

project1

February 28, 2025

1 Machine Learning in Python - Project 1

Due Friday, Feb 28th by 4 pm.

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1.1 Setup

To begin the analysis, we first import the necessary data processing, visualization, and modeling libraries.

```
[1]: import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
plt.rcParams['figure.figsize'] = (5,3)
plt.rcParams['figure.dpi'] = 80
from sklearn.model_selection import train_test_split, GridSearchCV, KFold
from sklearn.linear_model import LinearRegression, Ridge
from sklearn.metrics import mean_squared_error, r2_score
from sklearn.preprocessing import OneHotEncoder, StandardScaler
from sklearn.compose import ColumnTransformer
from sklearn.pipeline import make_pipeline

[2]: # Load data
url = "https://raw.githubusercontent.com/AwuoeZYC/Project_1/main/"
d = pd.read_csv(f"{url}adnidata.csv", index_col=0)

[3]: # Code from workshop
def model_fit(m, X, y, plot = False):
    """Returns the mean squared error, root mean squared error and  $R^2$  value of
    a fitted model based
    on provided  $X$  and  $y$  values.

    Args:
        m: sklearn model object
        X: model matrix to use for prediction
        y: outcome vector to use to calculating rmse and residuals
        plot: boolean value, should fit plots be shown
```

```

"""

y_hat = m.predict(X)
MSE = mean_squared_error(y, y_hat)
RMSE = np.sqrt(mean_squared_error(y, y_hat))
Rsqr = r2_score(y, y_hat)

Metrics = (round(MSE, 4), round(RMSE, 4), round(Rsqr, 4))

res = pd.DataFrame(
    data = {'y': y, 'y_hat': y_hat, 'resid': y - y_hat}
)

if plot:
    plt.figure()

    plt.subplot(121)
    sns.lineplot(x='y', y='y_hat', color="grey", data = pd.
↳DataFrame(data={'y': [min(y),max(y)], 'y_hat': [min(y),max(y)]}))
    sns.scatterplot(x='y', y='y_hat', data=res).set_title("Observed vs_
↳Fitted values")

    plt.subplot(122)
    sns.scatterplot(x='y_hat', y='resid', data=res).set_title("Fitted_
↳values vs Residuals")
    plt.hlines(y=0, xmin=np.min(y), xmax=np.max(y), linestyle='dashed',
↳alpha=0.3, colors="black")

    plt.subplots_adjust(left=0.0)

    plt.suptitle("Model (MSE, RMSE, Rsq) = " + str(Metrics), fontsize=14)
    plt.show()

return MSE, RMSE, Rsqr

```

2 Introduction

Alzheimer’s disease (AD) is a progressive neurodegenerative disorder that leads to cognitive decline, making early prediction crucial for identifying at-risk individuals and enabling timely interventions. This study develops a machine learning model to predict ADAS-Cog 13 scores at a 24-month follow-up using baseline features from the Alzheimer’s Disease Neuroimaging Initiative (ADNI) dataset.

The dataset includes demographic factors, genetic risk markers (APOE4 genotype), cognitive assessments, and Magnetic Resonance Imaging (MRI)-derived brain volumetric features (e.g., hippocampal volume, ventricular volume, and whole brain volume). To ensure model robustness, we preprocess the data by handling missing values, normalizing MRI volumes relative to intracranial volume (ICV), and encoding categorical variables. We then conduct exploratory data analysis

(EDA) to examine feature distributions and correlations before applying various regression models, including linear regression, ridge regression, lasso regression, polynomial regression, and elastic net, with hyperparameter tuning via cross-validation.

Our findings indicate that the baseline ADAS13 score is the strongest predictor of cognitive decline, while APOE4 genotype, age, and structural brain features—such as hippocampal and ventricular volumes—also play key roles. Among the models tested, Ridge Regression demonstrated the best overall performance, achieving the lowest test MSE (32.18) and the most stable coefficient estimates, making it the most accurate and reliable model for predicting cognitive decline. While Polynomial Regression captured potential nonlinear relationships, it introduced higher variance, making it less robust. Ridge Regression effectively reduced overfitting while preserving key predictor relationships, confirming its suitability for clinical applications.

3 Exploratory Data Analysis and Feature Engineering

Before proceeding with feature selection, we check for missing values and duplicate entries, as they can impact model performance.

```
[4]: # Checking for missing values
missing_values = d.isnull().sum()
print("Missing values per column:\n", missing_values[missing_values > 0])

# Check duplicate rows
duplicates = d.duplicated()
num_duplicates = duplicates.sum()
print(f"Number of duplicate rows: {num_duplicates}")
```

```
Missing values per column:
APOE4          5
Ventricles     147
Hippocampus    147
WholeBrain     148
Entorhinal     147
Fusiform       147
MidTemp        147
ICV            8
dtype: int64
Number of duplicate rows: 0
```

The dataset contains several columns with missing values, including Ventricles, Hippocampus, WholeBrain, and other clinical measurements. Additionally, no duplicate rows were found in the dataset.

To evaluate model performance, we split the dataset into training (80%) and test (20%) sets.

```
[5]: random_seed = 2 # Fix random seed
# Define the target and features (we will refine feature selection later)
target = 'ADAS13.m24'
```

```

features = d.columns.drop(['RID', 'ADAS13.m24']) # Exclude person identifier
↳ and target

# Drop rows with missing values (or consider imputation strategies)
d_clean = d.dropna().copy().drop(columns=['RID'])

# Create normalized volume features
volume_cols = ['Ventricles', 'Hippocampus', 'WholeBrain', 'Entorhinal',
↳ 'Fusiform', 'MidTemp']
for col in volume_cols:
    new_col = col + '_norm'
    d_clean.loc[:, new_col] = d_clean[col] / d_clean['ICV']

# Create training and testing sets
train_df, test_df = train_test_split(d_clean, test_size=0.2,
↳ random_state=random_seed)
print("Training set size:", train_df.shape)
print("Testing set size:", test_df.shape)

```

Training set size: (708, 23)

Testing set size: (177, 23)

