

Predicting Alzheimer's Disease using Socioeconomic and MRI Imaging Data from Demented and Nondemented Adults

Applying Random Forest machine learning algorithm to classify
Alzheimer's patients

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Introduction

The **Open Access Series of Imaging Studies (OASIS)** is a project aimed at making neuroimaging data sets of the brain freely available to the scientific community. This freely available neuroimaging longitudinal data consists of **150 subjects aged 60 to 96**. Each subject was scanned on two or more visits, separated by at least one year for a total of 373 imaging sessions on T1-weighted MRI scanner. 72 of the subjects were characterized as nondemented throughout the study. 64 of the subjects were characterized as demented at the time of their initial visits and remained so for subsequent scans. Another 14 subjects were characterized as nondemented at the time of their initial visit and were subsequently characterized as demented at a later visit.

The data contains the following attributes:

Column name	Information
Subject.ID	Unique ID of the patient
MRI.ID	Unique Id generated after conducting MRI on patient (This information combines subject ID with visit number, therefore it was removed from the analysis)
Group	Includes three subject categories. i) Nondemented (Normal), ii) Demented (Patients with mild to severe dementia), and iii) Converted (Previously Normal but developed dementia later)
Visit	Number of follow-up visit for each MRI scan
MR.Delay	The number of day between two medical visits
M.F	Gender (The column was renamed to gender for better readability)

Column name	Information
Hand	Handedness (All subjects are right-handed so the column was removed from the analysis)
Age	Age in years
EDUC	Years of education (This column was renamed as education)
SES	Socioeconomic status assessed by the Hollingshead Index of Social Position (1 = highest status to 5 = lowest status)
MMSE	Mini-Mental State Examination score (0 = worst to 30 = best)
CDR	[Clinical Dementia Rating](https://knightadrc.wustl.edu/professionals-clinicians/cdr-dementia-staging-instrument/#::~text=The%20Clinical%20Dementia%20Rating%20(CDR,Affairs%2C%) (0 = no dementia, 0.5 = very mild AD, 1 = mild AD, 2 = moderate AD)
eTIV	Estimated total intracranial volume (mm ³)
nWBV	Normalized whole-brain volume
ASF	Atlas scaling factor (unitless). Calculated by transforming native-space brain and skull to the atlas target

Loading and Understanding data

```
df <- read_csv(here("oasis_longitudinal.csv")) |>
  clean_names() |>
  select(-c(hand, mri_id)) |>
  rename(gender = m_f)

long <- data.table(df)
head(long)
```

```
      subject_id      group visit mr_delay gender age educ ses mmse cdr e_tiv
1:  OAS2_0001 Nondemented    1         0      M  87  14   2   27 0.0  1987
2:  OAS2_0001 Nondemented    2        457      M  88  14   2   30 0.0  2004
3:  OAS2_0002   Demented    1         0      M  75  12  NA   23 0.5  1678
4:  OAS2_0002   Demented    2        560      M  76  12  NA   28 0.5  1738
5:  OAS2_0002   Demented    3       1895      M  80  12  NA   22 0.5  1698
6:  OAS2_0004 Nondemented    1         0      F  88  18   3   28 0.0  1215
      n_wbv  asf
1: 0.696 0.883
```

```
2: 0.681 0.876
3: 0.736 1.046
4: 0.713 1.010
5: 0.701 1.034
6: 0.710 1.444
```

Data Exploration and Cleaning

```
data_summary <- describe(df)
data_summary
```

df

```
13 Variables      373 Observations
```

subject_id

```
  n missing distinct
373      0      150
```

```
lowest : OAS2_0001 OAS2_0002 OAS2_0004 OAS2_0005 OAS2_0007
```

```
highest: OAS2_0182 OAS2_0183 OAS2_0184 OAS2_0185 OAS2_0186
```

group

```
  n missing distinct
373      0         3
```

```
Value      Converted      Demented Nondemented
Frequency          37          146          190
Proportion      0.099      0.391      0.509
```

visit

```
  n missing distinct      Info      Mean      Gmd
373      0         5      0.874      1.882      0.9552
```

```
Value      1      2      3      4      5
Frequency    150    144    58    15     6
Proportion 0.402 0.386 0.155 0.040 0.016
```

For the frequency table, variable is rounded to the nearest 0

mr_delay

```
  n missing distinct      Info      Mean      Gmd      .05      .10
373      0      201      0.935      595.1      682.6        0        0
```

.25	.50	.75	.90	.95
0	552	873	1561	1828

lowest : 0 182 212 248 352, highest: 2386 2400 2508 2517 2639

gender

n	missing	distinct
373	0	2

Value	F	M
Frequency	213	160
Proportion	0.571	0.429

age

n	missing	distinct	Info	Mean	Gmd	.05	.10
373	0	39	0.998	77.01	8.703	65.0	67.2
.25	.50	.75	.90	.95			
71.0	77.0	82.0	87.8	90.0			

lowest : 60 61 62 63 64, highest: 94 95 96 97 98

educ

n	missing	distinct	Info	Mean	Gmd	.05	.10
373	0	12	0.962	14.6	3.183	11	12
.25	.50	.75	.90	.95			
12	15	16	18	18			

