CS109A Project Milestone 4: Models

Group 29

- · Tatyana Zyabkina
- · Joanna Guo
- · John Liang
- · Ray Ortigas

Our models are partial reproductions of the models described in the Ritter et al. 2015 paper, "Multimodal prediction of conversion to Alzheimer's disease based on incomplete biomarkers". (https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4877756/?report=reader), with some adjustments based on experimentation.

Using the ADNIMERGE data set, we used the following process:

- Select analysis cohort, participants who completed a 36-month or later follow-up
- · Identify "converters" who transitioned from non-AD to AD diagnosis sometime in the first 36 months of their study participation
- Identify features that based on our research are likely to be predictive
- · Impute missing values with mean
- · Dummy-encode and scale features
- Fit SVM, Random Forest, and Logistic Regression models and evaluate their predictive powers

Styling

```
In [1]: #RUN THIS CELL
    import requests
    from IPython.core.display import HTML
    styles = requests.get("https://raw.githubusercontent.com/Harvard-IACS/2018-CS109A/master/content/styles/c:
    HTML(styles)
Out[1]:
```

Imports

```
In [2]: import warnings
    warnings.filterwarnings('ignore')
    import numpy as np
    import pandas as pd
    import scipy
    import matplotlib
    import matplotlib.pyplot as plt
    import seaborn as sns
In [3]: import itertools
    from sklearn.base import clone
    from sklearn.impute import SimpleImputer
    from sklearn.preprocessing import StandardScaler
```

In [4]: from sklearn.model_selection import train_test_split
 from sklearn.model_selection import StratifiedKFold
 from sklearn.model_selection import GridSearchCV

```
In [5]: from sklearn.metrics import auc
from sklearn.metrics import accuracy_score
from sklearn.metrics import balanced_accuracy_score
from sklearn.metrics import confusion_matrix
from sklearn.metrics import roc_curve

In [6]: from sklearn.svm import SVC
from sklearn.ensemble import RandomForestClassifier
from sklearn.linear_model import LogisticRegressionCV
```

Loading

```
In [7]: adni_df = pd.read_csv("../data/ADNIMERGE.csv")
In [8]: adni_df.shape
Out[8]: (13017, 94)
In [9]: adni_df.head()
Out[9]:
             RID
                      PTID VISCODE SITE COLPROT ORIGPROT EXAMDATE DX_bl AGE PTGENDER ... EcogSPDivatt_bl EcogSPTotal_bl I
          0
               2 011_S_0002
                                  bl
                                       11
                                              ADNI1
                                                        ADNI1
                                                              2005-09-08
                                                                           CN
                                                                               74.3
                                                                                          Male ...
                                                                                                            NaN
                                                                                                                          NaN 1
               3 011_S_0003
                                              ADNI1
                                                       ADNI1
                                                              2005-09-12
                                  bl
                                      11
                                                                           AD 81.3
                                                                                          Male ...
                                                                                                            NaN
                                                                                                                          NaN 1
               3 011_S_0003
                                m06
                                       11
                                             ADNI1
                                                       ADNI1
                                                              2006-03-13
                                                                           AD 81.3
                                                                                          Male ...
                                                                                                            NaN
                                                                                                                          NaN 1
               3 011_S_0003
                                              ADNI1
                                                       ADNI1
                                m12
                                       11
                                                              2006-09-12
                                                                           AD
                                                                              81.3
                                                                                          Male ...
                                                                                                            NaN
                                                                                                                          NaN 1
               3 011_S_0003
                                m24
                                      11
                                             ADNI1
                                                       ADNI1 2007-09-12
                                                                           AD 81.3
                                                                                          Male ...
                                                                                                            NaN
                                                                                                                          NaN 1
```

5 rows × 94 columns

In [10]: adni_df.dtypes

```
Out[10]: RID
                                      int64
         PTID
                                     object
         VISCODE
                                     object
         SITE
                                     int64
         COLPROT
                                     object
         ORIGPROT
                                    object
         EXAMDATE
                                    object
         DX bl
                                    object
         AGE
                                    float64
         PTGENDER
                                    object
         PTEDUCAT
                                     int64
                                    object
         PTETHCAT
         PTRACCAT
                                    object
                                    object
         PTMARRY
         APOE4
                                    float64
         FDG
                                    float64
         PIB
                                   float64
         AV45
                                   float64
         CDRSB
                                   float64
                                   float64
         ADAS11
         ADAS13
                                    float64
         MMSE
                                   float64
         RAVLT immediate
                                   float64
         RAVLT learning
                                   float64
                                   float64
         RAVLT_forgetting
         RAVLT_perc_forgetting
                                   float64
                                   float64
         MOCA
                                   float.64
         EcogPtMem
                                   float64
         EcogPtLang
                                   float64
                                     . . .
         Ventricles bl
                                    float64
         Hippocampus_bl
                                   float64
         WholeBrain bl
                                   float64
         Entorhinal bl
                                   float64
         Fusiform bl
                                   float64
         MidTemp bl
                                   float64
         ICV_bl
                                   float64
         MOCA bl
                                   float64
         EcogPtMem_bl
                                   float64
                                   float64
         EcogPtLang_bl
         EcogPtVisspat_bl
                                   float64
         EcogPtPlan_bl
                                   float64
         EcogPtOrgan_bl
                                   float64
         EcogPtDivatt bl
                                   float64
         EcogPtTotal_bl
                                   float64
         EcogSPMem_bl
                                   float64
         EcogSPLang_bl
                                   float64
         EcogSPVisspat_bl
                                   float64
         EcogSPPlan bl
                                   float64
         EcogSPOrgan_bl
                                   float64
         EcogSPDivatt_bl
                                   float64
         EcogSPTotal_bl
                                    float64
         FDG_bl
                                   float64
         PIB bl
                                   float64
         AV45_bl
                                   float64
         Years_bl
                                   float64
         Month bl
                                    float64
         Month
                                      int64
                                      int64
         update stamp
                                     object
         Length: 94, dtype: object
```

```
In [11]: adni df.describe()
```

Out[11]:

| | RID | SITE | AGE | PTEDUCAT | APOE4 | FDG | PIB | AV45 | CDRSB | ADA |
|-------|--------------|--------------|--------------|--------------|--------------|-------------|------------|-------------|-------------|----------|
| count | 13017.000000 | 13017.000000 | 13017.000000 | 13017.000000 | 12958.000000 | 3353.000000 | 223.000000 | 2161.000000 | 9016.000000 | 8959.000 |
| mean | 2285.200584 | 73.892064 | 73.767220 | 15.994930 | 0.535654 | 1.208225 | 1.783161 | 1.195504 | 2.163598 | 11.398 |
| std | 1871.013213 | 110.533877 | 6.979685 | 2.824862 | 0.655480 | 0.160972 | 0.422511 | 0.227999 | 2.805879 | 8.616 |
| min | 2.000000 | 2.000000 | 54.400000 | 4.000000 | 0.000000 | 0.636804 | 1.095000 | 0.814555 | 0.000000 | 0.000 |
| 25% | 631.000000 | 21.000000 | 69.500000 | 14.000000 | 0.000000 | 1.109730 | 1.361250 | 1.010140 | 0.000000 | 5.330 |
| 50% | 1301.000000 | 41.000000 | 73.700000 | 16.000000 | 0.000000 | 1.219870 | 1.850000 | 1.114670 | 1.000000 | 9.000 |
| 75% | 4353.000000 | 116.000000 | 78.600000 | 18.000000 | 1.000000 | 1.314320 | 2.127500 | 1.364980 | 3.000000 | 15.000 |
| max | 6094.000000 | 941.000000 | 91.400000 | 20.000000 | 2.000000 | 1.753320 | 2.927500 | 2.669210 | 18.000000 | 70.000 |

8 rows × 77 columns

EDA

We perform a short EDA specifically for this baseline model, with Section 2.1.1 of the Ritter paper in mind:

For this study, patients with a baseline diagnosis of MCI and a follow-up time of at least 36 months were extracted from the ADNI database. Patients who were diagnosed with MCI, NL or MCI to NL at all visits during the 3-year follow-up were included in the MCI-stable group, whereas patients whose diagnosis changed to AD during the 3-year follow-up were regarded as MCI-converters. After this procedure, 237 patients were selected, 151 of which belonged to the MCI-stable group, and 86 to the MCI-converter group (see Table 1).

