PROJECT SPECIFICATION - BENCHMARK (Neural Network Model)

Machine Learning Capstone Project

This capstone project involves machine learning modeling and analysis of clinical, demographic, and brain related derived anatomic measures from human MRI (magnetic resonance imaging) tests (http://www.oasis-brains.org/ (http://www.oasis-brains.org/)). The objectives of these measurements are to diagnose the level of Dementia in the individuals and the probability that these individuals may have Alzheimer's Disease (AD).

In published studies, Machine Learning has been applied to Alzheimer's/Dementia identification from MRI scans and related data in the academic papers/theses in References 10 and 11 listed in the References Section below. Recently, a close relative of mine had to undergo a sequence of MRI tests for cognition difficulties.The motivation for choosing this topic for the Capstone project arose from the desire to understand and analyze potential for Dementia and AD from MRI related data. Cognitive testing, clinical assessments and demographic data related to these MRI tests are used in this project. This Capstone project does not use the MRI "imaging" data and does not focus on AD, focusses only on Dementia.

Problem Statement

[The problem which needs to be solved is clearly defined. A strategy for solving the problem, including discussion of the expected solution, has been made.]

• Cross-Sectional and longitudinal OASIS MRI structural and demographic data (clinical, demographic, and brain related derived anatomic measures) from human MRI (magnetic resonance imaging) tests (http://www.oasis-brains.org/ (http://www.oasis-brains.org/)) will be used to train a set of linear and non-linear machine learning classification models.

• Clinical Dementia Rating (CDR) values provided in the data set will be used as "labels" for training the classification models. [Clinical Dementia Ratings (CDR values: 0=nondemented; 0.5 = very mild dementia; 1 = mild dementia; 2 = moderate dementia)].

• Pandas will be used for data loading and Python scikit-learn library for modeling.

• The goal is to train machine learning models to predict whether the individuals in the cross-validation set (test set) have dementia (CDR>0), and if they do, the severity level of dementia (CDR values of 0.5, 1, and 2). The problem will be formulated both as a binary classification problem (CDR=0, and CDR>0), and multiclass classification problem (CDR values in the dataset: 0, 0.5, 1, and 2). In the binary classification formulation, the CDR>0 the values in the sliced dataset will be relabeled as CDR=1.

• Classification Accuracy will be used as the primary metric. Additionally, for binary classification AUC/ROC values will be reported. For multi- class classification (multiple CDR labels) F-1 score will be reported. The results from the best model will be reported along with those from the other models.

• About 80% of the data in the dataset will be used for training the models. About 20% of data will used prediction of the CDR label for the k-fold cross-validation with k=10. Sensitivity studies with proportion other than 80:20, e.g. 70:30, will be used to test sensitivity of this split on the accuracy.

• The base case uses a dataset that combines the cross-sectional and the longitudinal MRI datasets. This has the benefit of having a larger dataset. The cross-sectional and the longitudinal datasets will also be trained/cross-validated separately, and classification accuracy will be reported.

• Data cleaning (e.g. removal of NaN values), data exploration, data preparation, data visualization, and data preprocessing will be described, as appropriate, and the impact of the latter on prediction metrics will discussed.

References

1. The Open Access Series of Imaging Studies (OASIS), http://www.oasis-brains.org/app/template/Index.vm;jsessionid=6926BBF18A3D5CD974E750FAC8ED01CE (http://www.oasis-brains.org/app/template/Index.vm;jsessionid=6926BBF18A3D5CD974E750FAC8ED01CE)
2. OASIS Fact Sheet (rev. 2007-8-20) Cross-Sectional Data Across the Adult Lifespan, Marcus et al., 2007, http://www.oasis-brains.org/pdf/oasis_cross-sectional_facts.pdf (http://www.oasis-brains.org/pdf/oasis_cross-sectional_facts.pdf)
3. MRI Reliability data across the adult lifespan, http://www.oasis- (http://www.oasis-) brains.org/app/action/BundleAction/bundle/OAS1_RELIABILITY
4. Buckner, RL, Head, D, Parker, J, Fotenos, AF, Marcus, D, Morris, JC, Snyder, AZ, 2004, "A unified approach for morphometric and functional data analysis in young, old, and demented adults using automated atlas-based head size normalization: reliability and validation against manual measurement of total intracranial volume", Neuroimage 23, 724-38.
5. Fotenos, AF, Snyder, AZ, Girton, LE, Morris, JC, and Buckner, RL, 2005, "Normative estimates of crosssectional and longitudinal brain volume decline in aging and AD", Neurology, 64: 1032-1039.
6. Marcus, DS, Wang, TH, Parker, J, M, Csernansky, JG, Morris, JC, Buckner, RL, 2007. "Open Access Series of Imaging Studies (OASIS): Cross-Sectional MRI Data in Young, Middle Aged, Nondemented and Demented Older Adults", Journal of Cognitive Neuroscience, 19, 1498-1507.
7. Morris, JC, 1993. "The Clinical Dementia Rating (CDR): current version and scoring rules", Neurology 43, 2412b-2414b.
8. Rubin, EH, Storandt, M, Miller, JP, Kinscherf, DA, Grant, EA, Morris, JC, Berg, L, "A prospective study of cognitive function and onset of dementia in cognitively healthy elders". Arch Neurol. 55, 395- 401.
9. Zhang, Y, Brady, M, Smith, S, "Segmentation of brain MR images through a hidden Markov random field model and the expectation maximization algorithm". IEEE Trans. on Medical Imaging, 20(1):45-57.
10. "Diagnosis of Alzheimer's Disease Based on Structural MRI Images Using a Regularized Extreme Learning Machine and PCA Feature", https://www.hindawi.com/journals/jhe/2017/5485080/ (https://www.hindawi.com/journals/jhe/2017/5485080/)

11. "Use of Machine Learning Technology in the Diagnosis of Alzheimer's Disease", http://doras.dcu.ie/21356/1/Noel_s_Master_s_thesis__Copy_(1).pdf (http://doras.dcu.ie/21356/1/Noel_s_Master_s_thesis__Copy_(1).pdf)
12. Scikit-learn, http://scikit-learn.org/stable/index.html (http://scikit-learn.org/stable/index.html)
13. Model evaluation: quantifying the quality of predictions, http://scikit-learn.org/stable/modules/model_evaluation.html (http://scikit-learn.org/stable/modules/model_evaluation.html)).
14. Precision and Recall, http://scikit-learn.org/stable/auto_examples/model_selection/plot_precision_recall.html#sphx-glr-auto-examples-model-selection-plot-precision-recall-py (http://scikit-learn.org/stable/auto_examples/model_selection/plot_precision_recall.html#sphx-glr-auto-examples-model-selection-plot-precision-recall-py)
15. Confusion Matrix, http://scikit-learn.org/stable/modules/model_evaluation.html#confusion-matrix (http://scikit-learn.org/stable/modules/model_evaluation.html#confusion-matrix)
16. Support, http://scikit-learn.org/stable/modules/generated/sklearn.metrics.precision_recall_fscore_support.html (http://scikit-learn.org/stable/modules/generated/sklearn.metrics.precision_recall_fscore_support.html)
17. F1-score, http://scikit-learn.org/stable/modules/generated/sklearn.metrics.f1_score.html (http://scikit-learn.org/stable/modules/generated/sklearn.metrics.f1_score.html)
18. "Conditional data slicing in a Pandas dataframe", https://stackoverflow.com/questions/17071871/select-rows-from-a-dataframe-based-on-values-in-a-column-in-pandas (https://stackoverflow.com/questions/17071871/select-rows-from-a-dataframe-based-on-values-in-a-column-in-pandas)
19. "Matplotlib colormap examples and color schemes for using in heatmap", http://pyhogs.github.io/colormap-examples.html (http://pyhogs.github.io/colormap-examples.html); https://matplotlib.org/examples/color/colormaps_reference.html (https://matplotlib.org/examples/color/colormaps_reference.html)
20. "Usefulness of data from magnetic resonance imaging to improve prediction of dementia: population based cohort study" http://www.bmj.com/content/350/bmj.h2863 (http://www.bmj.com/content/350/bmj.h2863)
21. C - Statistics: http://www.statisticshowto.com/c-statistic/ (http://www.statisticshowto.com/c-statistic/)
22. The Use of MRI and PET for Clinical Diagnosis of Dementia and Investigation of Cognitive Impairment: A Consensus Report https://www.alz.org/national/documents/imaging_consensus_report.pdf (https://www.alz.org/national/documents/imaging_consensus_report.pdf)
23. Knopman DS, DeKosky ST, Cummings JL, Chui H, Corey-Bloom J, Relkin N, et al. Practice parameter: Diagnosis of dementia (anevidence-based review). Report of the Quality Standards Subcommittee of the American Academy of Neurology. Neurology 2001;56(9):1143–1153.
24. Machine Learning Mastery, https://machinelearningmastery.com/ (https://machinelearningmastery.com/)
25. "The Role of Balanced Training and Testing Data Sets for Binary Classifiers in Bioinformatics", https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3706434/ (https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3706434/)
26. "8 Proven Ways for improving the "Accuracy" of a Machine Learning Model", https://www.analyticsvidhya.com/blog/2015/12/improve-machine-learning-results/ (https://www.analyticsvidhya.com/blog/2015/12/improve-machine-learning-results/)

27. “A Gentle Introduction to the Gradient Boosting Algorithm for Machine Learning”, https://machinelearningmastery.com/gentle-introduction-gradient-boosting-algorithm-machine-learning/ (https://machinelearningmastery.com/gentle-introduction-gradient-boosting-algorithm-machine-learning/)
28. "Gradient Boosting Tree vs. Random Forest", https://stats.stackexchange.com/questions/173390/gradient-boosting-tree-vs-random-forest (https://stats.stackexchange.com/questions/173390/gradient-boosting-tree-vs-random-forest)
29. "Does the dataset size influence a machine learning algorithm?", https://stackoverflow.com/questions/25665017/does-the-dataset-size-influence-a-machine-learning-algorithm?rq=1 (https://stackoverflow.com/questions/25665017/does-the-dataset-size-influence-a-machine-learning-algorithm?rq=1)
30. http://scikit-learn.org/stable/modules/generated/sklearn.feature_selection.SelectKBest.html#sklearn.feature_ (http://scikit-learn.org/stable/modules/generated/sklearn.feature_selection.SelectKBest.html#sklearn.feature_

Metrics

*[Metrics used to measure performance of a model or result are clearly defined. Metrics are justified based on the characteristics of the problem.]