Value	6	8	11	12	13	14	15	16	17	18	20
Frequency	3	9	11	103	27	33	17	81	9	64	13
Proportion	0.008	0.024	0.029	0.276	0.072	0.088	0.046	0.217	0.024	0.172	0.035

Value	23
Frequency	3
Proportion	0.008

For the frequency table, variable is rounded to the nearest 0

ses

n	missing	distinct	Info	Mean	Gmd
354	19	5	0.938	2.46	1.266

Value	1	2	3	4	5
Frequency	88	103	82	74	7
Proportion	0.249	0.291	0.232	0.209	0.020

For the frequency table, variable is rounded to the nearest 0

```

-----
mmse
      n  missing distinct      Info      Mean      Gmd      .05      .10
    371      2      18    0.954    27.34    3.417      20      22
    .25    .50    .75    .90    .95
    27     29     30     30     30

Value      4      7     15     16     17     18     19     20     21     22     23
Frequency    1      1      2      3      5      2      3      7     11      7     11
Proportion 0.003 0.003 0.005 0.008 0.013 0.005 0.008 0.019 0.030 0.019 0.030

Value      24     25     26     27     28     29     30
Frequency    4     12     20     32     45     91    114
Proportion 0.011 0.032 0.054 0.086 0.121 0.245 0.307

```

For the frequency table, variable is rounded to the nearest 0

```

-----
cdr
      n  missing distinct      Info      Mean      Gmd
    373      0         4    0.794    0.2909    0.3683

Value      0.0     0.5     1.0     2.0
Frequency   206    123     41      3
Proportion 0.552 0.330 0.110 0.008

```

For the frequency table, variable is rounded to the nearest 0

```

-----
e_tiv
      n  missing distinct      Info      Mean      Gmd      .05      .10
    373      0     286      1    1488    197.7    1234    1289
    .25    .50    .75    .90    .95
   1357   1470   1597   1731   1817

```

lowest : 1106 1123 1143 1151 1154, highest: 1928 1931 1957 1987 2004

```

-----
n_wbv
      n  missing distinct      Info      Mean      Gmd      .05      .10
    373      0     136      1    0.7296    0.04232    0.6746    0.6822
    .25    .50    .75    .90    .95
    0.7000  0.7290  0.7560  0.7796  0.7940

```

lowest : 0.644 0.646 0.652 0.657 0.66 , highest: 0.817 0.819 0.822 0.827 0.837

```

-----
asf
      n  missing distinct      Info      Mean      Gmd      .05      .10
    373      0     265      1    1.195    0.1563    0.9656    1.0134

```

```

      .25      .50      .75      .90      .95
1.0990  1.1940  1.2930  1.3618  1.4222

lowest : 0.876 0.883 0.897 0.909 0.91 , highest: 1.521 1.525 1.535 1.563 1.587
-----

```

Handling missing values in the data

```

# Get a summary of missing (NA) values in the data
colSums(is.na(df))

```

```

subject_id    group    visit  mr_delay    gender    age    educ
      0         0         0         0         0         0         0
      ses      mmse      cdr      e_tiv      n_wbv      asf
      19         2         0         0         0         0

```

```

NA_rows <- df[!complete.cases(df), ]

unique(NA_rows$subject_id)

```

```

[1] "OAS2_0002" "OAS2_0007" "OAS2_0063" "OAS2_0099" "OAS2_0114" "OAS2_0160"
[7] "OAS2_0181" "OAS2_0182"

```

Out of 150 subject data, 8 subject data has NA values in the ses (socioeconomic status), mmse (mini mental examination score) columns. Because there are enough data points in the analysis, rows with missing ses and mmse values were removed from the analysis **instead of imputing mean or median values**. This strengthens data modeling without diminishing statistical power.

```

df_new <- df[complete.cases(df), ]
colSums(is.na(df_new)) # there are no NA values

```

```

subject_id    group    visit  mr_delay    gender    age    educ
      0         0         0         0         0         0         0
      ses      mmse      cdr      e_tiv      n_wbv      asf
      0         0         0         0         0         0

```

```

df_new$gender <- as.factor(df_new$gender)
df_new$group <- as.factor(df_new$group)
df_new$visit <- as.factor(df_new$visit)
df_new$ses <- as.factor(df_new$ses)