DX gives the diagnosis at any particular visit:

```
In [12]: adni_df["DX"].unique()
Out[12]: array(['CN', 'Dementia', 'MCI', nan], dtype=object)
```

DX b1 gives the diagnosis at baseline:

```
In [13]: adni_df["DX_bl"].unique()
Out[13]: array(['CN', 'AD', 'LMCI', 'SMC', 'EMCI', nan], dtype=object)
```

The codes differ slightly from the DX codes, but for the purposes of this milestone, we will consider Dementia and AD to be synonymous.

VISCODE in ADNIMERGE is the cleaned up visit code:

b1 indicates baseline, and then there are varying month markers. These have been cleaned and extracted with Month:

```
In [15]: HTML(adni_df["Month"].value_counts().to_frame().reset_index().sort_values("index").to_html(index=False))
Out[15]:
           index Month
              0
                   1784
              3
                   795
              6
                   1613
                   1472
              12
              18
                   1299
              24
                   1301
              30
                   768
              36
                   823
              42
                   332
              48
              54
                   224
              60
                   398
              66
                   295
              72
                   305
              78
                   238
                   207
              84
              90
                    137
              96
                    142
             102
                    19
             108
                    102
             114
                    15
             120
                    79
             126
                     6
                     5
             132
```

Data Preparation

Exclude Entries for Respondents with Alzheimer's at Baseline

Since we want to predict conversion to Alzheimer's Disease, we will remove all entries for respondents for which AD was their baseline diagnosis.

```
In [16]: def select_non_AD_DX_bl(adni_df):
    return adni_df[adni_df["DX_bl"] != "AD"]
```

```
In [17]: adni_non_AD_DX_bl_df = select_non_AD_DX_bl(adni_df)
adni_non_AD_DX_bl_df.head()
```

Out[17]:

| | RID | PTID | VISCODE | SITE | COLPROT | ORIGPROT | EXAMDATE | DX_bl | AGE | PTGENDER | EcogSPDivatt_bl | EcogSPTotal_bl | F |
|---|-----|------------|---------|------|---------|----------|------------|-------|------|----------|---------------------|----------------|---|
| 0 | 2 | 011_S_0002 | bl | 11 | ADNI1 | ADNI1 | 2005-09-08 | CN | 74.3 | Male | NaN | NaN | 1 |
| 5 | 4 | 022_S_0004 | bl | 22 | ADNI1 | ADNI1 | 2005-11-08 | LMCI | 67.5 | Male | NaN | NaN | |
| 6 | 4 | 022_S_0004 | m06 | 22 | ADNI1 | ADNI1 | 2006-05-02 | LMCI | 67.5 | Male | NaN | NaN | |
| 7 | 4 | 022_S_0004 | m12 | 22 | ADNI1 | ADNI1 | 2006-11-14 | LMCI | 67.5 | Male | NaN | NaN | |
| 8 | 4 | 022_S_0004 | m18 | 22 | ADNI1 | ADNI1 | 2007-05-14 | LMCI | 67.5 | Male | NaN | NaN | |

5 rows × 94 columns

Select Respondents with Data at 36 Months or Later

The Ritter paper focused on respondents with data points at 36 months or later. This boundary seems to have been chosen to permit experimentation around conversion time and how that affected sensitivity (true positive rates):

The sensitivity for patients converting after different time frames (i.e., 12–36 months) is shown in Fig. 3D. As expected, the onset of AD could be best predicted for patients converting after 12 months and worst for patients converting after 36 months.

| | RID | PTID | VISCODE | SITE | COLPROT | ORIGPROT | EXAMDATE | DX_bl | AGE | PTGENDER | EcogSPDivatt_bl | EcogSPTotal_bl | F |
|---|-----|------------|---------|------|---------|----------|------------|-------|------|----------|---------------------|----------------|---|
| 0 | 2 | 011_S_0002 | bl | 11 | ADNI1 | ADNI1 | 2005-09-08 | CN | 74.3 | Male | NaN | NaN | 1 |
| 5 | 4 | 022_S_0004 | bl | 22 | ADNI1 | ADNI1 | 2005-11-08 | LMCI | 67.5 | Male | NaN | NaN | |
| 6 | 4 | 022_S_0004 | m06 | 22 | ADNI1 | ADNI1 | 2006-05-02 | LMCI | 67.5 | Male | NaN | NaN | |
| 7 | 4 | 022_S_0004 | m12 | 22 | ADNI1 | ADNI1 | 2006-11-14 | LMCI | 67.5 | Male | NaN | NaN | |
| 8 | 4 | 022_S_0004 | m18 | 22 | ADNI1 | ADNI1 | 2007-05-14 | LMCI | 67.5 | Male | NaN | NaN | |

5 rows × 94 columns

Annotate Respondents Converted from Non-AD to AD through 36 Months

For the purposes of this project, we will only look at conversions that happen anytime through to the 36 month mark of a respondent's participation in the study.

Select Predictor Values Recorded at Baseline

To approximate the model in the Ritter paper, we will use some of the candidate predictors the Ritter paper used, and specifically the values for those predictors recorded at baseline.

Note that although some baseline predictors in ADNIMERGE are suffixed with _bl , others are not. To simplify our usage of ADNIMERGE , we'll only use the non- bl -suffixed columns, and then take the rows where VISCODE is bl to get the baseline-coded values.

In [23]: adni_annotated_converted_non_AD_to_AD_through_m36_bl_df.describe()

Out[23]:

| | RID | SITE | AGE | PTEDUCAT | APOE4 | FDG | PIB | AV45 | CDRSB | ADAS11 | |
|-------|-------------|-------------|-------------|-------------|-------------|------------|----------|------------|-------------|-------------|--|
| count | 1009.000000 | 1009.000000 | 1009.000000 | 1009.000000 | 1009.000000 | 767.000000 | 9.000000 | 542.000000 | 1009.000000 | 1008.000000 | |
| mean | 2505.576809 | 76.570862 | 73.379485 | 16.141724 | 0.473736 | 1.278575 | 1.566944 | 1.173215 | 0.920218 | 8.338899 | |
| std | 1874.221531 | 116.408026 | 6.905936 | 2.730765 | 0.626430 | 0.129538 | 0.315631 | 0.208780 | 0.980124 | 4.374082 | |
| min | 2.000000 | 2.000000 | 55.000000 | 6.000000 | 0.000000 | 0.782496 | 1.180000 | 0.838537 | 0.000000 | 0.000000 | |
| 25% | 702.000000 | 22.000000 | 68.900000 | 14.000000 | 0.000000 | 1.194700 | 1.360000 | 1.012010 | 0.000000 | 5.000000 | |
| 50% | 2146.000000 | 51.000000 | 73.400000 | 16.000000 | 0.000000 | 1.280300 | 1.490000 | 1.088980 | 0.500000 | 7.670000 | |
| 75% | 4419.000000 | 123.000000 | 78.300000 | 18.000000 | 1.000000 | 1.359995 | 1.672500 | 1.315997 | 1.500000 | 11.000000 | |
| max | 5290.000000 | 941.000000 | 90.100000 | 20.000000 | 2.000000 | 1.707170 | 2.232500 | 2.025560 | 5.500000 | 27.670000 | |

8 rows × 41 columns

```
In [24]: adni annotated converted non AD to AD through m36 bl na sum = \
             adni_annotated_converted_non_AD_to_AD_through_m36_bl_df.isna().sum()
         adni_annotated_converted_non_AD_to_AD_through_m36_bl_na_pct = \
             adni annotated converted non AD to AD through m36 bl na sum / \
                 adni_annotated_converted_non_AD_to_AD_through_m36_bl_df.shape[0]
         adni_annotated_converted_non_AD_to_AD_through_m36_bl_na_pct[
             adni annotated converted non AD to AD through m36 bl na pct > 0
Out[24]: FDG
                                  0.239841
                                 0.991080
         PIB
         AV45
                                 0.462834
         ADAS11
                                 0.000991
                                0.002973
         ADAS13
         RAVLT_immediate 0.001982
RAVLT_learning 0.001982
RAVLT_forgetting 0.001982
         RAVLT_perc_forgetting 0.001982
         FAO
                                 0.003964
         MOCA
                                 0.466799
         EcogPtMem
                                 0.461843
         EcogPtLang
                                 0.461843
         EcogPtVisspat
                                0.463826
         EcogPtPlan
                                0.461843
                                 0.468781
         EcogPtOrgan
         EcogPtDivatt
                                 0.462834
         EcogPtTotal
                                0.461843
         EcogSPMem
                                0.463826
         EcogSPLang
                                0.463826
                                0.471754
         EcogSPVisspat
         EcogSPPlan
                                 0.467790
         EcogSPOrgan
                                 0.490585
         EcogSPDivatt
                                0.477701
         EcogSPTotal
                                0.464817
         FLDSTRENG
                                 0.127849
         FSVERSION
                                 0.007929
         Ventricles
                                 0.037661
         Hippocampus
                                0.128840
         WholeBrain
                                0.015857
         Entorhinal
                                0.135778
         Fusiform
                                 0.135778
         MidTemp
                                 0.135778
         ICV
                                  0.007929
         dtype: float64
```

Almost all of the features have missing values for some percentage of the respondents.

