

```
In [59]: '''  
This jupyter notebook includes code taken from the following nilearn project,  
"8.3.10. Voxel-Based Morphometry on Oasis dataset", which predicts age from  
grey matter morphometry. Feature redux = k-best ANOVA, prediction function = SVM  
  
I am tweaking the code to the following analysis:  
Feature redux = PCA, prediction function = SVM.  
I've included various plots.  
'''
```

```
In [ ]: # Let's keep our notebook clean, so it's a little more readable!  
import warnings  
warnings.filterwarnings('ignore')
```

```
In [99]: from nilearn import datasets  
import os  
import numpy as np  
import pandas as pd  
import seaborn as sns  
import matplotlib  
%matplotlib inline  
import matplotlib.pyplot as plt  
from nilearn.input_data import NiftiMasker
```

```
In [60]: from nilearn import plotting
```

```
In [53]: oasis_dataset = datasets.fetch_oasis_vbm()  
gray_matter_map_filenames = oasis_dataset.gray_matter_maps  
age = oasis_dataset.ext_vars['age'].astype(float, None)
```

```
In [74]: #Checking to see where the dataset is downloaded onto my computer
oasis_dataset
```

```
Out[74]: {'gray_matter_maps': ['C:\\Users\\rwick\\nilearn_data\\oasis1\\OAS1_0001_MR1_
\\mwrc1OAS1_0001_MR1_mpr_anon_fslswapdim_bet.nii.gz',
'C:\\Users\\rwick\\nilearn_data\\oasis1\\OAS1_0002_MR1\\mwrc1OAS1_0002_MR1_
mpr_anon_fslswapdim_bet.nii.gz',
'C:\\Users\\rwick\\nilearn_data\\oasis1\\OAS1_0003_MR1\\mwrc1OAS1_0003_MR1_
mpr_anon_fslswapdim_bet.nii.gz',
'C:\\Users\\rwick\\nilearn_data\\oasis1\\OAS1_0004_MR1\\mwrc1OAS1_0004_MR1_
mpr_anon_fslswapdim_bet.nii.gz',
'C:\\Users\\rwick\\nilearn_data\\oasis1\\OAS1_0005_MR1\\mwrc1OAS1_0005_MR1_
mpr_anon_fslswapdim_bet.nii.gz',
'C:\\Users\\rwick\\nilearn_data\\oasis1\\OAS1_0006_MR1\\mwrc1OAS1_0006_MR1_
mpr_anon_fslswapdim_bet.nii.gz',
'C:\\Users\\rwick\\nilearn_data\\oasis1\\OAS1_0007_MR1\\mwrc1OAS1_0007_MR1_
mpr_anon_fslswapdim_bet.nii.gz',
'C:\\Users\\rwick\\nilearn_data\\oasis1\\OAS1_0009_MR1\\mwrc1OAS1_0009_MR1_
mpr_anon_fslswapdim_bet.nii.gz',
'C:\\Users\\rwick\\nilearn_data\\oasis1\\OAS1_0010_MR1\\mwrc1OAS1_0010_MR1_
mpr_anon_fslswapdim_bet.nii.gz',
'C:\\Users\\rwick\\nilearn_data\\oasis1\\OAS1_0011_MR1\\mwrc1OAS1_0011_MR1_
mpr_anon_fslswapdim_bet.nii.gz']}
```

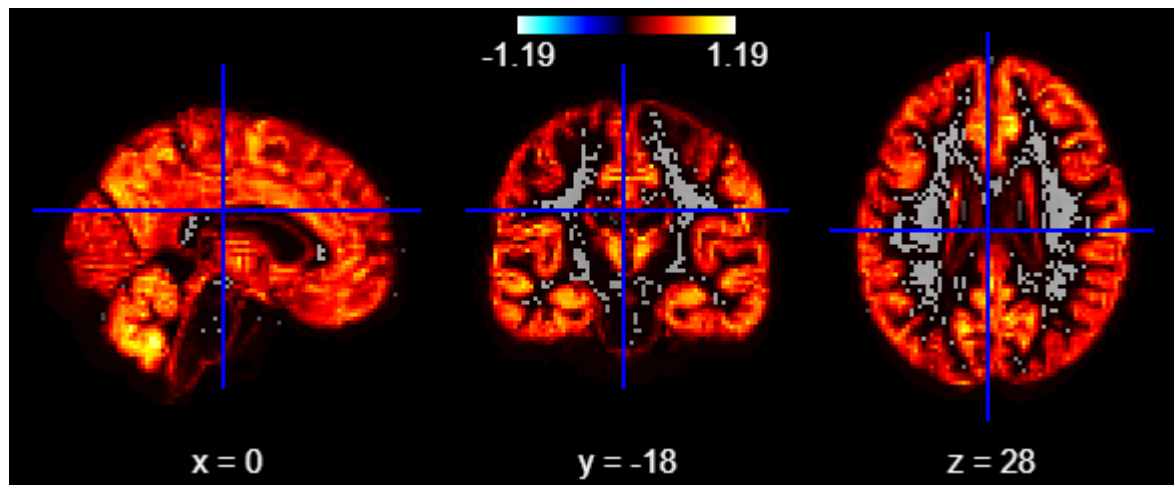
```
In [55]: '''
#for later if I decide to look at white matter
#Note to self: make sure the nifti masker is adapted for white matter, with correct