```

```
df_new$cdm <- as.factor(df_new$cdm)
```

Perform Univariate and Bivariate Exploratory Data Analysis

There are two objectives for performing exploratory data analysis. First is to explore data distribution and understand if specific variables are under- or over-represented in the dataset. Second objective is to determine relationship between variables that will help make assumptions in the modeling step.

```
P1 <- df_new |>
  mutate(group = fct_relevel(group, c("Demented", "Nondemented", "Converted"))) |>
  ggplot(aes(x = gender, fill = gender)) +
  geom_bar(alpha = 0.7, width = 0.9) +
  facet_wrap(~group) +
  scale_y_continuous(limits = c(0, 150),
                     breaks = seq(0, 150, 25)) +
  scale_x_discrete(labels = c("Female", "Male")) +
  coord_cartesian(expand = FALSE,
                  clip = "off") +
  labs(x = "Gender",
       y = "Number of Individuals",
       title = "Men are more likely to have dementia than women") +
  theme_classic() +
  theme(strip.background = element_blank(),
        strip.text = element_text(size = 12),
        axis.text = element_text(size = 10),
        axis.line = element_blank(),
        axis.ticks = element_blank(),
        panel.grid.major.y = element_line(color = "grey90", size = 0.5),
        panel.background = element_rect(fill = NA, color = "grey90"),
        legend.position = "none")

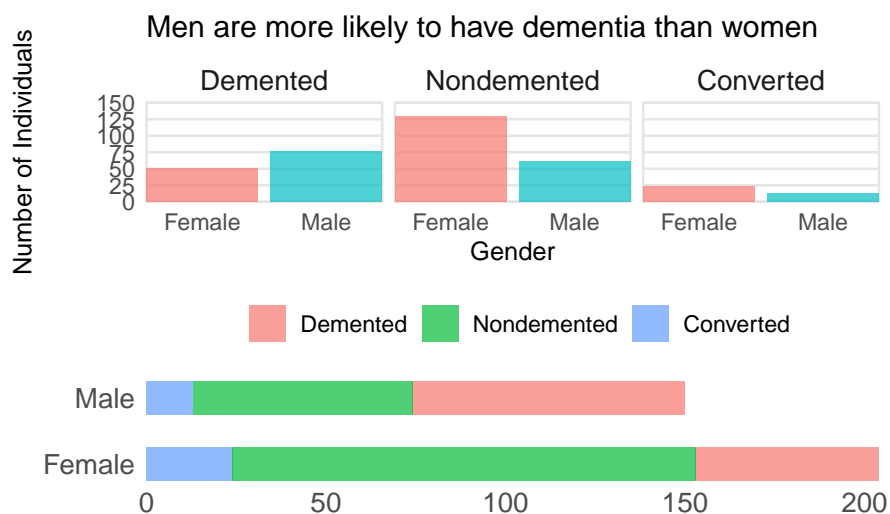
P2 <- df_new |>
  group_by(gender, group) |>
  summarise(count = n()) |>
  mutate(prop = count / sum(count)) |>
  mutate(group = fct_relevel(group, c("Demented", "Nondemented", "Converted"))) |>
  ungroup() |>
  ggplot(aes(x = count, y = gender, fill = group)) +
  geom_col(width = 0.5, alpha = 0.7) +
  coord_cartesian(expand = FALSE) +
  scale_y_discrete(labels = c("Female", "Male")) +
```

```

labs(x = "",
     y = "",
     fill = "") +
theme_classic() +
theme(axis.line = element_blank(),
      axis.ticks = element_blank(),
      legend.position = "top",
      axis.text = element_text(size = 12),
      legend.text = element_text(size = 10))

```

P1/P2



```

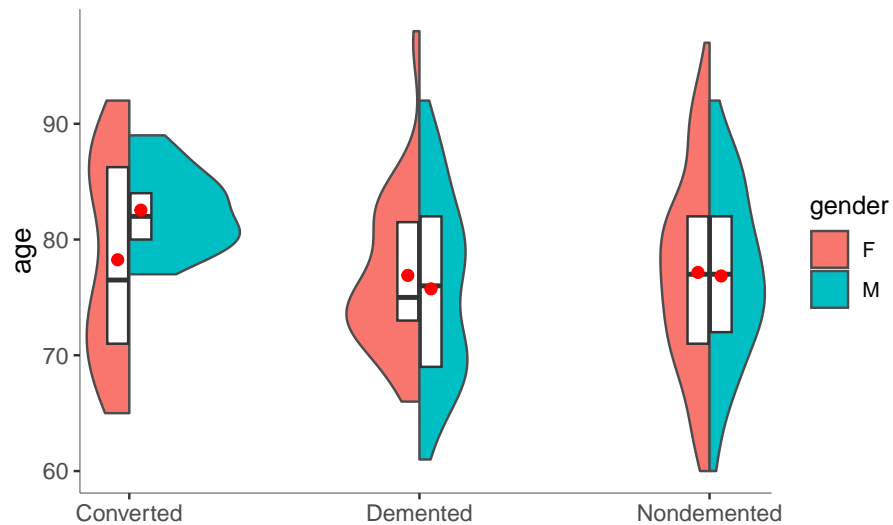
df_new |>
  select(group, gender, age) |>
  ggcraviola(craviola.width = 0.1,
             lines.col = "grey30",
             bins.quantiles = seq(0.25, 0.75, 0.25)) +
  scale_fill_manual(values = c("M" = "#00BFC4",
                              "F" = "#F8766D")) +
  labs(title = "There is no obvious relationship between age/sex and dementia diagnosis")
theme_classic() +
theme(axis.title.x = element_blank(),
      axis.line = element_line(size = 0.1, color = "grey30"),
      axis.text = element_text(size = 10),