Utility Functions

Imputation

As discussed in the previous section, and as noted in the Ritter paper, various datasets and predictors are missing data for respondents to varying degrees.

In class we learned about mean imputation, which was also applied in the Ritter paper.

```
In [25]: def impute_missing_values_with_mean(df, columns, missing_values):
    imputed_df = df.copy()
    for column in columns:
        imputed_df[f"{column}"] = impute_column_missing_values_with_mean(df, column, missing_values)
    return imputed_df

def impute_column_missing_values_with_mean(df, column, missing_values):
    imputer = SimpleImputer(copy=True, missing_values=missing_values, strategy="mean")
    imputed = pd.Series(
        imputer.fit_transform(df[column].astype(float).values.reshape(-1, 1)).reshape(-1),
        index=df[column].index
    )
    return imputed
```

Dummy Encoding

Some features like PTGENDER are categorical, so we need to encode these properly.

```
In [26]: def dummy_encode_predictors(df, predictors):
    return pd.get_dummies(df, columns=predictors, drop_first=True)
```

Scaling

We will scale our non-categorical data, to let us apply algorithms to the ADNI data which assume or work best with scaled data (e.g. <u>SVM</u> with RBF kernel (https://scikit-learn.org/stable/modules/generated/sklearn.preprocessing.StandardScaler.html)).

Creating Design Matrixes

As with our assignments, we have a utility function to split datasets into training and test datasets, creating response vectors and design matrixes where imputation, dummy encoding, and scaling have been applied.

```
In [28]: def create_design_mats(
             df,
             test size,
             response,
             predictors,
             predictors_to_scale,
             predictors to dummy encode
             X = df[predictors]
             y = df[response]
             X_train, X_test, y_train, y_test = train_test_split(
                 impute_missing_values_with_mean(
                     dummy_encode_predictors(X, predictors_to_dummy_encode),
                     predictors_to_scale,
                     np.nan),
                 test size=test size,
                 stratify=y
             )
             scaler = create_scaler(X_train, predictors_to_scale)
             X train = scale predictors(X train, predictors to scale, scaler)
             X_test = scale_predictors(X_test, predictors_to_scale, scaler)
             return X_train, y_train, X_test, y_test
```

Plotting Confusion Matrix

Since we are framing this as a classification problem, we have a utility method to get our confusion matrix (from scikit-learn examples). The matrix can help us calculate true positive rate (sensitivity/recall) and true negative rate (specificity), among other things.

```
In [29]: CLASS_NAMES = ["Cognitively Normal (CN)", "Dementia"]
```

```
In [30]: # https://scikit-learn.org/stable/auto examples/model selection/plot confusion matrix.html#sphx-qlr-auto
         def plot_confusion_matrix_without_and_with_normalization(cnf_matrix, title):
             np.set_printoptions(precision=2)
             fig, axs = plt.subplots(1, 2, figsize=(16, 10), sharex=False, sharey=False)
             fig.suptitle(title, fontsize=24)
             plot_confusion_matrix(axs[0], cnf_matrix, CLASS_NAMES,
                                   title="Confusion matrix, without normalization")
             plot_confusion_matrix(axs[1], cnf_matrix, CLASS_NAMES, normalize=True,
                                   title="Confusion matrix, with normalization")
             plt.tight_layout()
             plt.show()
         def plot_confusion_matrix(ax, cnf_matrix, class_names,
                                   normalize=False,
                                   title='Confusion matrix',
                                   cmap=plt.cm.Blues):
             if normalize:
                 cnf_matrix = cnf_matrix.astype('float') / cnf_matrix.sum(axis=1)[:, np.newaxis]
             ax.imshow(cnf matrix, interpolation='nearest', cmap=cmap)
             ax.set_title(title, fontsize=24)
             tick_marks = np.arange(len(class_names))
             ax.set_xticks(tick_marks)
             ax.set xticklabels(class names)
             ax.set_xticklabels(ax.get_xticklabels(), rotation=45)
             ax.set_yticks(tick_marks)
             ax.set_yticklabels(class_names)
             ax.set yticklabels(ax.get yticklabels(), rotation=45)
             fmt = '.2f' if normalize else 'd'
             thresh = cnf matrix.max() / 2.
             for i, j in itertools.product(range(cnf_matrix.shape[0]), range(cnf_matrix.shape[1])):
                 ax.text(j, i, format(cnf_matrix[i, j], fmt),
                         horizontalalignment="center",
                         color="white" if cnf matrix[i, j] > thresh else "black",
                         fontsize=24)
             ax.set_xlabel("Predicted Label", fontsize=14)
             ax.set_ylabel("True Label", fontsize=14)
```

Plotting ROC Curves

In this project, we will attempt to tune our models, as Ritter et al. did, using ROC curves. In the same spirit of going beyond just looking at overall classification accuracy, we will use the ROC curve to optimize for balanced accuracy--mean of TPR and TNR (or 1 - FPR)--and find a suitable classification probability threshold.

```
In [33]: # Adapted from https://scikit-learn.org/stable/auto examples/model selection/plot roc crossval.html
         def plot_augmented_roc_curves(augmented_roc_curves):
             fig, ax = plt.subplots(figsize=(16, 16))
             ax.set_xlabel("False Positive Rate")
             ax.set_ylabel("True Positive Rate")
             for i, (fpr, tpr, threshold, balanced accuracy) in enumerate(augmented roc curves):
                 roc auc = auc(fpr, tpr)
                 ax.plot(fpr, tpr, alpha=0.3, label=f"ROC fold {i} (AUC = {roc_auc:.2f})")
                 idx_best_balanced_accuracy = balanced_accuracy.argmax()
                 fpr best balanced accuracy = fpr[idx best balanced accuracy]
                 tpr_best_balanced_accuracy = tpr[idx_best_balanced_accuracy]
                 threshold_best_balanced_accuracy = threshold[idx_best_balanced_accuracy]
                 ax.scatter(fpr_best_balanced_accuracy,
                            tpr_best_balanced_accuracy,
                            marker="*",
                            label=f"best balanced accuracy fold {i} (threshold = {threshold_best_balanced_accuracy
             ax.legend()
             plt.show()
```