Classification Accuracy is used as the primary metric. This metric is applicable for binary classification where the number of records for the two labels are balanced. As shown later in this notebook, the ratio of the number of processed records with CDR=0 and CDR=1 is 60% to 40%, and is considered balanced. Classification accuracy is defined as the number of records correctly classified divided by the total number of records classified. Additionally, for binary classification here, AUC/ROC values are reported. Accuracy results are also be reported in sklearn Confusion Matrix format to evaluate classifier output quality, and in Classification Report format (provides, precision, recall, and f1-score) which are quite appropriate for the dataset used to train models for CDR classification. References 13 through 17 have details and discussion of these sklearn metrics.

Benchmark

[Student clearly defines a benchmark result or threshold for comparing performances of solutions obtained.\

My primary benchmark is a neural network model (Appendix 1) based on the same data discussed above and as used in this problem: Keras is used as the frontend with tensorflow backend. My secondary benchmark will be results of the study in the two papers below:

** Paper title: Usefulness of data from magnetic resonance imaging to improve prediction of dementia: population based cohort study, Reference 20

"Results During 10 years of follow-up, there were 119 confirmed cases of dementia, 84 of which were Alzheimer’s disease. The conventional risk model incorporated age, sex, education, cognition, physical function, lifestyle (smoking, alcohol use), health (cardiovascular disease, diabetes, systolic blood pressure), and the apolipoprotein genotype (C statistic for discrimination performance was

0.77, 95% confidence interval 0.71 to 0.82). No significant differences were observed in the discrimination performance of the conventional risk model compared with models incorporating data from MRI including white matter lesion volume (C statistic 0.77, 95% confidence interval 0.72 to 0.82; P=0.48 for difference of C statistics, Reference 21), brain volume (0.77, 0.72 to 0.82; P=0.60), hippocampal volume (0.79, 0.74 to 0.84; P=0.07), or all three variables combined (0.79, 0.75 to 0.84; P=0.05). Inclusion of hippocampal volume or all three MRI variables combined in the conventional model did, however, lead to significant improvement in reclassification measured by using the integrated discrimination improvement index (P=0.03 and P=0.04) and showed increased net benefit in decision curve analysis. Similar results were observed when the outcome was restricted to Alzheimer's disease."

**Paper Title: The Use of MRI and PET for Clinical Diagnosis of Dementia and Investigation of Cognitive Impairment: A Consensus Report, Reference 22.

"Once the presence of dementia has been established, the role of imaging in the diagnosis of dementia subtypes is very much a function of the clinical diagnosis. The accuracy of the clinical diagnosis of Alzheimer's disease (AD) is quite good. Pathological AD has a prevalence of about 70% (range 50% to above 80% depending upon whether the AD occurs in isolation or with other entities) among all dementias (see evidence Table 1 in Reference 23); thus, even clinicians with limited neurological expertise should have a diagnostic accuracy, for AD at least, at about that level. A review of 13 published studies gave average values for sensitivity and specificity of the clinical diagnosis of AD of 81% and 70%, respectively(Reference 23). The overall accuracy of the clinical diagnosis of AD versus not-AD compared with the neuropathological standard based on those values for prevalence, sensitivity, and specificity, is 78%. "

Datasets and Inputs

Reference 1 provides the downloadable MRI related data in csv format. Reference 2 provides metadata and additional facts about the cross-sectional MRI.

OASIS Cross-sectional MRI Data in Young, Middle Aged, Non-demented and Demented Older Adults

• This dataset consists of a cross-sectional collection for 416 persons aged 18 to 96

• For each person, 3 to 4 T1-weighted MRI scans that were obtained in single scan sessions are included.

• The persons include both men and women, and are all right-handed.

• In this dataset, one hundred persons over the age of 60 have been clinically diagnosed with very mild to moderate Alzheimer's disease (AD).

• Also, a reliability data set , Reference 3, is included which contains 20 non-demented subjects imaged on a subsequent visit within 90 days of their initial session.

• Dementia related Additional Data below for the cross-sectional MRI cases used this project. Features based on these Additional Data will be used to train classification models to predict the labels for the outcome (CDR).

OASIS: Longitudinal MRI Data in Non-demented and Demented Older Adults

This set consists of a longitudinal collection of 150 subjects aged 60 to 96. Each subject was scanned on two or more visits, separated by at least one year for a total of 373 imaging sessions. For each subject, 3 or 4 individual T1-weighted MRI scans obtained in single scan sessions are included.

Note: MRI image pixel data are NOT used in this problem, only related features prefixed with @ sign (below) will be used.

• The subjects are all right-handed and include both men and women.

• 72 of the subjects were characterized as non-demented throughout the study.

• 64 of the included subjects were characterized as demented at the time of their initial visits and remained so for subsequent scans, including 51 individuals with mild to moderate Alzheimer's disease.

• Another 14 subjects were characterized as non-demented at the time of their initial visit and were subsequently characterized as demented at a later visit.

• Dementia related **Additional Data** below for the longitudinal MRI cases are used this project.

Features based on the **Additional Data** are relevant to finding machine learning solutions to the problem defined above, and will be used to train classification models to predict the labels for the outcome (Critical Dementia Rating, CDR).

Additional Data: Specific References in parentheses below covering features are from Reference 2. These features include Demographic, clinical, and derived anatomic measures related to brain that are located in the file oasis_crosssectional.csv. Features prefixed with @ will be used for the problem.

Demographic data:

```
- @Gender (M/F), categorical data
- Handedness (Right or Left Handed), categorical data, all of which are r
ight handed in the dataset.
- @Age (numeric),
- @Education (Educ, categorical). Education codes correspond to the follo
wing levels of education:
    1=Less than high school graduate.
    2=High school graduate.
    3=Some college education
    4=College graduate.
    5=Beyond college.
```

Clinical data:

```
- @Mini-Mental State Examination (MMSE, Reference 8),

- @Clinical Dementia Rating (CDR, Reference 7)
    0 = non-demented (341 data points)
    0.5 = very mild dementia (193 data points)
    1 = mild dementia (69 data points)
    2 = moderate dementia (5 data points)
```

There are some records with NaN values in one or more fields; these records will be removed from datasets prior to analysis. All participants with dementia (CDR >0) were diagnosed with probable Alzheimer's Disease.

Derived anatomic volumes data:

```
- @Estimated total intracranial volume (eTIV, mm3), Reference 4
- @Atlas scaling factor (ASF), Reference 4
- @Normalized whole brain volume (nWBV, mm3), Reference 5
```

Load Libraries

In [1]:
```
# Load libraries
import numpy as np
from pandas import read_csv
from pandas.tools.plotting import scatter_matrix
from matplotlib import pyplot
from sklearn.model_selection import train_test_split
from sklearn.model_selection import KFold

from sklearn.model_selection import cross_val_score
from sklearn.metrics import classification_report
from sklearn.metrics import confusion_matrix
from sklearn.metrics import accuracy_score
from sklearn.linear_model import LogisticRegression
from sklearn.tree import DecisionTreeClassifier
from sklearn.neighbors import KNeighborsClassifier
from sklearn.discriminant_analysis import LinearDiscriminantAnalysis
from sklearn.naive_bayes import GaussianNB
from sklearn.svm import SVC
from sklearn.ensemble import GradientBoostingClassifier
from sklearn.ensemble import RandomForestClassifier
```

Load CSV data to Pandas Dataframes

In [2]:
```
# Read a local csvfile in Pandas for the OASIS cross-sectional MRI dataset downlo
import pandas as pd
dfoasx=pd.read_csv('oasis_cross-sectional.csv')
dfoasx.shape
```

Out[2]: (436, 12)

436 rows and 12 columns of data

In [3]:
```
# Read a csvfile in Pandas for the OASIS longitudinal MRI dataset downloaded from
import pandas as pd
dfoasl=pd.read_csv('oasis_longitudinal.csv')
dfoasl.shape
```

Out[3]:
```
(373, 15)
```

373 rows and 15 columns of data.