```



```
axis.title = element_text(size = 12))
```

There is no obvious relationship between age/sex and dementia



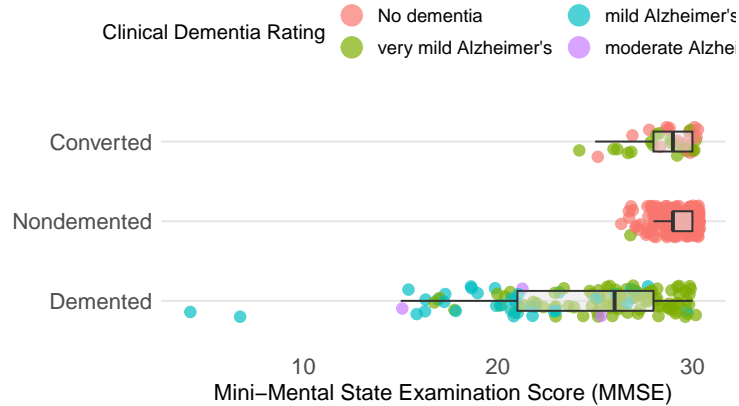
```
df_new |>
  select(group, mmse, cdr) |>
  mutate(group = fct_relevel(group, c("Demented", "Nondemented", "Converted"))) |>
  ggplot(aes(x = group, y = mmse)) +
  geom_point(aes(color = cdr), alpha = 0.7, size = 2.5, position = position_jitter(width = 0.5)) +
  geom_boxplot(fill = "grey90", width = 0.25, outlier.shape = NA, alpha = 0.5) +
  scale_color_discrete(labels = c("No dementia", "very mild Alzheimer's", "mild Alzheimer's")) +
  coord_flip() +
  labs(x = "",
       y = "Mini-Mental State Examination Score (MMSE)",
       title = "Nondemented individuals have higher MMSE score compared to Dementia patients",
       color = "Clinical Dementia Rating") +
  theme_classic() +
  theme(plot.title = element_text(size = 12),
        plot.title.position = "plot",
        axis.title.y = element_blank(),
        axis.ticks = element_blank(),
        axis.line = element_blank(),
        axis.text = element_text(size = 12),
        axis.title.x = element_text(size = 12),
        panel.grid.major.y = element_line(color = "grey90", linewidth = 0.5),
```

```

    legend.position = "top",
    legend.text = element_text(size = 10)) +
guides(color = guide_legend(ncol = 2, override.aes = list(size = 5)))

```

Nondemented individuals have higher MMSE score compared to Dementi



```

P3 <- df_new |>
  select(group, educ, cdr) |>
  mutate(group = fct_relevel(group, c("Demented", "Nondemented", "Converted"))) |>
  ggplot(aes(x = group, y = educ)) +
  geom_point(aes(color = cdr), alpha = 0.7, size = 2, position = position_jitter(width = 0.5)) +
  geom_boxplot(fill = "grey90", width = 0.25, outlier.shape = NA, alpha = 0.5) +
  scale_color_discrete(labels = c("No dementia", "very mild Alzheimer's", "mild Alzheimer's", "moderate Alzheimer's")) +
  coord_flip() +
  labs(x = "",
       y = "Education (in years)",
       color = "Clinical Dementia Rating") +
  theme_classic() +
  theme(axis.title.y = element_blank(),
        axis.ticks = element_blank(),
        axis.line = element_blank(),
        axis.text = element_text(size = 8),
        axis.title.x = element_text(size = 10),
        panel.grid.major.y = element_line(color = "grey90", linewidth = 0.5),
        legend.position = "top",
        legend.text = element_text(size = 8),
        legend.title = element_text(size = 8)) +
  guides(color = guide_legend(ncol = 2, override.aes = list(size = 5)))

