Analysing the data according to the mmse scale

Upload the libraries:

```
library(rstatix)
library(tidyr)
library(dplyr)
library(ggplot2)
library(patchwork)
library(ggpubr)
library(tidyverse)
library(ggpmisc)
```

Upload the data:

```
scales <- read.csv("scales_small_charlson.csv", header = FALSE,
    stringsAsFactors = FALSE)
lipids <- read.csv("lipids_small_charlson.csv", header = FALSE,
    stringsAsFactors = FALSE)
colnames(lipids) <- lipids[1, ]
lipids <- lipids[-1, ]
colnames(scales) <- scales[1, ]
scales <- scales[-1, ]
scales_lipids <- merge(scales, lipids, by = "MS ID")
```

Let's convert the data to the required type:

```
columns_to_convert <- which(names(scales_lipids) != "sex" & names(scales_lipids) !=
    "MS ID")
scales_lipids[, columns_to_convert] <- lapply(scales_lipids[,
    columns_to_convert], as.numeric)
```

We divide the patients' data into the group of patients with and without dementia according to the mmse scale:

Let's create a new dataset with the 50% worse values according to mmse. This group will include patients with dementia.

```
n_rows <- 495
sorted_mmse <- scales_lipids[order(scales_lipids$mmse), ]
worse_mmse <- sorted_mmse[1:n_rows, ]
worse_mmse$mmse_dementia <- rep("Dementia", 495)
```

Let's create a new dataset with the 50% best values.This group will include patients without dementia.

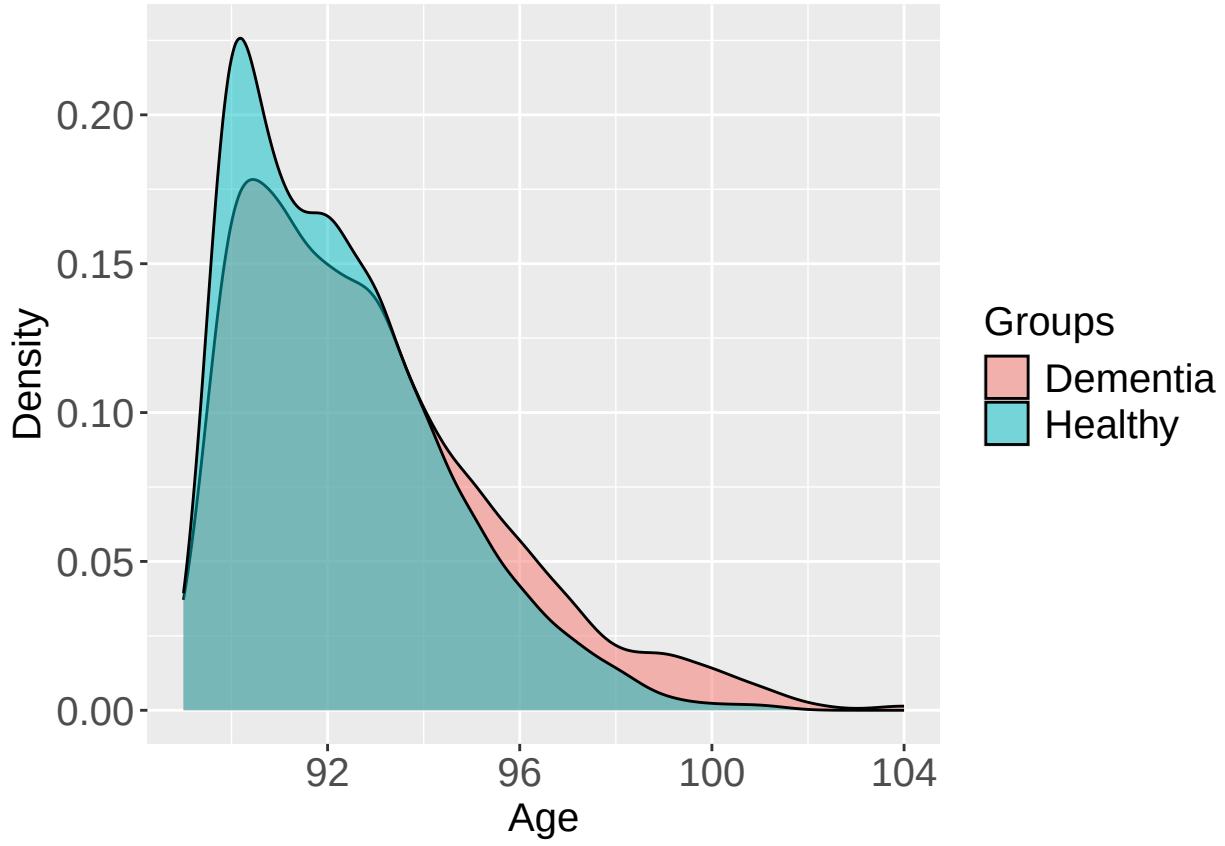
```
sorted_mmse_best <- scales_lipids[order(scales_lipids$mmse, decreasing = TRUE),
    ]
best_mmse <- sorted_mmse_best[1:n_rows, ]
best_mmse$mmse_dementia <- rep("Healthy", 495)
```

Then we combine both dataframes into one:

```
mmse <- rbind(worse_mmse, best_mmse)
mmse_long <- pivot_longer(mmse, cols = 10:230, names_to = "lipid_features",
    values_to = "values")
mmse_long$values <- as.numeric(mmse_long$values)
```

Let's look at the distribution of data in two groups:

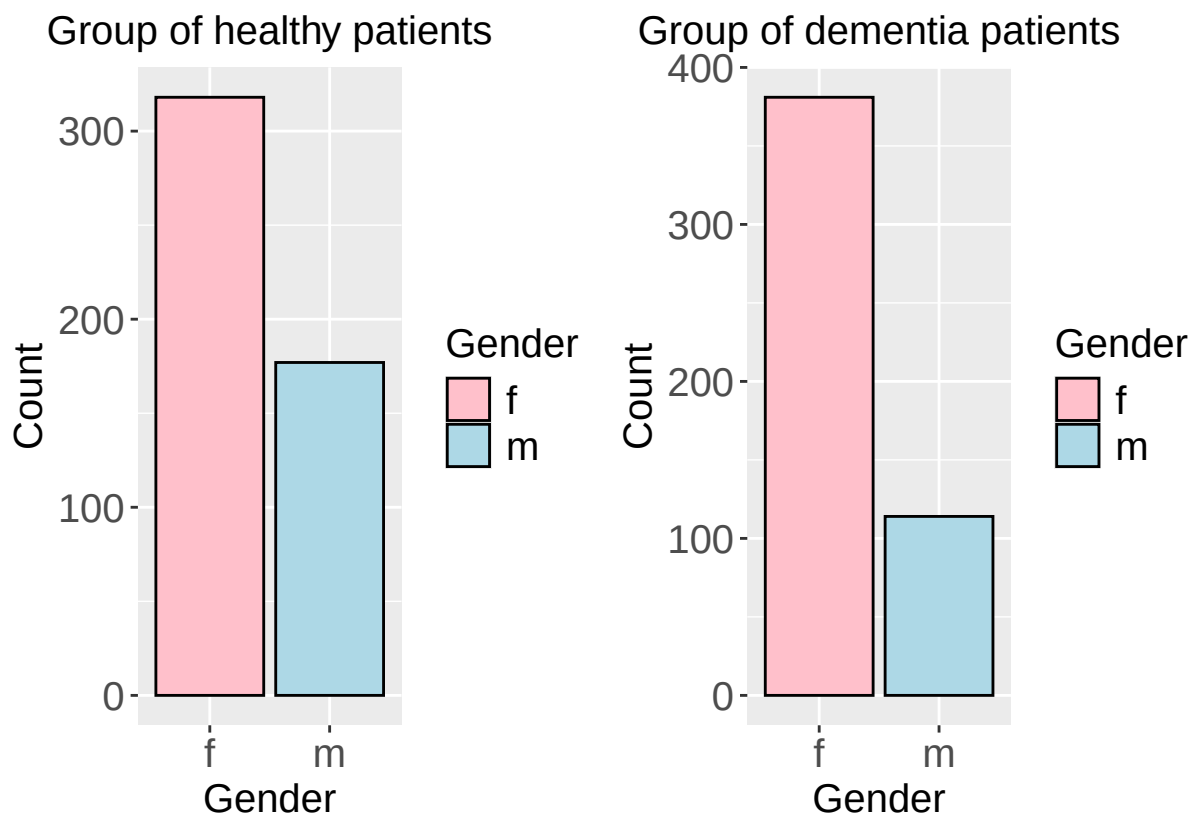
```
ggplot(data = mmse, aes(x = age, fill = mmse_dementia)) + geom_density(alpha = 0.5) +
    labs(x = "Age", y = "Density", fill = "Groups") + theme(plot.title = element_text(hjust = 0.5,
    size = 15), axis.title.x = element_text(size = 15), axis.title.y = element_text(size = 15),
    legend.text = element_text(size = 15), legend.title = element_text(size = 15)) +
    theme(axis.text.x = element_text(size = 15), axis.text.y = element_text(size = 15))
```



It can be seen that the age distribution of the data is similar in the dementia patient and healthy groups.

Let's look at the distribution of genders in the resulting patient groups

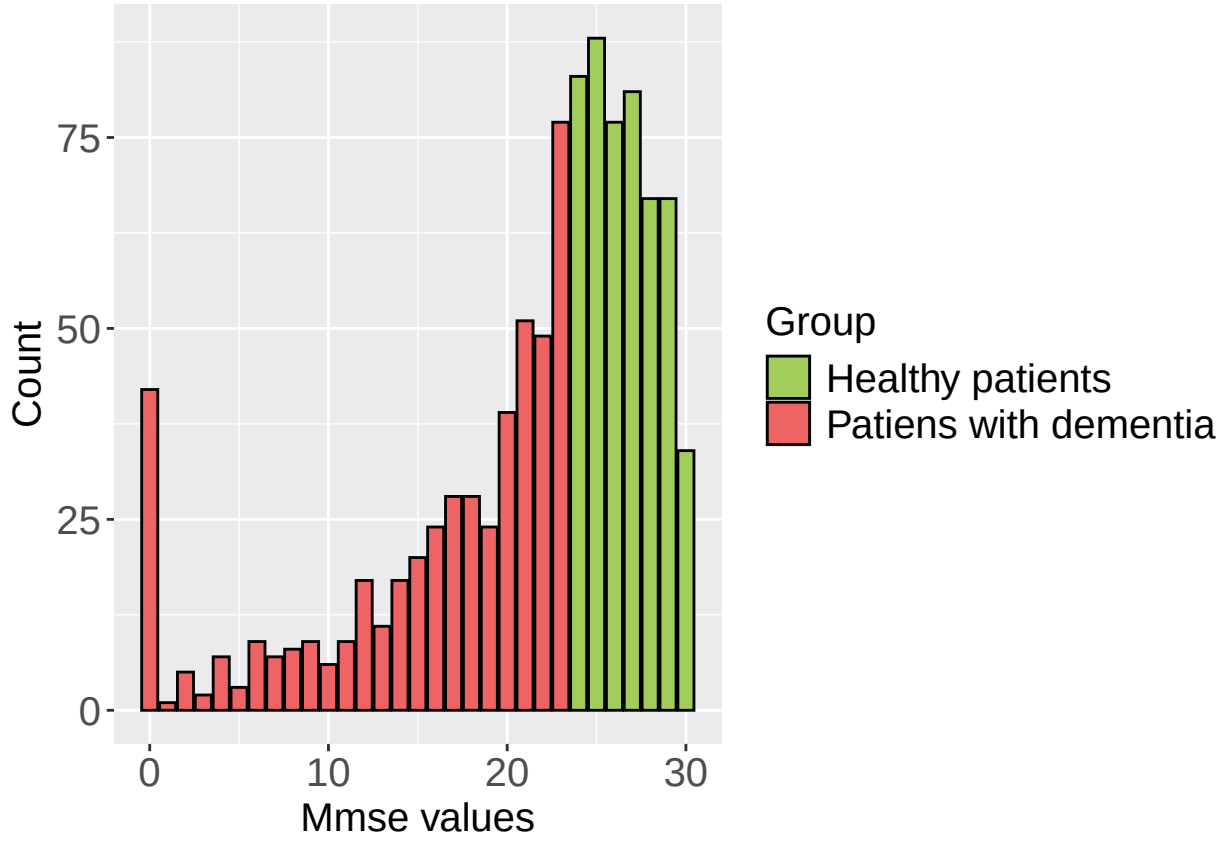
```
m1 <- ggplot(best_mmse, aes(x = factor(sex))) + geom_histogram(aes(fill = factor(sex)),
    color = "black", bins = 20, stat = "count") + scale_fill_manual(values = c(f = "pink",
    m = "lightblue")) + labs(x = "Gender", y = "Count", title = "Group of healthy patients",
    fill = "Gender") + theme(plot.title = element_text(hjust = 0.5,
    size = 15), axis.title.x = element_text(size = 15), axis.title.y = element_text(size = 15),
    legend.text = element_text(size = 15), legend.title = element_text(size = 15)) +
    theme(axis.text.x = element_text(size = 15), axis.text.y = element_text(size = 15))

m2 <- ggplot(worse_mmse, aes(x = factor(sex))) + geom_histogram(aes(fill = factor(sex)),
    color = "black", bins = 20, stat = "count") + scale_fill_manual(values = c(f = "pink",
    m = "lightblue")) + labs(x = "Gender", y = "Count", title = "Group of dementia patients",
    fill = "Gender") + theme(plot.title = element_text(hjust = 0.5,
    size = 15), axis.title.x = element_text(size = 15), axis.title.y = element_text(size = 15),
    legend.text = element_text(size = 15), legend.title = element_text(size = 15)) +
    theme(axis.text.x = element_text(size = 15), axis.text.y = element_text(size = 15))

m1 + m2
```



There are more men in the group of healthy patients than in the group of patients with dementia

Let's look at the distribution of mmse scale values in the resulting groups:

```
ggplot(scales_lipids, aes(x = mmse)) + geom_histogram(aes(fill = ifelse(mmse %in%
    best_mmse$mmse, "Healthy patients", ifelse(mmse %in% worse_mmse$mmse,
    "Patiens with dementia", "Data not included \n in analysis"))),
    color = "black", bins = 20, stat = "count") + scale_fill_manual(values = c("darkolivegreen3",
    "#EE6363")) + labs(x = "Mmse values", y = "Count", fill = "Group") +
    theme(axis.title.x = element_text(size = 15), axis.title.y = element_text(size = 15),
        legend.text = element_text(size = 15), legend.title = element_text(size = 15)) +
    theme(axis.text.x = element_text(size = 15), axis.text.y = element_text(size = 15))
```



Let's perform t-test between the lipids of the 50% best and 50% worst samples according to the mmse scale