Analysis

OASIS Cross-sectional Data Exploration

In [4]:
```
# Column names in the dataset, eleven columns, including the index column (ID)
list(dfoasx.columns.values)
```

Out[4]:
```
['ID',
 'M/F',
 'Hand',
 'Age',
 'Educ',
 'SES',
 'MMSE',
 'CDR',
 'eTIV',
 'nWBV',
 'ASF',
 'Delay']
```

In [5]:
```
# Summary statistics for cross-sectionalMRI related dataset.
dfoasx.describe()
```

Out[5]:

	Age	Educ	SES	MMSE	CDR	eTIV	nWBV	
count	436.000000	235.000000	216.000000	235.00000	235.000000	436.000000	436.000000	436.00
mean	51.357798	3.178723	2.490741	27.06383	0.285106	1481.919725	0.791670	1.19
std	25.269862	1.311510	1.120593	3.69687	0.383405	158.740866	0.059937	0.12
min	18.000000	1.000000	1.000000	14.00000	0.000000	1123.000000	0.644000	0.88
25%	23.000000	2.000000	2.000000	26.00000	0.000000	1367.750000	0.742750	1.11
50%	54.000000	3.000000	2.000000	29.00000	0.000000	1475.500000	0.809000	1.19
75%	74.000000	4.000000	3.000000	30.00000	0.500000	1579.250000	0.842000	1.28
max	96.000000	5.000000	5.000000	30.00000	2.000000	1992.000000	0.893000	1.56

We note from demographic and clinical features and cognitive test data for the cross-sectional MRI data, the following:

Mean Age for cross-sectional MRI data is about 51 years, mean for Education is 3.2 years, SES about 2.5, MMSE 27, eTIV 1481, nWBV 0.79, ASF 1.2.

Also note the missing (NaN) data from the count values. Those columns that have count of 436 have missing (NaN) data. The Delay column has most missing data followed by Educ, SES, MMSE, and the label (CDR) which have mising data in many rows. An option is to remove rows with missing column values, and that option will be chosen as seen later in this notebook. Another option, not used here, is to replace the NaN values with mean values listed for colmuns below. That latter choice would be appropriate if the column values have a normal or an uniform distribution. Also note that the values in the different columns are of different orders of magnitude, Some on the order of unity (SES, CDR, nWBV, and ASF), and other column values of higher of magnitude (Age and eTIV). Later in the notebook, rescaling or normalizing the columns(features) will be chosen as sensitivity studies for impact on accuracy and results,

In [6]:
```
# Note that the column data types are object, float64, and int64 data types.
dfoasx.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 436 entries, 0 to 435
Data columns (total 12 columns):
ID       436 non-null object
M/F      436 non-null object
Hand     436 non-null object
Age      436 non-null int64
Educ     235 non-null float64
SES      216 non-null float64
MMSE     235 non-null float64
CDR      235 non-null float64
eTIV     436 non-null int64
nWBV     436 non-null float64
ASF      436 non-null float64
Delay    20 non-null float64
dtypes: float64(7), int64(2), object(3)
memory usage: 40.9+ KB
```

In [7]:
```
dfoasx.head(5)
```

Out[7]:

	ID	M/F	Hand	Age	Educ	SES	MMSE	CDR	eTIV	nWBV	ASF	Delay
0	OAS1_0001_MR1	F	R	74	2.0	3.0	29.0	0.0	1344	0.743	1.306	NaN
1	OAS1_0002_MR1	F	R	55	4.0	1.0	29.0	0.0	1147	0.810	1.531	NaN
2	OAS1_0003_MR1	F	R	73	4.0	3.0	27.0	0.5	1454	0.708	1.207	NaN
3	OAS1_0004_MR1	M	R	28	NaN	NaN	NaN	NaN	1588	0.803	1.105	NaN
4	OAS1_0005_MR1	M	R	18	NaN	NaN	NaN	NaN	1737	0.848	1.010	NaN

Note categorical data for gender M/F, and label (CDR) vlues >=0.0, and NaN.Cross-sectional MRI dataset has many rows with NaN values in multiple columns. These NaN values will be removed after merging the dataset with the Longitudinal MRI dataset.

In [8]:
```
# Determine the count of various values for the label CDR
print (dfoasx.CDR[(dfoasx.CDR == 0.0)].count(),",", dfoasx.CDR[(dfoasx.CDR == 0.5
print (dfoasx.CDR[(dfoasx.CDR == 1.0)].count(),",", dfoasx.CDR[(dfoasx.CDR == 2)]
```

```
(135, ',', 70)
(28, ',', 2)
```

Data frequency for CDR label: There are 135, 70, 28, and 2 rows with CDR label values 0, 0.5, 1.0, and 2. We see very few data points with CDR=2. This is a potential limitation in modeling the classification problem as multi-label (not binary) classification since the some cross validation sets may have very few or even no data points. Metrics for multi-label clasification may not be meaningful for CDR=2 data. An alternative is to not include the few CDR=2 data points in the multi-label classification case.

In [9]:
```
import pandas as pd
## dfoasx cross-sectional MRI data frame
## Calculate number of records with missing label(CDR) values..
sum(pd.isnull(dfoasx['CDR']))
```

Out[9]: 201

We see that for the cross-sectional dataset there are 201 records with NaN values, or about 46% of the records in the data set.

OASIS Longitudinal Data Exploration

In [10]:
```
list(dfoasl.columns.values)
```

Out[10]:
```
['Subject ID',
 'MRI ID',
 'Group',
 'Visit',
 'MR Delay',
 'M/F',
 'Hand',
 'Age',
 'EDUC',
 'SES',
 'MMSE',
 'CDR',
 'eTIV',
 'nWBV',
 'ASF']
```

The three additional columns (Subject ID, Group, and Visit) in dfoasl dataset are not in the dfoasx dataset. These three columns are not meaningful for the CDR classification, and will be dropped before merging the dloasx and dfoasl datasets. The MR Delay and Delay columns in the two datasets have same meaning and the MR Delay column will be repositioned to be in the same column order as the Delay column.

In [11]:
```
dfoasl.describe()
```

Out[11]:

	Visit	MR Delay	Age	EDUC	SES	MMSE	CDR	
count	373.000000	373.000000	373.000000	373.000000	354.000000	371.000000	373.000000	373.
mean	1.882038	595.104558	77.013405	14.597855	2.460452	27.342318	0.290885	1488.
std	0.922843	635.485118	7.640957	2.876339	1.134005	3.683244	0.374557	176.
min	1.000000	0.000000	60.000000	6.000000	1.000000	4.000000	0.000000	1106.
25%	1.000000	0.000000	71.000000	12.000000	2.000000	27.000000	0.000000	1357.
50%	2.000000	552.000000	77.000000	15.000000	2.000000	29.000000	0.000000	1470.
75%	2.000000	873.000000	82.000000	16.000000	3.000000	30.000000	0.500000	1597.
max	5.000000	2639.000000	98.000000	23.000000	5.000000	30.000000	2.000000	2004.

Mean Age for cross-sectional MRI data is about 77 years, mean for Education is 15.6 years, SES about 2.5, MMSE 27, eTIV 1488, nWBV 0.73, ASF 1.2. Also note the missing (NaN) data from the count values. Those columns that have count of 436 have missing (NaN) data. The Delay column has most missing data followed by Educ, SES, MMSE, and the label (CDR) which have mising data in many rows. Another option, not used here, is to replace the NaN values with mean values listed for colmuns below. That latter choice would be appropriate if the column values have a normal or an uniform distribution. Also note that the values in the different columns are of different orders of magnitude, some on the order of unity (SES, CDR, nWBV, and ASF), and other column values of higher of magnitude (Age and eTIV). Rescaling or normalizing the columns(features) will be chosen as sensitivity studies for impact on accuracy and resuls, later in the notebook.

In [12]:
```
dfoasl.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 373 entries, 0 to 372
Data columns (total 15 columns):
Subject ID    373 non-null object
MRI ID        373 non-null object
Group         373 non-null object
Visit         373 non-null int64
MR Delay      373 non-null int64
M/F           373 non-null object
Hand          373 non-null object
Age           373 non-null int64
EDUC          373 non-null int64
SES           354 non-null float64
MMSE          371 non-null float64
CDR           373 non-null float64
eTIV          373 non-null int64
nWBV          373 non-null float64
ASF           373 non-null float64
dtypes: float64(5), int64(5), object(5)
memory usage: 43.8+ KB
```

In [13]:
```
dfoasl.head(5)
```

Out[13]:

	Subject ID	MRI ID	Group	Visit	MR Delay	M/F	Hand	Age	EDUC	SES	MMSE
0	OAS2_0001	OAS2_0001_MR1	Nondemented	1	0	M	R	87	14	2.0	27.0
1	OAS2_0001	OAS2_0001_MR2	Nondemented	2	457	M	R	88	14	2.0	30.0
2	OAS2_0002	OAS2_0002_MR1	Demented	1	0	M	R	75	12	NaN	23.0
3	OAS2_0002	OAS2_0002_MR2	Demented	2	560	M	R	76	12	NaN	28.0
4	OAS2_0002	OAS2_0002_MR3	Demented	3	1895	M	R	80	12	NaN	22.0

Longitudinal MRI dataset has many rows with NaN values in multiple columns. These NaN values will be removed after merging the dataset with the Cross-sectional MRI dataset.

In [14]:
```
typesl=dfoasx.dtypes
print(typesl)
```

```
ID        object
M/F       object
Hand      object
Age        int64
Educ     float64
SES      float64
MMSE     float64
CDR      float64
eTIV       int64
nWBV     float64
ASF      float64
Delay    float64
dtype: object
```

In [15]:
```
# Determine the count of various values for the label CDR
print (dfoasl.CDR[(dfoasl.CDR == 0.0)].count(),",", dfoasl.CDR[(dfoasl.CDR == 0.5
print (dfoasl.CDR[(dfoasl.CDR == 1.0)].count(),",", dfoasl.CDR[(dfoasl.CDR == 2)]
```

```
(206, ',', 123)
(41, ',', 3)
```

Data frequency for CDR label: In the longitudinal MRI dataset, there are 206, 123, 41, and 3 rows with CDR label values 0, 0.5, 1.0, and 2, respectively. Similar to the cross sectional MRI dataset. We see very few data points with CDR=2. This is a potential limitation in modeling the classification problem as multi-label (not binary) classification since the some cross validation sets may have very few or even no data points. Metrics for multi-label clasification may not be meaningful for CDR=2 data. An alternative is to not include the few CDR=2 data points in the multi-label classification case.