```

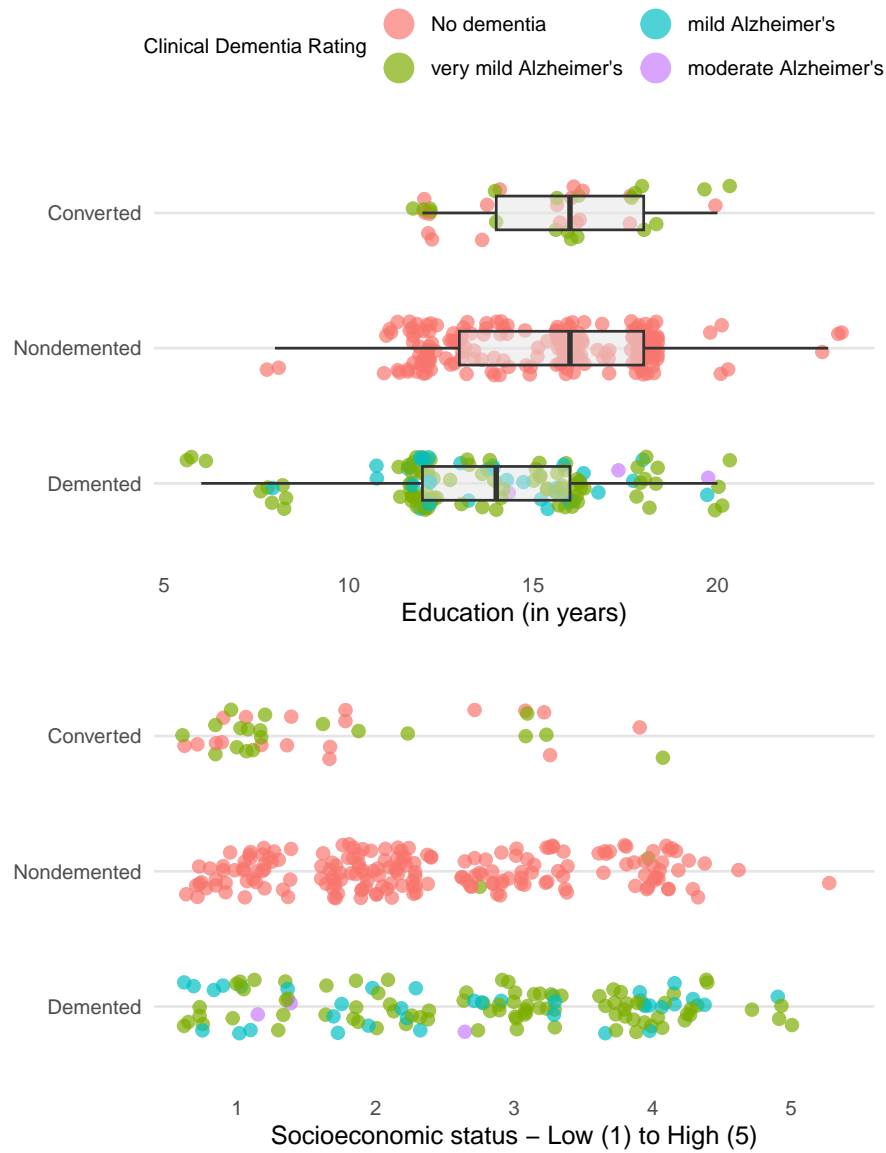
```

P4 <- df_new |>
  select(group, ses, cdr) |>
  mutate(group = fct_relevel(group, c("Demented", "Nondemented", "Converted"))) |>
  ggplot(aes(x = group, y = ses)) +
  geom_point(aes(color = cdr), alpha = 0.7, size = 2, position = position_jitter(width =
  scale_color_discrete(labels = c("No dementia", "very mild Alzheimer's", "mild Alzheimer
  coord_flip() +
  labs(x = "",
       y = "Socioeconomic status - Low (1) to High (5)",
       color = "Clinical Dementia Rating") +
  theme_classic() +
  theme(axis.title.y = element_blank(),
        axis.ticks = element_blank(),
        axis.line = element_blank(),
        axis.text = element_text(size = 8),
        axis.title.x = element_text(size = 10),
        panel.grid.major.y = element_line(color = "grey90", linewidth = 0.5),
        legend.position = "top",
        legend.text = element_text(size = 8),
        legend.title = element_text(size = 8)) +
  guides(color = guide_legend(ncol = 2, override.aes = list(size = 5)))

P3 / P4 +
  plot_annotation(title = "Education and Socioeconomic status has no impact on \nClinical
                 theme = theme(legend.position = "top",
                               plot.title = element_text(size = 10))) +
  plot_layout(guides = "collect")