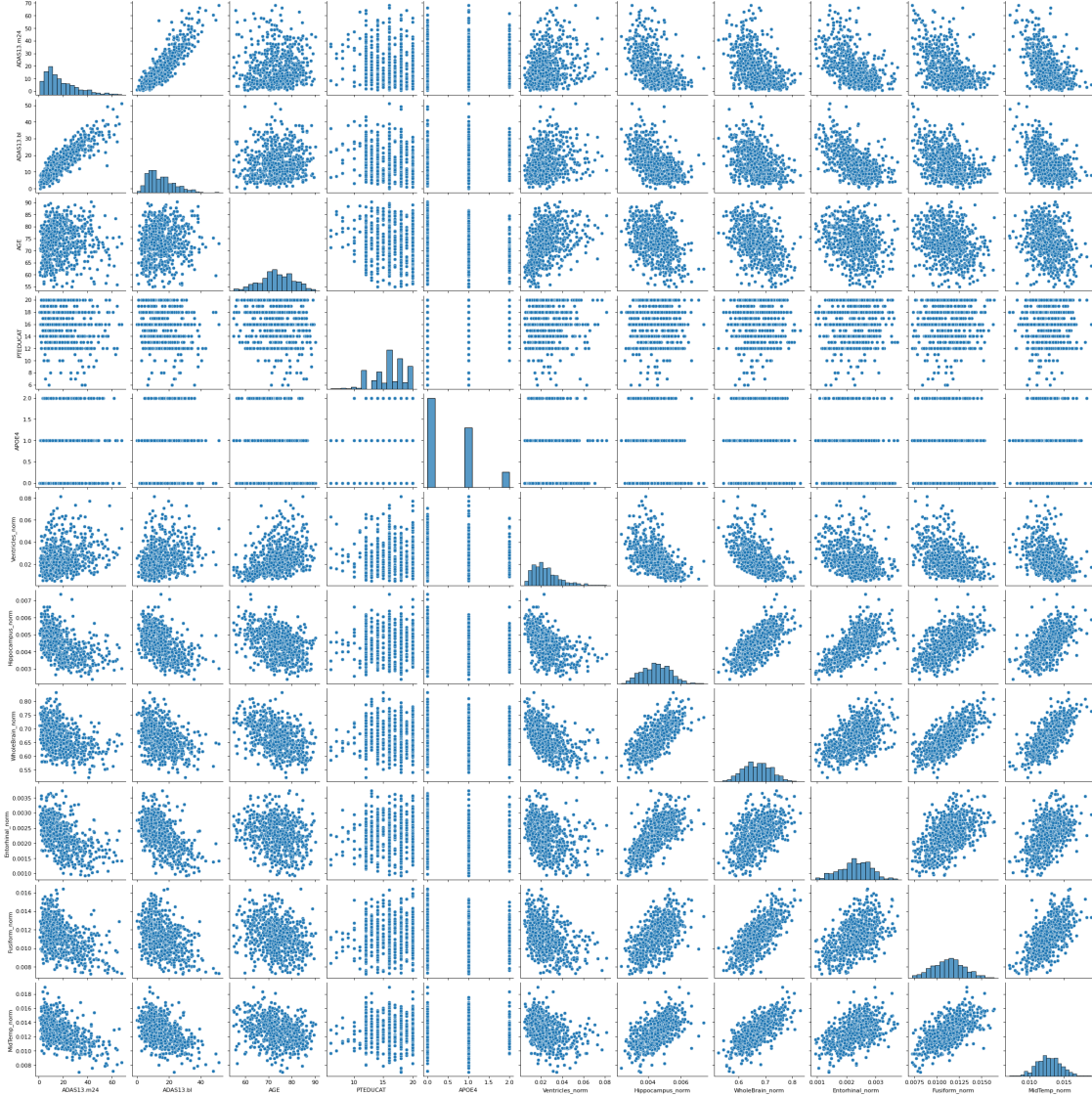
The training set contains 80% of the data, providing enough samples for model learning, while the test set consists of 20%, allowing evaluation on unseen data. Additionally, rows with missing values were removed, resulting in a clean dataset.

To visualize relationships between baseline cognitive scores, demographic variables, and normalized volumetric features, we then generate a pairplot.

```

[6]: sns.pairplot(train_df[['ADAS13.m24', 'ADAS13.b1', 'AGE', 'PTEDUCAT', 'APOE4',
↳ 'Ventricles_norm', 'Hippocampus_norm',
                                'WholeBrain_norm', 'Entorhinal_norm', 'Fusiform_norm',
↳ 'MidTemp_norm']])
plt.show()

```



ADAS13.bl and ADAS13.m24 show a strong linear correlation, reinforcing the idea that baseline cognitive assessment is a crucial predictor of future cognitive decline. Hippocampus_norm is negatively correlated with ADAS13.m24, suggesting that smaller hippocampal volumes are associated with greater cognitive deterioration. On the other hand, Ventricle_norm is positively correlated with ADAS13.m24, indicating that larger ventricular volumes are linked to increased brain atrophy and cognitive impairment. Meanwhile, Age and education (PTEDUCAT) do not exhibit strong correlations.

We compute a correlation matrix for numerical features to identify key predictors of cognitive decline.

```
[7]: numeric_df = train_df.select_dtypes(include=[np.number])
    corr_matrix = numeric_df.corr()
```