In [16]:
```
import pandas as pd
# CDR is name of column for which you want to calculate the NaN values
sum(pd.isnull(dfoasx['CDR'])), sum(pd.isnull(dfoasl['CDR']))
```

Out[16]: (201, 0)

We find 201 missing CDR values in the cross-sectional dataset (dfoasx), and no missing values in the longitudinal MRI dataset)dfoasl).

The count of various CDR labels for the two datasets and the total values are shown in the Table below. Again we see that the total number of records for the combined dataset would be 5, a small number of datarecords to calculate meaningful

- CDR = 0, 0.5, 1.0, 2, NaN
- dfoasx= 135, 70, 28, 2, 201
- dfoasl= 206, 123, 41, 3, 0
- Total = 341, 193, 69, 5, 201

Methodology

Data Preprocessing

[All preprocessing steps have been clearly documented. Abnormalities or characteristics about the data or input that needed to be addressed have been corrected. If no data preprocessing is necessary, it has been clearly justified.]

Wikipedia: "If there is much irrelevant and redundant information present or noisy and unreliable data, then knowledge discovery during the training phase is more difficult. Data pre-processing includes cleaning, instance selection, normalization, transformation, feature extraction and selection, etc. The product of data pre-processing is the final training set."

- Replace gender categorical data (M, F) with numerical values (0, 1).
- Select longitudinal dataset (dfoasl) columns that have data similar to the dataset for cross-sectional dataset (dfoasx). This will facilitate combining the two datasets to create a merged dataset (dfoas_merge).
- Explore the merged dataset
- Remove NaN rows; drop rows with NaN values (missing data) in at least one column. This will make classification metrics meaningful.

In [17]:
```
# Cross-sectional MRI data preparation and preprocessing
# Replace gender data "M" and "F" with numerical inputs 0, and 1
dfoasx['M/F'] = dfoasx['M/F'].replace('F', 1)
dfoasx['M/F'] = dfoasx['M/F'].replace('M', 0)

# Convert CDR>0 values to 1 to make this a binary classification problem (CDR val
# Leave CDR values of 0 as is
# Convert CDR values >0 to 1

dfoasx['CDR'] = dfoasx['CDR'].replace(0.5, 1)
dfoasx['CDR'] = dfoasx['CDR'].replace(2, 1)
dfoasx.head(10)
```

Out[17]:

	ID	M/F	Hand	Age	Educ	SES	MMSE	CDR	eTIV	nWBV	ASF	Delay
0	OAS1_0001_MR1	1	R	74	2.0	3.0	29.0	0.0	1344	0.743	1.306	NaN
1	OAS1_0002_MR1	1	R	55	4.0	1.0	29.0	0.0	1147	0.810	1.531	NaN
2	OAS1_0003_MR1	1	R	73	4.0	3.0	27.0	1.0	1454	0.708	1.207	NaN
3	OAS1_0004_MR1	0	R	28	NaN	NaN	NaN	NaN	1588	0.803	1.105	NaN
4	OAS1_0005_MR1	0	R	18	NaN	NaN	NaN	NaN	1737	0.848	1.010	NaN
5	OAS1_0006_MR1	1	R	24	NaN	NaN	NaN	NaN	1131	0.862	1.551	NaN
6	OAS1_0007_MR1	0	R	21	NaN	NaN	NaN	NaN	1516	0.830	1.157	NaN
7	OAS1_0009_MR1	1	R	20	NaN	NaN	NaN	NaN	1505	0.843	1.166	NaN
8	OAS1_0010_MR1	0	R	74	5.0	2.0	30.0	0.0	1636	0.689	1.073	NaN
9	OAS1_0011_MR1	1	R	52	3.0	2.0	30.0	0.0	1321	0.827	1.329	NaN

In [18]:
```
# Determine the count of various values for the label CDR
print (dfoasx.CDR[(dfoasx.CDR == 0.0)].count(),",", dfoasx.CDR[(dfoasx.CDR == 0.5
print (dfoasx.CDR[(dfoasx.CDR == 1.0)].count(),",", dfoasx.CDR[(dfoasx.CDR == 2)]
```

```
(135, ',', 0)
(100, ',', 0)
```

In [19]:
```
# Longitudinal  MRI data preparation
# Replace gender data "M" and "F" with numerical inputs 0, and 1
# Convert CDR>0 values to 1 to make this a binary classification problem (CDR val
dfoasl['M/F'] = dfoasl['M/F'].replace('F', 1)
dfoasl['M/F'] = dfoasl['M/F'].replace('M', 0)
# Leave CDR values of 0 as is
# Convert CDR values >0 to 1

dfoasl['CDR'] = dfoasl['CDR'].replace(0.5, 1)
dfoasl['CDR'] = dfoasl['CDR'].replace(2, 1)
dfoasl.head(10)
```

Out[19]:

	Subject ID	MRI ID	Group	Visit	MR Delay	M/F	Hand	Age	EDUC	SES	MMSE
0	OAS2_0001	OAS2_0001_MR1	Nondemented	1	0	0	R	87	14	2.0	27.0
1	OAS2_0001	OAS2_0001_MR2	Nondemented	2	457	0	R	88	14	2.0	30.0
2	OAS2_0002	OAS2_0002_MR1	Demented	1	0	0	R	75	12	NaN	23.0
3	OAS2_0002	OAS2_0002_MR2	Demented	2	560	0	R	76	12	NaN	28.0
4	OAS2_0002	OAS2_0002_MR3	Demented	3	1895	0	R	80	12	NaN	22.0
5	OAS2_0004	OAS2_0004_MR1	Nondemented	1	0	1	R	88	18	3.0	28.0
6	OAS2_0004	OAS2_0004_MR2	Nondemented	2	538	1	R	90	18	3.0	27.0
7	OAS2_0005	OAS2_0005_MR1	Nondemented	1	0	0	R	80	12	4.0	28.0
8	OAS2_0005	OAS2_0005_MR2	Nondemented	2	1010	0	R	83	12	4.0	29.0
9	OAS2_0005	OAS2_0005_MR3	Nondemented	3	1603	0	R	85	12	4.0	30.0

In [20]:
```
# Determine the count of various values for the label CDR
print (dfoasl.CDR[(dfoasl.CDR == 0.0)].count(),",", dfoasl.CDR[(dfoasl.CDR == 0.5
print (dfoasl.CDR[(dfoasl.CDR == 1.0)].count(),",", dfoasl.CDR[(dfoasl.CDR == 2)]
```

```
(206, ',', 0)
(167, ',', 0)
```

In [21]:
```
# Select longitudinal dataset columns that are similar to the dataset for cross-s
dfoasl2=dfoasl[['MRI ID','M/F','Hand','Age',
 'EDUC','SES','MMSE','CDR','eTIV','nWBV','ASF', 'MR Delay']]
dfoasl2.head(6)
```

Out[21]:

	MRI ID	M/F	Hand	Age	EDUC	SES	MMSE	CDR	eTIV	nWBV	ASF	MR Delay
0	OAS2_0001_MR1	0	R	87	14	2.0	27.0	0.0	1987	0.696	0.883	0
1	OAS2_0001_MR2	0	R	88	14	2.0	30.0	0.0	2004	0.681	0.876	457
2	OAS2_0002_MR1	0	R	75	12	NaN	23.0	1.0	1678	0.736	1.046	0
3	OAS2_0002_MR2	0	R	76	12	NaN	28.0	1.0	1738	0.713	1.010	560
4	OAS2_0002_MR3	0	R	80	12	NaN	22.0	1.0	1698	0.701	1.034	1895
5	OAS2_0004_MR1	1	R	88	18	3.0	28.0	0.0	1215	0.710	1.444	0

In [22]:
```
# Rename columns:MRI ID to ID, EDUC to Educ, MR Delay to Delay similar to cross-s
dfoasl2=dfoasl2.rename(columns={'EDUC':'Educ', 'MRI ID':'ID', 'MR Delay':'Delay'}
dfoasl2.head(6)
```

Out[22]:

	ID	M/F	Hand	Age	Educ	SES	MMSE	CDR	eTIV	nWBV	ASF	Delay
0	OAS2_0001_MR1	0	R	87	14	2.0	27.0	0.0	1987	0.696	0.883	0
1	OAS2_0001_MR2	0	R	88	14	2.0	30.0	0.0	2004	0.681	0.876	457
2	OAS2_0002_MR1	0	R	75	12	NaN	23.0	1.0	1678	0.736	1.046	0
3	OAS2_0002_MR2	0	R	76	12	NaN	28.0	1.0	1738	0.713	1.010	560
4	OAS2_0002_MR3	0	R	80	12	NaN	22.0	1.0	1698	0.701	1.034	1895
5	OAS2_0004_MR1	1	R	88	18	3.0	28.0	0.0	1215	0.710	1.444	0

In [23]:
```
dfoasx.head(6)
```

Out[23]:

	ID	M/F	Hand	Age	Educ	SES	MMSE	CDR	eTIV	nWBV	ASF	Delay
0	OAS1_0001_MR1	1	R	74	2.0	3.0	29.0	0.0	1344	0.743	1.306	NaN
1	OAS1_0002_MR1	1	R	55	4.0	1.0	29.0	0.0	1147	0.810	1.531	NaN
2	OAS1_0003_MR1	1	R	73	4.0	3.0	27.0	1.0	1454	0.708	1.207	NaN
3	OAS1_0004_MR1	0	R	28	NaN	NaN	NaN	NaN	1588	0.803	1.105	NaN
4	OAS1_0005_MR1	0	R	18	NaN	NaN	NaN	NaN	1737	0.848	1.010	NaN
5	OAS1_0006_MR1	1	R	24	NaN	NaN	NaN	NaN	1131	0.862	1.551	NaN

Merge the cross-sectional and the Longitudinal MRI datasets

In [24]:
```
# Merge the cross-sectional and the longitudinal MRI datasets
dfoas_merge = dfoasx.append(dfoasl2, ignore_index=True)
dfoas_merge.shape
```

Out[24]: (809, 12)

In [25]:
```
dfoas_merge_with_NaN= dfoas_merge
```

The merged dataset dfoas_merge has 809 rows and 12 columns

Explore the merged dataset

In [26]:
```
dfoas_merge.describe()
```

Out[26]:

	M/F	Age	Educ	SES	MMSE	CDR	eTIV	nl
count	809.000000	809.000000	608.000000	570.00000	606.000000	608.000000	809.000000	809.00
mean	0.594561	63.186650	10.184211	2.47193	27.234323	0.439145	1484.782447	0.76
std	0.491280	23.117511	6.058388	1.12805	3.687980	0.496691	166.911689	0.05
min	0.000000	18.000000	1.000000	1.00000	4.000000	0.000000	1106.000000	0.64
25%	0.000000	49.000000	4.000000	2.00000	26.000000	0.000000	1361.000000	0.71
50%	1.000000	72.000000	12.000000	2.00000	29.000000	0.000000	1475.000000	0.75
75%	1.000000	80.000000	16.000000	3.00000	30.000000	1.000000	1583.000000	0.81
max	1.000000	98.000000	23.000000	5.00000	30.000000	1.000000	2004.000000	0.89

In [27]:
```
# Replace NaN values for the Delay column to dataset average of 555 to facilitate
dfoas_merge['Delay'] = dfoas_merge['Delay'].replace(np.NaN, 555)
```

In [28]:
```
dfoas_merge.head(10)
```

Out[28]:

	ID	M/F	Hand	Age	Educ	SES	MMSE	CDR	eTIV	nWBV	ASF	Delay
0	OAS1_0001_MR1	1	R	74	2.0	3.0	29.0	0.0	1344	0.743	1.306	555.0
1	OAS1_0002_MR1	1	R	55	4.0	1.0	29.0	0.0	1147	0.810	1.531	555.0
2	OAS1_0003_MR1	1	R	73	4.0	3.0	27.0	1.0	1454	0.708	1.207	555.0
3	OAS1_0004_MR1	0	R	28	NaN	NaN	NaN	NaN	1588	0.803	1.105	555.0
4	OAS1_0005_MR1	0	R	18	NaN	NaN	NaN	NaN	1737	0.848	1.010	555.0
5	OAS1_0006_MR1	1	R	24	NaN	NaN	NaN	NaN	1131	0.862	1.551	555.0
6	OAS1_0007_MR1	0	R	21	NaN	NaN	NaN	NaN	1516	0.830	1.157	555.0
7	OAS1_0009_MR1	1	R	20	NaN	NaN	NaN	NaN	1505	0.843	1.166	555.0
8	OAS1_0010_MR1	0	R	74	5.0	2.0	30.0	0.0	1636	0.689	1.073	555.0
9	OAS1_0011_MR1	1	R	52	3.0	2.0	30.0	0.0	1321	0.827	1.329	555.0

In [29]:
```
dfoas_merge.dtypes
```

Out[29]:
```
ID        object
M/F        int64
Hand      object
Age        int64
Educ     float64
SES      float64
MMSE     float64
CDR      float64
eTIV       int64
nWBV     float64
ASF      float64
Delay    float64
dtype: object
```

Drop rows in the merged dataset with NaN in any column. We see that there are 809-570=239 rows with NaN values (missing data) in at least one column.

In [30]:
```
# Drop rows with NaN
dfoas_merge=dfoas_merge.dropna(how='any')
```

In [31]:
```
dfoas_merge.shape
```

Out[31]:
```
(570, 12)
```

In [32]:
```
dfoas_merge.dtypes
```

Out[32]:
```
ID        object
M/F        int64
Hand      object
Age        int64
Educ     float64
SES      float64
MMSE     float64
CDR      float64
eTIV       int64
nWBV     float64
ASF      float64
Delay    float64
dtype: object
```

In [33]:
```
dfoas_merge.head(6)
```

Out[33]:

	ID	M/F	Hand	Age	Educ	SES	MMSE	CDR	eTIV	nWBV	ASF	Delay
0	OAS1_0001_MR1	1	R	74	2.0	3.0	29.0	0.0	1344	0.743	1.306	555.0
1	OAS1_0002_MR1	1	R	55	4.0	1.0	29.0	0.0	1147	0.810	1.531	555.0
2	OAS1_0003_MR1	1	R	73	4.0	3.0	27.0	1.0	1454	0.708	1.207	555.0
8	OAS1_0010_MR1	0	R	74	5.0	2.0	30.0	0.0	1636	0.689	1.073	555.0
9	OAS1_0011_MR1	1	R	52	3.0	2.0	30.0	0.0	1321	0.827	1.329	555.0
11	OAS1_0013_MR1	1	R	81	5.0	2.0	30.0	0.0	1664	0.679	1.055	555.0

In [34]:
```
dfoas_merge.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 570 entries, 0 to 808
Data columns (total 12 columns):
ID       570 non-null object
M/F      570 non-null int64
Hand     570 non-null object
Age      570 non-null int64
Educ     570 non-null float64
SES      570 non-null float64
MMSE     570 non-null float64
CDR      570 non-null float64
eTIV     570 non-null int64
nWBV     570 non-null float64
ASF      570 non-null float64
Delay    570 non-null float64
dtypes: float64(7), int64(3), object(2)
memory usage: 57.9+ KB
```

In [35]:
```
print (dfoas_merge.CDR[(dfoas_merge.CDR == 0.0)].count(),",", dfoas_merge.CDR[(df
```

```
(339, ',', 231)
```

We see from above exploratory results that the combined cross-sectional and longitudinal datasets have 339 records for CDR=0.0, and 231 records for CDR=1 (recall CDR values of 0.5 and 2.0 have been replaced by 1.0 to make it a binary classification problem. Thus the labels are "balanced", the number of records with CDR=0.0 and CDR=1.0 are 59% and 41% respectively.

Exploratory Visualization

[A visualization has been provided that summarizes or extracts a relevant characteristic or feature about the dataset or input data with thorough discussion. Visual cues are clearly defined.]

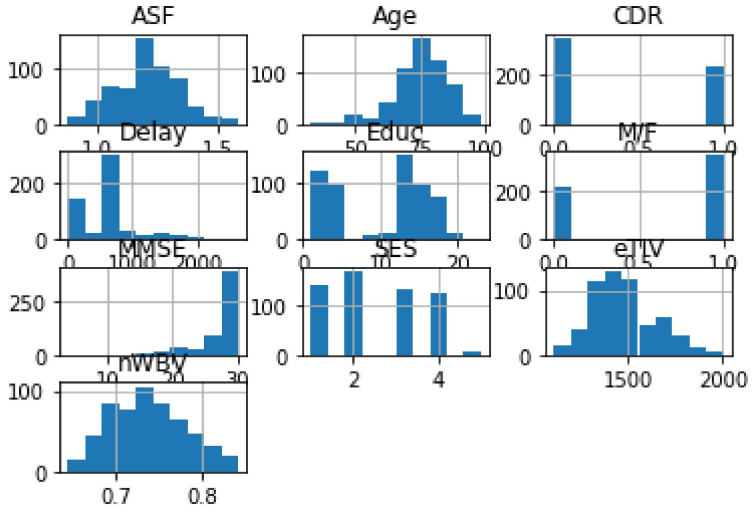
The following visualizations of the merged dataset (doafs_merge dataframe) have been provided below.