```

Education and Socioeconomic status has no impact on
Clinical Dementia Rating



```
# shapiro.test(df_new$e_tiv) # data not normally distributed
# shapiro.test(df_new$n_wbv) # data normally distributed
```

```

stat.test <- df_new |>
  dunn_test(e_tiv ~ group)

stat.test1 <- df_new |>
  tukey_hsd(n_wbv ~ group) |>
  add_xy_position(x = "group", dodge = 0.8)

P5 <- df_new |>
  select(group, e_tiv) |>
  mutate(group = fct_relevel(group, c("Demented", "Nondemented", "Converted"))) |>
  ggplot(aes(x = group, y = e_tiv, fill = group)) +
  geom_point(color = "grey30", alpha = 0.5, size = 2, position = position_jitter(width =
  geom_boxplot(width = 0.25, outlier.shape = NA, alpha = 0.5) +
  scale_y_continuous(limits = c(1000,2250),
                      breaks = seq(1000, 2250,250)) +
  labs(y = "Estimated total intracranial volume") +
  theme_classic() +
  theme(axis.title.x = element_blank(),
        axis.ticks = element_blank(),
        axis.line = element_blank(),
        axis.text = element_text(size = 12),
        axis.title.y = element_text(size = 12),
        panel.grid.major.y = element_line(color = "grey90", linewidth = 0.5),
        legend.position = "none") +
  stat_kruskal_test(group.by = "x.var", label = "p = {p.signif}")

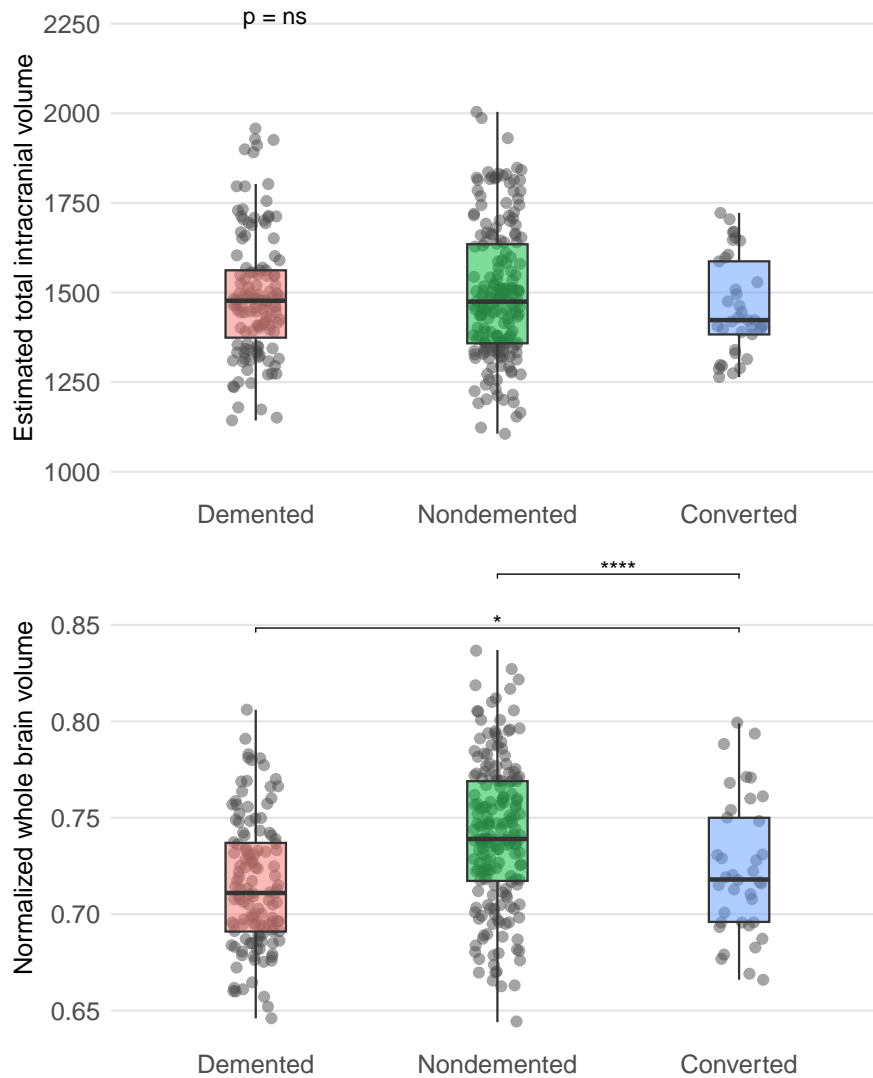
P6 <- df_new |>
  select(group, n_wbv) |>
  mutate(group = fct_relevel(group, c("Demented", "Nondemented", "Converted"))) |>
  ggplot(aes(x = group, y = n_wbv)) +
  geom_point(color = "grey30", alpha = 0.5, size = 2, position = position_jitter(width =
  geom_boxplot(aes(fill = group), width = 0.25, outlier.shape = NA, alpha = 0.5) +
  labs(y = "Normalized whole brain volume") +
  theme_classic() +
  theme(axis.title.x = element_blank(),
        axis.ticks = element_blank(),
        axis.line = element_blank(),
        axis.text = element_text(size = 12),
        axis.title.y = element_text(size = 12),
        panel.grid.major.y = element_line(color = "grey90", linewidth = 0.5),
        legend.position = "none") +
  stat_pvalue_manual(stat.test1, label = "p.adj.signif", hide.ns = TRUE, tip.length = 0.0

P5 / P6 +