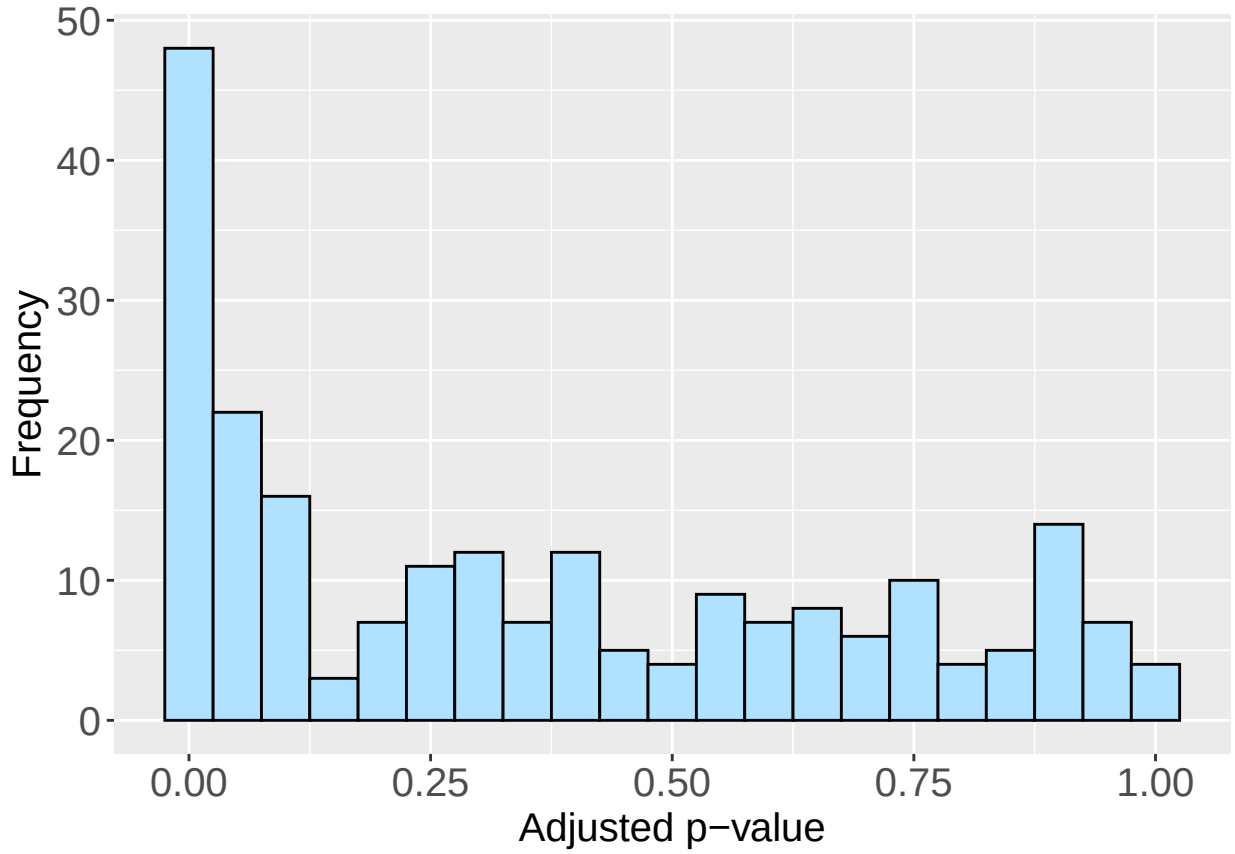
```
stat.test_mmse <- mmse_long %>%
    group_by(lipid_features) %>%
    t_test(values ~ mmse_dementia) %>%
    adjust_pvalue(method = "BH") %>%
    add_significance()
print(stat.test_mmse)
```

```
## # A tibble: 221 x 11
##    lipid_features .y.    group1   group2     n1    n2 statistic    df          p
##    <chr>          <chr>  <chr>    <chr>   <int> <int>     <dbl> <dbl>      <dbl>
##  1 CAR 10:1       values Dementia Healthy   495   495    -2.71   988.    6.84e-3
##  2 CAR 18:1       values Dementia Healthy   495   495    -1.30   988.    1.94e-1
##  3 CAR 18:2       values Dementia Healthy   495   495    -3.60   987.    3.4 e-4
##  4 CE 14:0        values Dementia Healthy   495   495     0.757  987.    4.49e-1
##  5 CE 15:0        values Dementia Healthy   495   495     1.17   928.    2.43e-1
##  6 CE 16:1        values Dementia Healthy   495   495     5.84   988.    7.02e-9
##  7 CE 17:1        values Dementia Healthy   495   495     2.60   987.    9.45e-3
##  8 CE 18:2        values Dementia Healthy   495   495     0.546  983.    5.85e-1
##  9 CE 18:3        values Dementia Healthy   495   495     0.622  988.    5.34e-1
```

```
## 10 CE 19:1        values Dementia Healthy   495   495     1.68   949.    9.34e-2
## # i 211 more rows
## # i 2 more variables: p.adj <dbl>, p.adj.signif <chr>
```

Let's plot the p-value distribution:

```
ggplot(data = stat.test_mmse, aes(x = p.adj)) + geom_histogram(binwidth = 0.05,
    fill = "#B0E2FF", color = "black", bins = 15) + labs(x = "Adjusted p-value",
    y = "Frequency") + theme(axis.title.x = element_text(size = 15),
    axis.title.y = element_text(size = 15), legend.text = element_text(size = 15),
    legend.title = element_text(size = 15)) + theme(axis.text.x = element_text(size = 15),
    axis.text.y = element_text(size = 15))
```



Based on the distribution of p-value values, it can be seen that the patient groups are significantly different from each other.

Let's look separately at lipids significantly different between patients with and without dementia

```
stat.test_mmse_significant <- stat.test_mmse[stat.test_mmse$p.adj <=
    0.05, ]
print(stat.test_mmse_significant)
```

```
## # A tibble: 63 x 11
##    lipid_features .y.    group1   group2     n1    n2 statistic    df          p
##    <chr>          <chr>  <chr>    <chr>   <int> <int>     <dbl> <dbl>      <dbl>
##  1 CAR 10:1       values Dementia Healthy   495   495     -2.71  988.    6.84e-3
##  2 CAR 18:2       values Dementia Healthy   495   495     -3.60  987.    3.4 e-4
##  3 CE 16:1        values Dementia Healthy   495   495      5.84  988.    7.02e-9
##  4 CE 17:1        values Dementia Healthy   495   495      2.60  987.    9.45e-3
##  5 CE 19:5        values Dementia Healthy   495   495      3.56  987.    3.95e-4
##  6 CE 20:5        values Dementia Healthy   495   495     -4.33  987.    1.62e-5
##  7 CE 21:1        values Dementia Healthy   495   495      3.23  964.    1.29e-3
##  8 CE 22:6        values Dementia Healthy   495   495     -2.81  986.    5.06e-3
##  9 Cer 34:1       values Dementia Healthy   495   495      4.45  984.    9.61e-6
## 10 LPC 14:0       values Dementia Healthy   495   495     -2.65  982.    8.27e-3
## # i 53 more rows
## # i 2 more variables: p.adj <dbl>, p.adj.signif <chr>
```

Let's parse the data on lipids:

```
stat.test_mmse$lipid_features <- gsub("LPC O-(\\d+):(\\d+)",
    "LPC-O \\1:\\2", stat.test_mmse$lipid_features)
stat.test_mmse_sep <- separate(stat.test_mmse, lipid_features,
    into = c("Class", "Other"), sep = " ", remove = FALSE)
stat.test_mmse_sep <- separate(stat.test_mmse_sep, Other, into = c("Chain_length",
    "Double_bounds"), sep = ":")

stat.test_mmse_significant$lipid_features <- gsub("LPC O-(\\d+):(\\d+)",
    "LPC-O \\1:\\2", stat.test_mmse_significant$lipid_features)
stat.test_mmse_signif_sep <- separate(stat.test_mmse_significant,
    lipid_features, into = c("Class", "Other"), sep = " ", remove = FALSE)
stat.test_mmse_signif_sep <- separate(stat.test_mmse_signif_sep,
    Other, into = c("Chain_length", "Double_bounds"), sep = ":")
```

Let's count the percentage of significant lipids by class:

```
stat.test_mmse_all_lipids <- as.data.frame(table(stat.test_mmse_sep$Class))
stat.test_mmse_all_lipid_signif <- as.data.frame(table(stat.test_mmse_signif_sep$Class))
lipids_stat.test_mmse <- merge(stat.test_mmse_all_lipids, stat.test_mmse_all_lipid_signif,
    by = "Var1")
lipids_stat.test_mmse$percentage <- (lipids_stat.test_mmse$Freq.y/lipids_stat.test_mmse$Freq.x) *
    100
colnames(lipids_stat.test_mmse)[1] <- "Class"
```

Let's perform enrichment analysis:

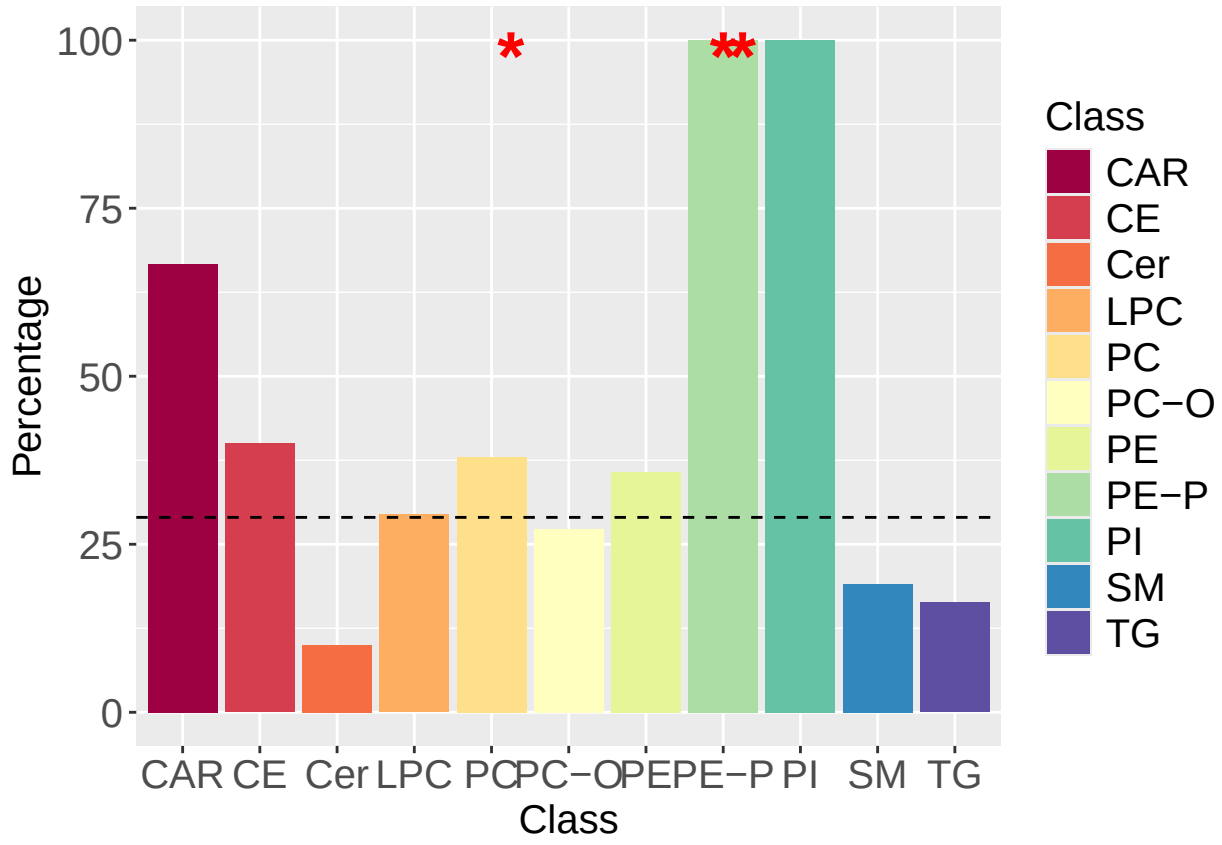
```
results_enrichment <- data.frame(Class = character(), p_value = numeric(),
    adjusted_p_value = numeric(), stringsAsFactors = FALSE)

lipid_classes <- unique(stat.test_mmse_signif_sep$Class)
```

```
for (lipid_class in lipid_classes) {
    q <- sum(stat.test_mmse_signif_sep$Class == lipid_class)
    m <- nrow(stat.test_mmse_signif_sep)
    n <- nrow(stat.test_mmse_sep) - m
    k <- sum(stat.test_mmse_sep$Class == lipid_class)

    p_value <- phyper(q - 1, m, n, k, lower.tail = FALSE, log.p = FALSE)

    adjusted_p_value <- p.adjust(p_value, method = "bonferroni")

    results_enrichment <- rbind(results_enrichment, data.frame(Class = lipid_class,
        p_value = p_value, adjusted_p_value = adjusted_p_value))
}

print(results_enrichment)
```

```
##    Class      p_value adjusted_p_value
## 1    CAR 0.1962578115     0.1962578115
## 2     CE 0.2291220505     0.2291220505
## 3    Cer 0.9679279659     0.9679279659
## 4    LPC 0.5630020508     0.5630020508
## 5     PC 0.0670781464     0.0670781464
## 6   PC-O 0.6395617745     0.6395617745
## 7     PE 0.3649453253     0.3649453253
## 8   PE-P 0.0004496393     0.0004496393
## 9     PI 0.2850678733     0.2850678733
## 10    SM 0.9010157712     0.9010157712
## 11    TG 0.9920125029     0.9920125029
```

Plot the results:

```
significant_results <- results_enrichment[results_enrichment$adjusted_p_value <
    0.05, ]
significant_results2 <- results_enrichment[results_enrichment$adjusted_p_value <
    0.1, ]

ggplot(lipids_stat.test_mmse, aes(x = Class, y = percentage,
    fill = Class)) + geom_bar(stat = "identity") + scale_fill_brewer(palette = "Spectral") +
    labs(x = "Class", y = "Percentage") + theme(axis.title.x = element_text(size = 15),
    axis.title.y = element_text(size = 15), legend.text = element_text(size = 15),
    legend.title = element_text(size = 15), axis.text.x = element_text(size = 15),
    axis.text.y = element_text(size = 15)) + geom_text(data = significant_results,
    aes(x = Class, y = 0, label = paste0("*")), vjust = -12.7,
    size = 9, color = "red", fontface = "bold") + geom_text(data = significant_results2,
    aes(x = Class, y = 0, label = paste0("  *")), vjust = -12.7,
    size = 9, color = "red", fontface = "bold") + geom_hline(yintercept = 29,
    linetype = "dashed", color = "black")
```



It can be seen that lipids differing significantly between the patient groups belong to different classes. In addition, compared to the expected lipid levels, there is enrichment of such lipid classes as PC and PE-P.

Let's explore differences in lipid content between groups:

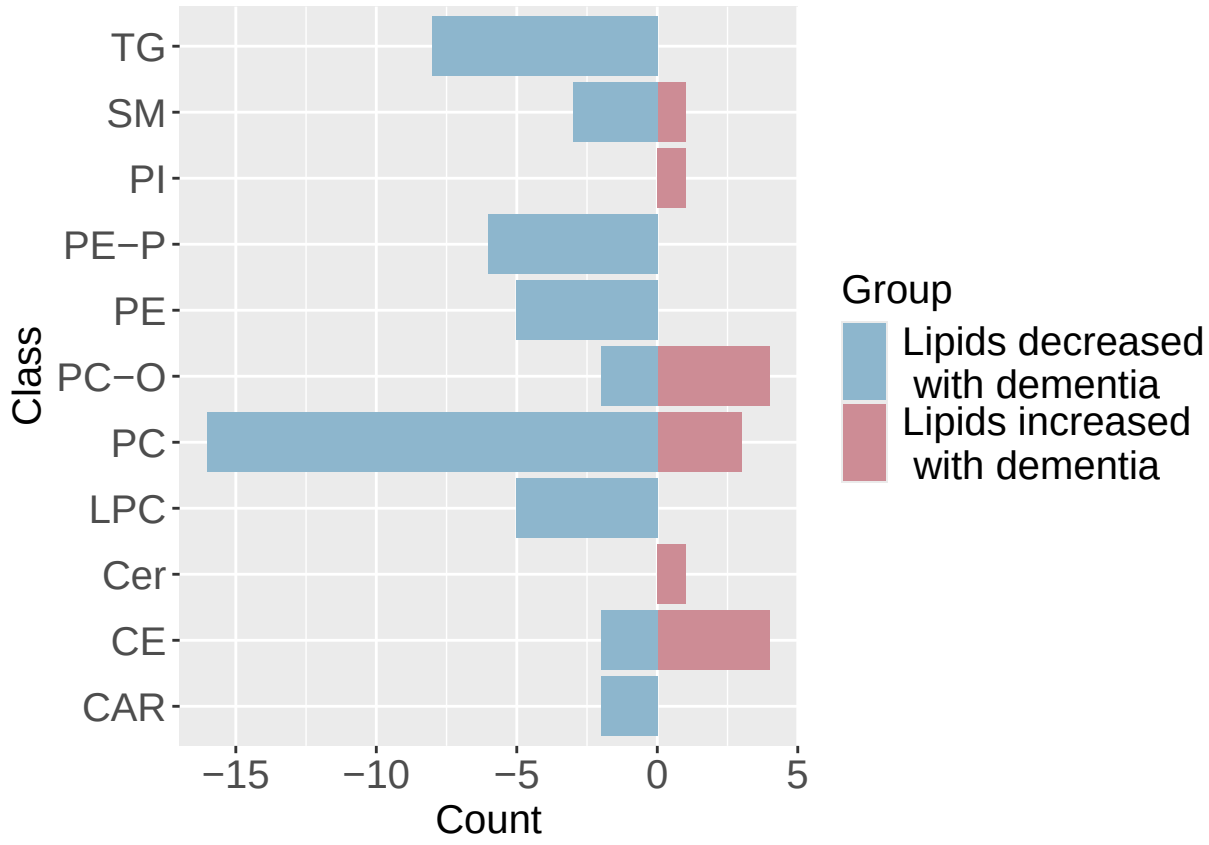
Prepare the data:

```
mmse_dementia <- mmse_long[mmse_long$mmse_dementia == "Dementia",
    ]
mmse_nodementia <- mmse_long[mmse_long$mmse_dementia == "Healthy",
    ]

mmse_dementia_mean <- mmse_dementia %>%
    group_by(lipid_features) %>%
    summarise(mean_dementia = mean(values))

mmse_nodementia_mean <- mmse_nodementia %>%
    group_by(lipid_features) %>%
    summarise(mean_nodementia = mean(values))

mean_mmse <- merge(mmse_dementia_mean, mmse_nodementia_mean,
    by = "lipid_features")
```

```
mean_mmse_filtered <- mean_mmse %>%
    filter(lipid_features %in% stat.test_mmse_significant$lipid_features)

mean_mmse_filtered$difference <- mean_mmse_filtered$mean_dementia -
    mean_mmse_filtered$mean_nodementia

mean_mmse_filtered$Sign <- ifelse(mean_mmse_filtered$difference >
    0, "Positive", "Negative")

mean_mmse_filtered$Count <- 1

mean_mmse_filtered$Value <- ifelse(mean_mmse_filtered$Sign ==
    "Negative", -mean_mmse_filtered$Count, mean_mmse_filtered$Count)

mean_mmse_filtered$lipid_features <- gsub("LPC O-(\\d+):(\\d+)",
    "LPC-O \\1:\\2", mean_mmse_filtered$lipid_features)
mean_mmse_filtered <- separate(mean_mmse_filtered, lipid_features,
    into = c("Class", "Other"), sep = " ", remove = FALSE)
mean_mmse_filtered <- separate(mean_mmse_filtered, Other, into = c("Chain_length",
    "Double_bounds"), sep = ":")
```

Plot the results:

```
ggplot(mean_mmse_filtered, aes(x = Class, y = Value, fill = Sign)) +
    geom_bar(stat = "identity") + scale_fill_manual(values = c(Positive = "#CD8C95",
    Negative = "#8DB6CD"), labels = c(Positive = "Lipids increased \n with dementia",
    Negative = "Lipids decreased \n with dementia")) + coord_flip() +
    labs(x = "Class", y = "Count", fill = "Group") + theme(axis.title.x = element_text(size = 15),
    axis.title.y = element_text(size = 15), legend.text = element_text(size = 15),
    legend.title = element_text(size = 15)) + theme(axis.text.x = element_text(size = 15),
    axis.text.y = element_text(size = 15))
```



We can see that the majority of lipids are reduced in patients with dementia.