Evaluating Models

In order to evaluate and compare various models, we have some utility functions to consolidate the metrics that concern us for a given model.

```
In [34]: def create_and_evaluate_model(base_model, X_train, y_train, X_test, y_test):
             model = clone(base_model).fit(X_train, y_train)
             y_predicted_train = model.predict(X_train)
             y_predicted_test = model.predict(X_test)
             cnf_matrix_train = confusion_matrix(y_train, y_predicted_train)
             tn_train, fp_train, fn_train, tp_train = cnf_matrix_train.ravel()
             cnf_matrix_test = confusion_matrix(y_test, y_predicted_test)
             tn_test, fp_test, fn_test, tp_test = cnf_matrix_test.ravel()
             return (
                 model,
                     cnf matrix train,
                     accuracy_score(y_train, y_predicted_train),
                     balanced_accuracy_score(y_train, y_predicted_train),
                     tn_train / (tn_train + fp_train),
                     tp_train / (tp_train + fn_train)
                     cnf_matrix_test,
                     accuracy_score(y_test, y_predicted_test),
                     balanced accuracy score(y test, y predicted test),
                     tn_test / (tn_test + fp_test),
                     tp_test / (tp_test + fn_test)
                 )
```

```
In [35]: def create_and_evaluate_probabilistic_model(base_model, X_train, y_train, X_test, y_test, threshold):
             model = clone(base_model).fit(X_train, y_train)
             y predicted train = model.predict proba(X train)[:, 1] > threshold
             y_predicted_test = model.predict_proba(X_test)[:, 1] > threshold
             cnf matrix train = confusion matrix(y train, y predicted train)
             tn_train, fp_train, fn_train, tp_train = cnf_matrix_train.ravel()
             cnf_matrix_test = confusion_matrix(y_test, y_predicted_test)
             tn_test, fp_test, fn_test, tp_test = cnf_matrix_test.ravel()
             return (
                 model,
                 (
                     cnf_matrix_train,
                     accuracy_score(y_train, y_predicted_train),
                     balanced_accuracy_score(y_train, y_predicted_train),
                     tn_train / (tn_train + fp_train),
                     tp_train / (tp_train + fn_train)
                 ),
                     cnf matrix test,
                     accuracy_score(y_test, y_predicted_test),
                     balanced_accuracy_score(y_test, y_predicted_test),
                     tn_test / (tn_test + fp_test),
                     tp_test / (tp_test + fn_test)
                 )
In [36]: def plot_model_results(model_results, base_title):
             confusion matrix, accuracy, balanced accuracy, tnr, tpr = model results
             plot_confusion_matrix_without_and_with_normalization(
                 confusion_matrix,
                 f"{base title}"
                 f"\n(accuracy: {accuracy:.2}, balanced accuracy: {balanced_accuracy:.2}"
                 f", specificity: {tnr:.2}, sensitivity: {tpr:.2})
In [37]: def model_results_to_dict(model_results, name):
             cnf_matrix, accuracy, balanced_accuracy, specificity, sensitivity = model_results
             return {
                 "model": name,
                 "confusion matrix": cnf matrix,
                  "accuracy": accuracy,
                 "balanced accuracy": balanced_accuracy,
                 "specificity": specificity,
                 "sensitivity": sensitivity
             }
```

Models

Response and Predictors

Similar to the models in the Ritter paper, our models will predict conversions to AD within the first 36 months.

```
In [38]: ADNI_RESPONSE = "converted_non_AD_to_AD_through_m36"
```

We also consider the predictors from the ADNIMERGE dataset.

```
In [39]: ADNI PREDICTORS = [
              "AGE",
              "PTGENDER",
              "PTEDUCAT",
              "PTETHCAT",
              "PTRACCAT",
              "APOE4",
              "FDG",
              "CDRSB",
              "ADAS11",
              "ADAS13",
              "MMSE",
              "RAVLT_immediate",
              "RAVLT_learning",
              "RAVLT_forgetting",
              "RAVLT_perc_forgetting",
              "FAQ",
              "Ventricles",
              "Hippocampus",
              "WholeBrain",
              "Entorhinal",
              "Fusiform",
              "MidTemp"
          ]
          ADNI_PREDICTORS_TO_DUMMY_ENCODE = [
              "PTGENDER",
              "PTEDUCAT",
              "PTETHCAT",
              "PTRACCAT"
          ]
          ADNI_PREDICTORS_TO_SCALE = [
              "AGE",
              "APOE4",
              "FDG",
              "CDRSB"
              "ADAS11",
              "ADAS13",
              "MMSE",
              "RAVLT_immediate",
"RAVLT_learning",
              "RAVLT_forgetting",
              "RAVLT_perc_forgetting",
              "FAQ",
              "Ventricles",
              "Hippocampus",
              "WholeBrain",
              "Entorhinal",
              "Fusiform",
              "MidTemp"
```

Now let's create the response vectors and design matrixes for training and test data.

In [41]: X_train.dtypes

Out[41]: AGE float64 float64 APOE4 FDG float64 CDRSB float64 ADAS11 float64 float64 ADAS13 MMSE float64 RAVLT immediate float64 RAVLT_learning float64 RAVLT_forgetting float64 RAVLT_perc_forgetting float64 float64 FAQ Ventricles float64 float64 Hippocampus WholeBrain float64 Entorhinal float64 Fusiform float64 MidTemp float64 PTGENDER_Male uint8 PTEDUCAT_7 uint8 PTEDUCAT 8 uint8 PTEDUCAT_9 uint8 PTEDUCAT 10 uint8 PTEDUCAT 11 uint8 PTEDUCAT_12 uint8 PTEDUCAT_13 uint8 $PTEDUCAT_14$ uint8 PTEDUCAT 15 uint8 PTEDUCAT 16 uint8 PTEDUCAT_17 uint8 PTEDUCAT_18 uint8 PTEDUCAT 19 uint8 PTEDUCAT_20 uint8 PTETHCAT_Not Hisp/Latino uint8 PTETHCAT_Unknown uint8 PTRACCAT_Asian uint8 PTRACCAT_Black uint8 ${\tt PTRACCAT_More\ than\ one}$ uint8 PTRACCAT Unknown uint8 PTRACCAT_White uint8 dtype: object

In [42]: X_train.head()

Out[42]:

| | AGE | APOE4 | FDG | CDRSB | ADAS11 | ADAS13 | MMSE | RAVLT_immediate | RAVLT_learning | RAVLT_forgetting | ı |
|------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------------|----------------|------------------|-------|
| 5140 | -1.092857 | -0.754233 | -1.757299 | 0.079418 | 0.384719 | 0.856182 | 0.472756 | -0.810281 | -1.472742 | -0.101169 | _ |
| 1616 | 1.677218 | 0.865654 | 0.016445 | 0.079418 | 0.076826 | 0.206824 | -0.693324 | -1.808000 | -1.855653 | -1.642129 | |
| 3258 | -0.748392 | 0.865654 | -1.922720 | 0.592577 | 0.384719 | 0.406281 | -0.693324 | -0.447474 | -0.324009 | -0.486409 | |
| 9006 | -0.518748 | -0.754233 | -0.783912 | 1.105737 | 0.847714 | 1.156116 | -1.276364 | -1.263789 | -0.706920 | -0.486409 | |
| 9592 | 0.729938 | 0.865654 | 0.010164 | -0.946902 | -1.235766 | -1.093390 | 1.055796 | 1.275860 | 0.824725 | -0.486409 | |

5 rows × 40 columns

```
In [43]: X_train.describe()
```

Out[43]:

| | AGE | APOE4 | FDG | CDRSB | ADAS11 | ADAS13 | MMSE | RAVLT_immediate | RAVLT_le |
|-------|---------------|-------------------|---------------|-------------------|---------------|---------------|---------------|-----------------|----------|
| count | 7.560000e+02 | 7.560000e+02 | 7.560000e+02 | 7.560000e+02 | 7.560000e+02 | 7.560000e+02 | 7.560000e+02 | 7.560000e+02 | 7.56000 |
| mean | -3.614099e-16 | 1.806315e-16 | -1.986947e-16 | -5.844825e- 17 | 5.081179e-17 | 7.049035e-17 | -5.658319e-16 | 9.633681e-17 | 1.8268 |
| std | 1.000662e+00 | 1.000662e+00 | 1.000662e+00 | 1.000662e+00 | 1.000662e+00 | 1.000662e+00 | 1.000662e+00 | 1.000662e+00 | 1.00066 |
| min | -2.628598e+00 | -7.542334e- 01 | -4.400249e+00 | -9.469015e- 01 | -1.930260e+00 | -1.843225e+00 | -3.025484e+00 | -2.442912e+00 | -2.62147 |
| 25% | -6.909810e-01 | -7.542334e- 01 | -5.224032e-01 | -9.469015e- 01 | -7.727707e-01 | -7.934559e-01 | -6.933239e-01 | -8.102805e-01 | -7.0691 |
| 50% | 5.125972e-03 | -7.542334e- 01 | 1.644479e-02 | -4.337420e- 01 | -1.546715e-01 | -1.935877e-01 | 4.727559e-01 | -7.745651e-03 | 5.8902 |
| 75% | 7.155856e-01 | 8.656542e-01 | 4.634479e-01 | 5.925771e-01 | 6.162164e-01 | 6.690979e-01 | 1.055796e+00 | 7.316493e-01 | 8.2472 |
| max | 2.409207e+00 | 2.485542e+00 | 3.531468e+00 | 4.697853e+00 | 4.475286e+00 | 3.956001e+00 | 1.055796e+00 | 2.817790e+00 | 2.73928 |