white_matter_map_filenames = oasis_dataset.white_matter_maps
wm_maps_masked = nifti_masker.fit_transform(white_matter_map_filenames)
'''
```

```
In [ ]: nifti_masker = NiftiMasker(
        standardize=False,
        smoothing_fwhm=2,
        memory='nilearn_cache') # cache options
gm_maps_masked = nifti_masker.fit_transform(gray_matter_map_filenames)

n_samples, n_features = gm_maps_masked.shape
print("%d samples, %d features" % (n_samples, n_features))
```

```
In [61]: subject1 = oasis_dataset.gray_matter_maps[0]
plotting.view_img(subject1)
```

Out[61]:



```
In [58]: print("ANOVA + SVR")
# Define the prediction function to be used.
# Here we use a Support Vector Classification, with a linear kernel
from sklearn.svm import SVR
svr = SVR(kernel='linear')

# Dimension reduction
from sklearn.feature_selection import VarianceThreshold, SelectKBest, \
    f_regression

# Remove features with too low between-subject variance
variance_threshold = VarianceThreshold(threshold=.01)

# Here we use a classical univariate feature selection based on F-test,
# namely Anova.
feature_selection = SelectKBest(f_regression, k=2000)

# We have our predictor (SVR), our feature selection (SelectKBest), and now,
# we can plug them together in a *pipeline* that performs the two operations
# successively:
from sklearn.pipeline import Pipeline
anova_svr = Pipeline([
    ('variance_threshold', variance_threshold),
    ('anova', feature_selection),
    ('svr', svr)])

### Fit and predict
anova_svr.fit(gm_maps_masked, age)
age_pred = anova_svr.predict(gm_maps_masked)
```

ANOVA + SVR

```

In [131]: print("PCA + SVR")
          # Define the prediction function to be used.
          # Here we use a Support Vector Classification, with a linear kernel
          from sklearn.svm import SVR
          svr = SVR(kernel='linear')

          # Dimension reduction

          from sklearn.decomposition import PCA
          #from sklearn.preprocessing import MinMaxScaler -
          #not needed because values are between 0 and 1, as they are tissue probabilities
          pca = PCA() # Here I'm not setting any hyperparameters on the number of components
          pca.fit(gm_maps_masked) # Fit the data.

          #These components are in an array called pca.explained_variance_ratio_
          #What if I want to see factor loadings? This would basically show every single variable
          #and how it correlates with each loading, which would be a huge figure.