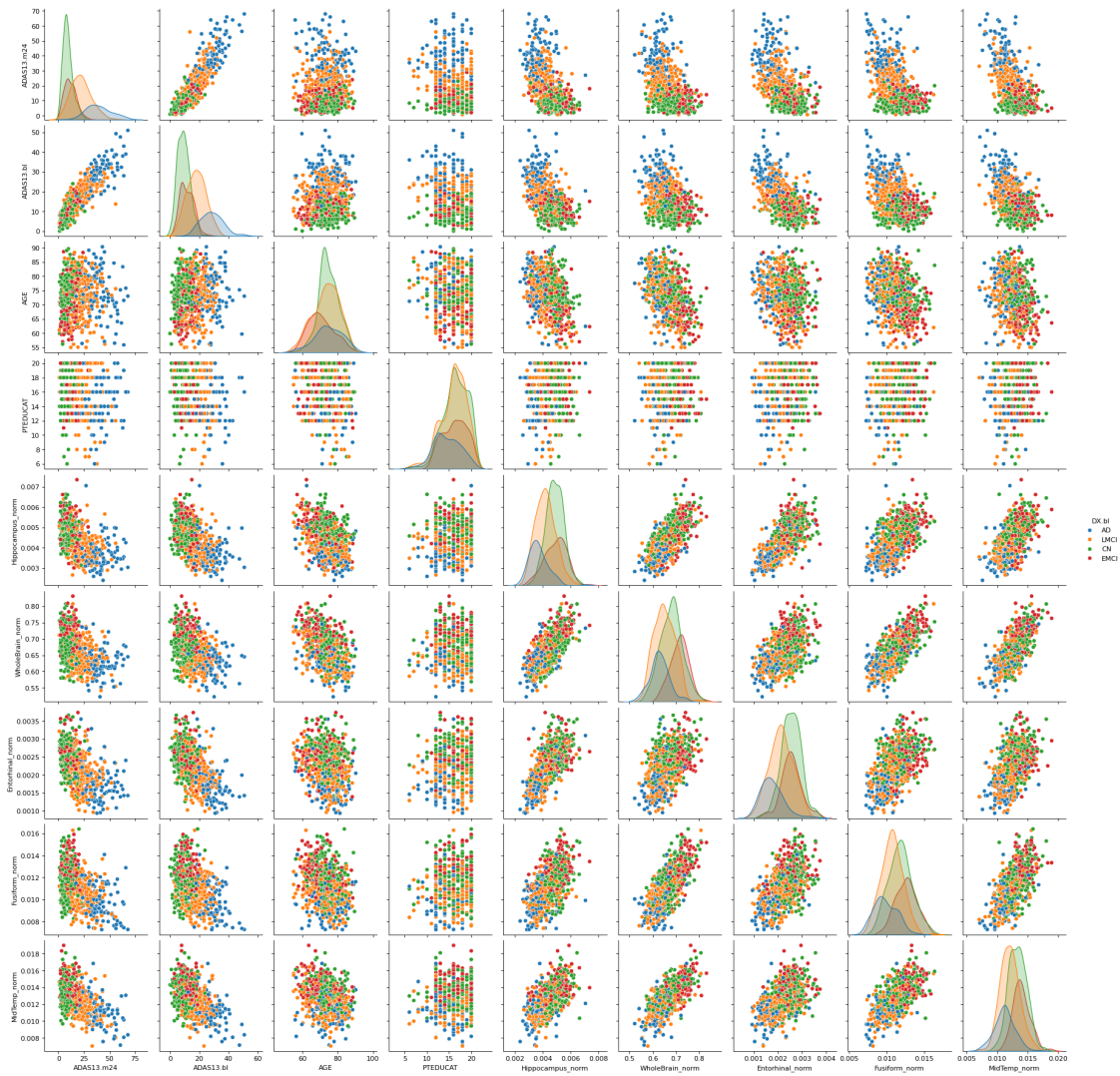
```
subset_corr = corr_matrix.loc['ADAS13.m24'] # Only show the correlation with
↳target
print(subset_corr)
```

```
ADAS13.bl          0.882006
ADAS13.m24         1.000000
AGE                0.063524
PTEDUCAT          -0.207972
APOE4              0.352586
Ventricles         0.270433
Hippocampus        -0.527248
WholeBrain         -0.258306
Entorhinal         -0.527313
Fusiform           -0.424442
MidTemp            -0.458689
ICV                0.067017
Ventricles_norm    0.290048
Hippocampus_norm   -0.537560
WholeBrain_norm    -0.453800
Entorhinal_norm    -0.546310
Fusiform_norm      -0.486201
MidTemp_norm       -0.553484
Name: ADAS13.m24, dtype: float64
```

ADAS13.bl has the highest positive correlation ($r = 0.882$) with ADAS13.m24, establishing it as a key predictor of cognitive decline. Hippocampus_norm shows a strong negative correlation ($r = -0.537$) with ADAS13.m24, suggesting that reduced hippocampal volume is associated with greater cognitive deterioration. Ventricles_norm has a moderate positive correlation ($r = 0.290$) with ADAS13.m24, indicating that larger ventricles are linked to cognitive impairment. ICV exhibits a very weak correlation ($r = 0.067$) with ADAS13.m24, suggesting that intracranial volume has little influence on cognitive decline. Additionally, AGE shows a minimal correlation ($r = 0.063$), while APOE4 has a moderate positive correlation ($r = 0.352$) with cognitive decline. Other brain regions such as WholeBrain_norm, Entorhinal_norm, and MidTemp_norm also demonstrate significant negative correlations, further supporting their role in cognitive deterioration.

After testing all categorical variables, we found that DX.bl had the greatest impact on the data. Therefore, to compare cognitive decline across different diagnostic groups, we generate a boxplot of ADAS13.m24 for CN, EMCI, LMCI, and AD, which are the categories derived from DX.bl.

```
[8]: sns.pairplot(train_df[['ADAS13.m24', 'ADAS13.bl', 'AGE', 'PTEDUCAT',
↳ 'Hippocampus_norm', 'WholeBrain_norm', 'Entorhinal_norm',
↳ 'Fusiform_norm', 'MidTemp_norm',
                                'DX.bl']], hue='DX.bl')
plt.show()
```

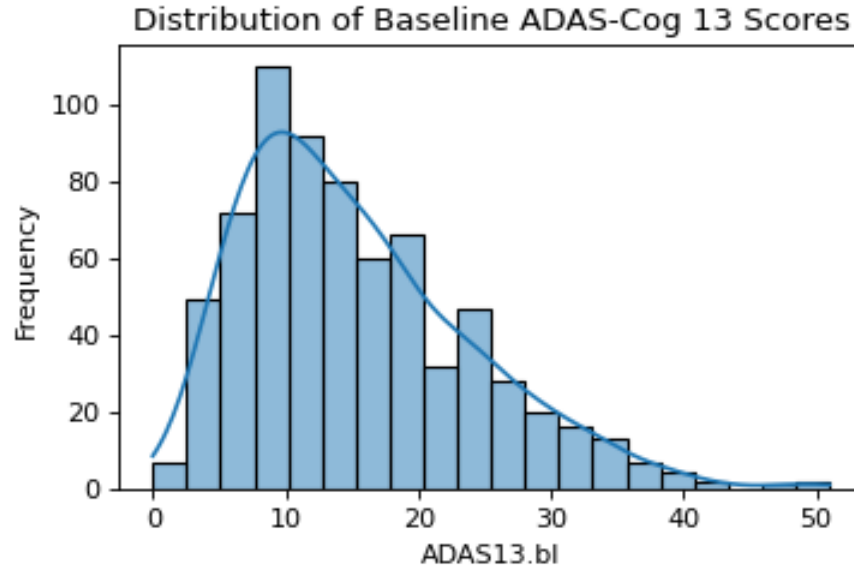



The results indicate that patients diagnosed with Alzheimer's disease (AD) exhibit the highest cognitive decline, as reflected by their significantly higher ADAS13.m24 scores. In contrast, individuals classified as cognitively normal (CN) have the lowest scores, confirming that they experience minimal cognitive deterioration over 24 months. Participants with early mild cognitive impairment (EMCI) and late mild cognitive impairment (LMCI) show a wider distribution of scores, suggesting that cognitive decline in these groups varies significantly between individuals.