8 rows × 40 columns

The proportion of non-AD respondents in the training set is:

```
In [44]: y_train[~y_train].count() / y_train.count()
Out[44]: 0.8042328042328042
```

The proportion of non-AD respondents in the test set is:

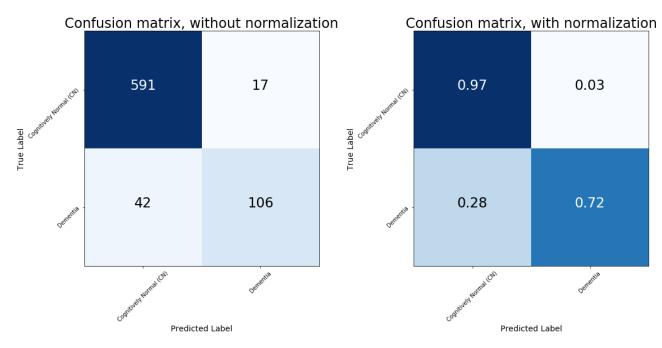
```
In [45]: y_test[~y_test].count() / y_test.count()
```

Out[45]: 0.8023715415019763

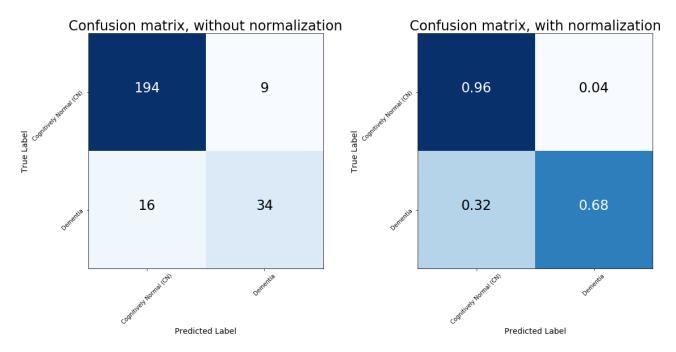
If you just guessed non-AD for all respondents, you'd be 80% correct.

SVM

SVC Baseline (Train) (accuracy: 0.92, balanced accuracy: 0.84, specificity: 0.97, sensitivity: 0.72)

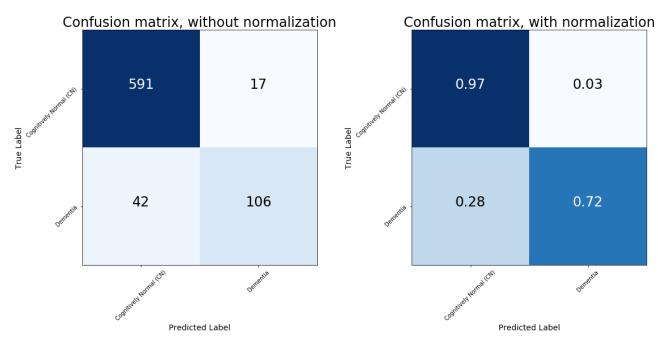


SVC Baseline (Test) (accuracy: 0.9, balanced accuracy: 0.82, specificity: 0.96, sensitivity: 0.68)

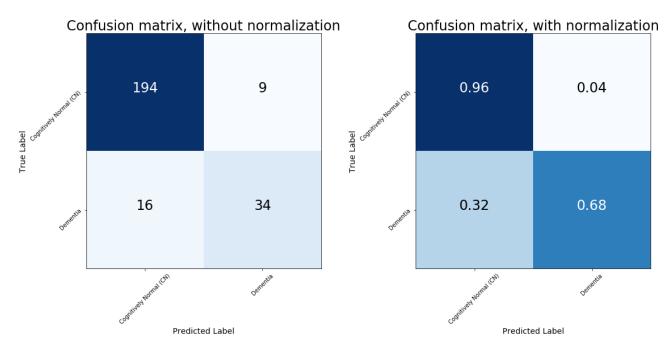


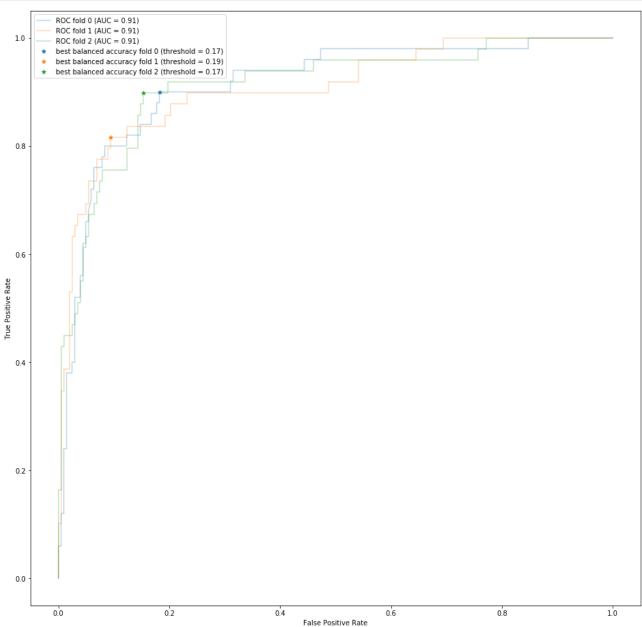
Adjusting SVM with ROC

SVC with Probabilty (Train) (accuracy: 0.92, balanced accuracy: 0.84, specificity: 0.97, sensitivity: 0.72)

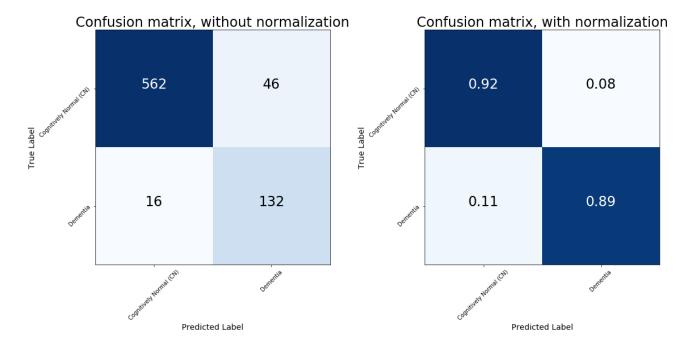


SVC with Probabilty (Test) (accuracy: 0.9, balanced accuracy: 0.82, specificity: 0.96, sensitivity: 0.68)

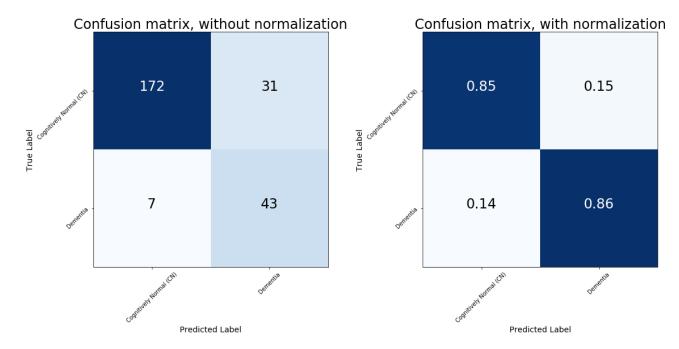




SVC with Probabilty, Tuned with ROC to Threshold 0.18 (Train) (accuracy: 0.92, balanced accuracy: 0.91, specificity: 0.92, sensitivity: 0.89)

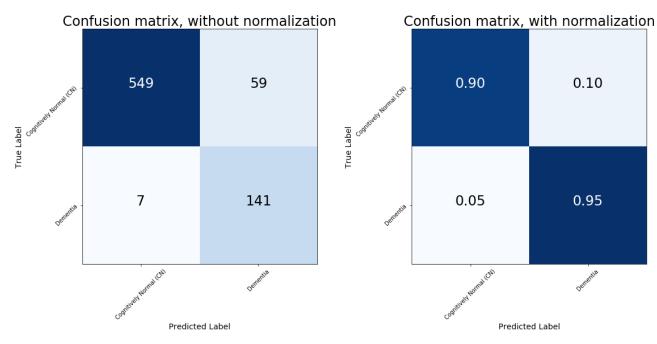


SVC with Probabilty, Tuned with ROC to Threshold 0.18 (Test) (accuracy: 0.85, balanced accuracy: 0.85, specificity: 0.85, sensitivity: 0.86)