          #What if I want to see a covariance/correlation matrix between all of my components?

          #Plotting the Cumulative Summation of the Explained Variance
          plt.figure()
          plt.plot(np.cumsum(pca.explained_variance_ratio_))
          plt.xlabel('Number of Components')
          plt.ylabel('Variance (%)') #for each component
          plt.title('PCA - Oasis Grey Matter Explained Variance')
          plt.show()

          #Scree plot: a line plot of the eigenvalues of factors or principal components in order
          #Try later

          ...

          We have our predictor (SVR), our feature selection (PCA), and now,
          we can plug them together in a *pipeline* that performs the two operations
          successively:
          ...

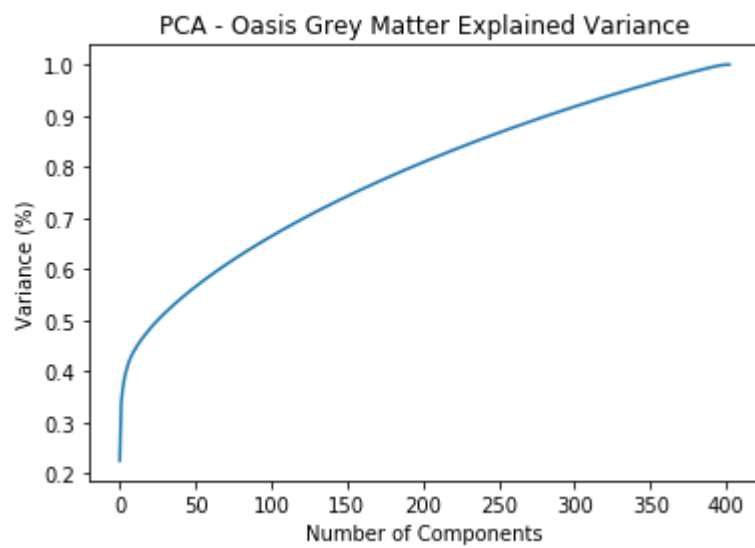
          # Remove components with too low between-subject variance
          variance_threshold = VarianceThreshold(threshold=.001)

          from sklearn.pipeline import Pipeline
          pca_svr = Pipeline([
              ('variance_threshold', variance_threshold),
              ('PCA', pca),
              ('svr', svr)])

          # Fit and predict
          pca_svr.fit(gm_maps_masked, age)
          age_pred = pca_svr.predict(gm_maps_masked)

```

PCA + SVR



```
In [130]: pca.explained_variance_ratio_
```

```
Out[130]: array([2.2584088e-01, 1.1436371e-01, 2.6626622e-02, 1.7880067e-02,
 1.3828022e-02, 1.0346623e-02, 9.5663518e-03, 7.4550672e-03,
 6.2674419e-03, 5.5455039e-03, 5.1566600e-03, 5.0084377e-03,
 4.4522383e-03, 4.3732417e-03, 4.2156246e-03, 3.9440263e-03,
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 3.4652401e-03, 3.4333770e-03, 3.2579077e-03, 3.2121697e-03,
 3.1870520e-03, 3.1186503e-03, 3.0648196e-03, 2.9737179e-03,
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 2.2153966e-03, 2.1884532e-03, 2.1630446e-03, 2.1581594e-03,
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 2.0426018e-03, 2.0294755e-03, 2.0136640e-03, 1.9954494e-03,
 1.9905095e-03, 1.9788677e-03, 1.9669503e-03, 1.9592512e-03,
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 1.4456082e-03, 1.4369712e-03, 1.4313423e-03, 1.4245587e-03,
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 1.3922962e-03, 1.3872288e-03, 1.3846006e-03, 1.3789861e-03,
 1.3745185e-03, 1.3691484e-03, 1.3637854e-03, 1.3618452e-03,
 1.3573989e-03, 1.3554659e-03, 1.3522484e-03, 1.3455915e-03,