Let's look at the number of double bonds in significant lipids and their differences in the patient groups:

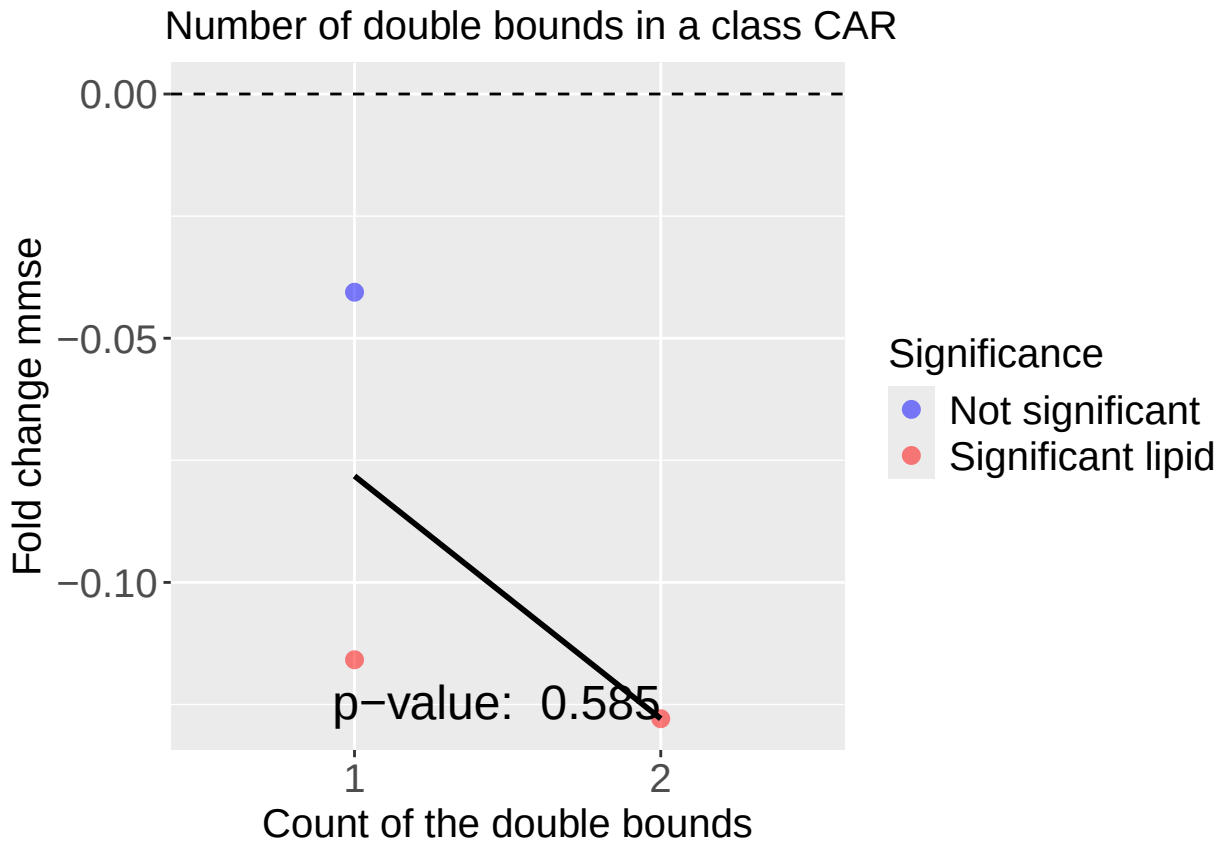
Count the fold change:

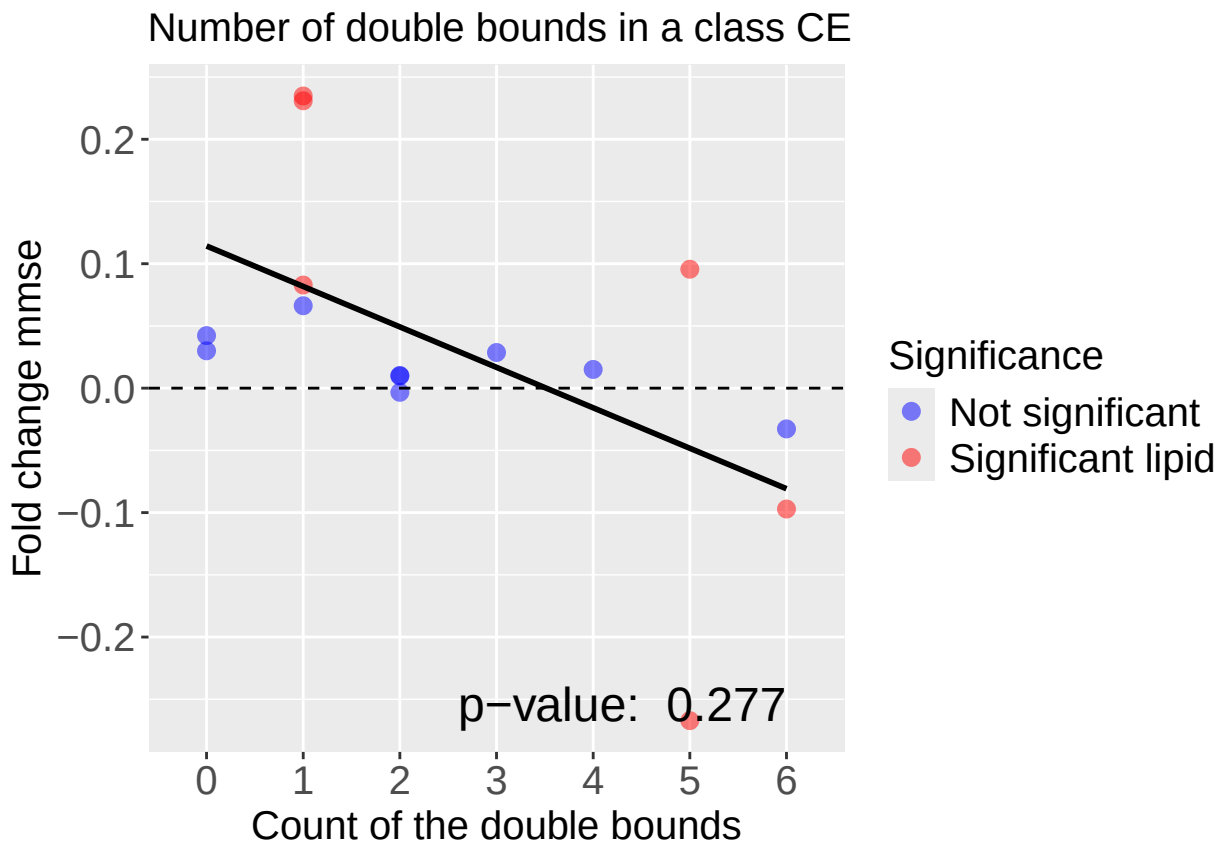
```
best_mmse_long <- pivot_longer(best_mmse, cols = 10:230, names_to = "lipid_features",
    values_to = "values")
worse_mmse_long <- pivot_longer(worse_mmse, cols = 10:230, names_to = "lipid_features",
    values_to = "values")

best_mmse_mean <- best_mmse_long %>%
    group_by(lipid_features) %>%
    summarise(mean_mmse_high = mean(values))

worse_mmse_mean <- worse_mmse_long %>%
    group_by(lipid_features) %>%
    summarise(mean_mmse_low = mean(values))

mean_mmse <- merge(best_mmse_mean, worse_mmse_mean, by = "lipid_features")
mean_mmse$FC_mmse <- mean_mmse$mean_mmse_low - mean_mmse$mean_mmse_high
```

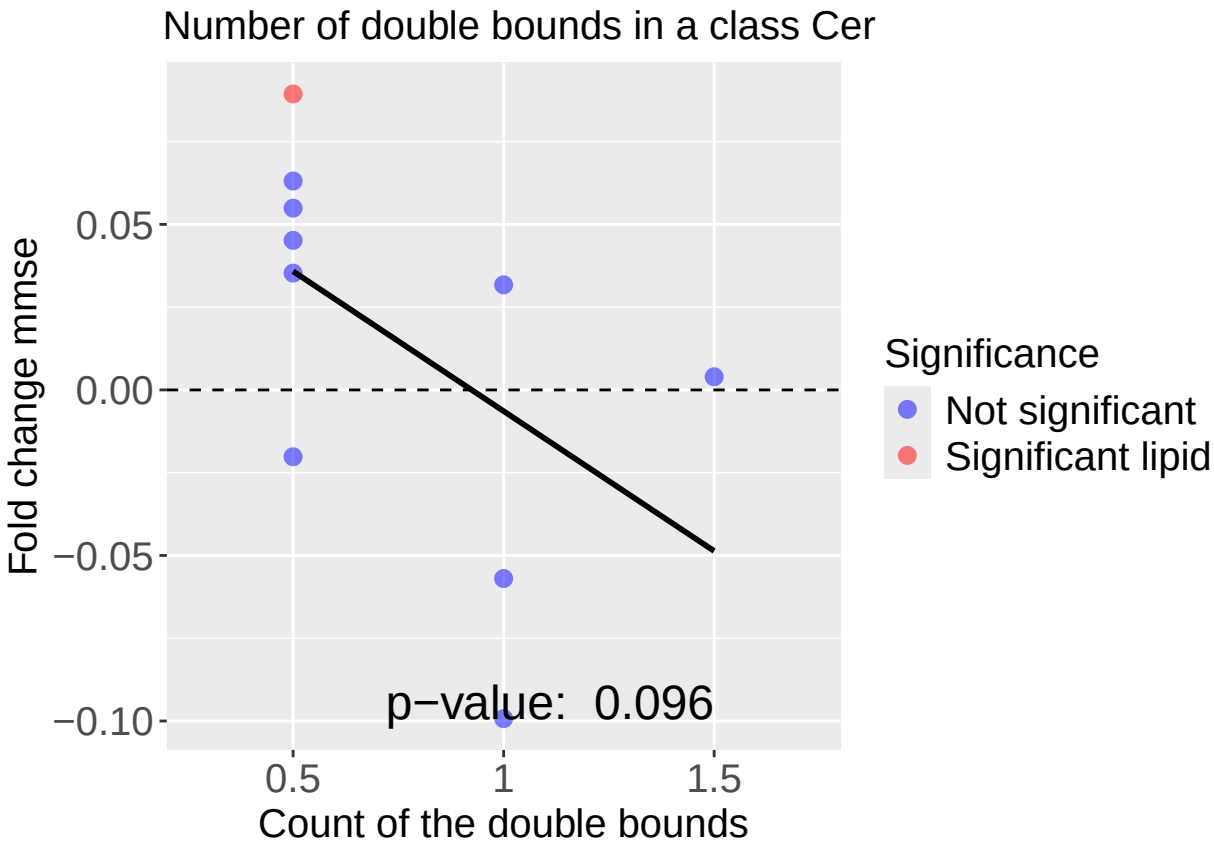
Plot the results:

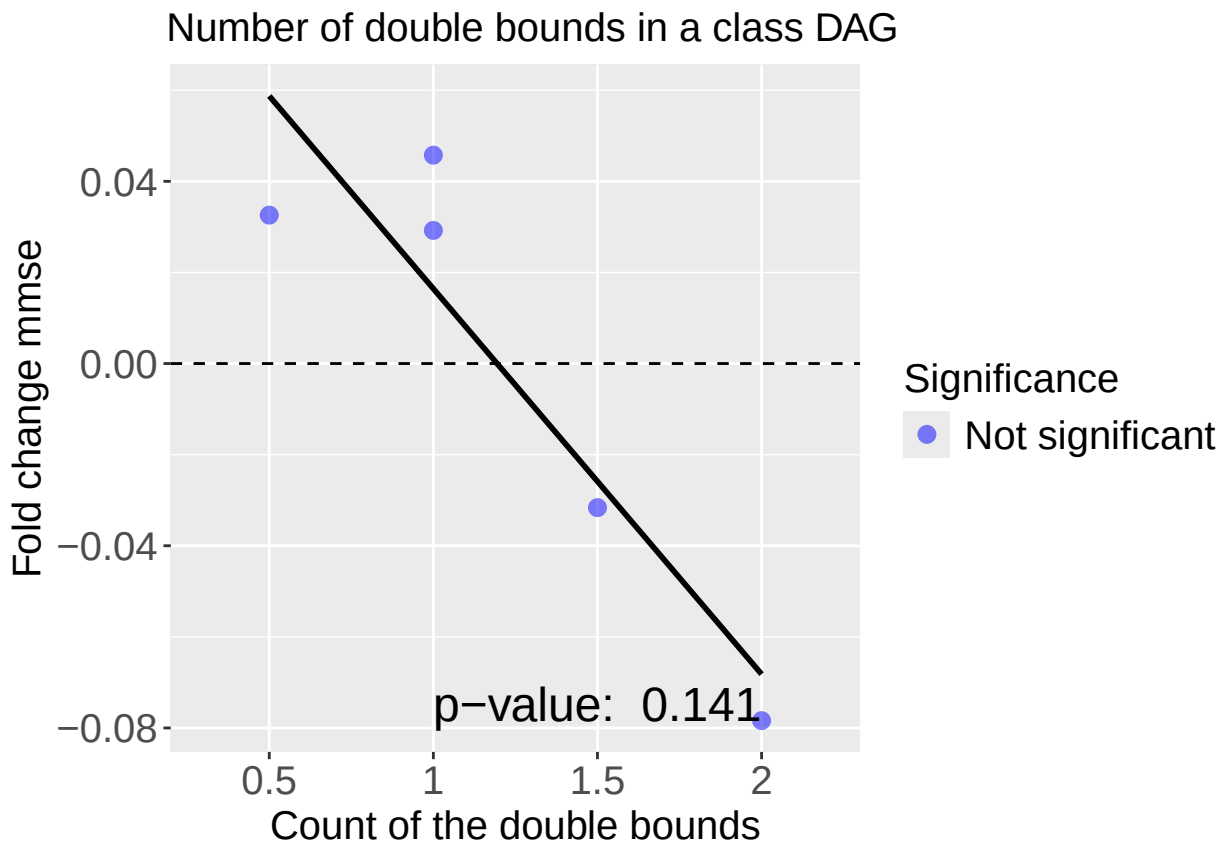
```
unique_classes <- unique(stat.test_mmse_sep$Class)
stat.test_mmse_sep$lipid_features <- gsub("LPC O-(\\d+):(\\d+)",
    "LPC-O \\1:\\2", stat.test_mmse_sep$lipid_features)
mean_mmse$lipid_features <- gsub("LPC O-(\\d+):(\\d+)", "LPC-O \\1:\\2",
    mean_mmse$lipid_features)


for (current_class in unique_classes) {

    stat.test_mmse_lipid <- stat.test_mmse_sep[stat.test_mmse_sep$Class ==
        current_class, ]

    merged_bounds_FC <- merge(mean_mmse, stat.test_mmse_lipid,
        by = "lipid_features")

    if (current_class %in% c("CAR", "CE", "LPC", "LPE", "LPC-O")) {
        merged_bounds_FC$bounds_correct <- round(as.numeric(as.character(merged_bounds_FC$Double_bounds
            1)
    } else if (current_class %in% c("SM", "Cer", "PC", "PE", "DAG",
        "PC-O", "PE-P")) {
        merged_bounds_FC$bounds_correct <- round(as.numeric(as.character(merged_bounds_FC$Double_bounds
            1)
    } else if (current_class == "TG") {
        merged_bounds_FC$bounds_correct <- round(as.numeric(as.character(merged_bounds_FC$Double_bounds
            1)
    } else if (current_class == "PI") {
        merged_bounds_FC$bounds_correct <- round(as.numeric(as.character(merged_bounds_FC$Double_bounds
            2)
    } else {

        next
    }

    merged_bounds_FC$bounds_correct <- as.character(merged_bounds_FC$bounds_correct)

    if (nrow(merged_bounds_FC) >= 2) {

        model <- lm(FC_mmse ~ bounds_correct, data = merged_bounds_FC)

        summary_result <- summary(model)

        f <- summary_result$fstatistic
        p_value <- pf(f[1], f[2], f[3], lower.tail = F)

        plot <- ggplot(merged_bounds_FC, aes(x = bounds_correct,
            y = FC_mmse, color = ifelse(lipid_features %in% stat.test_mmse_signif_sep$lipid_features,
                "TRUE", "FALSE"))) + geom_point(shape = 16, size = 3,
            alpha = 0.5) + labs(x = "Count of the double bounds",
            y = "Fold change mmse", title = paste("Number of double bounds in a class",
                current_class)) + geom_vline(xintercept = 0,
            linetype = "dashed", color = "black") + geom_hline(yintercept = 0,
```