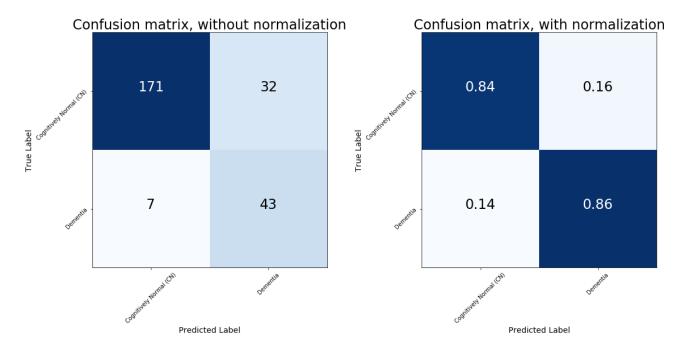


Adjusting SVM with Class Weights

SVC with Class Weights (1:4) (Train) (accuracy: 0.91, balanced accuracy: 0.93, specificity: 0.9, sensitivity: 0.95)



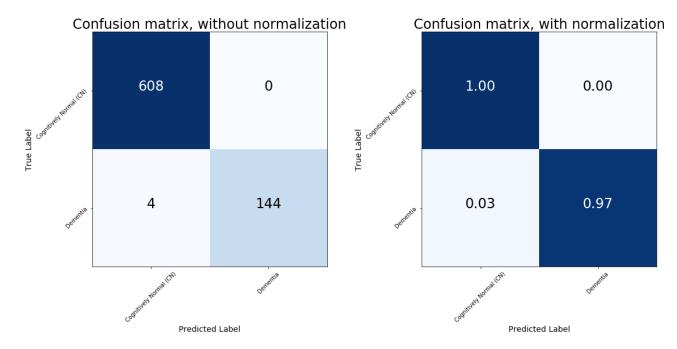
SVC with Class Weights (1:4) (Test) (accuracy: 0.85, balanced accuracy: 0.85, specificity: 0.84, sensitivity: 0.86)



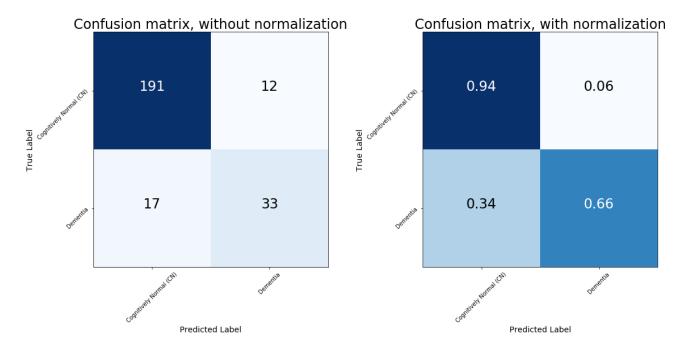
```
In [ ]:
```

Random Forest

Random Forest (Train) (accuracy: 0.99, balanced accuracy: 0.99, specificity: 1.0, sensitivity: 0.97)



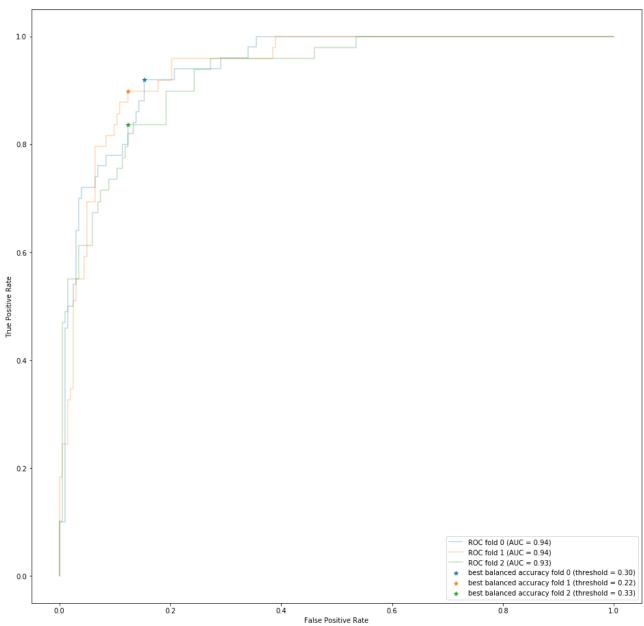
Random Forest (Test) (accuracy: 0.89, balanced accuracy: 0.8, specificity: 0.94, sensitivity: 0.66)



Top Feature Counts for Random Forest

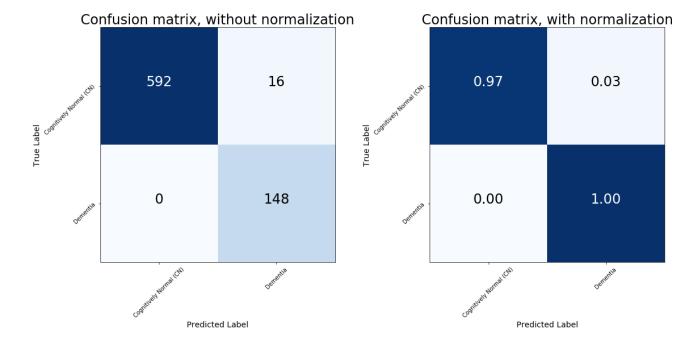
| | count |
|-----------------------|-------|
| feature | |
| FAQ | 15 |
| RAVLT_immediate | 14 |
| RAVLT_perc_forgetting | 13 |
| ADAS13 | 13 |
| ADAS11 | 8 |
| CDRSB | 6 |
| Hippocampus | 6 |
| MMSE | 4 |
| APOE4 | 4 |
| Entorhinal | 4 |
| RAVLT_forgetting | 2 |
| FDG | 2 |
| Ventricles | 2 |
| PTRACCAT_Black | 1 |
| RAVLT_learning | 1 |
| PTEDUCAT_9 | 1 |
| Fusiform | 1 |
| MidTemp | 1 |
| PTEDUCAT_8 | 1 |
| AGE | 1 |

Adjusting Random Forest with ROC

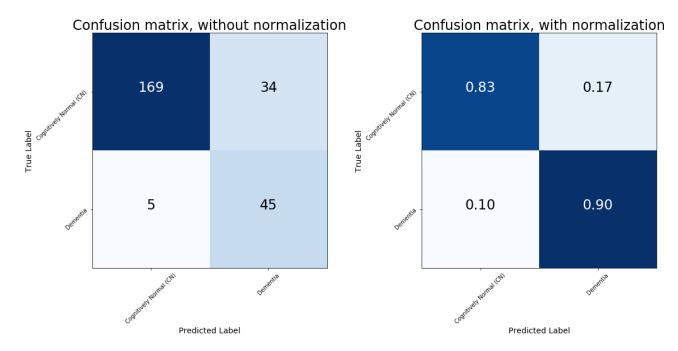


```
In [54]: rf_roc_tuned_model, rf_roc_tuned_results_train, rf_roc_tuned_results_test = \
             create_and_evaluate_probabilistic_model(
                 rf_model,
                 X train,
                 y_train,
                 X_test,
                 y test,
                 rf_roc_tuned_threshold
         plot_model_results(
             rf_roc_tuned_results_train,
             f"Random Forest, Tuned with ROC to Threshold {rf roc tuned threshold:.2} (Train)"
         plot_model_results(
             rf roc tuned results test,
             f"Random Forest, Tuned with ROC to Threshold {rf_roc_tuned_threshold:.2} (Test)"
         display(HTML(f"<h4>Top Feature Counts for Random Forest, Tuned with ROC to Threshold {rf_roc_tuned_threshold }
         display(rf_top_feature_counts(rf_roc_tuned_model, X_train.columns))
```