 1.3406917e-03, 1.3390647e-03, 1.3323993e-03, 1.3307688e-03,
 1.3280221e-03, 1.3223292e-03, 1.3179997e-03, 1.3137892e-03,
 1.3106659e-03, 1.3068999e-03, 1.3033262e-03, 1.3005041e-03,
 1.2965433e-03, 1.2919662e-03, 1.2891974e-03, 1.2825729e-03,
 1.2807273e-03, 1.2772733e-03, 1.2750929e-03, 1.2723877e-03,
 1.2677106e-03, 1.2652477e-03, 1.2621434e-03, 1.2561048e-03,
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 1.1989798e-03, 1.1968840e-03, 1.1942502e-03, 1.1930905e-03,
```

```

1.1908448e-03, 1.1838028e-03, 1.1835219e-03, 1.1779685e-03,
1.1746801e-03, 1.1728758e-03, 1.1686299e-03, 1.1665858e-03,
1.1643243e-03, 1.1604020e-03, 1.1552661e-03, 1.1529251e-03,
1.1510504e-03, 1.1470491e-03, 1.1460664e-03, 1.1438235e-03,
1.1409966e-03, 1.1387529e-03, 1.1371174e-03, 1.1327459e-03,
1.1287875e-03, 1.1264761e-03, 1.1226551e-03, 1.1196607e-03,
1.1154821e-03, 1.1145177e-03, 1.1075584e-03, 1.1058630e-03,
1.1012587e-03, 1.1001255e-03, 1.0975766e-03, 1.0972272e-03,
1.0951937e-03, 1.0914726e-03, 1.0900162e-03, 1.0861802e-03,
1.0840353e-03, 1.0830464e-03, 1.0811270e-03, 1.0777710e-03,
1.0755782e-03, 1.0691205e-03, 1.0672041e-03, 1.0635090e-03,
1.0617800e-03, 1.0609117e-03, 1.0571751e-03, 1.0546790e-03,
1.0533786e-03, 1.0514263e-03, 1.0500281e-03, 1.0476074e-03,
1.0432813e-03, 1.0409728e-03, 1.0375225e-03, 1.0368954e-03,
1.0343557e-03, 1.0332770e-03, 1.0305531e-03, 1.0290233e-03,
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1.0036835e-03, 1.0023044e-03, 1.0013669e-03, 9.9791889e-04,
9.9393202e-04, 9.9041429e-04, 9.8958844e-04, 9.8861451e-04,
9.8543265e-04, 9.8320865e-04, 9.8036614e-04, 9.7900617e-04,
9.7519025e-04, 9.7234739e-04, 9.7157952e-04, 9.6790551e-04,
9.6686563e-04, 9.6319115e-04, 9.6008438e-04, 9.5921673e-04,
9.5648045e-04, 9.5345109e-04, 9.4933936e-04, 9.4838301e-04,
9.4600307e-04, 9.4302365e-04, 9.4043498e-04, 9.4030437e-04,
9.3636307e-04, 9.3427306e-04, 9.3210937e-04, 9.3088619e-04,
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9.0827199e-04, 9.0613757e-04, 9.0295123e-04, 9.0134458e-04,
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8.4407255e-04, 8.4299617e-04, 8.3928474e-04, 8.3767000e-04,
8.3487103e-04, 8.3178765e-04, 8.2918518e-04, 8.2712906e-04,
8.2564267e-04, 8.2237856e-04, 8.2021224e-04, 8.1944047e-04,
8.1401371e-04, 8.1189093e-04, 8.0952351e-04, 8.0669700e-04,
8.0116687e-04, 8.0072938e-04, 7.9862331e-04, 7.9565437e-04,
