn.decomposition import TruncatedSVD
```

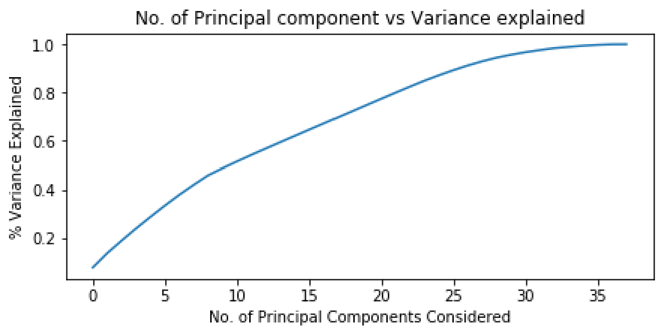
```
In [56]: comps = Xsc.shape[1] - 1

         svd = TruncatedSVD(n_components=comps)
         X_svd = svd.fit_transform(Xsc)
         var = svd.explained_variance_ratio_
         c_var = var.cumsum()
         c_var;
```

The variance or "information" explained per feature in the dimensionally-reduced matrix is shown in the first plot below. Notice that the first few features or principal components explain majority of the information. The second plot shows the cumulative information explained.

95% of the information or variance is explained by 29 principal components.

```
In [57]: plt.figure(figsize = (7, 3))
         plt.plot(var)
         plt.xlabel('Principal Component')
         plt.ylabel('% Variance Explained')
         plt.title('Principal component vs Variance explained')
         plt.show()
         plt.figure(figsize = (7, 3))
         plt.plot(c_var)
         plt.xlabel('No. of Principal Components Considered')
         plt.title('No. of Principal component vs Variance explained')
         plt.ylabel('% Variance Explained');
```





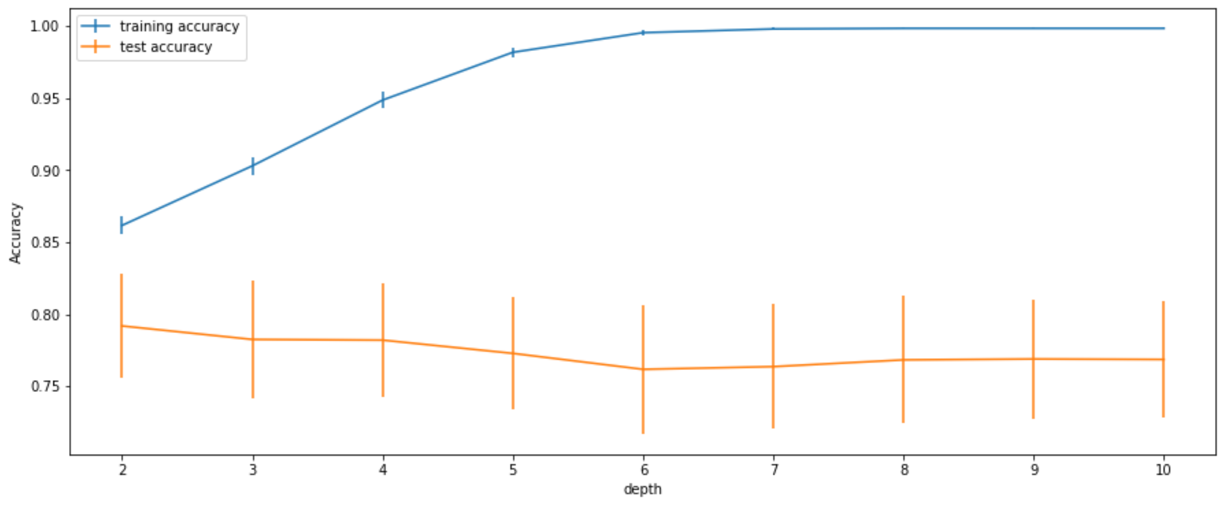
```
In [58]: n_95 = [c_var < 0.95][0].sum()
         n_95