Random Forest, Tuned with ROC to Threshold 0.28 (Train) (accuracy: 0.98, balanced accuracy: 0.99, specificity: 0.97, sensitivity: 1.0)



Random Forest, Tuned with ROC to Threshold 0.28 (Test) (accuracy: 0.85, balanced accuracy: 0.87, specificity: 0.83, sensitivity: 0.9)



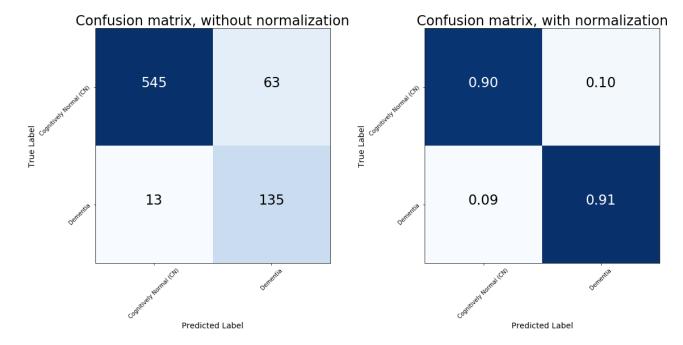
Top Feature Counts for Random Forest, Tuned with ROC to Threshold 0.28

| | count |
|-----------------------|-------|
| feature | |
| FAQ | 12 |
| RAVLT_perc_forgetting | 12 |
| ADAS13 | 11 |
| RAVLT_immediate | 11 |
| ADAS11 | 8 |
| Entorhinal | 7 |
| Hippocampus | 7 |
| MMSE | 6 |
| RAVLT_learning | 6 |
| CDRSB | 5 |
| FDG | 5 |
| WholeBrain | 2 |
| MidTemp | 2 |
| PTEDUCAT_9 | 2 |
| PTEDUCAT_19 | 1 |
| PTEDUCAT_12 | 1 |
| PTEDUCAT_14 | 1 |
| PTRACCAT_White | 1 |

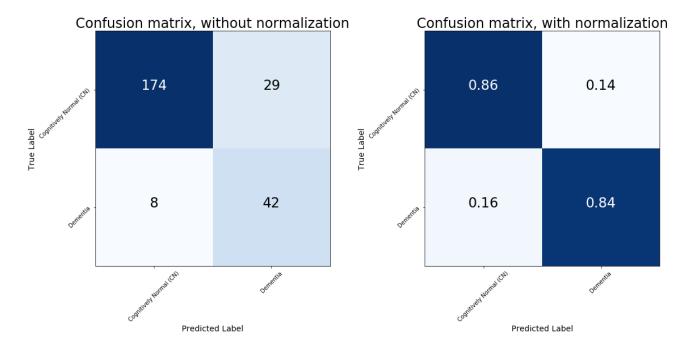
Adjusting Random Forest with Class Weights

```
In [55]: rf_weighted_model, rf_weighted_results_train, rf_weighted_results_test = \
             create_and_evaluate_model(
                 GridSearchCV(
                     RandomForestClassifier(n estimators=100, class weight={0: 1, 1: 4}),
                         "max_depth": range(3, 20)
                     },
                     scoring="balanced_accuracy",
                     cv=3
                 ).fit(X_train, y_train).best_estimator_,
                 X_train,
                 y_train,
                 X_test,
                 y_test
         plot_model_results(rf_weighted_results_train, "Random Forest with Class Weights (1:4) (Train)")
         plot_model_results(rf_weighted_results_test, "Random Forest with Class Weights (1:4) (Test)")
         display(HTML(f"<h4>Top Feature Counts for Random Forest with Class Weights (1:4)</h4>"))
         display(rf_top_feature_counts(rf_weighted_model, X_train.columns))
```

Random Forest with Class Weights (1:4) (Train) (accuracy: 0.9, balanced accuracy: 0.9, specificity: 0.9, sensitivity: 0.91)



Random Forest with Class Weights (1:4) (Test) (accuracy: 0.85, balanced accuracy: 0.85, specificity: 0.86, sensitivity: 0.84)



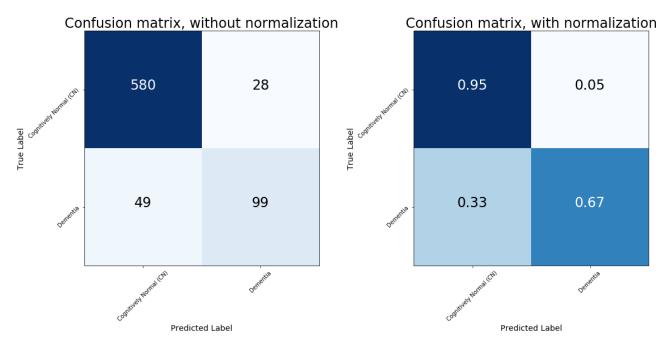
Top Feature Counts for Random Forest with Class Weights (1:4)

| | count |
|------------------------|-------|
| feature | |
| RAVLT_immediate | 19 |
| ADAS13 | 17 |
| ADAS11 | 13 |
| FAQ | 9 |
| CDRSB | 6 |
| RAVLT_perc_forgetting | 6 |
| RAVLT_learning | 5 |
| Entorhinal | 4 |
| MMSE | 4 |
| RAVLT_forgetting | 3 |
| APOE4 | 2 |
| AGE | 2 |
| Hippocampus | 2 |
| PTEDUCAT_8 | 2 |
| PTEDUCAT_11 | 1 |
| Ventricles | 1 |
| Fusiform | 1 |
| MidTemp | 1 |
| FDG | 1 |
| PTRACCAT_More than one | 1 |

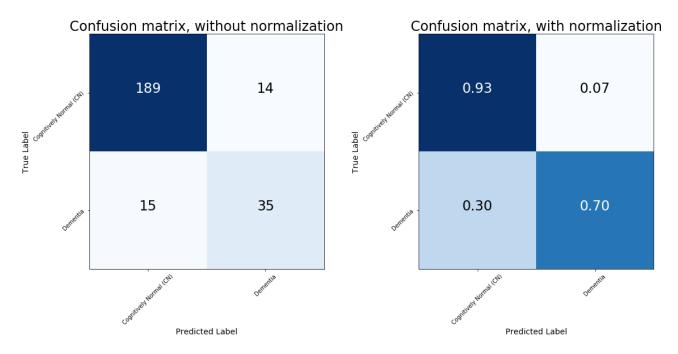
| In []: | |
|---------|--|
| | |
| In []: | |

Logistic Regression (Train)

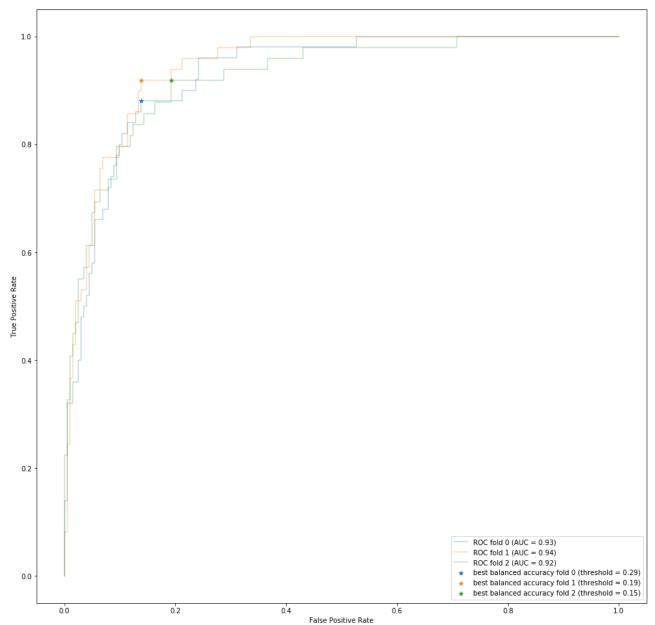
(accuracy: 0.9, balanced accuracy: 0.81, specificity: 0.95, sensitivity: 0.67)