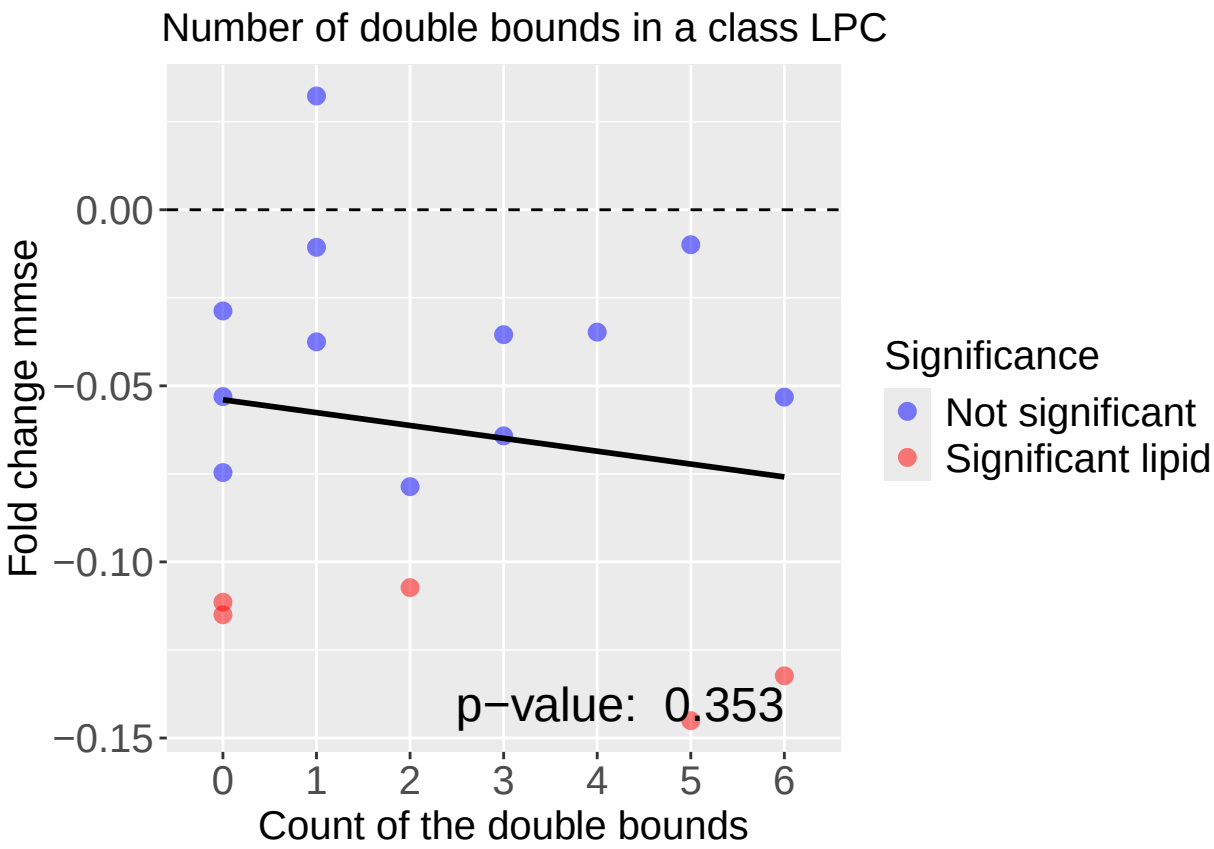
```
            linetype = "dashed", color = "black") + scale_color_manual(values = c(`TRUE` = "red",
            `FALSE` = "blue"), name = "Significance", labels = if (all(merged_bounds_FC$lipid_features %
            stat.test_mmse_signif_sep$lipid_features))
            c("Significant lipid", "Significant lipid") else c("Not significant", "Significant lipid"))
            size = 15), axis.title.x = element_text(size = 15),
            axis.title.y = element_text(size = 15), legend.text = element_text(size = 15),
            legend.title = element_text(size = 15), axis.text.x = element_text(size = 15),
            axis.text.y = element_text(size = 15)) + geom_smooth(aes(group = 1),
            method = "lm", se = FALSE, color = "black", show.legend = FALSE) +
            stat_regline_equation(label.x = "left", label.y = "bottom",
                show.legend = FALSE) + annotate("text", x = max(merged_bounds_FC$bounds_correct),
            y = min(merged_bounds_FC$FC_mmse), label = paste("p-value: ",
                formatC(p_value, digits = 3, format = "f")),
            hjust = 1, vjust = 0, size = 6.5, color = "black")
        print(plot)

    }
}
```

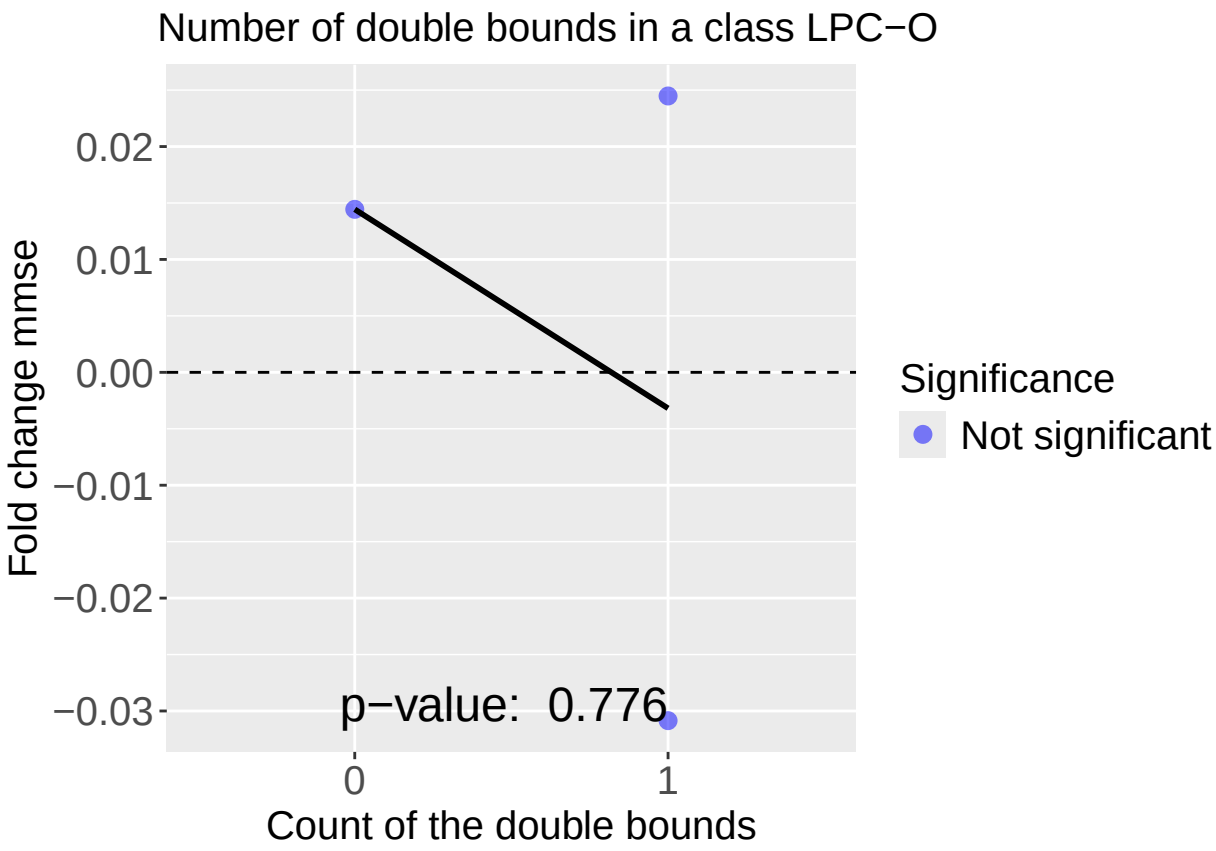


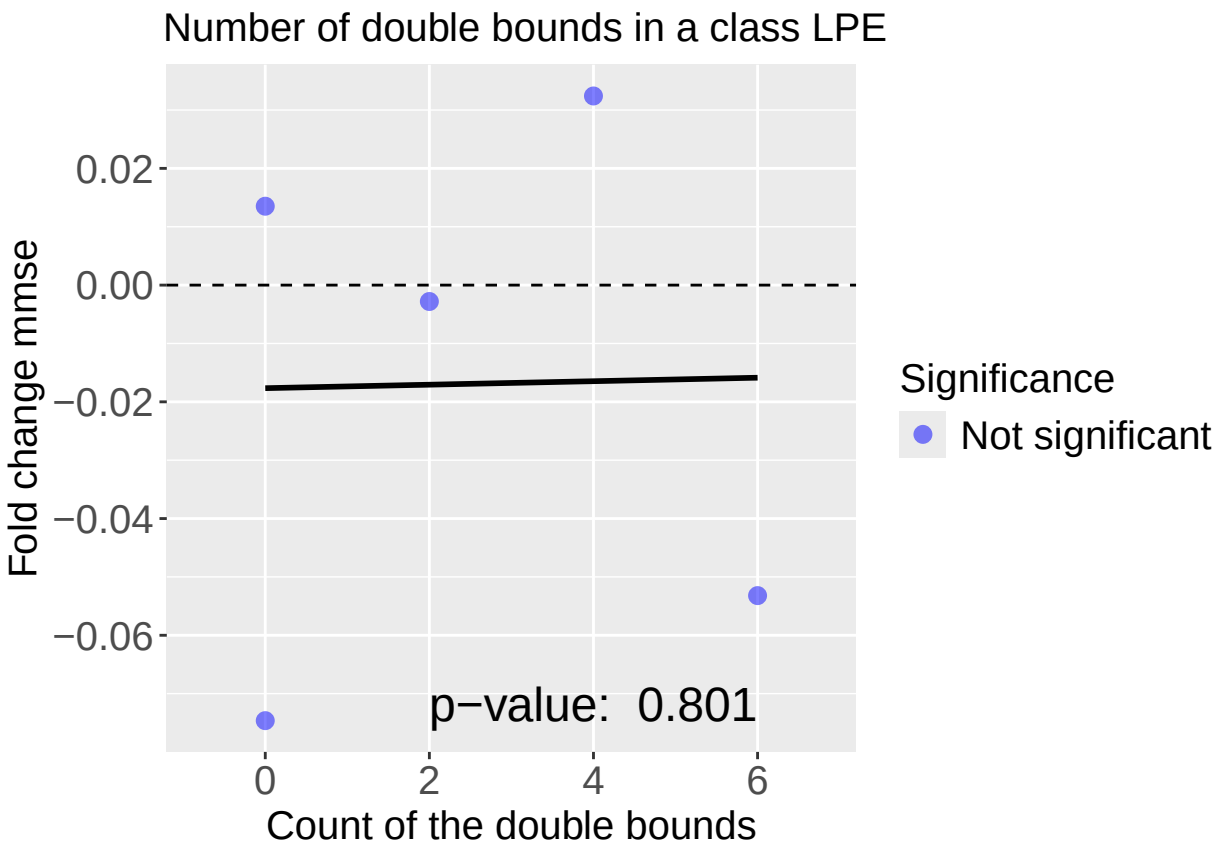

Number of double bounds in a class CE
Fold change mmse
0.2
0.1
0.0
−0.1
−0.2
p−value: 0.277
0
1
2
3
4
5
6
Count of the double bounds
Significance
Not significant
Significant lipid

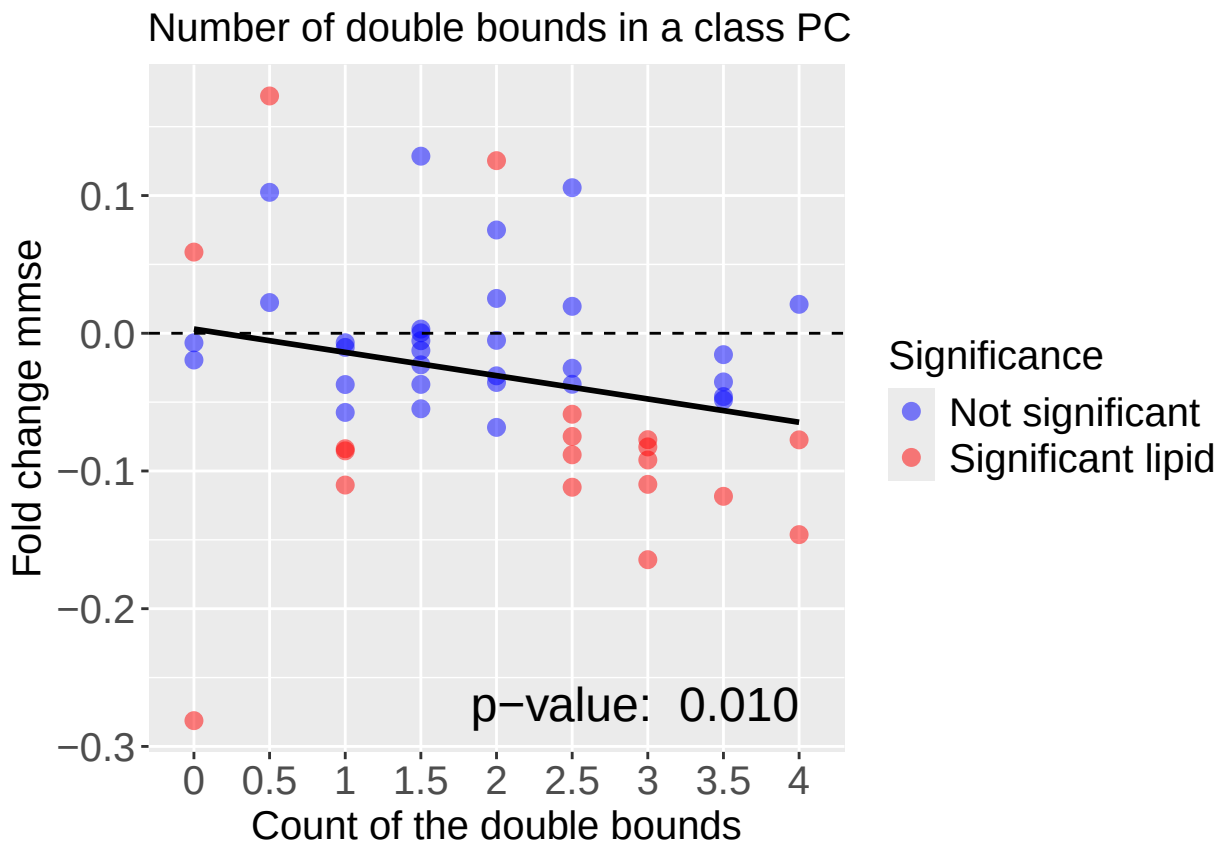

Number of double bounds in a class Cer
Fold change mmse
0.05
0.00
−0.05
−0.10
p−value: 0.096
0.5
1
1.5
Count of the double bounds
Significance
Not significant
Significant lipid