```

```
plot_annotation(title = "There is no difference in estimated intracranial volume and
```

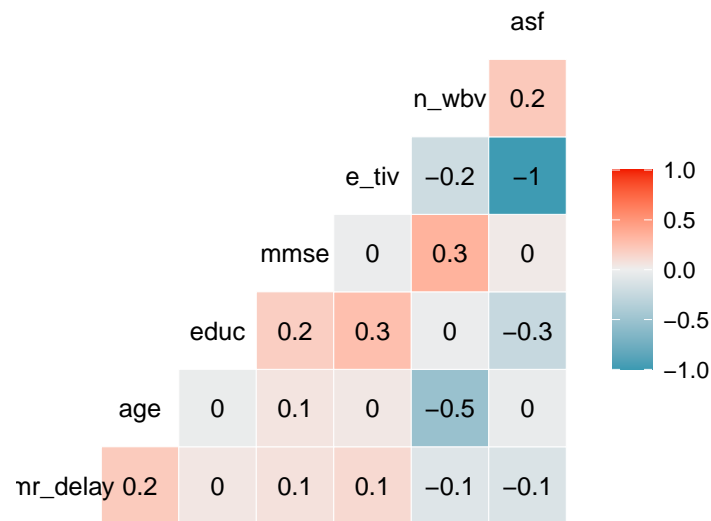
There is no difference in estimated intracranial volume and nomrmalized whole brain volume between dementia patients and non-dementia individuals



Second, we measure correlation between variables. The correlation matrix suggests weak or no correlation between numericals variables.

*There is a strong negative correlation between estimated total intracranial volume (eTIV) and Atlas Scaling Factor (ASF). The **ASF** is a one-parameter scaling factor that allows for comparison of the estimated total intracranial volume (**eTIV**) based on differences in human brain volume, therefore, the correlation is expected and not meaningful for the analysis. **I will drop ASF from the modeling to avoid multicollinearity.**

```
ggcorr(df_new,
       label = TRUE,
       legend.size = 10)
```



Conclusion I

Based on the exploratory data analysis, we derive the following conclusions.

1. Men are more likely to have dementia.
2. There is no obvious relationship between age/sex and dementia diagnosis.
3. Non-demented individuals have higher MMSE score compared to Dementia patients.
4. Education and Socioeconomic status has no impact on Clinical Dementia Rating.
5. There is no difference in estimated intracranial volume and normalized whole brain volume between dementia patients and non-dementia individuals.

6. There is no correlation between MMSE score and estimated intracranial volume/normalized whole brain volume

Random Forest Classification Model

Based on the given data, can we predict dementia and Alzheimer's disease? This is a classification problem. We will employ decision tree which is a supervised learning algorithm to predict Alzheimer's disease based on socioeconomic factors.

```
model_data <- df_new |>
  select(-asf)

# partition data
set.seed(500)
ind <- sample(2, nrow(model_data), replace = T, prob = c(0.8, 0.2))
train <- df_new[ind == 1, ]
test <- df_new[ind == 2, ]

rf <- randomForest(group ~.,
                    data=train,
                    proximity=TRUE,
                    importance=TRUE,
                    predicted = TRUE)

print(rf)
```

Call:

```
randomForest(formula = group ~ ., data = train, proximity = TRUE, importance = TRUE, p
              Type of random forest: classification
              Number of trees: 500
```

No. of variables tried at each split: 3

OOB estimate of error rate: 10.22%

Confusion matrix:

	Converted	Demented	Nondemented	class.error
Converted	3	11	14	0.892857143
Demented	1	105	0	0.009433962
Nondemented	0	2	138	0.014285714

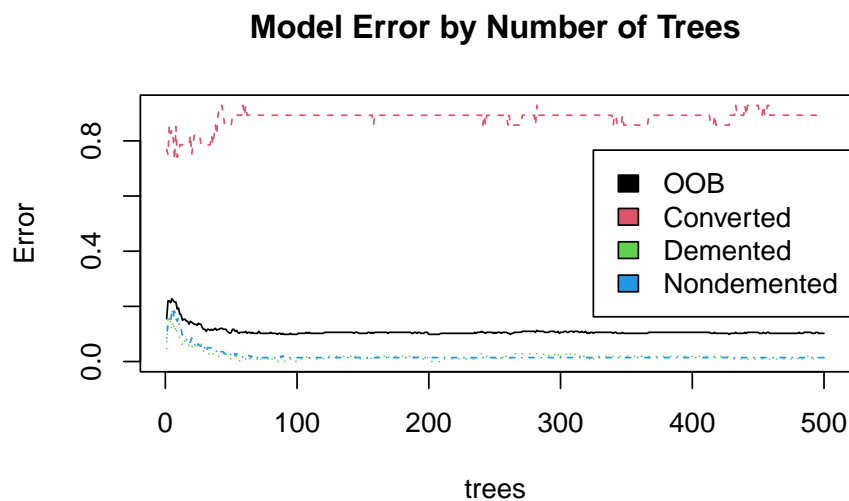
Model cross-validation on test data


```
test_pred <- predict(rf,
                     newdata = test)

accuracy <- mean(test_pred == test$group)*100
cat('Accuracy on testing data: ', round(accuracy, 2), '%', sep='')
```