- Histogram

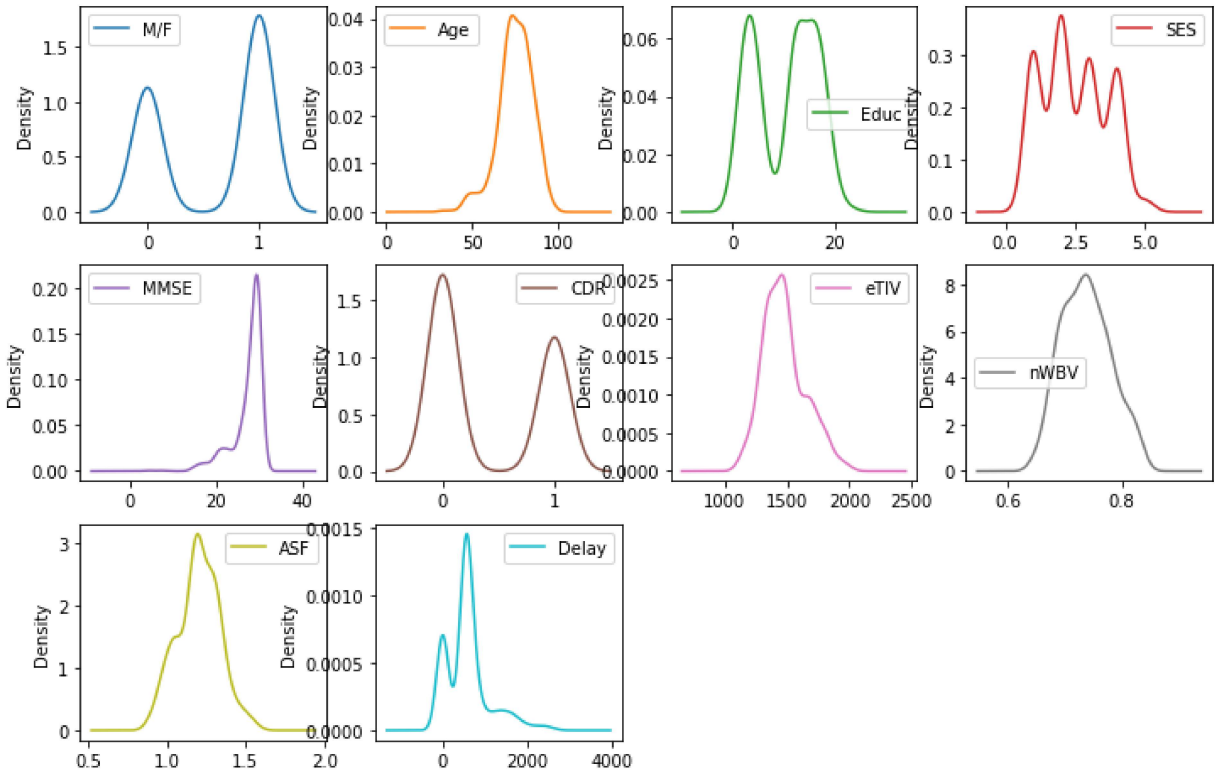
- Density Plots
- Box Plots
- Scatter Plots
- Correlation matrix

From the histogram. density plots, and box plots for the feature variables, we note the following: Age, eTIV, nWBV, and ASF have approximately normal distribution. The feature variables, Educ, and SES have bi-modal or multimodal distribution. As expected CDR after transformation of CDR>0 values to 1, indicates binary distribution (0, and 1). The gender variable M/F indicates transformed numerical values of 0 and 1 as expected.

In [36]:
```
from matplotlib import pyplot
dfoas_merge.hist()
fig_size = pyplot.rcParams["figure.figsize"]
fig_size[0] = 9
fig_size[1] = 12
pyplot.rcParams["figure.figsize"] = fig_size
pyplot.show();
```

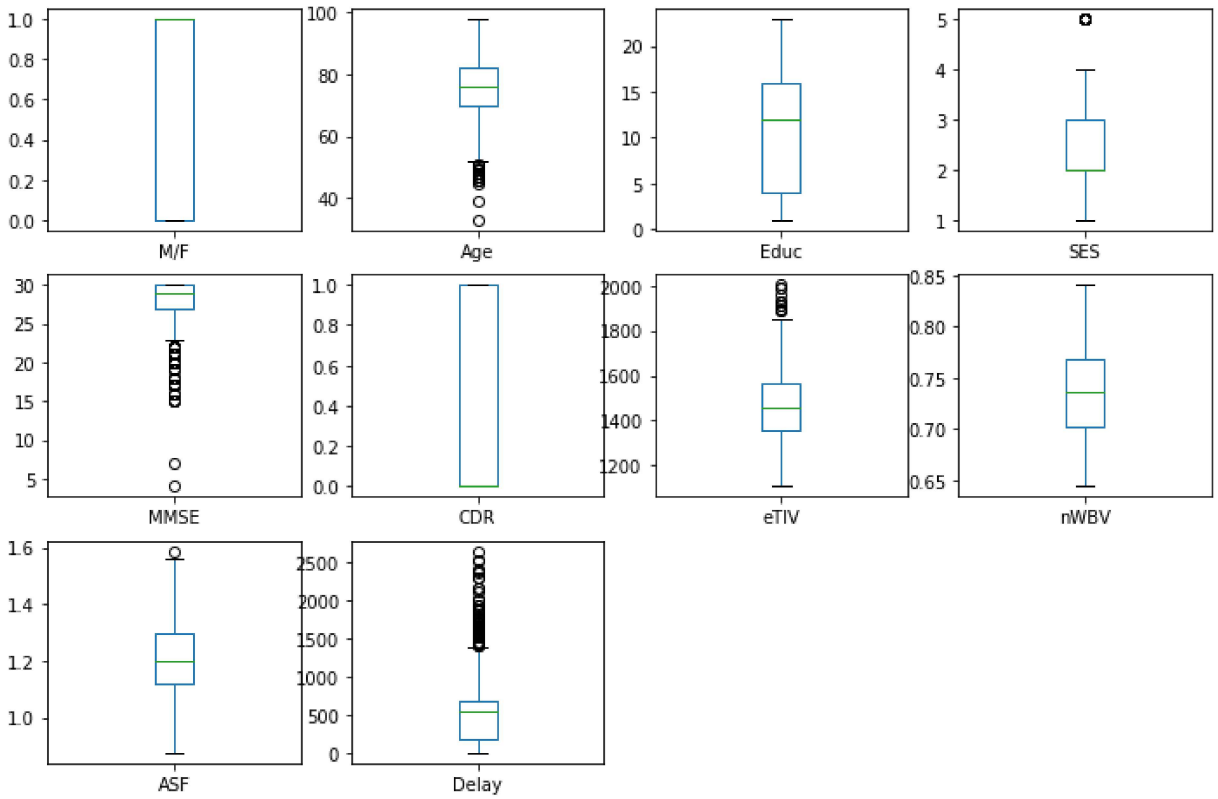


In [37]:
```
# http://pandas.pydata.org/pandas-docs/stable/generated/pandas.DataFrame.plot.htm
# Univariate Density Plots
from matplotlib import pyplot
dfoas_merge.plot(kind='density', subplots=True, layout=(3, 4), figsize=(12, 8), s
pyplot.show();
```



Outliers (data that are values that have values at that are located, outside the bandsdefined by 1.5 times greater than the size of spread of the middle 50% of the data. Age, SES, eTIV, MMSE, and Delay have some outliers.

In [38]:
```
dfoas_merge.plot(kind='box', subplots=True, layout=(3, 4), figsize=(12, 8), share
pyplot.show();
```

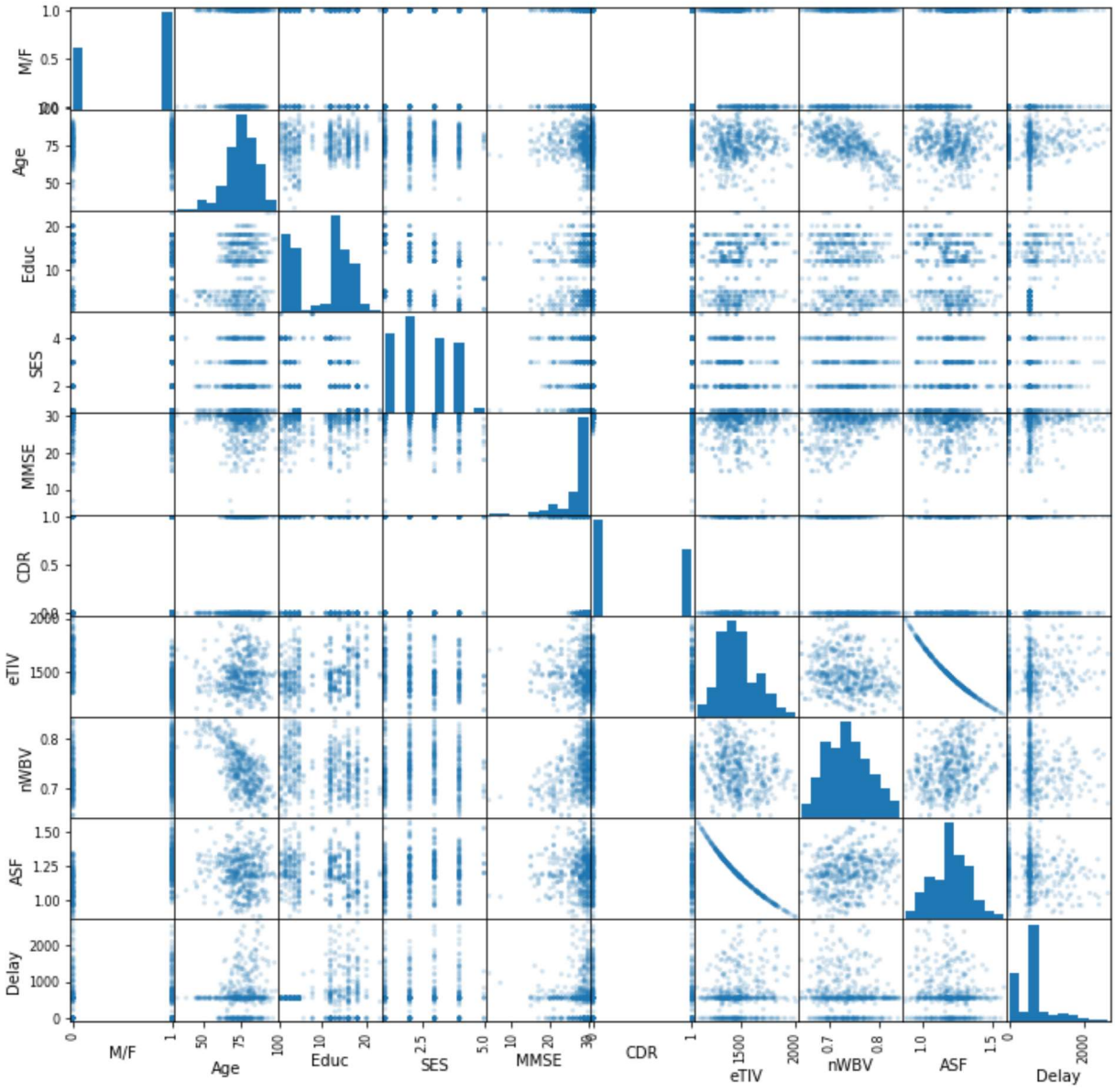


Outliers are column values located, outside the bands defined by 1.5 times greater than the size of spread of the middle 50% of the data. We see from the box and whiskers plots that Age, SES, eTIV, MMSE, and Delay columns have some outliers. The base classification case will be run without removing the outliers. A sensitivity study option is to train the model by removing the outliers.