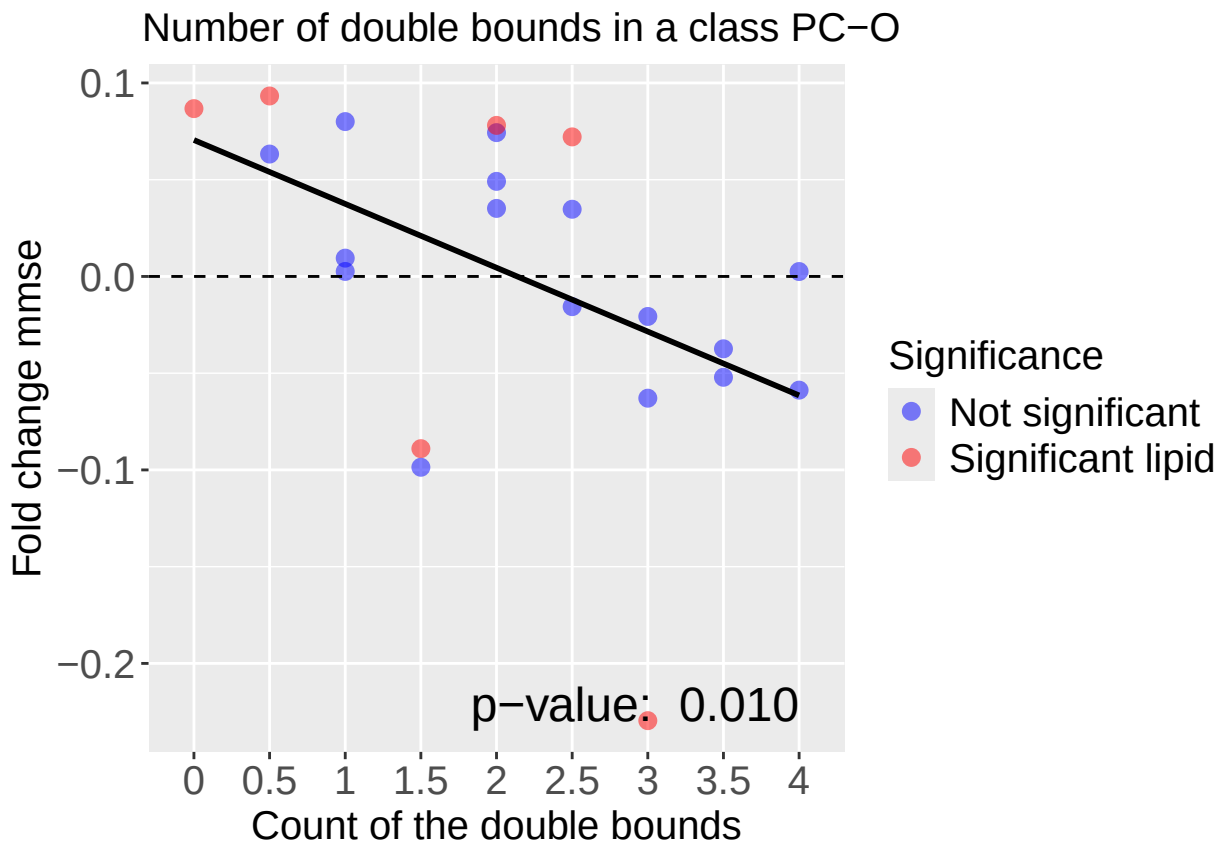

Number of double bounds in a class DAG
Fold change mmse
0.04
0.00
−0.04
−0.08
p−value: 0.141
0.5
1
1.5
2
Count of the double bounds
Significance
Not significant

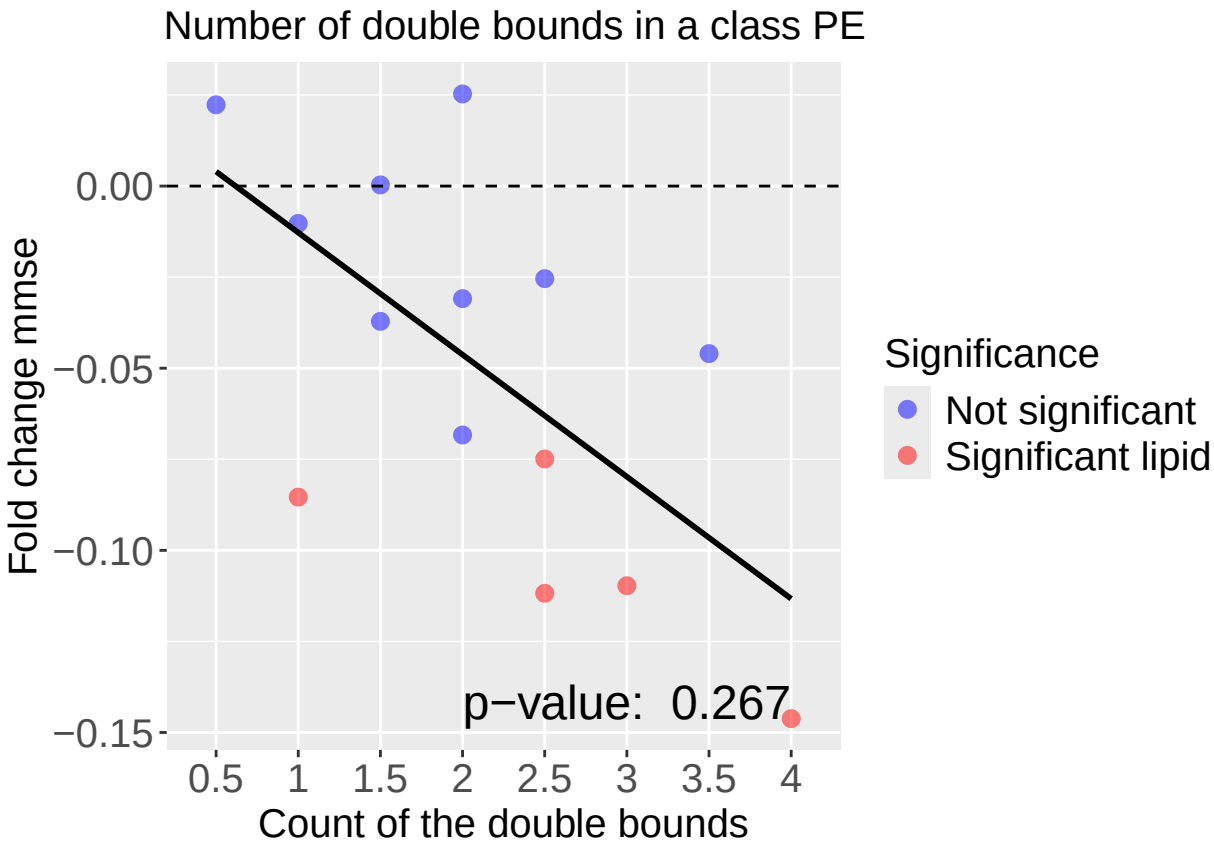

Number of double bounds in a class LPC
Fold change mmse
0.00
−0.05
−0.10
−0.15
p−value: 0.353
0
1
2
3
4
5
6
Count of the double bounds
Significance
Not significant
Significant lipid

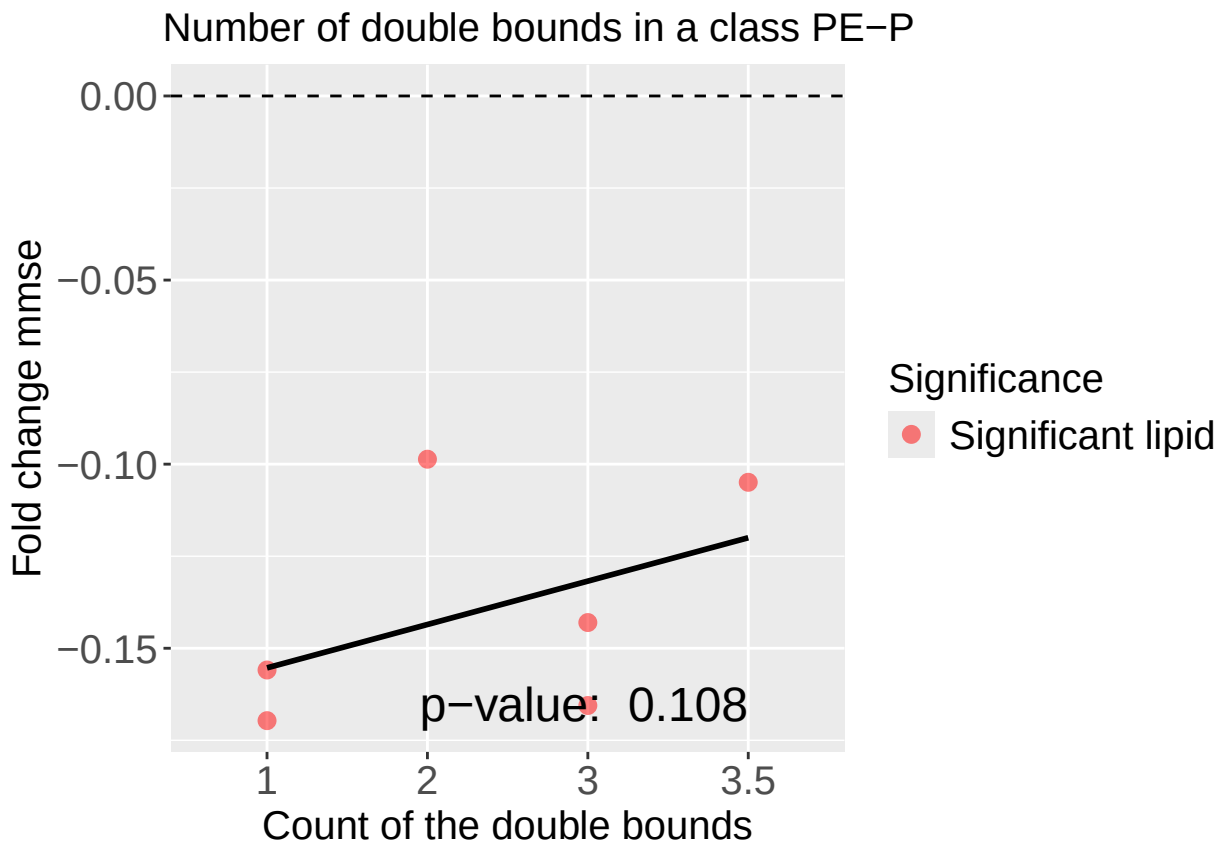

Number of double bounds in a class LPC−O
Fold change mmse
0.02
0.01
0.00
−0.01
−0.02
−0.03
p−value: 0.776
0
1
Count of the double bounds
Significance
Not significant

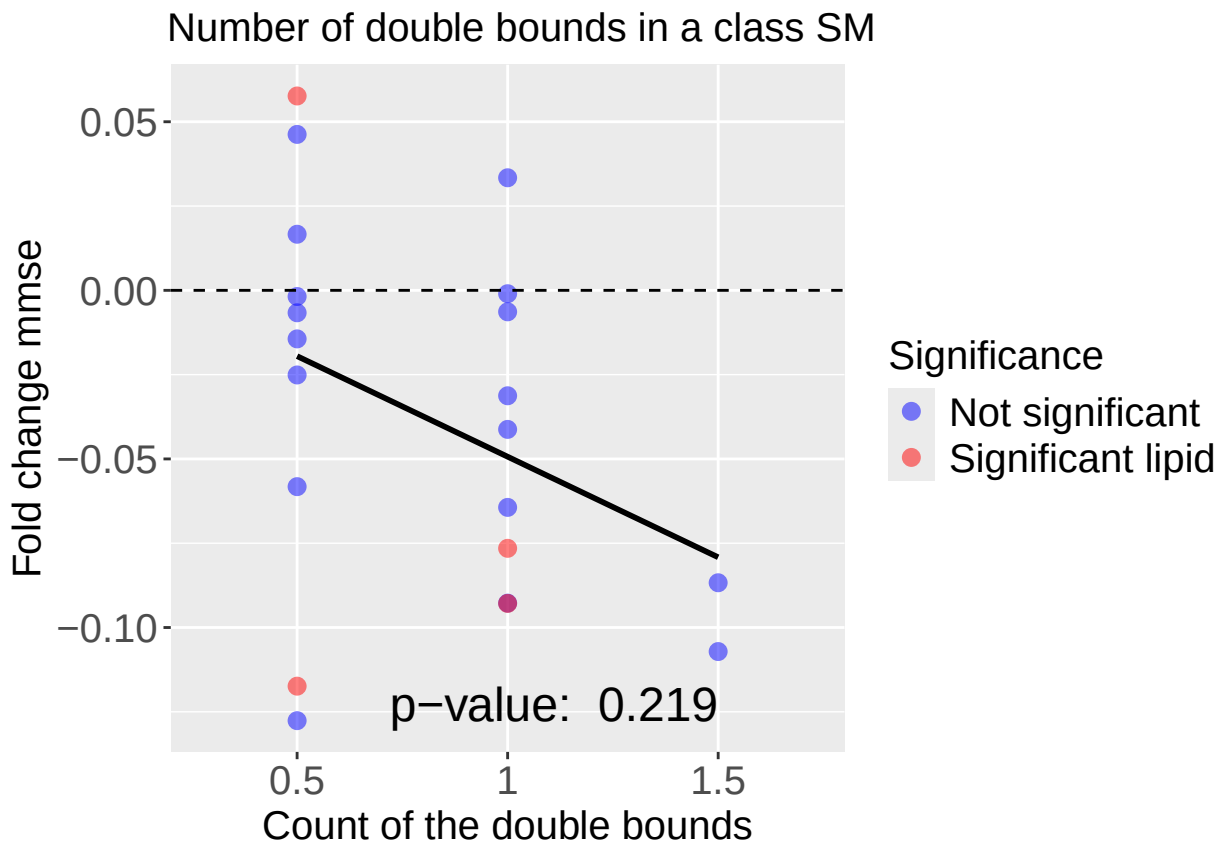

Number of double bounds in a class LPE
Fold change mmse
0.02
0.00
−0.02
−0.04
−0.06
p−value: 0.801
0
2
4
6
Count of the double bounds
Significance
Not significant

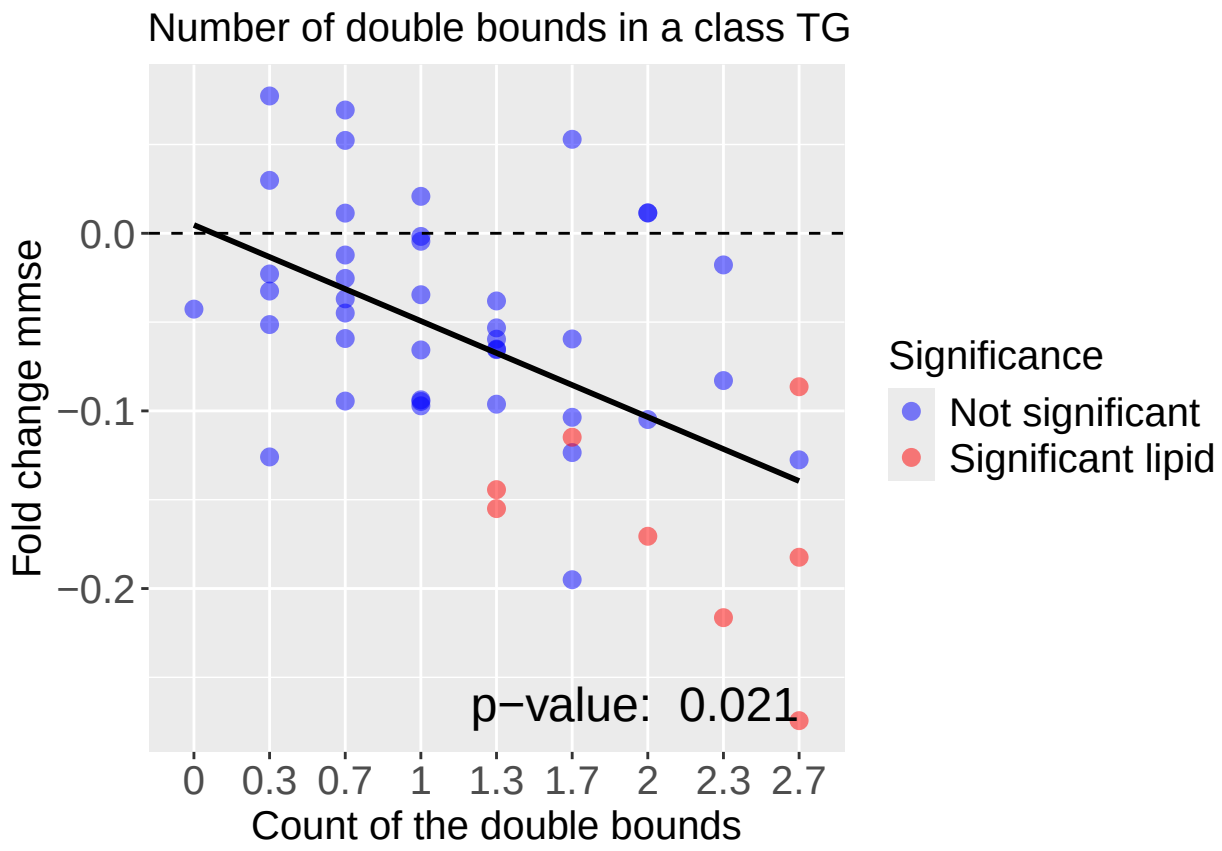

Number of double bounds in a class PC
Fold change mmse
0.1
0.0
−0.1
−0.2
−0.3
p−value: 0.010
0
0.5
1
1.5
2
2.5
3
3.5
4
Count of the double bounds
Significance
Not significant
Significant lipid


Number of double bounds in a class PC−O
Fold change mmse
0.1
0.0
−0.1
−0.2
p−value: 0.010
0
0.5
1
1.5
2
2.5
3
3.5
4
Count of the double bounds
Significance
Not significant
Significant lipid