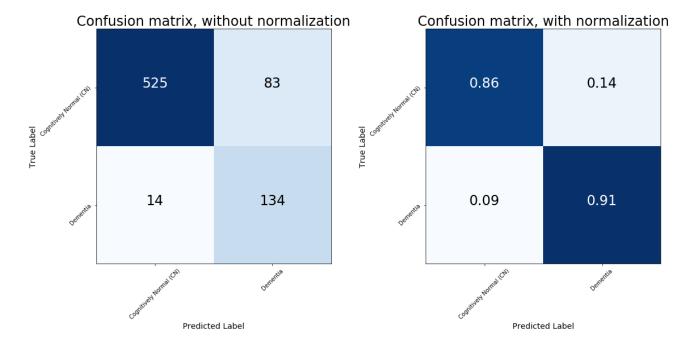
Logistic Regression (Test) (accuracy: 0.89, balanced accuracy: 0.82, specificity: 0.93, sensitivity: 0.7)



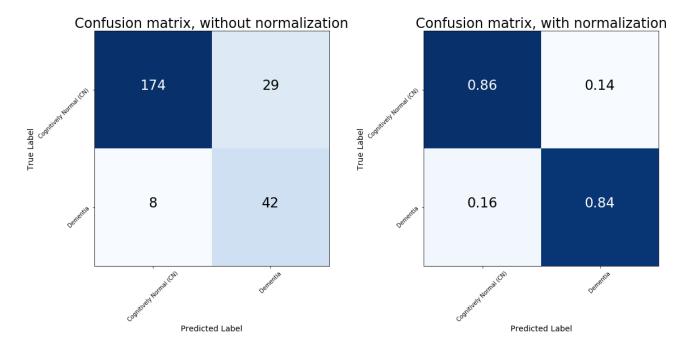
Adjusting Logistic Regression with ROC



Logistic Regression, Tuned with ROC to Threshold 0.21 (Train) (accuracy: 0.87, balanced accuracy: 0.88, specificity: 0.86, sensitivity: 0.91)

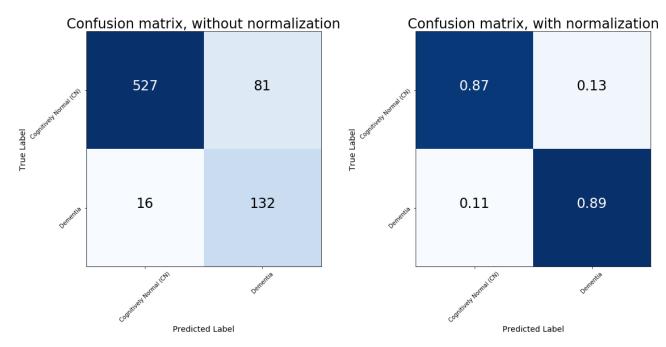


Logistic Regression, Tuned with ROC to Threshold 0.21 (Test) (accuracy: 0.85, balanced accuracy: 0.85, specificity: 0.86, sensitivity: 0.84)

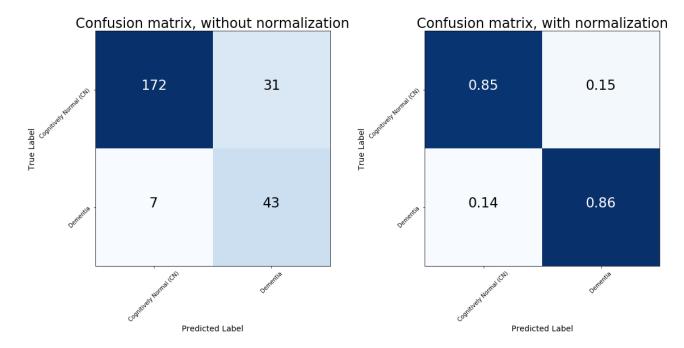


Adjusting Logistic Regression with Class Weights

SVC with Class Weights (1:4) (Train) (accuracy: 0.87, balanced accuracy: 0.88, specificity: 0.87, sensitivity: 0.89)



SVC with Class Weights (1:4) (Test) (accuracy: 0.85, balanced accuracy: 0.85, specificity: 0.85, sensitivity: 0.86)



Summary

```
In [60]: train_results = pd.DataFrame(
               list(map(
                    model_results_to_dict,
                    *zip(*[
                        (svc baseline results train, "SVC"),
                        (svc_probabilistic_results_train, "SVC with Probability Outputs"),
                        (rf_results_train, "Random Forest"),
                        (logreg_results_train, "Logistic Regression"),
                        (svc_roc_tuned_results_train, "SVC Tuned with ROC"),
(rf_roc_tuned_results_train, "Random Forest Tuned with ROC"),
                        (logreg_roc_tuned_results_train, "Logistic Regression Tuned with ROC"),
                        (svc_weighted_results_train, "SVC with Class Weights"),
(rf_weighted_results_train, "Random Forest with Class Weights"),
                         (logreg_weighted_results_train, "Logistic Regression with Class Weights")
                    ])
               )),
               columns=["model", "accuracy", "specificity", "sensitivity", "balanced accuracy"]
           ).set index("model")
          with pd.option_context("precision", 3):
               display(HTML("<h3>Model Performance on Training Data</h3>"))
               print(train_results.to_string())
```

Model Performance on Training Data

| | accuracy | specificity | sensitivity | balanced accuracy |
|--|----------|-------------|-------------|-------------------|
| model | | | | |
| SVC | 0.922 | 0.972 | 0.716 | 0.844 |
| SVC with Probability Outputs | 0.922 | 0.972 | 0.716 | 0.844 |
| Random Forest | 0.995 | 1.000 | 0.973 | 0.986 |
| Logistic Regression | 0.898 | 0.954 | 0.669 | 0.811 |
| SVC Tuned with ROC | 0.918 | 0.924 | 0.892 | 0.908 |
| Random Forest Tuned with ROC | 0.979 | 0.974 | 1.000 | 0.987 |
| Logistic Regression Tuned with ROC | 0.872 | 0.863 | 0.905 | 0.884 |
| SVC with Class Weights | 0.913 | 0.903 | 0.953 | 0.928 |
| Random Forest with Class Weights | 0.899 | 0.896 | 0.912 | 0.904 |
| Logistic Regression with Class Weights | 0.872 | 0.867 | 0.892 | 0.879 |

```
In [61]: test_results = pd.DataFrame(
               list(map(
                    model_results_to_dict,
                    *zip(*[
                         (svc_baseline_results_test, "SVC"),
                        (svc_probabilistic_results_test, "SVC with Probability Outputs"),
                        (rf results test, "Random Forest"),
                        (logreg_results_test, "Logistic Regression"),
                        (svc_roc_tuned_results_test, "SVC Tuned with ROC"),
(rf_roc_tuned_results_test, "Random Forest Tuned with ROC"),
                        (logreg_roc_tuned_results_test, "Logistic Regression Tuned with ROC"),
                        (svc_weighted_results_test, "SVC with Class Weights"),
(rf_weighted_results_test, "Random Forest with Class Weights"),
                        (logreg_weighted_results_test, "Logistic Regression with Class Weights")
                    ])
               )),
               columns=["model", "accuracy", "specificity", "sensitivity", "balanced accuracy"]
           ).set_index("model")
          with pd.option context("precision", 3):
               display(HTML("<h3>Model Performance on Test Data</h3>"))
               print(test_results.to_string())
```

Model Performance on Test Data

| | accuracy | specificity | sensitivity | balanced accuracy |
|--|----------|-------------|-------------|-------------------|
| model | | | | |
| SVC | 0.901 | 0.956 | 0.68 | 0.818 |
| SVC with Probability Outputs | 0.901 | 0.956 | 0.68 | 0.818 |
| Random Forest | 0.885 | 0.941 | 0.66 | 0.800 |
| Logistic Regression | 0.885 | 0.931 | 0.70 | 0.816 |
| SVC Tuned with ROC | 0.850 | 0.847 | 0.86 | 0.854 |
| Random Forest Tuned with ROC | 0.846 | 0.833 | 0.90 | 0.866 |
| Logistic Regression Tuned with ROC | 0.854 | 0.857 | 0.84 | 0.849 |
| SVC with Class Weights | 0.846 | 0.842 | 0.86 | 0.851 |
| Random Forest with Class Weights | 0.854 | 0.857 | 0.84 | 0.849 |
| Logistic Regression with Class Weights | 0.850 | 0.847 | 0.86 | 0.854 |

```
In [ ]:
```