Out[58]: 29
```

Using 29 principal components, the new matrix is saved in `X_svd_2`.

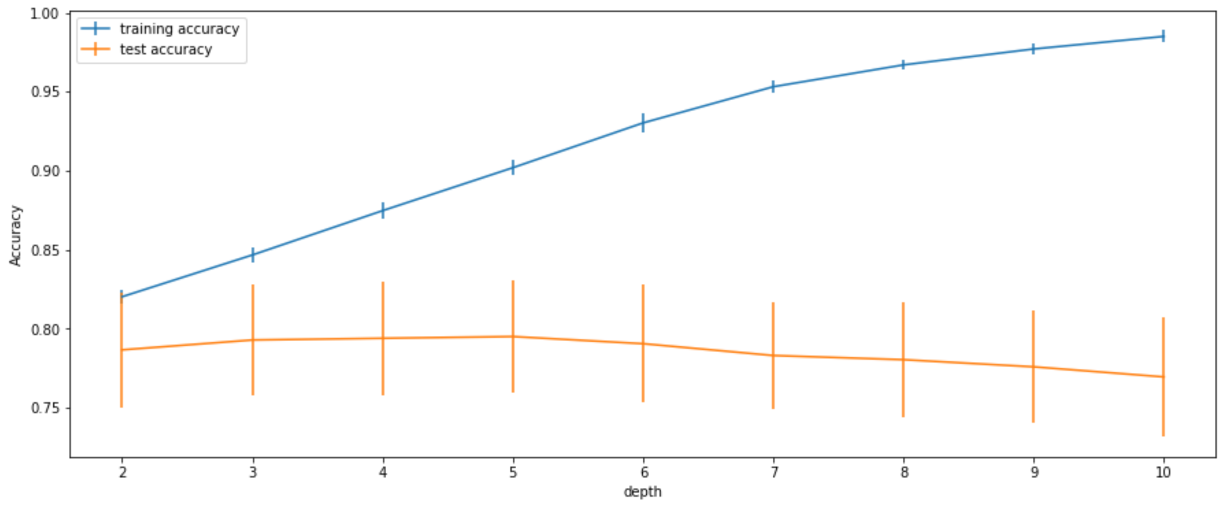
```
In [59]: svd = TruncatedSVD(n_components = n_95)
         X_svd_2 = svd.fit_transform(Xsc)
         X_svd_2.shape

Out[59]: (1309, 29)
```

```
In [60]: X_train, X_test, y_train, y_test = train_test_split(X_svd_2, y, random_state=42)
         forest = RandomForestClassifier(n_estimators=1000, random_state=42)
         forest.fit(X_train, y_train)
         print("accuracy on training set: %f" % forest.score(X_train, y_train))
         print("accuracy on test set: %f" % forest.score(X_test, y_test))

         accuracy on training set: 0.997961
         accuracy on test set: 0.759146
```

```
In [62]: run_gbm(0.5, X_svd_2)

         Highest Average Test Set Achieved = 0.792024
         Best Depth Parameter = 1

         /Users/fernandojavier/anaconda3/lib/python3.6/site-packages/numpy/core/fromnumeric.py:52: FutureW
         arning: 'argmax' is deprecated, use 'idxmax' instead. The behavior of 'argmax'
         will be corrected to return the positional maximum in the future.
         Use 'series.values.argmax' to get the position of the maximum now.
           return getattr(obj, method)(*args, **kwds)
```

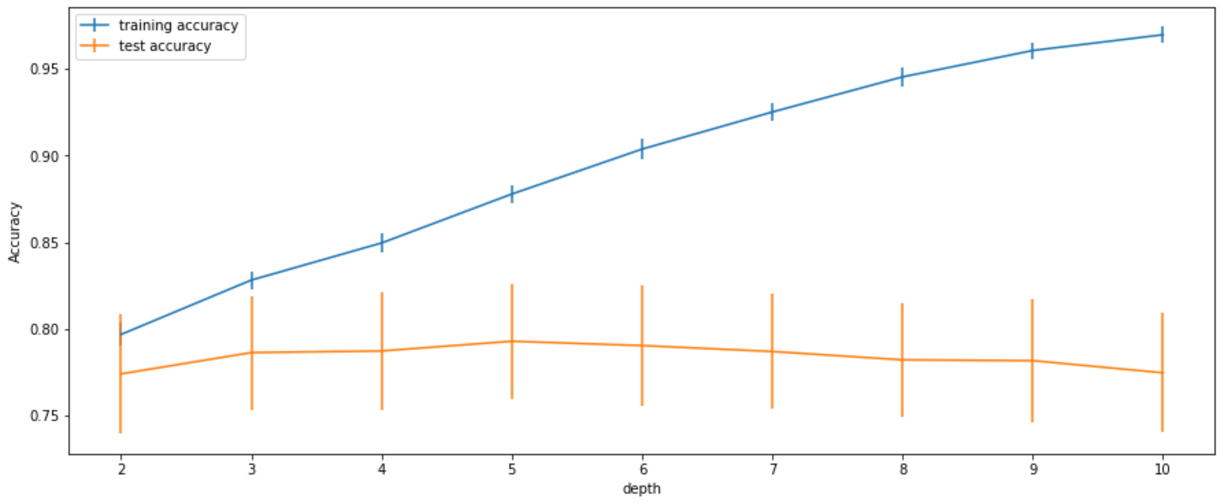