Number of double bounds in a class PE
Fold change mmse
0.00
−0.05
−0.10
−0.15
0.5
1
1.5
2
2.5
3
3.5
4
Count of the double bounds
p−value: 0.267
Significance
Not significant
Significant lipid


Number of double bounds in a class PE−P
0.00
−0.05
−0.10
−0.15
Fold change mmse
p−value: 0.108
1
2
3
3.5
Count of the double bounds
Significance
Significant lipid


Number of double bounds in a class SM
Fold change mmse
0.05
0.00
−0.05
−0.10
p−value: 0.219
0.5
1
1.5
Count of the double bounds
Significance
Not significant
Significant lipid

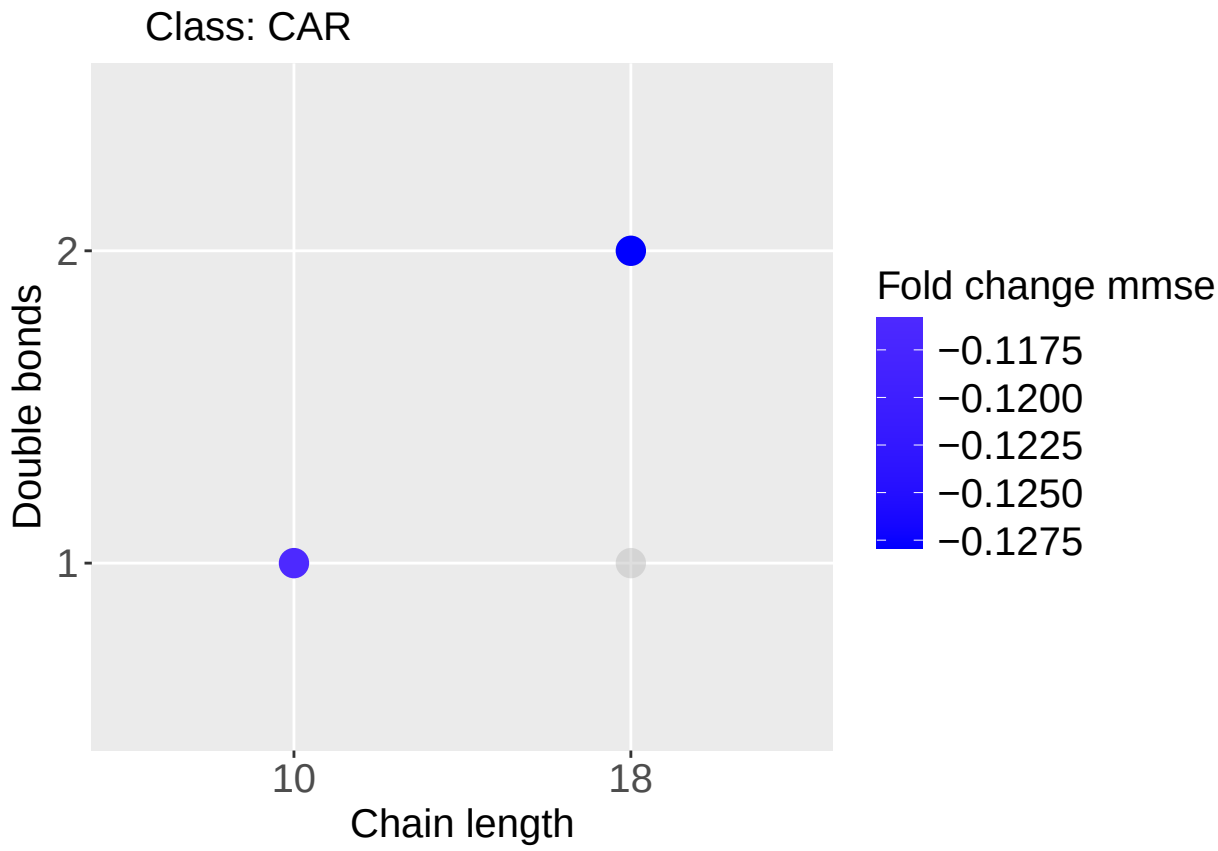


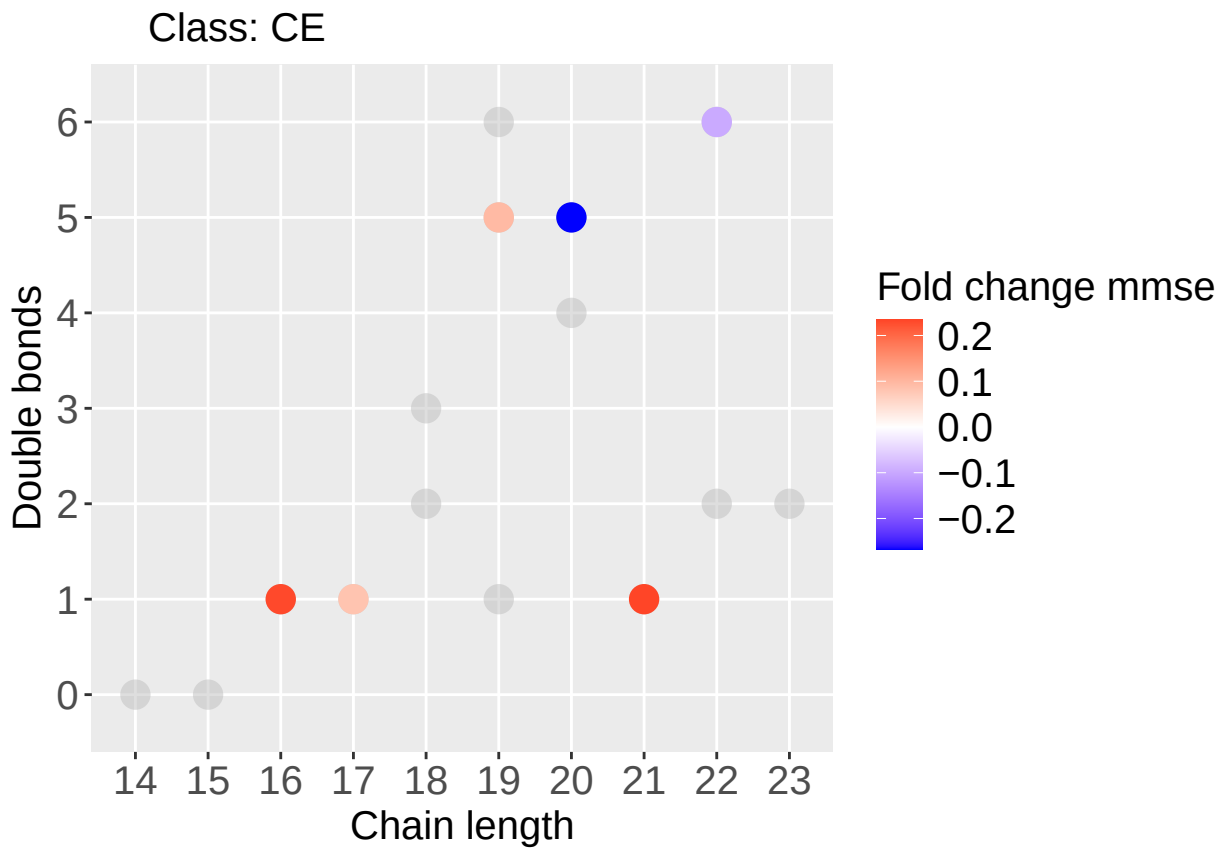
Based on these plots, we can conclude that the level of polyunsaturated lipids is reduced among patients with dementia

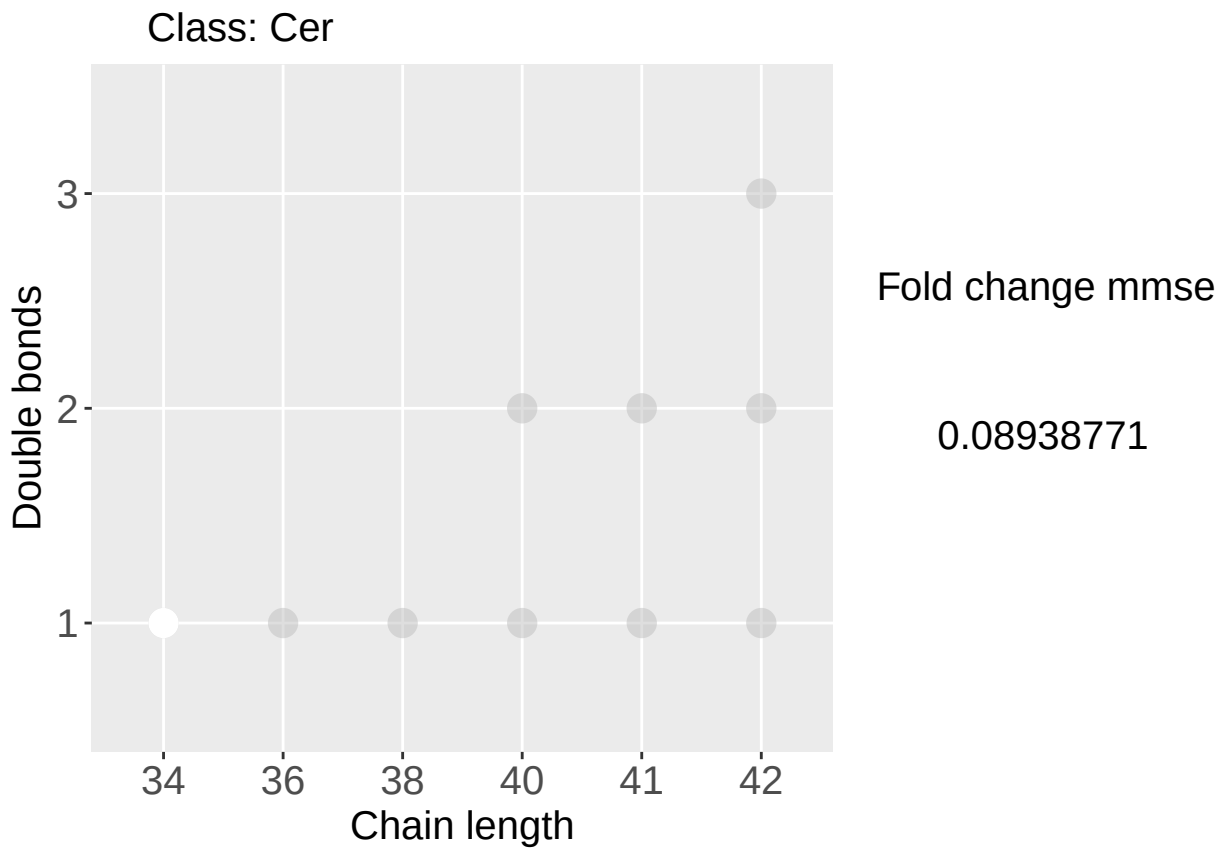
Let's look at the number of double bonds as well as chain lengths in the significant lipids and their differences in the patient groups:

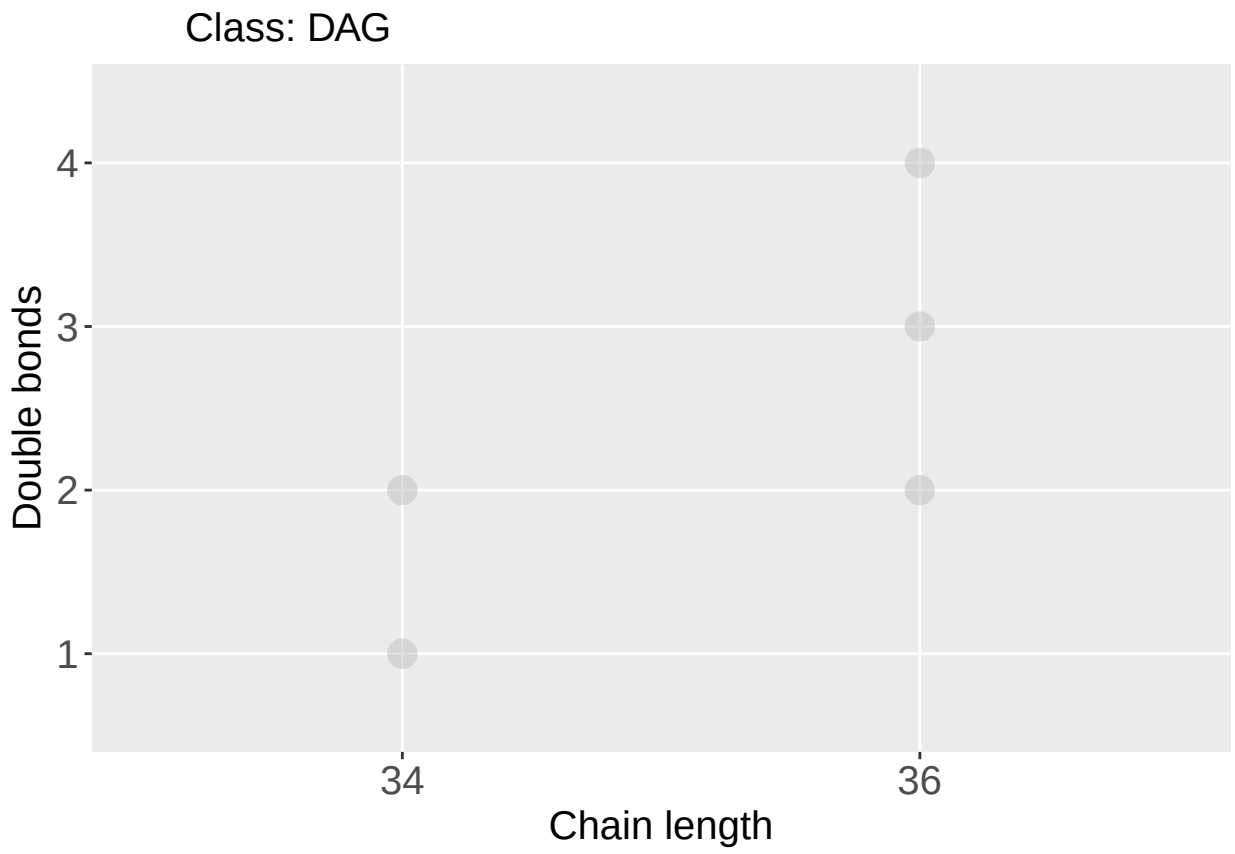
```
unique_classes <- unique(stat.test_mmse_sep$Class)
for (current_class in unique_classes) {

    stat.test_mmse_lipid <- stat.test_mmse_sep[stat.test_mmse_sep$Class ==
        current_class, ]
    merged_bounds_FC <- merge(mean_mmse, stat.test_mmse_lipid,
        by = "lipid_features")

    stat.test_mmse_lipid_signif <- stat.test_mmse_signif_sep[stat.test_mmse_signif_sep$Class ==
        current_class, ]
    merged_bounds_FC_signif <- merge(mean_mmse, stat.test_mmse_lipid_signif,
        by = "lipid_features")

    data1 <- merged_bounds_FC
    data2 <- merged_bounds_FC_signif

    d2 <- ggplot() + geom_point(data = data1, aes(x = Chain_length,
        y = Double_bounds), color = "grey", pch = 16, cex = 5,
```