To analyze the distribution of baseline cognitive scores (ADAS13.bl) and their relationship with future cognitive decline (ADAS13.m24), we generate a histogram to assess the distribution of ADAS13.bl and a scatterplot to visualize the relationship between ADAS13.bl and ADAS13.m24 over 24 months.

```
[9]: # Histogram for baseline ADAS-Cog 13 scores
plt.figure()
sns.histplot(train_df['ADAS13.bl'], bins=20, kde=True)
```

```
plt.title('Distribution of Baseline ADAS-Cog 13 Scores')
plt.xlabel('ADAS13.bl')
plt.ylabel('Frequency')
plt.show()
```



ADAS13.bl follows a right-skewed distribution, meaning most participants have mild impairment, with fewer experiencing severe decline.

4 Model Fitting and Tuning

We explored polynomial, Ridge, Lasso, and ElasticNet regression, ultimately selecting Ridge for its superior performance and interpretability.

4.1 Baseline Model

We select ADAS13.bl, AGE, PTEDUCAT, and MRI volumetric features (e.g., Ventricles_norm, Hippocampus_norm) as key predictors of ADAS13.m24, based on their clinical relevance to cognitive decline and Alzheimer's progression. These features ensure effective model training and evaluation.

```
[10]: # Define a basic set of features for the baseline model
features_baseline = ['ADAS13.bl', 'AGE', 'PTEDUCAT'] + [col for col in d_clean.
    ↪columns if '_norm' in col]
print(features_baseline)

X_train_baseline = train_df[features_baseline]
y_train_baseline = train_df[target]
X_test_baseline = test_df[features_baseline]
```



```
y_test_baseline = test_df[target]
```

```
['ADAS13.bl', 'AGE', 'PTEDUCAT', 'Ventricles_norm', 'Hippocampus_norm',  
'WholeBrain_norm', 'Entorhinal_norm', 'Fusiform_norm', 'MidTemp_norm']
```

Linear regression is selected as the benchmark model due to its interpretability and efficiency in estimating the relationship between cognitive decline and predictor variables. The model follows the equation:

$$\text{ADAS13.m24} = \beta_0 + \beta_1(\text{ADAS13.bl}) + \beta_2(\text{AGE}) + \beta_3(\text{PTEDUCAT}) + \dots + \beta_n(\text{MRIFeatures}) + \epsilon$$

where β represents the estimated coefficients, and ϵ is the residual error. This model serves as a reference point for evaluating more complex techniques, such as Ridge Regression, in subsequent steps. The primary goal is to determine how well a simple linear model can predict future cognitive scores based on baseline characteristics.

To understand feature importance, we extract coefficient values from the baseline model.

```
[11]: # Fit the baseline model
baseline_model = LinearRegression()
baseline_model.fit(X_train_baseline, y_train_baseline)
# Calculate coefficients
bcoefs = baseline_model.coef_
bcoefs_ = pd.DataFrame(
    np.copy(baseline_model.coef_),
    columns=["Coefficients"],
    index=features_baseline,
)

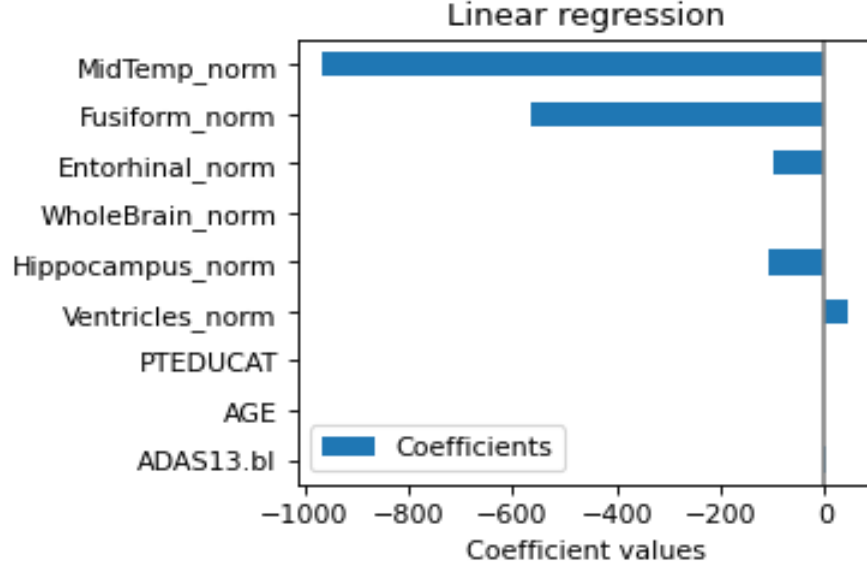
print(bcoefs_)

bcoefs_.plot.barh()
plt.title("Linear regression")
plt.axvline(x=0, color=".5")
plt.xlabel("Coefficient values")
plt.subplots_adjust(left=0.3)
# Model performance
train_MSE, train_RMSE, train_R2 = model_fit(baseline_model, X_train_baseline,
    ↪ y_train_baseline, plot=False)
print(f"Training Data - MSE: {train_MSE}, RMSE: {train_RMSE}, R²: {train_R2}")

test_MSE, test_RMSE, test_R2 = model_fit(baseline_model, X_test_baseline,
    ↪ y_test_baseline, plot=False)
print(f"Test Data - MSE: {test_MSE}, RMSE: {test_RMSE}, R²: {test_R2}")
```

	Coefficients
ADAS13.bl	1.182755
AGE	-0.208472
PTEDUCAT	-0.135640
Ventricles_norm	42.086665

Hippocampus_norm -110.292635
 WholeBrain_norm -2.603836
 Entorhinal_norm -98.776700
 Fusiform_norm -563.941724
 MidTemp_norm -964.546785
 Training Data - MSE: 32.57577372900131, RMSE: 5.70751905200511, R²: 0.8122828654570748
 Test Data - MSE: 39.233348681268886, RMSE: 6.263652982187701, R²: 0.7469974212066837



The model analysis reveals that ADAS13.bl (with a coefficient of 1.18) is the strongest predictor of future cognitive scores. Negative coefficients for hippocampal and entorhinal volumes indicate a link between brain atrophy and cognitive decline, while the positive coefficient for Ventricles_norm (42.08) suggests that ventricular enlargement is associated with disease progression. In terms of model performance, the training data yields an MSE of 32.58, RMSE of 5.71, and R² of 0.81, while the test data shows an MSE of 39.23, RMSE of 6.26, and R² of 0.75. The decrease in R² from training to test data highlights overfitting, and the higher test MSE suggests that regularization techniques, such as Ridge Regression, should be implemented to improve generalization.