Accuracy on testing data: 92.5%

```
plot(rf, main = "Model Error by Number of Trees")
legend(x = "right",
       legend = colnames(rf$err.rate),
       fill = 1:ncol(rf$err.rate))
```



```
pred <- as.data.frame(predict(rf))

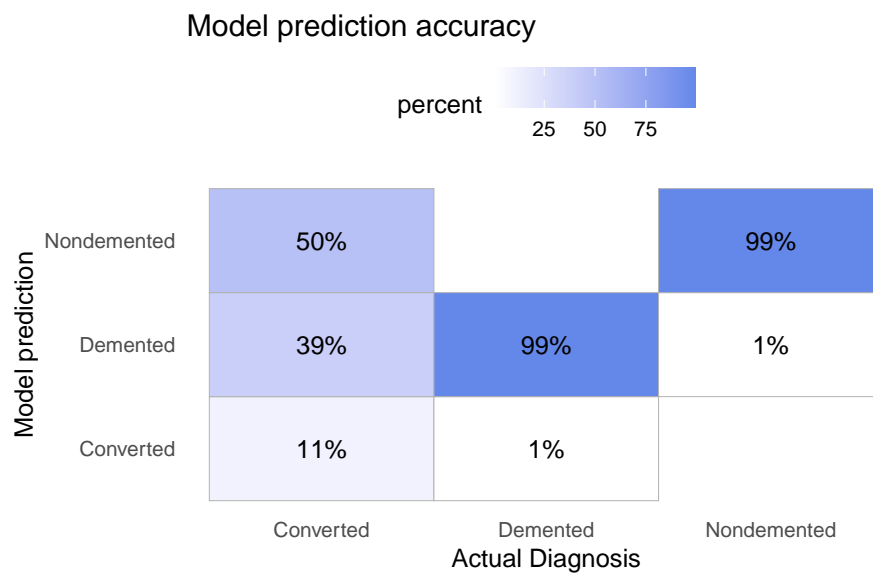
a <- train |>
  cbind(pred) |>
  group_by(group, predict(rf)) |>
  summarise(n = n()) |>
  mutate(freq = n/sum(n)) |>
  ungroup() |>
  rename("predict" = "predict(rf)") |>
```

```

mutate(percent = round(freq, digits = 2) * 100)

a |>
  ggplot(aes(x = group, y = predict)) +
  geom_tile(aes(fill = percent), color = "grey70") +
  geom_text(aes(label = paste0(percent, "%"))) +
  scale_fill_gradient(low = "white", high = "#6488ea") +
  labs(x = "Actual Diagnosis",
       y = "Model prediction",
       title = "Model prediction accuracy") +
  theme_classic() +
  theme(axis.line = element_blank(),
        axis.ticks = element_blank(),
        legend.position = "top")

```

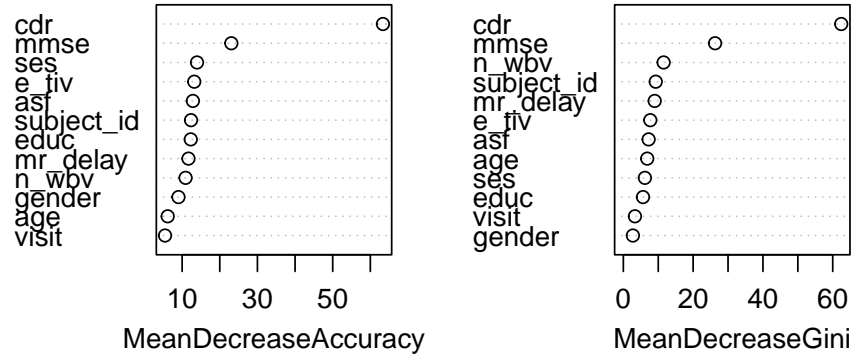


```

varImpPlot(rf, main = "Importance of variables")

```

Importance of variables



Conclusion II

The Random Forest model shows great accuracy in predicting Alzheimer's disease diagnosis based on socioeconomic and brain imaging data. Among all the variables, clinical dementia rating (CDR) and mini-mental state examination score show greater reliability in accurately predicting dementia. While the prediction accuracy is 98% in classifying demented and nondemented individuals, the model performance reflects well on the data for converted patients. It is difficult to diagnose dementia in individuals when their CDR and MMSE scores do not suggest any cognitive decline. While Alzheimer's is a complex disease, features such as CDR and MMSE can be valuable in timely diagnosis.