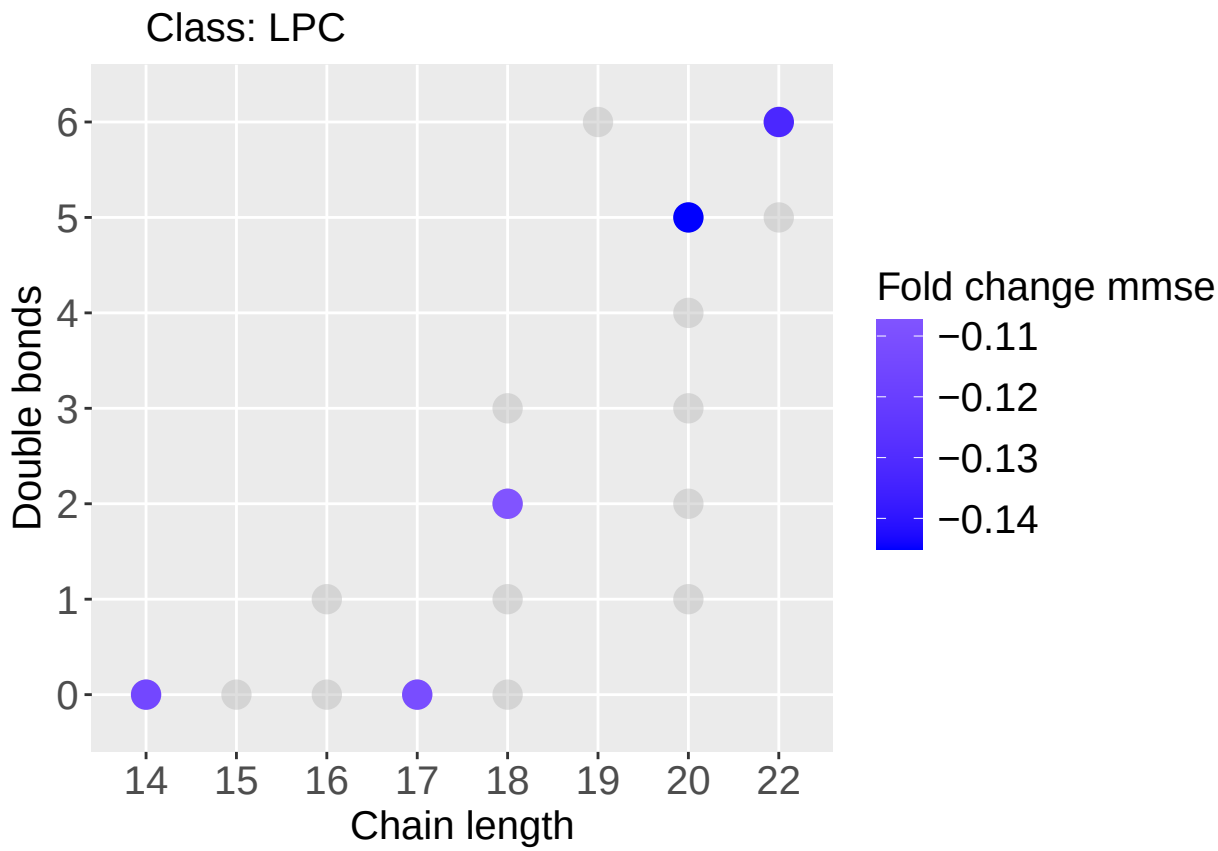
```
        alpha = 0.5) + geom_point(data = data2, aes(x = Chain_length,
        y = Double_bounds, color = FC_mmse), pch = 16, cex = 5,
        alpha = 1) + labs(x = "Chain length", y = "Double bonds",
        color = "FC_mmse") + ggtitle(paste("Class:", current_class)) +
        scale_color_gradient2(low = "blue", mid = "white", high = "red",
            midpoint = 0, name = "Fold change mmse") + theme(plot.title = element_text(hjust = 0.1,
        size = 15), axis.title.x = element_text(size = 15), axis.title.y = element_text(size = 15),
        legend.text = element_text(size = 15), legend.title = element_text(size = 15),
        axis.text.x = element_text(size = 15), axis.text.y = element_text(size = 15))

    print(d2)

}
```

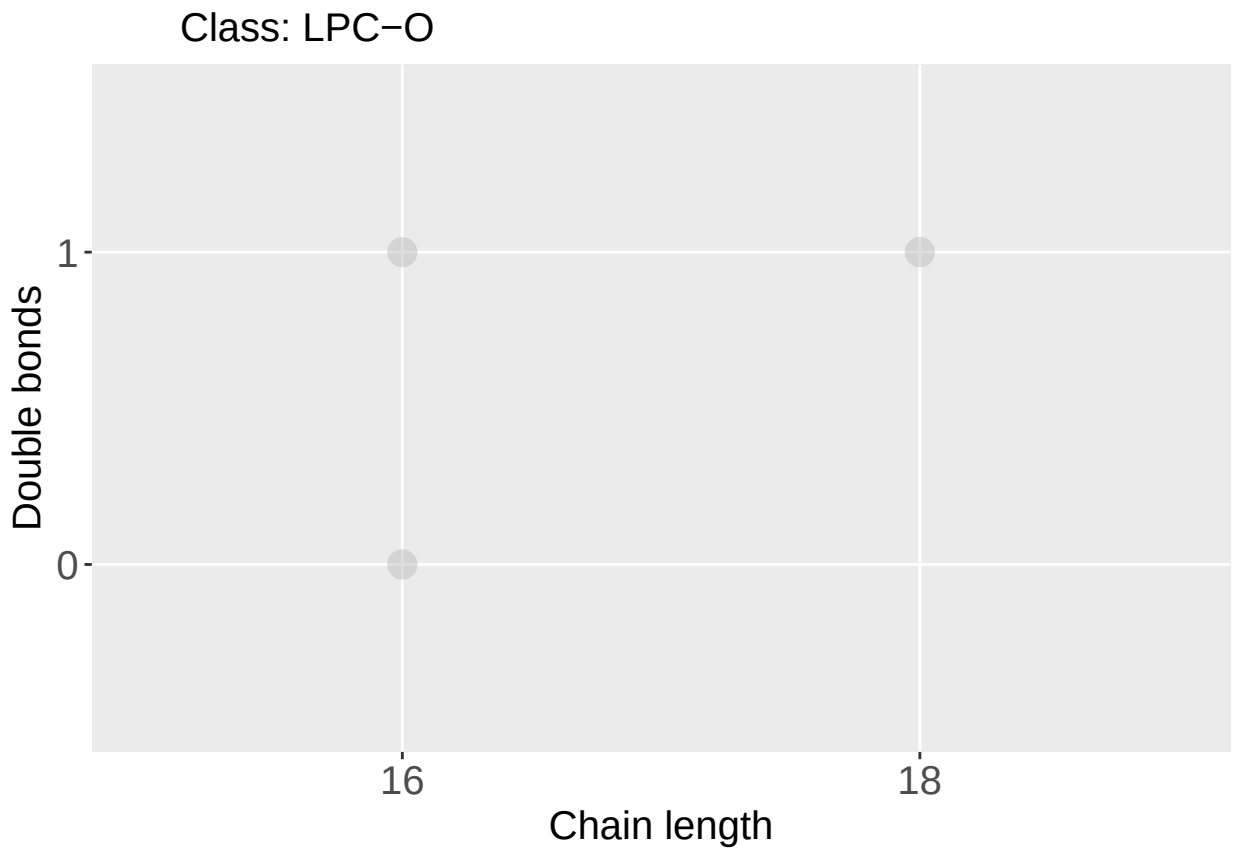


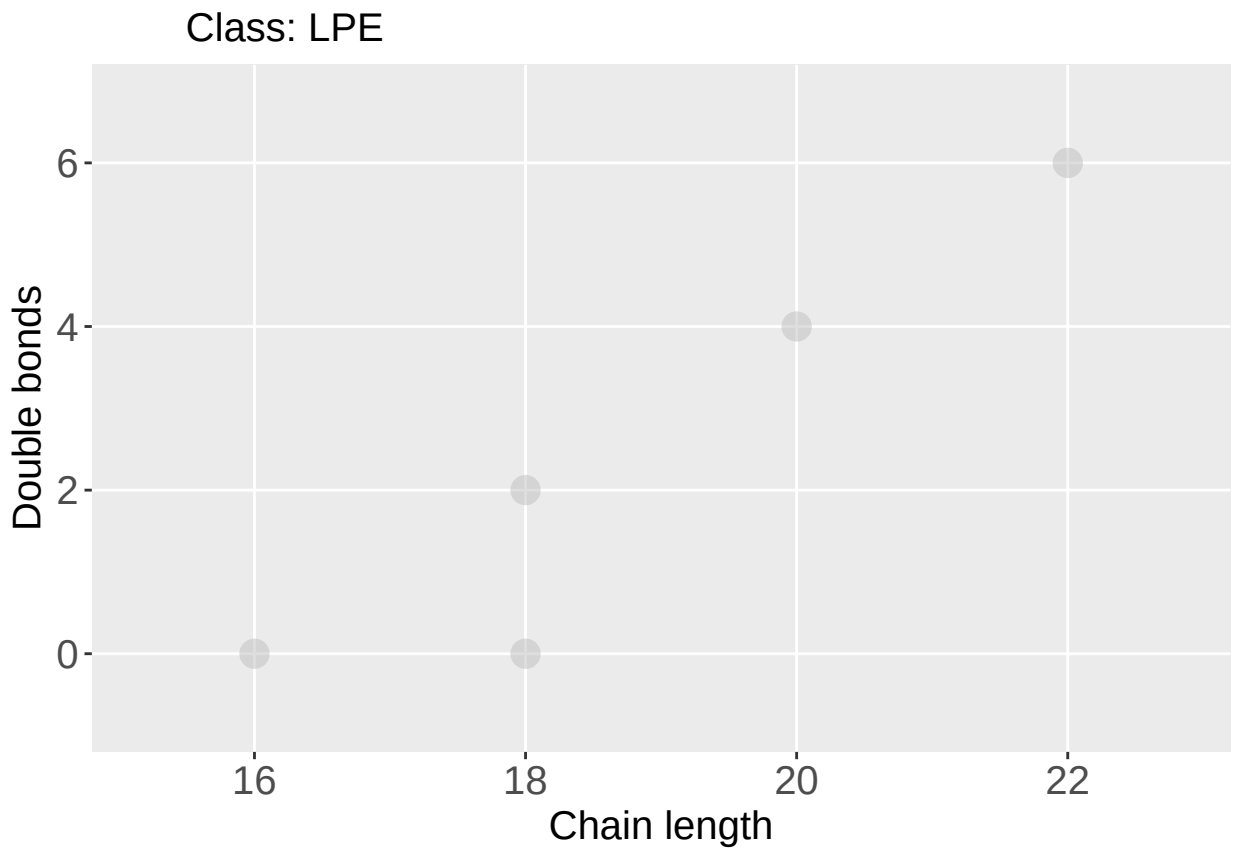

Class: CE
Double bonds
0
1
2
3
4
5
6
14
15
16
17
18
19
20
21
22
23
Chain length
Fold change mmse
0.2
0.1
0.0
−0.1
−0.2

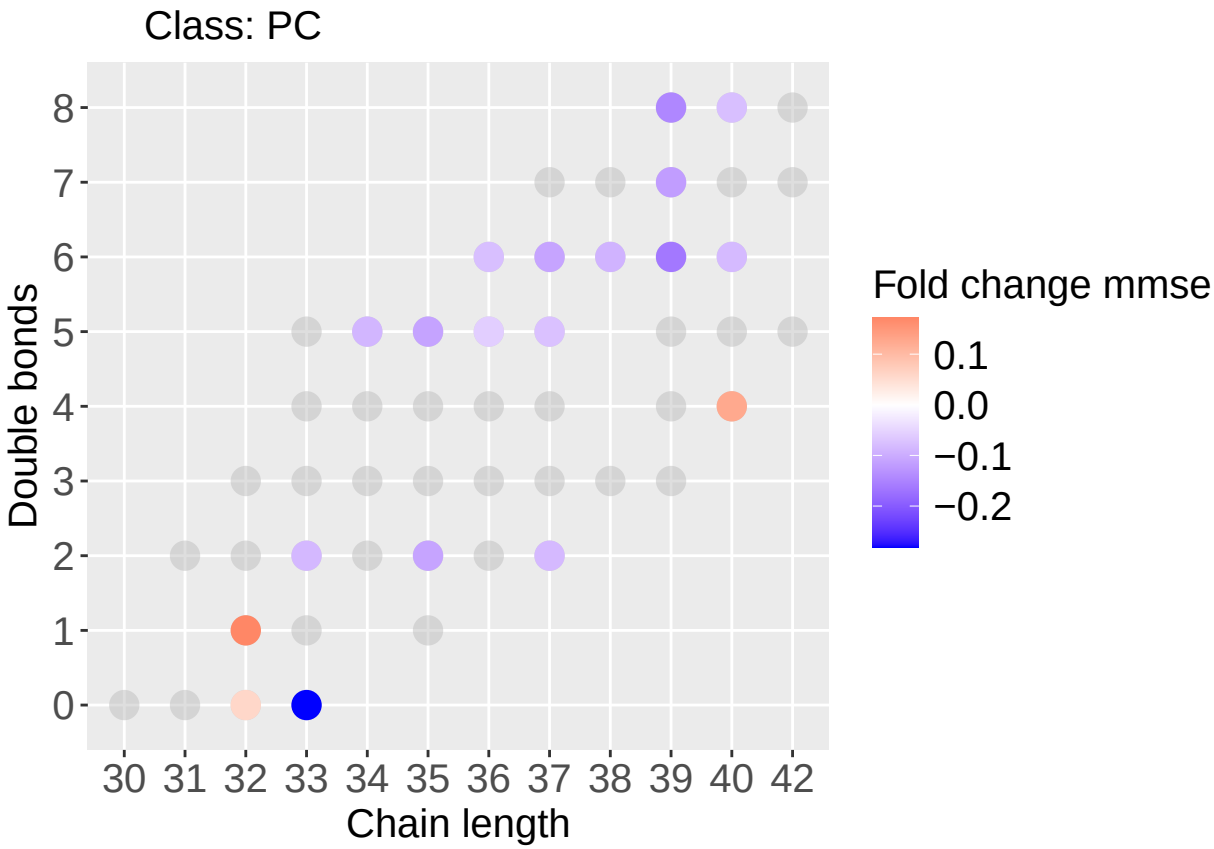

Class: Cer
Double bonds
3
2
1
34
36
38
40
41
42
Chain length
Fold change mmse
0.08938771