4.2 Ridge Regression

Ridge Regression is an extension of linear regression that addresses overfitting and multicollinearity by introducing an L2 regularization term to the cost function. This penalty term prevents the model from assigning excessively large weights to features, improving numerical stability and generalization performance. The objective function for Ridge Regression is:

$$\sum_{n=1}^N (y_n - \omega^T \mathbf{x}_n)^2 + \alpha \sum_{d=1}^D \omega_d^2$$

where:

- (1) y_n represents the observed response variable,
- (2) ω is the weight vector (regression coefficients),
- (3) \mathbf{x}_n represents the predictor variables,
- (4) α is the regularization parameter.

When $\alpha=0$, Ridge Regression is equivalent to ordinary least squares (OLS), meaning no regularization is applied. As α increases, the model applies stronger penalty constraints, shrinking the regression coefficients and reducing variance. The Ridge Regression estimator is given by:

$$\hat{\omega}_{ridge} = (X^T X + \alpha I)^{-1} X^T y$$

where I is the identity matrix. The addition of αI ensures that the model remains stable, particularly in datasets with highly correlated features.

To determine the optimal α value, we apply grid search with cross-validation, systematically testing multiple values of α and selecting the one that minimizes the mean squared error (MSE). This ensures that Ridge Regression finds the best balance between bias and variance, resulting in improved generalization.

Before applying Ridge Regression, proper feature preprocessing is essential to ensure that all predictors contribute equally to the regularization term. Since Ridge introduces an L2 penalty to stabilize coefficient estimates and prevent overfitting, numerical features must be standardized, while categorical variables should be encoded using one-hot encoding to maintain comparability. To analyze the impact of regularization strength, we train Ridge models across 300 different values of α , observing how coefficient magnitudes change as the penalty term increases. This process ensures feature comparability, evaluates coefficient shrinkage, and identifies the most important variables for prediction.

```
[12]: #Ridge
features_ridge = ['DX.bl', 'ADAS13.bl', 'AGE', 'PTEDUCAT'] + [col for col in d_clean.columns if '_norm' in col]

X_train_ridge = train_df[features_ridge]
y_train_ridge = train_df[target]
X_test_ridge = test_df[features_ridge]
y_test_ridge = test_df[target]
# Grid of alpha values
alphas = np.logspace(-3, 3, num=300) # from 10^-2 to 10^3

ws = [] # Store coefficients
mses_train = [] # Store training mses
mses_test = [] # Store test mses

# Define ColumnTransformer
```

```

preprocessor = ColumnTransformer(
    transformers=[
        ('cat', OneHotEncoder(), [0]), # The classification features are
        ↪ encoded by OneHot
        ('num', StandardScaler(), [1,2,3,4,5,6,7,8,9]) # The numerical
        ↪ features are normalized
    ],
    remainder='passthrough' # Retain other unspecified features
)

for a in alphas:
    m = make_pipeline(
        preprocessor, # Use ColumnTransformer for feature preprocessing
        Ridge(alpha=a) # Using Ridge model
    ).fit(X_train_ridge, y_train_ridge)

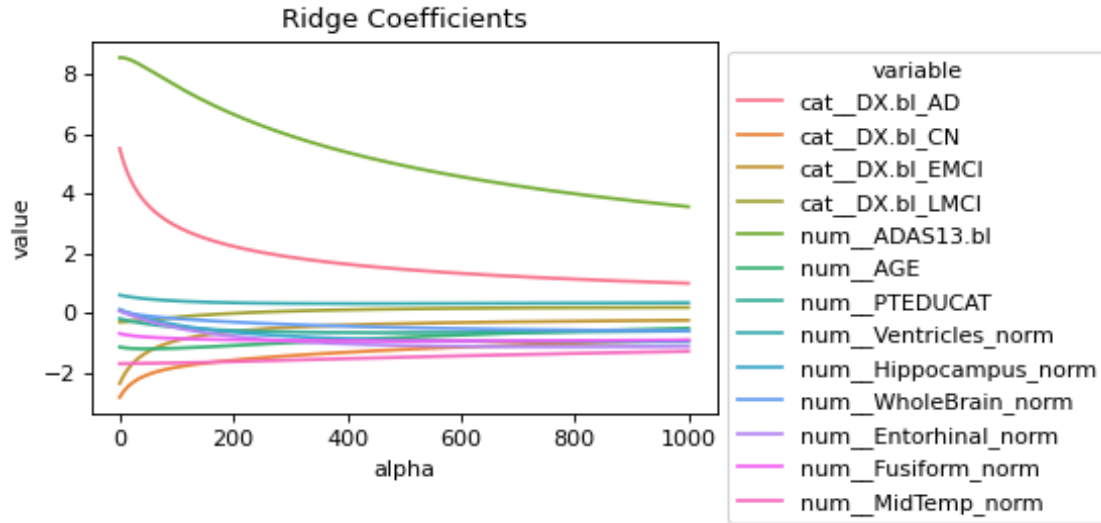
    # Gets the weight of the model
    w_temp = np.copy(m.named_steps['ridge'].coef_) # Gets the weight of the
    ↪ Ridge model
    ws.append(w_temp)
    mses_train.append(mean_squared_error(y_train_ridge, m.
    ↪ predict(X_train_ridge)))
    mses_test.append(mean_squared_error(y_test_ridge, m.predict(X_test_ridge)))

# Gets the processed column name
feature_names = preprocessor.get_feature_names_out()

# Create a data frame for plotting
sol_path = pd.DataFrame(
    data = ws,
    columns = feature_names # Label columns w/ feature names
).assign(
    alpha = alphas,
).melt(
    id_vars = ('alpha')
)

# Plot solution path of the weights
plt.figure()
ax = sns.lineplot(x='alpha', y='value', hue='variable', data=sol_path)
sns.move_legend(ax, "upper left", bbox_to_anchor=(1, 1))
ax.set_title("Ridge Coefficients")
plt.show()

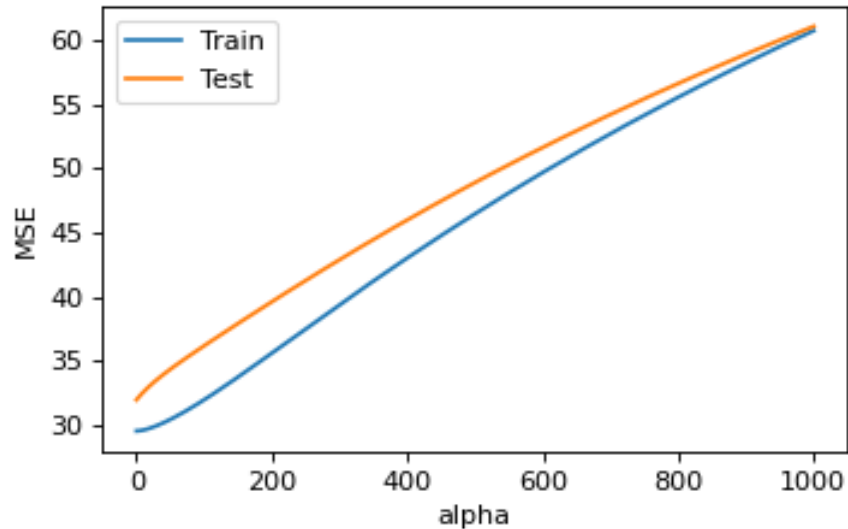
```