```
In [63]: run_gbm(0.1, X_svd_2)

         Highest Average Test Set Achieved = 0.795139
         Best Depth Parameter = 4

         /Users/fernandojavier/anaconda3/lib/python3.6/site-packages/numpy/core/fromnumeric.py:52: FutureW
         arning: 'argmax' is deprecated, use 'idxmax' instead. The behavior of 'argmax'
         will be corrected to return the positional maximum in the future.
         Use 'series.values.argmax' to get the position of the maximum now.
           return getattr(obj, method)(*args, **kwds)
```



```
In [64]: run_gbm(0.05, X_svd_2)
```

```
Highest Average Test Set Achieved = 0.792803
Best Depth Parameter = 4

/Users/fernandojavier/anaconda3/lib/python3.6/site-packages/numpy/core/fromnumeric.py:52: FutureW
arning: 'argmax' is deprecated, use 'idxmax' instead. The behavior of 'argmax'
will be corrected to return the positional maximum in the future.
Use 'series.values.argmax' to get the position of the maximum now.
  return getattr(obj, method)(*args, **kwds)
```



GBM and random forest classifier on dimensionally-reduced data reduced the accuracy of the classification model.

Summary

Titanic dataset was provided by AIM ACCESS lab. The dataset was cleaned and run on multiple classification models with the goal of finding whether a person would survive in the Titanic accident or not.

The model that yielded the highest accuracy was GBM with around 81% accuracy using learning rate of 0.1 and maximum depth of 6. However, the downside was it lacked interpretability.

The model that yielded second best accuracy was random forest with accuracy of 80.8%. The highest predictors were ticket number and sex.

The third was nonlinear SVM with RBF kernel and C=0.75 and min-max scaled dataset which yielded 80.8% accuracy. However, the best predictors were not determined for this model.

Fourth, decision tree yielded 80.3% accuracy at maximum depth of 3. The advantage of the decision tree was its interpretability as a tree diagram could be constructed of the step-by-step process in classification process.

Finally, the dataset was dimensionally reduced using SVD. GBM and random forest were rerun but it was shown that accuracies for both decreased.

From this analysis, it was found that sex was the highest predictor of whether or not a person would survive the accident. The proportion of females in the survivors were higher than the males, whereas the proportion of females in the non-survivors were much less than the males.

For the models, GBM proved most accurate in classifying and may be used if the goal is merely for prediction. However, for the balance between interpretability and prediction, decision trees classifier is deemed preferrable.

Limitations and Recommendations

Feature engineering to improve accuracy may be explored in future analyses.

References

https://github.com/awesomedata/awesome-public-datasets/issues/351 (https://github.com/awesomedata/awesome-public-datasets/issues/351)
http://web.mit.edu/be.400/www/SVD/Singular_Value_Decomposition.htm
(http://web.mit.edu/be.400/www/SVD/Singular_Value_Decomposition.htm)

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