7.9355080e-04, 7.8953465e-04, 7.8892265e-04, 7.8466174e-04,
7.8022201e-04, 7.7700464e-04, 7.7279302e-04, 7.7202613e-04,
7.6655636e-04, 7.6456275e-04, 7.6151220e-04, 7.5811159e-04,
7.4963906e-04, 7.4570614e-04, 7.4139284e-04, 7.3910563e-04,
7.3581678e-04, 7.2715903e-04, 7.2551757e-04, 7.1492733e-04,
7.0619286e-04, 6.8900490e-04, 6.3116988e-04, 5.5659632e-04,
5.4640311e-04, 4.6178058e-04, 3.8572747e-04, 2.5240699e-04,
1.8324256e-04, 1.5303958e-04, 4.2368989e-13], dtype=float32)

```

```
In [140]: type(pca.explained_variance_ratio_)
```

```
Out[140]: numpy.ndarray
```

```
In [ ]: pca.explained_variance
```

```
In [143]: sorted_components = np.sort(pca.explained_variance_ratio_, axis=-1, kind=None, order=None)
shortened_components=sorted_components[:20]
```

```
-----
TypeError                                Traceback (most recent call last)
<ipython-input-143-a8e5af444712> in <module>
----> 1 sorted_components = np.sort(pca.explained_variance_ratio_, axis=-1, kind=None, order=None)
      2 shortened_components=sorted_components[:20]

~\Anaconda3\lib\site-packages\numpy\core\fromnumeric.py in sort(a, axis, kind, order)
    932     else:
    933         a = asanyarray(a).copy(order="K")
--> 934     a.sort(axis=axis, kind=kind, order=order)
    935     return a
    936
```

TypeError: expected bytes, NoneType found

```
In [124]: shortened_components
```

```
Out[124]: array([0.22507139, 0.11385646, 0.0272289 , 0.01823406, 0.0138927 ,
                 0.01038271, 0.00970589, 0.0074357 , 0.00624059, 0.00552639,
                 0.00517382, 0.0050704 , 0.00452513, 0.00435713, 0.00424785,
                 0.00397213, 0.00386279, 0.0038356 , 0.00375894, 0.00366369],
                dtype=float32)
```

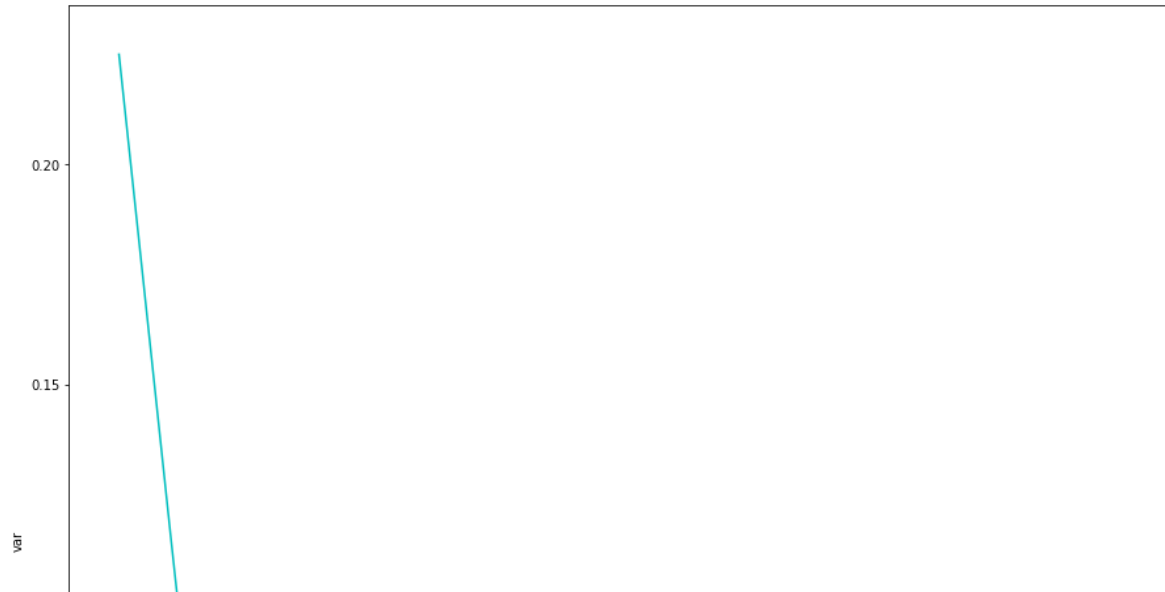
```
In [127]: mylist = []
          for i in range(20):
              mylist.append("PCA%i" % i)
          mylist
```

```
Out[127]: ['PCA0',
            'PCA1',
            'PCA2',
            'PCA3',
            'PCA4',
            'PCA5',
            'PCA6',
            'PCA7',
            'PCA8',
            'PCA9',
            'PCA10',
            'PCA11',
            'PCA12',
            'PCA13',
            'PCA14',
            'PCA15',
            'PCA16',
            'PCA17',
            'PCA18',
            'PCA19']
```



```
In [149]: #Creating a scree plot with the first 20 components.  