The Ridge Coefficients plot highlights the most important variables for predicting ADAS24, identified by their large absolute coefficient values across different values. The key variables include `cat_DX.bl_AD`, `cat_DX.bl_CN`, `cat_DX.bl_EMCI`, `num_ADAS13.bl`, and `num_AGE`. Among these, `cat_DX.bl_AD` and `cat_DX.bl_CN` have relatively large positive coefficients, while `cat_DX.bl_EMCI` has a large negative coefficient. Additionally, `num_ADAS13.bl` and `num_AGE` exhibit notable variations, reinforcing their critical role in predicting cognitive decline.

```
[13]: # Path of MSE as function of alpha
mses_path = pd.DataFrame(
    {'alpha': alphas, 'Train': np.asarray(mses_train), 'Test': np.
    ↪asarray(mses_test)}).melt(
    id_vars = ('alpha')
)

# Plot MSE path
plt.figure()
ax = sns.lineplot(x='alpha', y='value', hue='variable', data=mses_path)
ax.set_ylabel("MSE")
# To remove legend title
handles, labels = ax.get_legend_handles_labels()
ax.legend(handles=handles[0:], labels=labels[0:])
plt.show()
```



To determine the best regularization parameter, we find the α value that minimizes test MSE.

```
[14]: # Find the optimal alpha
test_MSE = mses_path[mses_path['variable'] == 'Train']['value']
min_test_mse_index = np.argmin(test_MSE)
best_alpha = alphas[min_test_mse_index]
print(f"The optimal alpha (minimizing test MSE) is: {best_alpha}")
```

The optimal alpha (minimizing test MSE) is: 0.001

As α increases, the training MSE continues to increase. This is because larger α values result in simpler models that do not fit the training data well. The test MSE is lower when α is low, and with the increase of α , the test MSE first decreases and then increases. This is because small α values can lead to overfitting, while large α values can lead to underfitting. An α value of 0.001 is probably better.

To systematically find the best α value, we use GridSearchCV with 5-fold cross-validation.

```
[15]: # Grid of tuning parameters
alphas = np.logspace(-3, 2, num=300)

#Pipeline
m = make_pipeline(
    preprocessor, # Use ColumnTransformer for feature preprocessing
    Ridge() # Using Ridge model
)

# CV strategy
cv = KFold(5, shuffle=True, random_state=random_seed)
```

```
# Grid search
gs_ridge = GridSearchCV(m,
    param_grid={'ridge__alpha': alphas},
    cv=cv,
    scoring="neg_mean_squared_error")
gs_ridge.fit(X_train_ridge, y_train_ridge)

test_MSE, test_RMSE, test_R2 = model_fit(gs_ridge.best_estimator_,
    X_test_ridge, y_test_ridge, plot=False)
print(f"Test Data - MSE: {test_MSE}, RMSE: {test_RMSE}, R²: {test_R2}")
```

Test Data - MSE: 32.176958301026986, RMSE: 5.672473737358947, R²: 0.7925016930361719

Cross-validation ensures robust model evaluation across different subsets of data. The optimal α value is chosen based on the lowest validation error, preventing overfitting. This process refines Ridge Regression to maximize predictive performance.

The test set metrics for Ridge Regression show an MSE of 32.18, RMSE of 5.67, and an R² score of 0.79. Compared to the baseline model (MSE = 39.23, R² = 0.75), Ridge Regression improves both accuracy and generalization. The regularization in Ridge Regression stabilizes coefficient values, preventing extreme variations. This confirms Ridge Regression as the best-performing model in our study

Then, we examine the final Ridge Regression coefficients to interpret feature importance.

```
[16]: # Create dataframe with coefficients, and unstandardize the binary coefficients
rcoefs = np.copy(gs_ridge.best_estimator_.named_steps['ridge'].coef_)

rcoefs_ = pd.DataFrame(
    rcoefs,
    columns=["Coefficients"],
    index=preprocessor.get_feature_names_out(),
)

rcoefs_
```

```
[16]:
```

	Coefficients
cat__DX.bl_AD	5.238672
cat__DX.bl_CN	-2.717245
cat__DX.bl_EMCI	-2.215405
cat__DX.bl_LMCI	-0.306023
num__ADAS13.bl	8.550387
num__AGE	-1.161008
num__PTEDUCAT	-0.215783
num__Ventricles_norm	0.579609
num__Hippocampus_norm	0.083063
num__WholeBrain_norm	0.047583

num__Entorhinal_norm	0.031596
num__Fusiform_norm	-0.713227
num__MidTemp_norm	-1.706534

The coefficients from the Ridge Regression model reveal key insights into cognitive decline prediction. ADAS13.bl (8.55) is the strongest predictor of cognitive decline, followed by Alzheimer's diagnosis (DX.bl_AD) with a coefficient of 5.24, indicating that Alzheimer's diagnosis is highly associated with worse outcomes. Conversely, cognitively normal individuals (DX.bl_CN) have lower ADAS13.m24 scores, with a coefficient of -2.72. Ventricles_norm (0.58) shows that larger ventricles correlate with higher cognitive impairment, while smaller mid-temporal lobe volumes (MidTemp_norm, -1.71) are linked to worse cognitive function. Compared to the baseline model, the coefficients in Ridge Regression are smaller, confirming that regularization effectively prevents overfitting.