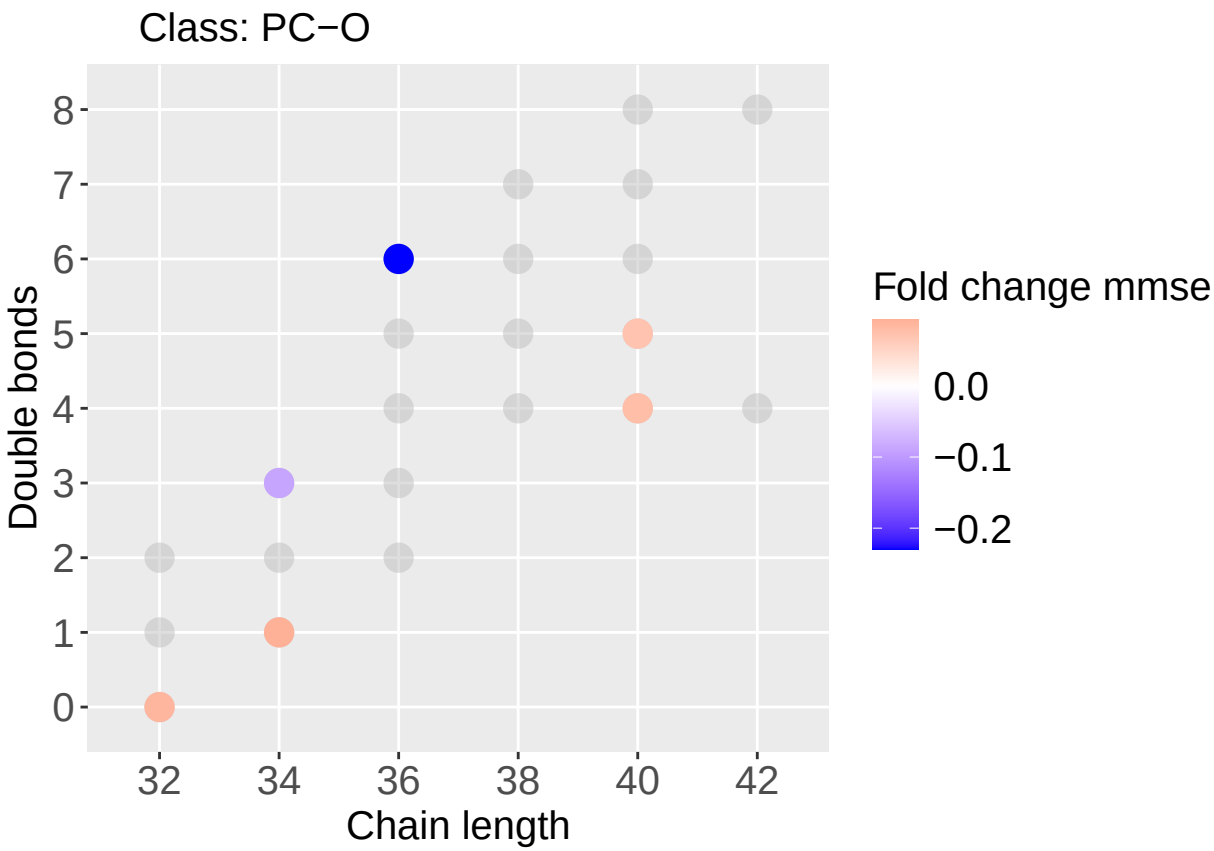

Class: DAG
Double bonds
4
3
2
1
34
36
Chain length

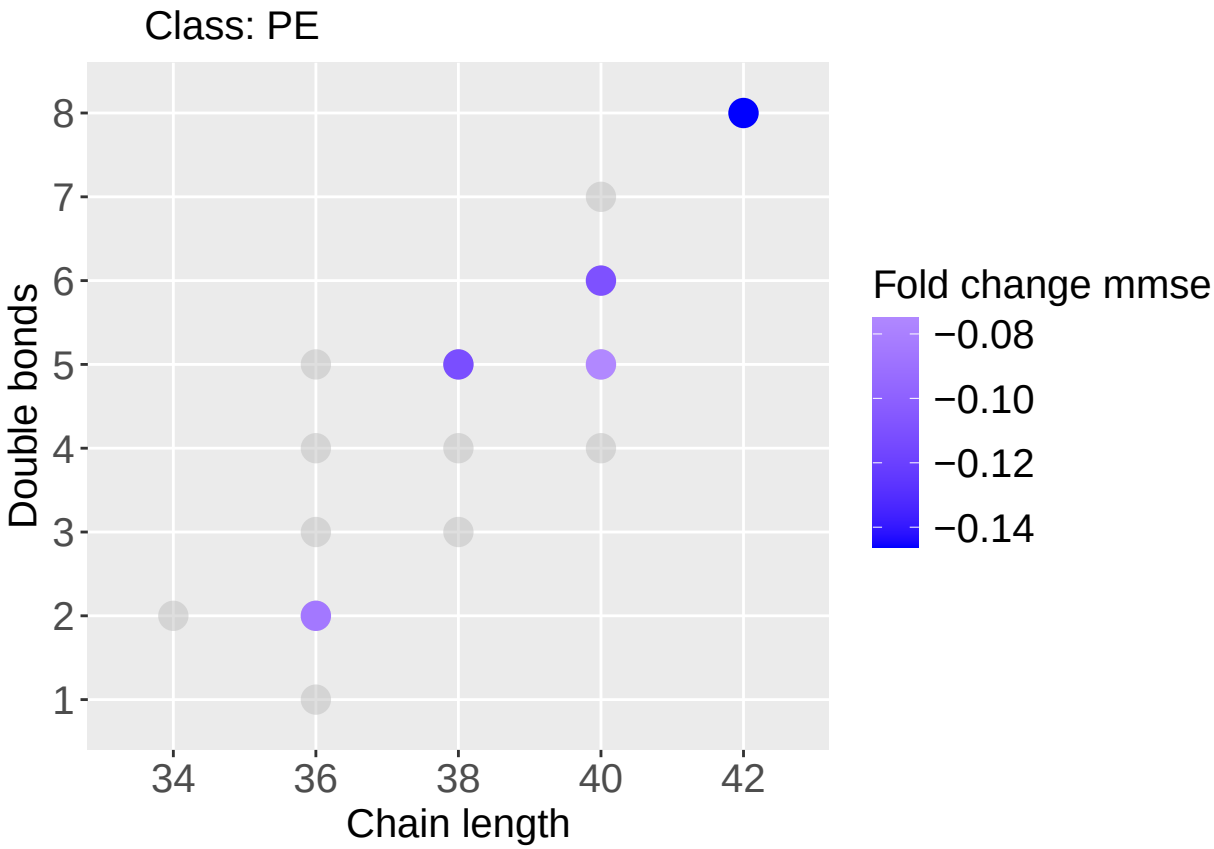

Class: LPC
Double bonds
0
1
2
3
4
5
6
14
15
16
17
18
19
20
22
Chain length
Fold change mmse
−0.11
−0.12
−0.13
−0.14

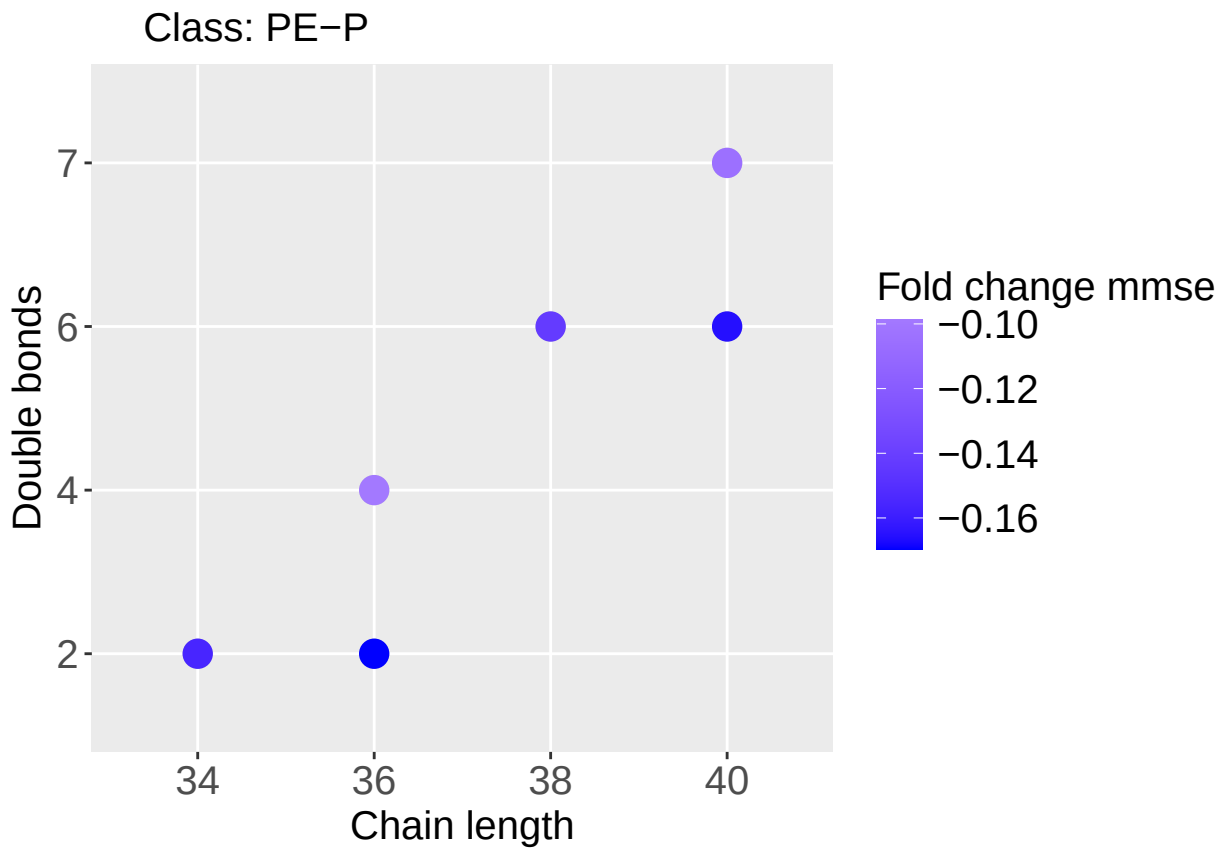

Class: LPC−O
Double bonds
1
0
16
18
Chain length

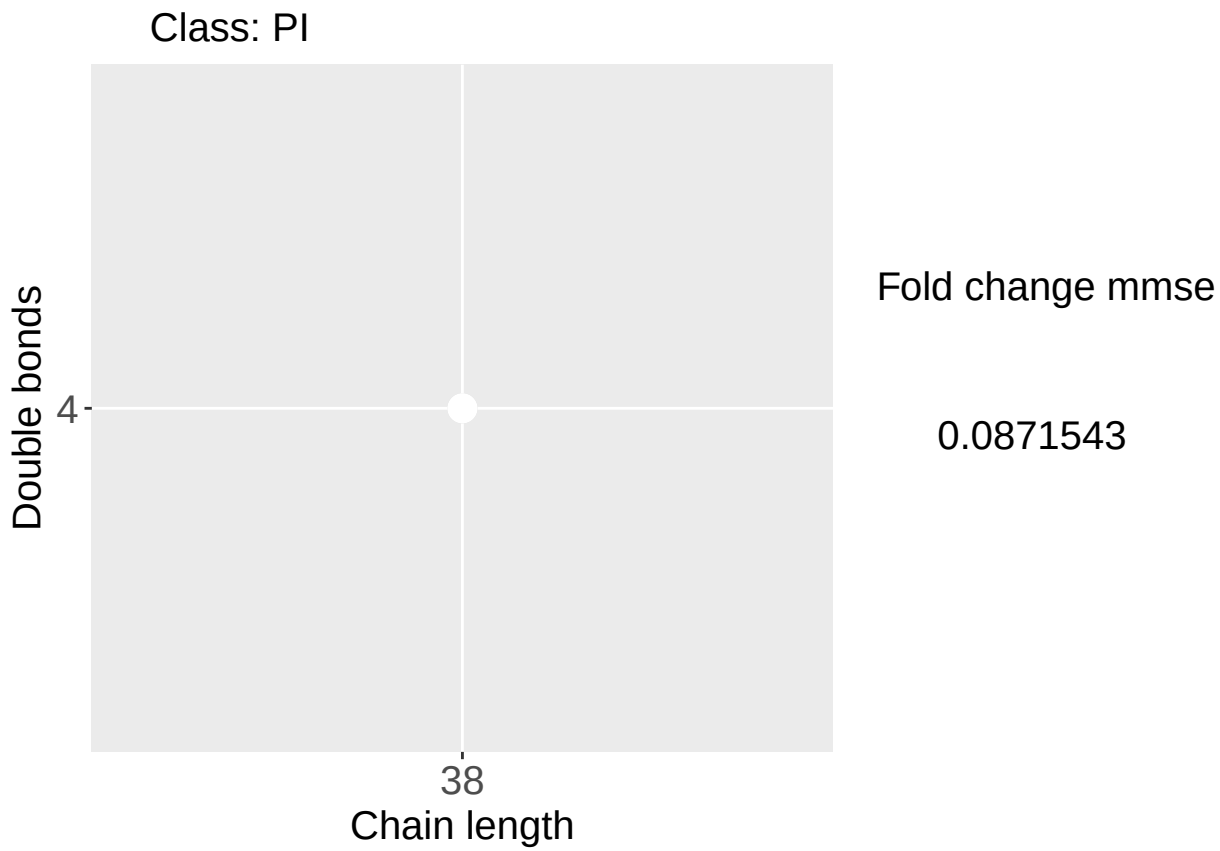

Class: LPE
Double bonds
6
4
2
0
16
18
20
22
Chain length

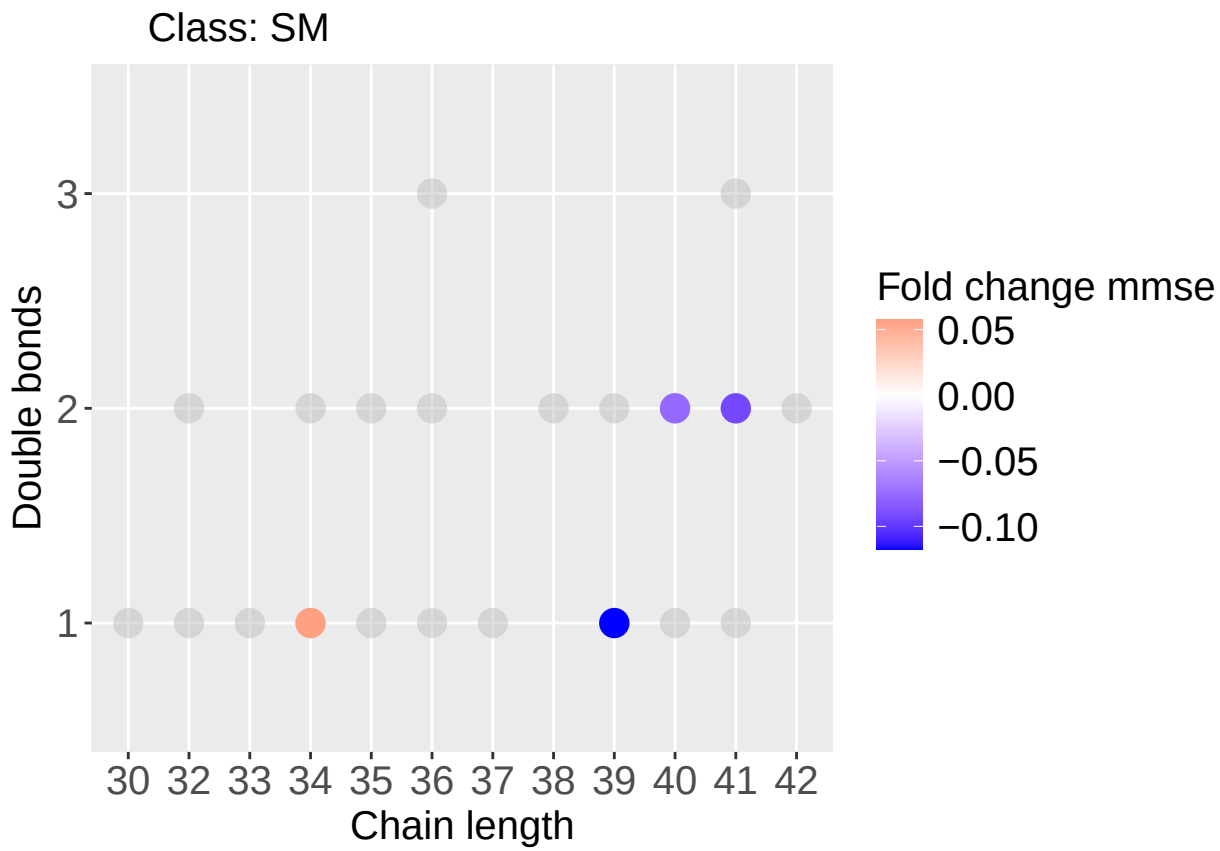

Class: PC
Double bonds
0
1
2
3
4
5
6
7
8
30 31 32 33 34 35 36 37 38 39 40 42
Chain length
Fold change mmse
0.1
0.0
−0.1
−0.2

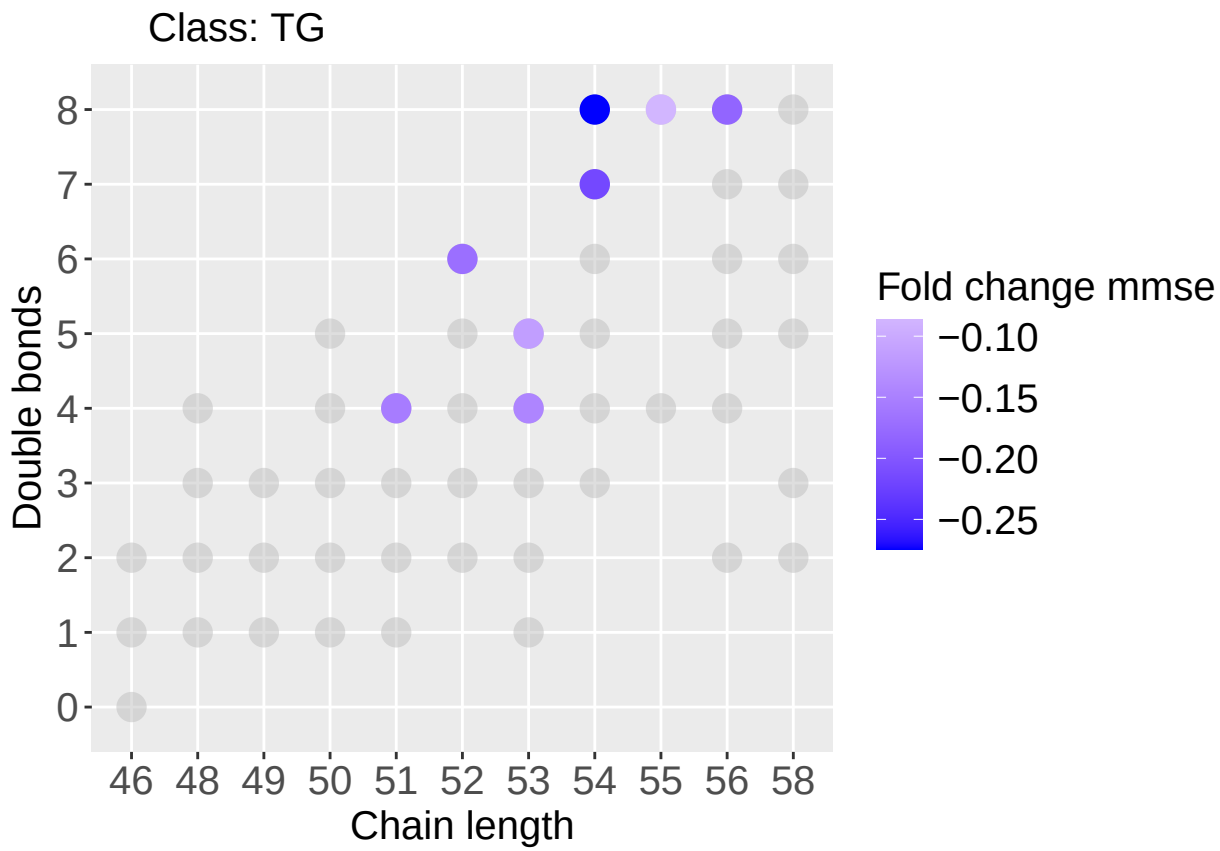

Class: PC−O
Double bonds
Chain length
Fold change mmse
0.0
−0.1
−0.2


Class: PE
Double bonds
8
7
6
5
4
3
2
1
34
36
38
40
42
Chain length
Fold change mmse
−0.08
−0.10
−0.12
−0.14


Class: PE−P
Double bonds
7
6
4
2
34
36
38
40
Chain length
Fold change mmse
−0.10
−0.12
−0.14
−0.16


Class: PI
Double bonds
4
38
Chain length
Fold change mmse
0.0871543


Class: SM
Double bonds
3
2
1
30 32 33 34 35 36 37 38 39 40 41 42
Chain length
Fold change mmse
0.05
0.00
−0.05
−0.10



So we can also say that the number of long chain lipids is also reduced in patients with dementia.