Two multivariate plots are displayed below. The Scatter plot and the Correlation plot. These plots indicate whether there are any dependencies/interactions and correlation between the features in the dataset. For example, the scatter plot shows that eTIV and ASF have interactions/negative depenence, whereas the features Age has negative correlation with nWBV.

In [39]:
```
# Scatterplot Matrix
from matplotlib import pyplot
from pandas import read_csv
from pandas.tools.plotting import scatter_matrix
scatter_matrix(dfoas_merge, alpha=0.2, figsize=(12, 12))
pyplot.show();
```

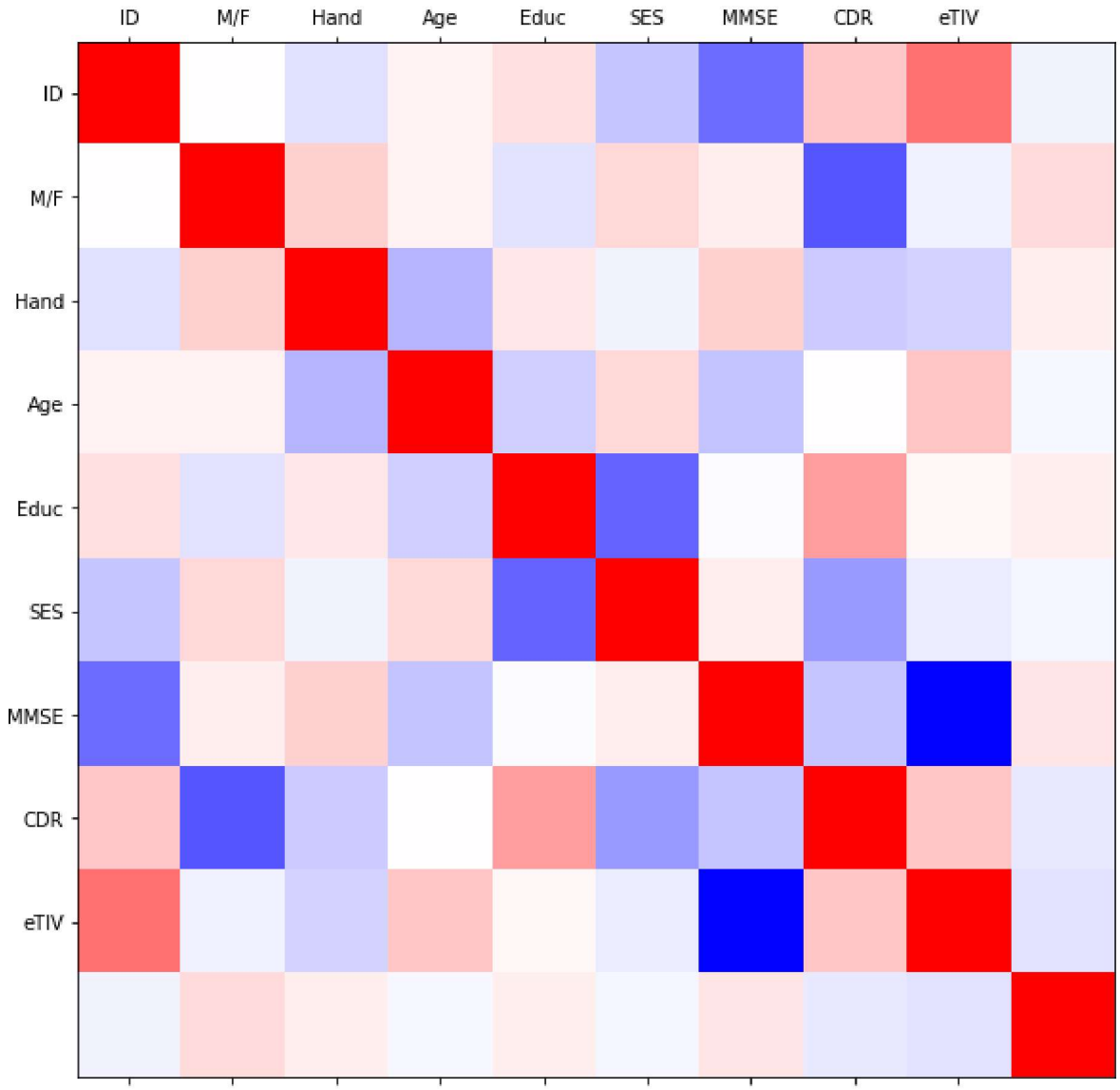
```
/usr/local/lib/python2.7/site-packages/ipykernel_launcher.py:5: FutureWarning:
'pandas.tools.plotting.scatter_matrix' is deprecated, import 'pandas.plotting.s
catter_matrix' instead.
  """
```



Feature Selection Methodology

In [40]:
```
# Correlation Matrix Plot
from matplotlib import pyplot
from matplotlib import cm
import numpy as np
correlations = dfoas_merge.corr()
# plot correlation matrix
figoasx = pyplot.figure()
cm = pyplot.cm.bwr
fig = pyplot.figure()
ax = fig.add_subplot(111);
cax = ax.matshow(correlations, cmap=cm, vmin=-1, vmax=1);
ticks = np.arange(0,9,1);
names= list(dfoas_merge.columns.values)
ax.set_xticks(ticks)
ax.set_yticks(ticks)
ax.set_xticklabels(names)
ax.set_yticklabels(names)
fig.set_figheight(10)
fig.set_figwidth(10)
pyplot.show();
```

```
<matplotlib.figure.Figure at 0x7f9913580290>
```



In [ ]:

Methodology- Solution

Results

Binary Classification accuracy for a neural network with 4 input features(nodes), 2 hidden layers with 8 nodes each, and an output layer with one node, is 75.6%. Relu activation is used for the hidden layers, and sigmoid activation for the output layer.

Conclusion

So, this benchmark accuracy of 75.6% is less than that obtained in the analysis with Gradient Boosting Machine (GBM) and Random Forest classifier (RFC) which is ~87%, showing an improvement over the benchmark.