plt.figure(figsize=(15,15))  
df = pd.DataFrame({'var':shortened_components,  
                  'PC':mylist})  
sns.lineplot(x='PC',y="var",  
            data=df, color="c")
```

Out[149]: <matplotlib.axes._subplots.AxesSubplot at 0x12185f6fc50>



```
In [133]: #Well that's very bizarre. These are totally out of order.
```

```

In [ ]: coef = svr.coef_
# reverse feature selection
coef = feature_selection.inverse_transform(coef)
# reverse variance threshold
coef = variance_threshold.inverse_transform(coef)
# reverse masking
weight_img = nifti_masker.inverse_transform(coef)

# Create the figure
from nilearn.plotting import plot_stat_map, show
bg_filename = gray_matter_map_filenames[0]
z_slice = 0

fig = plt.figure(figsize=(5.5, 7.5), facecolor='k')
# Hard setting vmax to highlight weights more
display = plot_stat_map(weight_img, bg_img=bg_filename,
                        display_mode='z', cut_coords=[z_slice],
                        figure=fig, vmax=1)
display.title('SVM weights', y=1.2)

# Measure accuracy with cross validation
from sklearn.model_selection import cross_val_score
cv_scores = cross_val_score(anova_svr, gm_maps_masked, age)

# Return the corresponding mean prediction accuracy
prediction_accuracy = np.mean(cv_scores)
print("=== ANOVA ===")
print("Prediction accuracy: %f" % prediction_accuracy)
print("")

### Inference with massively univariate model #####
print("Massively univariate model")

# Statistical inference
from nilearn.mass_univariate import permuted_ols
data = variance_threshold.fit_transform(gm_maps_masked)
neg_log_pvals, t_scores_original_data, _ = permuted_ols(
    age, data, # + intercept as a covariate by default
    n_perm=2000, # 1,000 in the interest of time; 10000 would be better
    n_jobs=1) # can be changed to use more CPUs
signed_neg_log_pvals = neg_log_pvals * np.sign(t_scores_original_data)
signed_neg_log_pvals_unmasked = nifti_masker.inverse_transform(
    variance_threshold.inverse_transform(signed_neg_log_pvals))

# Show results
threshold = -np.log10(0.1) # 10% corrected

fig = plt.figure(figsize=(5.5, 7.5), facecolor='k')

display = plot_stat_map(signed_neg_log_pvals_unmasked, bg_img=bg_filename,
                        threshold=threshold, cmap=plt.cm.RdBu_r,
                        display_mode='z', cut_coords=[z_slice],
                        figure=fig)
title = ('Negative  $\log_{10}$  p-values'
        '\n(Non-parametric + max-type correction)')

```

```
display.title(title, y=1.2)

n_detections = (signed_neg_log_pvals_unmasked.get_data() > threshold).sum()
print('\n%d detections' % n_detections)

show()
```

```
In [69]: #All k-fold cross-validation stuff here
from sklearn.model_selection import train_test_split
```