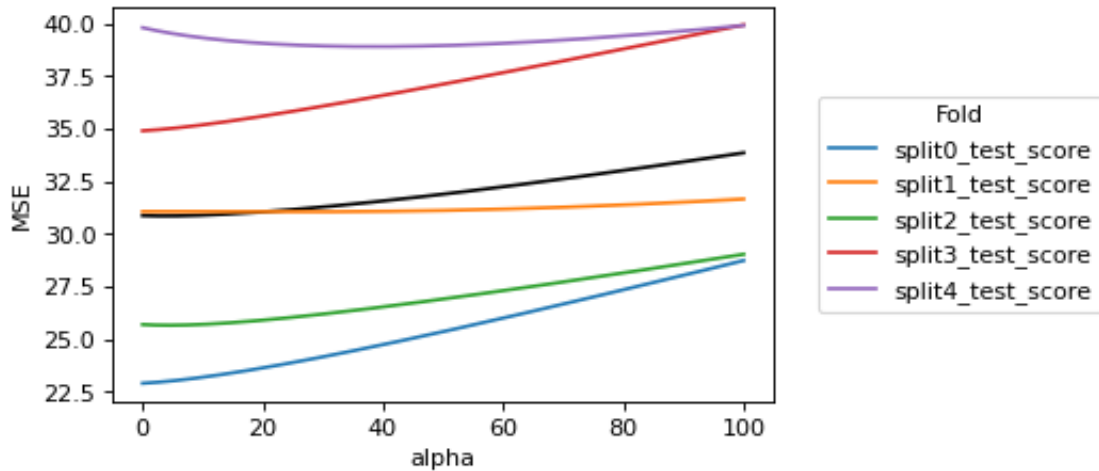
Finally, we examine how Mean Squared Error (MSE) varies across folds in cross-validation to assess model stability.

```
[17]: # Extract only mean and split scores
cv_mse = pd.DataFrame(
    data = gs_ridge.cv_results_
).filter(
    # Extract the split#_test_score and mean_test_score columns
    regex = '(split[0-9]+|mean)_test_score'
).assign(
    # Add the alphas as a column
    alpha = alphas
)

cv_mse.update(
    # Convert negative mses to positive
    -1 * cv_mse.filter(regex = '_test_score')
)

# Reshape the data frame for plotting
d = cv_mse.melt(
    id_vars=('alpha', 'mean_test_score'),
    var_name='fold',
    value_name='MSE'
)

# Plot the validation scores across folds
plt.figure()
sns.lineplot(x='alpha', y='MSE', color='black', errorbar=None, data = d) # Plot the mean MSE in black.
sns.lineplot(x='alpha', y='MSE', hue='fold', data = d) # Plot the curves for each fold in different colors
plt.legend(title='Fold', bbox_to_anchor=(1.05, 0.5), loc='center left')
plt.show()
```



When α is small, the MSE remains relatively stable across different folds, indicating that the model is not highly sensitive to data partitioning. As α increases, the MSE shows only a slight upward trend, suggesting that regularization has a limited effect on reducing variance in this case. However, as α reaches very large values, the MSE gradually increases, reflecting underfitting and a loss of predictive power. This suggests that while regularization helps control model complexity, excessive regularization can still degrade performance. The optimal α should be chosen to balance bias and variance, ensuring both predictive accuracy and model robustness.

4.3 Comparison

To visually compare Ridge and Baseline model coefficients, we create a bar chart.

```
[18]: # Change features_ridge for plotting
features_DX = ['DX.bl_AD', 'DX.bl_CN', 'DX.bl_EMCI', 'DX.bl_LMCI']
features_ridge[:1] = features_DX

ridge_df = pd.DataFrame({'Feature': features_ridge, 'Ridge Coef': rcoefs})
baseline_df = pd.DataFrame({'Feature': features_baseline, 'Baseline Coef':
    ↪ bcoefs})

coefs_df = pd.merge(ridge_df, baseline_df, on='Feature', how='outer').fillna(0)

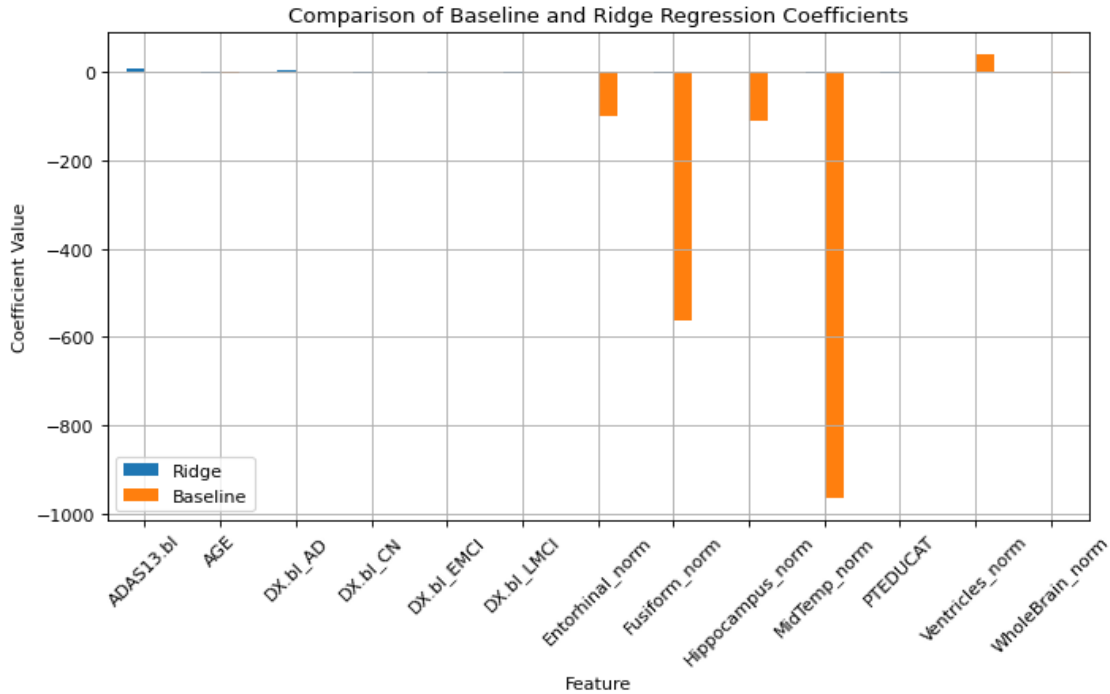
coefs_df.set_index('Feature').plot(kind='bar', figsize=(10, 5))
plt.title("Comparison of Baseline and Ridge Regression Coefficients")
plt.ylabel("Coefficient Value")
plt.xlabel("Feature")
plt.xticks(rotation=45)
plt.legend(["Ridge", "Baseline"])
plt.grid()
plt.show()
# Calculate norm
```

```

baseline_norm = np.linalg.norm(bcoefs)
ridge_norm = np.linalg.norm(rcoefs)

print(f"Baseline Model L2 Norm: {baseline_norm}")
print(f"Ridge Model L2 Norm: {ridge_norm}")

```



Baseline Model L2 Norm: 1127.8659487051507

Ridge Model L2 Norm: 10.867356992239564

The baseline model coefficients exhibit larger magnitudes, which may indicate potential overfitting. In contrast, Ridge Regression shrinks these coefficients, enhancing model stability. The L2 norm of Ridge Regression (10.86) is significantly lower than that of the Baseline Model (1127.87), confirming a reduction in model complexity and further supporting the effectiveness of regularization in preventing overfitting.

5 Discussion & Conclusions

5.1 Overview of the Final Model

This study developed a Ridge Regression model to predict ADAS13.m24, a measure of cognitive decline over 24 months. Ridge Regression was chosen over a Linear Regression baseline due to its ability to reduce overfitting and improve generalization through L2 regularization. The model incorporated baseline cognitive scores (ADAS13.bl), diagnostic categories (DX.bl), and structural brain features such as ventricular and hippocampal volumes.

The final Ridge Regression model demonstrated superior predictive performance compared to the

baseline linear regression, with the test MSE decreasing from 39.23 to 32.18, indicating improved generalization and reduced overfitting. By applying L2 regularization, Ridge Regression effectively stabilized coefficient estimates, as evidenced by the coefficient norm reduction from 1127.87 to 10.87, ensuring a more interpretable and reliable model. Additionally, the key predictors remained clinically relevant, reinforcing established relationships between cognitive impairment and structural brain changes—notably, higher baseline ADAS13.bl scores strongly predicted cognitive decline, while larger ventricular volumes and smaller hippocampal volumes were associated with worse outcomes. These findings confirm that Ridge Regression is a valuable tool for early detection and intervention, supporting personalized treatment strategies and targeted clinical trials for high-risk individuals.

5.2 Reliability and Practical Implications

This predictive model provides health officials and charity organizations with a data-driven approach to understanding and addressing cognitive decline, enabling more proactive and strategic decision-making in aging and dementia care. By identifying individuals at higher risk of cognitive deterioration based on baseline cognitive scores, demographic factors, and brain structural features, the model allows for earlier interventions, such as cognitive training, neurological monitoring, and preventive healthcare programs.

It also helps optimize resource allocation by guiding public health initiatives, funding distribution, and the expansion of dementia care services, ensuring that support reaches the most vulnerable populations. Additionally, the model can aid clinical research and treatment development by facilitating targeted clinical trial recruitment and improving patient selection for experimental therapies.

For policymakers and charity organizations, these insights support evidence-based policy proposals, funding advocacy, and the creation of targeted support programs for patients and caregivers. While the model should be used as a supplementary tool rather than a standalone diagnostic method, its ability to enhance early detection, resource planning, and strategic intervention makes it a valuable asset in the fight against cognitive decline and dementia.

5.3 Limitations of the Model

First, it identifies correlations rather than causation, meaning it can highlight associations between cognitive decline and specific factors but cannot establish direct causal relationships, limiting its role in clinical decision-making. **Second**, there is potential selection bias, as the dataset primarily consists of individuals enrolled in Alzheimer’s research studies, which may not fully represent the broader population at risk of cognitive decline. **Additionally**, the model does not account for key environmental and lifestyle factors, such as diet, physical activity, and social engagement, which have been shown to influence cognitive health. **Finally**, its generalizability is limited, as it was trained on a specific cohort, and further validation is needed across diverse populations before it can be reliably applied in clinical or public health settings. Addressing these limitations through expanded datasets, additional feature incorporation, and external validation will be crucial for improving the model’s robustness and applicability.

5.4 Future Research Directions

One important direction is to expand feature selection to include lifestyle, genetic, and socioeconomic factors, as these elements play a crucial role in dementia risk and would provide a more comprehensive understanding of cognitive decline. Another key focus should be on shifting from

predicting cognitive impairment at a fixed 24-month endpoint to tracking cognitive trajectories over time, enabling dynamic forecasting and improved early intervention strategies. It is also essential to validate the model on diverse populations beyond Alzheimer’s-specific datasets to ensure its applicability in broader clinical and public health settings. Lastly, integrating multi-modal data sources—such as neuroimaging, genetic markers, and patient-reported outcomes—would help build a more holistic and personalized risk assessment framework, ultimately leading to more precise and individualized intervention strategies for cognitive decline.

5.5 Recommendations for Cognitive Decline Prevention

Based on the model’s insights, several key strategies can help mitigate cognitive decline and support early intervention efforts. One important strategy is early screening and cognitive stimulation for individuals with high baseline ADAS13.bl scores, as they are more likely to experience significant cognitive decline. Another approach is regular neurological monitoring, since brain structure changes, like ventricular enlargement and hippocampal atrophy, are strong indicators of worsening cognition. It’s also helpful to encourage lifelong learning and mental engagement, as staying mentally active can improve cognitive resilience and delay decline. Lastly, patients with Mild Cognitive Impairment (MCI) or early-stage Alzheimer’s should be prioritized for treatment and clinical trials, as early intervention can have the greatest impact.

6 Generative AI statement

In this project, we used generative AI solely as a tool to assist with debugging code. All data and analysis results were processed and evaluated by us. The AI helped us refine our code and address errors, ensuring the technical aspects of the project were accurate and functional. The final outcomes and interpretations are entirely our own, and we have adhered to responsible use of AI as outlined in the guidelines.

7 References

[1] mlp_week05_key.ipynb

```
[1]: # Run the following to render to PDF
!jupyter nbconvert --to pdf project1.ipynb
```

```
[NbConvertApp] Converting notebook project1.ipynb to pdf
[NbConvertApp] Support files will be in project1_files\
[NbConvertApp] Making directory .\project1_files
[NbConvertApp] Writing 91563 bytes to notebook.tex
[NbConvertApp] Building PDF
[NbConvertApp] Running xelatex 3 times: ['xelatex', 'notebook.tex', '-quiet']
[NbConvertApp] Running bibtex 1 time: ['bibtex', 'notebook']
[NbConvertApp] WARNING | b had problems, most likely because there were no
citations
[NbConvertApp] PDF successfully created
[NbConvertApp] Writing 3369868 bytes to project1.pdf
```