Methodology - Select Training and Test/Validation Sets

In [41]:
```
# Split-out validation dataset
array = dfoas_merge.values
#X = array[:,[1, 3, 4, 5, 6, 8, 9, 10]]
X = array[:,[3, 6, 9, 10]] #Feature Extraction with RFE
Y = array[:,7] # all rows and CDR column
Y=Y.astype(np.str)
validation_size = 0.20
seed = 12345
X_train, X_validation, Y_train, Y_validation = train_test_split(X, Y,
test_size=validation_size, random_state=seed)
print (X)
print (Y)
```

```
[[74 29.0 0.743 1.306]
 [55 29.0 0.81 1.531]
 [73 27.0 0.708 1.207]
 ...,
 [61 30.0 0.8009999999999999 1.331]
 [63 30.0 0.7959999999999999 1.3230000000000002]
 [65 30.0 0.8009999999999999 1.317]]
['0.0' '0.0' '1.0' '0.0' '0.0' '0.0' '1.0' '0.0' '0.0' '0.0' '1.0' '1.0'
 '1.0' '0.0' '1.0' '0.0' '1.0' '0.0' '0.0' '0.0' '1.0' '1.0' '1.0' '0.0'
 '1.0' '1.0' '1.0' '0.0' '0.0' '0.0' '0.0' '1.0' '1.0' '0.0' '0.0' '0.0'
 '0.0' '0.0' '1.0' '0.0' '0.0' '1.0' '0.0' '0.0' '0.0' '1.0' '0.0' '0.0'
 '0.0' '0.0' '0.0' '0.0' '0.0' '1.0' '0.0' '1.0' '1.0' '1.0' '0.0' '0.0'
 '1.0' '0.0' '1.0' '0.0' '0.0' '1.0' '1.0' '0.0' '0.0' '1.0' '1.0' '1.0'
 '0.0' '0.0' '0.0' '0.0' '0.0' '1.0' '0.0' '0.0' '1.0' '0.0' '0.0' '0.0'
 '0.0' '0.0' '0.0' '0.0' '0.0' '0.0' '1.0' '0.0' '0.0' '0.0' '1.0' '0.0'
 '1.0' '0.0' '0.0' '1.0' '0.0' '0.0' '1.0' '0.0' '0.0' '1.0' '0.0' '1.0'
 '0.0' '1.0' '0.0' '0.0' '0.0' '0.0' '0.0' '0.0' '1.0' '0.0' '1.0' '1.0'
 '1.0' '0.0' '0.0' '1.0' '1.0' '0.0' '1.0' '0.0' '0.0' '0.0' '1.0' '1.0'
 '1.0' '0.0' '1.0' '1.0' '0.0' '0.0' '1.0' '0.0' '1.0' '0.0' '0.0' '1.0'
 '1.0' '1.0' '0.0' '1.0' '1.0' '0.0' '0.0' '0.0' '0.0' '1.0' '0.0' '0.0'
 '1.0' '0.0' '0.0' '0.0' '0.0' '0.0' '0.0' '1.0' '1.0' '0.0' '0.0' '0.0'
 '0.0' '0.0' '0.0' '0.0' '0.0' '0.0' '0.0' '0.0' '0.0' '1.0' '1.0' '0.0'
 '1.0' '0.0' '1.0' '1.0' '0.0' '1.0' '0.0' '1.0' '0.0' '1.0' '1.0' '1.0'
 '0.0' '0.0' '1.0' '1.0' '0.0' '0.0' '1.0' '1.0' '0.0' '0.0' '1.0' '1.0'
 '0.0' '0.0' '0.0' '1.0' '0.0' '1.0' '1.0' '1.0' '1.0' '0.0' '0.0' '0.0'
 '0.0' '0.0' '0.0' '0.0' '0.0' '1.0' '0.0' '0.0' '0.0' '1.0' '1.0' '1.0'
 '1.0' '0.0' '0.0' '0.0' '0.0' '0.0' '0.0' '1.0' '1.0' '1.0' '1.0' '0.0'
 '1.0' '0.0' '0.0' '0.0' '0.0' '1.0' '0.0' '1.0' '1.0' '1.0' '1.0' '0.0'
 '0.0' '1.0' '1.0' '1.0' '1.0' '0.0' '0.0' '0.0' '0.0' '1.0' '1.0' '0.0'
 '0.0' '0.0' '0.0' '0.0' '0.0' '1.0' '1.0' '1.0' '0.0' '0.0' '0.0' '0.0'
 '0.0' '0.0' '0.0' '0.0' '0.0' '0.0' '1.0' '1.0' '1.0' '1.0' '1.0' '1.0'
 '1.0' '1.0' '1.0' '0.0' '0.0' '1.0' '0.0' '0.0' '1.0' '1.0' '1.0' '1.0'
 '1.0' '0.0' '0.0' '1.0' '1.0' '0.0' '0.0' '1.0' '1.0' '1.0' '1.0' '1.0'
 '0.0' '0.0' '0.0' '1.0' '1.0' '0.0' '0.0' '0.0' '0.0' '0.0' '0.0' '0.0'
 '0.0' '1.0' '0.0' '0.0' '0.0' '0.0' '0.0' '0.0' '0.0' '1.0' '1.0' '1.0'
 '1.0' '1.0' '0.0' '0.0' '0.0' '0.0' '0.0' '0.0' '1.0' '1.0' '1.0' '1.0'
 '1.0' '0.0' '0.0' '0.0' '0.0' '0.0' '0.0' '0.0' '0.0' '0.0' '0.0' '0.0'
 '0.0' '0.0' '1.0' '1.0' '0.0' '0.0' '0.0' '0.0' '0.0' '1.0' '1.0' '0.0'
 '0.0' '0.0' '0.0' '0.0' '0.0' '0.0' '0.0' '1.0' '1.0' '1.0' '1.0' '1.0'
 '1.0' '1.0' '1.0' '0.0' '0.0' '0.0' '0.0' '1.0' '1.0' '1.0' '1.0' '1.0'
 '1.0' '0.0' '0.0' '0.0' '0.0' '0.0' '0.0' '1.0' '0.0' '0.0' '0.0' '0.0'
 '0.0' '0.0' '0.0' '0.0' '0.0' '1.0' '1.0' '0.0' '0.0' '0.0' '0.0' '0.0'
 '0.0' '1.0' '1.0' '1.0' '0.0' '1.0' '1.0' '1.0' '1.0' '0.0' '0.0' '1.0'
 '1.0' '1.0' '1.0' '0.0' '0.0' '1.0' '1.0' '1.0' '1.0' '1.0' '1.0' '1.0'
```

```
'1.0' '0.0' '0.0' '0.0' '0.0' '0.0' '1.0' '0.0' '0.0' '0.0' '1.0' '1.0'
'0.0' '0.0' '0.0' '0.0' '1.0' '1.0' '0.0' '0.0' '0.0' '0.0' '1.0' '1.0'
'1.0' '1.0' '0.0' '0.0' '0.0' '0.0' '0.0' '1.0' '0.0' '0.0' '1.0' '1.0'
'1.0' '0.0' '0.0' '1.0' '1.0' '0.0' '0.0' '1.0' '1.0' '1.0' '1.0' '1.0'
'0.0' '0.0' '0.0' '0.0' '0.0' '0.0' '0.0' '0.0' '1.0' '0.0' '1.0' '1.0'
'1.0' '0.0' '0.0' '0.0' '0.0' '0.0' '0.0' '1.0' '1.0' '0.0' '0.0' '0.0'
'0.0' '0.0' '0.0' '0.0' '1.0' '1.0' '0.0' '0.0' '1.0' '1.0' '0.0' '0.0'
'0.0' '1.0' '1.0' '1.0' '1.0' '1.0' '1.0' '0.0' '0.0' '0.0' '0.0' '0.0'
'1.0' '1.0' '0.0' '0.0' '0.0' '1.0' '1.0' '1.0' '0.0' '0.0' '1.0' '0.0'
'0.0' '0.0' '0.0' '0.0' '1.0' '1.0' '0.0' '0.0' '0.0' '0.0' '1.0' '1.0'
'1.0' '1.0' '1.0' '0.0' '0.0' '0.0']
```

We see the scores for each attribute and the 4 attributes chosen (those with the highest scores): Age, MMSE, and ASF. We can identify the names for the chosen attributes by matching/mapping the index of the 4 highest scores with the index of the attribute names.

Recursive Feature Elimination

The Recursive Feature Elimination (or RFE) works by recursively removing attributes and building a model on those attributes that remain. It uses the model accuracy to identify which attributes (and combination of attributes) contribute the most to predicting the target attribute. You can learn more about the RFE class in the scikit-learn documentation. The example below uses RFE with the logistic regression algorithm to select the top 3 features. The choice of algorithm does not matter too much as long as it is skillful and consistent. We see from feature ranking below, those with rank 1, e.g. columns Age, MMSE, NWBV, and ASF are the top four featutes.

In [42]:
```
# Feature Extraction with RFE
from sklearn.feature_selection import RFE
from sklearn.linear_model import LogisticRegression
# feature extraction
model = DecisionTreeClassifier()
rfe = RFE(model, 4)
fit = rfe.fit(X, Y)
print("Num Features: %d" % fit.n_features_)
print("Selected Features: %s" % fit.support_)
print("Feature Ranking: %s" % fit.ranking_)
```

```
Num Features: 4
Selected Features: [ True  True  True  True]
Feature Ranking: [1 1 1 1]
```

In [ ]:
```
```

Appendix 1: Neural Network Model with Keras+TensorFlow

A neural network model has been formulated based on the combined cross-sectional and the longitudinal MRI clinical/demographic dataset described earlier. The model is based on recommendations in Reference 24. The model is comprised of an input layer with 8 nodes, a hidden

(dense) layer with 12 nodes with Relu activation function, followed by another hidden (dense) layer with 8 nodes with Relu activation followed by an output layer with Sigmoid activation.

In [43]:
```
from keras.models import Sequential
from keras.layers import Dense
import numpy
# fix random seed for reproducibility
numpy.random.seed(3445)
```

```
Using TensorFlow backend.
```

In [44]:
```
# Keras Model withT ensorflow backend
from keras.models import Sequential
from keras.layers import Dense
import numpy
# fix random seed for reproducibility
numpy.random.seed(33456)
# load dataset arrays
array = dfoas_merge.values
#X = array[:,[1, 3, 4, 5, 6, 8, 9, 10]] # Original feature set
X = array[:,[3, 6, 9, 10]] # Reduced feature Extraction based on RFE analysis
Y = array[:,7] # all rows and CDR column
# create model
model = Sequential()
model.add(Dense(8, input_dim=4, activation='relu'))
model.add(Dense(8, activation='relu'))
model.add(Dense(1, activation='sigmoid'))
# Compile model
model.compile(loss='binary_crossentropy', optimizer='adam', metrics=['accuracy'])
# Fit the model
model.fit(X, Y, epochs=150, batch_size=10)
# evaluate the model
scores = model.evaluate(X, Y)
print("\n%s: %.2f%%" % (model.metrics_names[1], scores[1]*100))
```

```
570/570 [==============================] - 0s - loss: 0.5072 - acc: 0.7456

Epoch 109/150
570/570 [==============================] - 0s - loss: 0.5018 - acc: 0.7579

Epoch 110/150
570/570 [==============================] - 0s - loss: 0.5044 - acc: 0.7509

Epoch 111/150
570/570 [==============================] - 0s - loss: 0.5039 - acc: 0.7526

Epoch 112/150
570/570 [==============================] - 0s - loss: 0.5015 - acc: 0.7561

Epoch 113/150
570/570 [==============================] - 0s - loss: 0.5038 - acc: 0.7667

Epoch 114/150
570/570 [==============================] - 0s - loss: 0.5049 - acc: 0.7614
```

Results ¶

Binary Classification accuracy for a neural network with 4 input features(nodes), 2 hidden layers with 8 nodes each, and an output layer with one node, is 75.6%. Relu activation is used for the hidden layers, and sigmoid activation for the output layer.

Conclusion

So, this benchmark accuracy of 75.6% is less than that obtained in the analysis with Gradient Boosting Machine (GBM) and Random Forest classifier (RFC) which is ~87%, showing an improvement over the benchmark.

In [ ]: