

MicrobialBiotechnology_Project_Markdown

2024-03-05

#Install packages

```
options(repos = c(CRAN = "https://cran.rstudio.com/"))
install.packages("dplyr")

## Installing package into 'M:/R/Win-Library/4.2'
## (as 'lib' is unspecified)

## package 'dplyr' successfully unpacked and MD5 sums checked

## Warning: cannot remove prior installation of package 'dplyr'

## Warning in file.copy(savedcopy, lib, recursive = TRUE): problem copying
## M:\R\Win-Library\4.2\00LOCK\dplyr\libs\x64\dplyr.dll to
## M:\R\Win-Library\4.2\dplyr\libs\x64\dplyr.dll: Permission denied

## Warning: restored 'dplyr'

##
## The downloaded binary packages are in
## C:\Users\s2146807\AppData\Local\Temp\RtmpGEDx57\downloaded_packages

install.packages("lubridate")

## Installing package into 'M:/R/Win-Library/4.2'
## (as 'lib' is unspecified)

## package 'lubridate' successfully unpacked and MD5 sums checked

## Warning: cannot remove prior installation of package 'lubridate'

## Warning in file.copy(savedcopy, lib, recursive = TRUE): problem copying
## M:\R\Win-Library\4.2\00LOCK\lubridate\libs\x64\lubridate.dll to
## M:\R\Win-Library\4.2\lubridate\libs\x64\lubridate.dll: Permission denied

## Warning: restored 'lubridate'

##
## The downloaded binary packages are in
## C:\Users\s2146807\AppData\Local\Temp\RtmpGEDx57\downloaded_packages

install.packages("ggplot2")

## Installing package into 'M:/R/Win-Library/4.2'
## (as 'lib' is unspecified)
```

```
## package 'ggplot2' successfully unpacked and MD5 sums checked
##
## The downloaded binary packages are in
## C:\Users\s2146807\AppData\Local\Temp\RtmpGEDx57\downloaded_packages

install.packages("tidyr")

## Installing package into 'M:/R/Win-Library/4.2'
## (as 'lib' is unspecified)

## package 'tidyr' successfully unpacked and MD5 sums checked

## Warning: cannot remove prior installation of package 'tidyr'

## Warning in file.copy(savedcopy, lib, recursive = TRUE): problem copying
## M:\R\Win-Library\4.2\00LOCK\tidyr\libs\x64\tidyr.dll to
## M:\R\Win-Library\4.2\tidyr\libs\x64\tidyr.dll: Permission denied

## Warning: restored 'tidyr'

##
## The downloaded binary packages are in
## C:\Users\s2146807\AppData\Local\Temp\RtmpGEDx57\downloaded_packages

install.packages("scales")

## Installing package into 'M:/R/Win-Library/4.2'
## (as 'lib' is unspecified)

## package 'scales' successfully unpacked and MD5 sums checked
##
## The downloaded binary packages are in
## C:\Users\s2146807\AppData\Local\Temp\RtmpGEDx57\downloaded_packages

install.packages("MASS")

## Installing package into 'M:/R/Win-Library/4.2'
## (as 'lib' is unspecified)

## package 'MASS' successfully unpacked and MD5 sums checked

## Warning: cannot remove prior installation of package 'MASS'

## Warning in file.copy(savedcopy, lib, recursive = TRUE): problem copying
## M:\R\Win-Library\4.2\00LOCK\MASS\libs\x64\MASS.dll to
## M:\R\Win-Library\4.2\MASS\libs\x64\MASS.dll: Permission denied

## Warning: restored 'MASS'

##
## The downloaded binary packages are in
## C:\Users\s2146807\AppData\Local\Temp\RtmpGEDx57\downloaded_packages

#library import
```

```

library(dplyr)

## Warning: package 'dplyr' was built under R version 4.2.3
##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':
##
##   filter, lag

## The following objects are masked from 'package:base':
##
##   intersect, setdiff, setequal, union

library(lubridate)

## Warning: package 'lubridate' was built under R version 4.2.3
##
## Attaching package: 'lubridate'

## The following objects are masked from 'package:base':
##
##   date, intersect, setdiff, union

library(ggplot2)

## Warning: package 'ggplot2' was built under R version 4.2.3

library(tidyr)

## Warning: package 'tidyr' was built under R version 4.2.3

library(scales)

## Warning: package 'scales' was built under R version 4.2.3

library(MASS)

## Warning: package 'MASS' was built under R version 4.2.3
##
## Attaching package: 'MASS'

## The following object is masked from 'package:dplyr':
##
##   select

data <- read.csv ("datarecord.csv")
head(data)

##   Paper.No.
## 1         1

```

```

## 2      2
## 3      3
## 4      4
## 5      5
## 6      6
##
Title
## 1      A metabolomic landscape of maize plants treated with a microbial biostimulant under well-watered and drought conditions
## 2      Streamlined identification of strain engineering targets for bioprocess improvement using metabolic pathway enrichment analysis
## 3      On-line untargeted metabolomics monitoring of an Escherichia coli succinate fermentation process
## 4      A novel targeted/untargeted GC-Orbitrap metabolomics methodology applied to Candida albicans and Staphylococcus aureus biofilms
## 5      Glycolysis and pyrimidine biosynthesis are required for replication of adherent-invasive escherichia coli in macrophages
## 6 Substantial Extracellular Metabolic Differences Found Between Phylogenetically Closely Related Probiotic and Pathogenic Strains of Escherichia coli
##      DOI      ResGrp.PI Type Institution
## 1  10.3389/fpls.2021.676632 Karl Burgess IQB3      SBS
## 2  10.1038/s41598-023-39661-x Karl Burgess IQB3      SBS
## 3      10.1002/bit.28173 Karl Burgess IQB3      SBS
## 4  10.1007/s11306-016-1134-2 Karl Burgess IQB3      SBS
## 5      10.1099/mic.0.000289 Karl Burgess IQB3      SBS
## 6  10.3389/fmicb.2019.00252 Karl Burgess IQB3      SBS
##      Journal Year AnalysisPgrm CodeArchived DAS
## 1      Frontiers in Plant Science 2021      1      NA      1
## 2      Scientific reports 2023      1      NA      1
## 3 Biotechnology and Bioengineering 2022      1      NA      1
## 4      Metabolomics 2016      1      NA      NA
## 5 Biotechnology and Bioengineering 2016      1      NA      NA
## 6      Frontiers in Microbiology 2019      1      NA      1
##      CorresAuthor Preprint Complete Reuse Access Licence Image Genomics
## 1      1      0      2      3      4      4      NA      NA
## 2      1      0      4      4      4      4      NA      NA
## 3      1      0      3      4      4      4      NA      NA
## 4      1      0      4      4      2      4      NA      NA
## 5      1      0      2      2      2      4      0      NA
## 6      1      0      4      4      4      4      NA      NA
##      Proteometabolomic      Data.Storage Funding.Source
## 1      0      Supplementary material      1
## 2      1      Supplementary material, MetaboLights      0
## 3      0      Supplementary material, MetaboLights      0
## 4      1      Supplementary material      0
## 5      NA      Supplementary material      1
## 6      1 Supplementary material, GNPS repository      0
##      Number.of.times.cited.according.to.Google.Scholar CitationsPA
## 1      40      13.33333
## 2      2      2.00000

```

```
## 3                6      3.00000
## 4               56      7.00000
## 5                5      0.62500
## 6               29      5.80000
## Competing.interests PIGroupLeader
## 1                1          0
## 2                0          1
## 3               NA          1
## 4                1          1
## 5               NA          0
## 6                0          0
```

#1 - Descriptive Statistics

#How many papers in each type

```
type_frequency <- table(data$Type)
print(type_frequency)
```

```
##
## IQB3 Other
## 80 50
```

#frequency and percentage of paper in each year

```
total_counts_by_type <- data %>%
  group_by(Type) %>%
  summarise(Total = n(), .groups = "drop")

# Calculate frequency and percentage for each Type and Year
summarized_data <- data %>%
  group_by(Year, Type) %>%
  summarise(count = n(), .groups = "drop") %>%
  left_join(total_counts_by_type, by = "Type") %>%
  mutate(Percentage = (count / Total) * 100) # Removed the trailing %>%

print(summarized_data)
```

```
## # A tibble: 20 × 5
##   Year Type count Total Percentage
##   <int> <chr> <int> <int>      <dbl>
## 1 2014 IQB3     8     80        10
## 2 2014 Other    7     50        14
## 3 2015 IQB3     7     80        8.75
## 4 2015 Other    5     50        10
## 5 2016 IQB3     5     80        6.25
## 6 2016 Other    8     50        16
## 7 2017 IQB3     9     80       11.2
## 8 2017 Other    3     50         6
## 9 2018 IQB3     7     80        8.75
## 10 2018 Other    4     50         8
```

```
## 11 2019 IQB3      9    80    11.2
## 12 2019 Other     4    50      8
## 13 2020 IQB3      7    80    8.75
## 14 2020 Other     7    50    14
## 15 2021 IQB3      8    80    10
## 16 2021 Other     5    50    10
## 17 2022 IQB3     11    80   13.8
## 18 2022 Other     3    50     6
## 19 2023 IQB3      9    80   11.2
## 20 2023 Other     4    50     8
```

Calculate the total number of papers for each year

```
yearly_totals <- data %>%
  group_by(Year) %>%
  summarise(Total = n(), .groups = "drop")

# Calculate the grand total of all papers
grand_total <- sum(yearly_totals$Total)

# Add a column for the percentage of each year's total relative to the grand
total
yearly_totals <- yearly_totals %>%
  mutate(Percentage = (Total / grand_total) * 100)

# Print the yearly totals and percentages
print(yearly_totals)

## # A tibble: 10 × 3
##   Year Total Percentage
##   <int> <int>     <dbl>
## 1  2014     15     11.5
## 2  2015     12      9.23
## 3  2016     13     10
## 4  2017     12      9.23
## 5  2018     11      8.46
## 6  2019     13     10
## 7  2020     14    10.8
## 8  2021     13     10
## 9  2022     14    10.8
## 10 2023     13     10
```

#to categorize papers based on the year of publication compared to FAIR principles implementation 2016 (overall)

```
data <- data %>%
  mutate(Period = ifelse(Year <= 2016, "Before or in 2016", "After 2016"))

# Calculate the total number of papers for each period
period_totals <- data %>%
```

```

group_by(Period) %>%
  summarise(Total = n(), .groups = "drop")

# Calculate the grand total of all papers
grand_total <- sum(period_totals$Total)

# Add a column for the percentage of each period's total relative to the grand total
period_totals <- period_totals %>%
  mutate(Percentage = (Total / grand_total) * 100)

# Print the period totals and percentages
print(period_totals)

## # A tibble: 2 × 3
##   Period      Total Percentage
##   <chr>      <int>      <dbl>
## 1 After 2016      90      69.2
## 2 Before or in 2016  40      30.8

```

#to categorize papers based on the year of publication compared to FAIR principles implementation 2016 (depend on type)

```

#Frequency and Percentage of paper before and After FAIR principles (2016)
total_counts_by_type <- data %>%
  group_by(Type) %>%
  summarise(Total = n(), .groups = "drop")

# Categorize, calculate frequency and percentage for each Type based on year
summarized_data <- data %>%
  mutate(Category = ifelse(Year <= 2016, "On/Before 2016", "After 2020")) %>%
  group_by(Category, Type) %>%
  summarise(count = n(), .groups = "drop") %>%
  left_join(total_counts_by_type, by = "Type") %>%
  mutate(Percentage = (count / Total) * 100)

```

```

print(summarized_data)

## # A tibble: 4 × 5
##   Category      Type  count Total Percentage
##   <chr>      <chr> <int> <int>      <dbl>
## 1 After 2020    IQB3     60    80      75
## 2 After 2020   Other     30    50      60
## 3 On/Before 2016 IQB3     20    80      25
## 4 On/Before 2016 Other     20    50      40

```

#to categorise papers based on the year of publication compared to COVID 19 - 2020 (overall)

```

data <- data %>%
  mutate(Period = ifelse(Year <= 2020, "Before or in 2020", "After 2020"))

# Calculate the total number of papers for each period
period_totals <- data %>%
  group_by(Period) %>%
  summarise(Total = n(), .groups = "drop")

# Calculate the grand total of all papers
grand_total <- sum(period_totals$Total)

# Add a column for the percentage of each period's total relative to the grand total
period_totals <- period_totals %>%
  mutate(Percentage = (Total / grand_total) * 100)

# Print the period totals and percentages
print(period_totals)

## # A tibble: 2 × 3
##   Period          Total Percentage
##   <chr>          <int>     <dbl>
## 1 After 2020           40       30.8
## 2 Before or in 2020    90       69.2

```

#to categorise papers based on the year of publication compared to COVID 19 - 2020 (IQB3 vs Other)

```

total_counts_by_type <- data %>%
  group_by(Type) %>%
  summarise(Total = n(), .groups = "drop")

# Categorize, calculate frequency and percentage for each Type based on year
summarized_data <- data %>%
  mutate(Category = ifelse(Year <= 2020, "On/Before 2020", "After 2020")) %>%
  group_by(Category, Type) %>%
  summarise(count = n(), .groups = "drop") %>%
  left_join(total_counts_by_type, by = "Type") %>%
  mutate(Percentage = (count / Total) * 100)

print(summarized_data)

## # A tibble: 4 × 5
##   Category      Type  count Total Percentage
##   <chr>        <chr> <int> <int>     <dbl>
## 1 After 2020   IQB3     28    80       35
## 2 After 2020   Other    12    50       24
## 3 On/Before 2020 IQB3     52    80       65
## 4 On/Before 2020 Other    38    50       76

```


Frequency and Percentage of the papers that share data (Data Sharing= Data Completeness score >1) Overall

```
data <- data %>%
  mutate(Period = ifelse(Complete > 1, "Completeness > 1", "Completeness = 1"
))

# Calculate the total number of papers for each period
period_totals <- data %>%
  group_by(Period) %>%
  summarise(Total = n(), .groups = "drop")

# Calculate the grand total of all papers
grand_total <- sum(period_totals$Total)

# Add a column for the percentage of each period's total relative to the grand total
period_totals <- period_totals %>%
  mutate(Percentage = (Total / grand_total) * 100)

# Print the period totals and percentages
print(period_totals)

## # A tibble: 2 × 3
##   Period      Total Percentage
##   <chr>      <int>      <dbl>
## 1 Completeness = 1         6      4.62
## 2 Completeness > 1     124     95.4
```

Frequency and Percentage of the papers that share data (Data Sharing= Data Completeness score >1) by Type

```
total_counts_by_type <- data %>%
  group_by(Type) %>%
  summarise(Total = n(), .groups = "drop")

# Categorize based on Completeness, calculate frequency and percentage for each Type
summarized_data <- data %>%
  filter(Complete == 1 | Complete > 1) %>%
  mutate(Category = ifelse(Complete == 1, "Completeness = 1", "Completeness > 1")) %>%
  group_by(Category, Type) %>%
  summarise(count = n(), .groups = "drop") %>%
  left_join(total_counts_by_type, by = "Type") %>%
  mutate(Percentage = (count / Total) * 100)

print(summarized_data)
```

```
## # A tibble: 4 × 5
##   Category      Type count Total Percentage
##   <chr>      <chr> <int> <int>      <dbl>
## 1 Completeness = 1 IQB3      3     80       3.75
## 2 Completeness = 1 Other      3     50        6
## 3 Completeness > 1 IQB3     77     80      96.2
## 4 Completeness > 1 Other     47     50      94
```

#Chi square test to assess if there is any difference in data share between the two types (IQB3 vs Other)

```
# Create a contingency table
table_completeness <- table(data$Type, data$Complete > 1)

# Perform the Chi-square test
result <- chisq.test(table_completeness)

## Warning in chisq.test(table_completeness): Chi-squared approximation may be
## incorrect

#Print the chi-square results
print(result)

##
## Pearson's Chi-squared test with Yates' continuity correction
##
## data:  table_completeness
## X-squared = 0.027302, df = 1, p-value = 0.8688

# Get the expected values
expected_values <- result$expected

# Print the expected values
print(expected_values) ##in order to check the assumption of chi square test:
Each cell in the contingency table should have an expected count of 5 or more
.

##
##           FALSE      TRUE
## IQB3  3.692308 76.30769
## Other  2.307692 47.69231

#The assumptions of that test were met:

#### Sample Size: Each cell in the contingency table has an expected count of 5 or more.
#### Independence: The observations are independent of each other. This means that the selection of one observation should not influence or affect the selection of another observation.
#### Random Sampling: The data is a random sample.
```

Categorical Data: Both variables should be categorical (either nominal or ordinal).

#Frequency and percentage of Preprint

Calculate frequency and percentage for each Preprint category, across all types

```
Preprint_summary <- data %>%  
  group_by(Preprint) %>%  
  summarise(count = n(), .groups = "drop")
```

Calculate the overall total

```
overall_total <- sum(Preprint_summary$count)
```

Add a column for the percentage of each Preprint category relative to the overall total

```
Preprint_summary <- Preprint_summary %>%  
  mutate(percentage = (count / overall_total) * 100)
```

Print the summary

```
print(Preprint_summary)
```

```
## # A tibble: 2 × 3
```

```
##   Preprint count percentage
```

```
##   <int> <int>    <dbl>
```

```
## 1     0   110     84.6
```

```
## 2     1    20     15.4
```

Frequency and Percentage of the papers with Preprint

```
data %>%  
  group_by(Type, Preprint) %>%  
  summarise(count = n(), .groups = "drop") %>%  
  group_by(Type) %>%  
  mutate(total = sum(count),  
         percentage = (count/total)*100) %>%  
  ungroup() %>%  
  arrange(Type, Preprint)
```

```
## # A tibble: 4 × 5
```

```
##   Type Preprint count total percentage
```

```
##   <chr>    <int> <int> <int>    <dbl>
```

```
## 1 IQB3      0    69    80     86.2
```

```
## 2 IQB3      1    11    80     13.8
```

```
## 3 Other     0    41    50      82
```

```
## 4 Other     1     9    50      18
```

#Chi square test to assess if there is any difference in preprint between the two types (IQB3, Other)

Create a contingency table

```
table_preprint <- table(data$Type, data$Preprint)
```

```

# Perform the Chi-square test
result <- chisq.test(table_preprint)

#Print the chi-square results
print(result)

##
## Pearson's Chi-squared test with Yates' continuity correction
##
## data: table_preprint
## X-squared = 0.16287, df = 1, p-value = 0.6865

# Get the expected values
expected_values <- result$expected

# Print the expected values
print(expected_values) ##in order to check the assumption of chi square test:
Each cell in the contingency table should have an expected count of 5 or more
.

##
##           0           1
## IQB3  67.69231 12.307692
## Other 42.30769  7.692308

#The assumptions of that test were met:

#### Sample Size: Each cell in the contingency table has an expected count of
5 or more.
#### Independence: The observations are independent of each other. This mean
s that the selection of one observation should not influence or affect the se
lection of another observation.
#### Random Sampling: The data is a random sample.
#### Categorical Data: Both variables should be categorical (either nominal or
ordinal).

```

Calculate frequency and percentage for DAS

```

DAS_summary <- data %>%
  group_by(DAS) %>%
  summarise(count = n(), .groups = "drop")

# Calculate the overall total
overall_total <- sum(DAS_summary$count)

# Add a column for the percentage of each DAS category relative to the overal
l total
DAS_summary <- DAS_summary %>%
  mutate(percentage = (count / overall_total) * 100)

```

```

print(DAS_summary)

## # A tibble: 3 × 3
##   DAS count percentage
##   <int> <int>      <dbl>
## 1     0     8        6.15
## 2     1    48       36.9
## 3    NA    74       56.9

data$DAS <- as.factor(data$DAS)

# Frequency and Percentage of the papers with DAS in the publications
data %>%
  group_by(Type, DAS) %>%
  summarise(count = n(), .groups = "drop") %>%
  group_by(Type) %>%
  mutate(total = sum(count),
         percentage = (count/total)*100) %>%
  ungroup() %>%
  arrange(Type, DAS)

## # A tibble: 6 × 5
##   Type DAS   count total percentage
##   <chr> <fct> <int> <int>      <dbl>
## 1 IQB3  0         6    80        7.5
## 2 IQB3  1        28    80        35
## 3 IQB3 <NA>       46    80       57.5
## 4 Other 0         2    50         4
## 5 Other 1        20    50        40
## 6 Other <NA>      28    50        56

```

#Chi square test to assess if there is any difference in DAS between the two types (IQB3, Other)

```

# Create a contingency table
table_das <- table(data$Type, data$DAS)

# Perform the Chi-square test
result <- chisq.test(table_das)

## Warning in chisq.test(table_das): Chi-squared approximation may be incorrect

#Print the chi-square results
print(result)

##
## Pearson's Chi-squared test with Yates' continuity correction
##

```

```
## data: table_das
## X-squared = 0.25267, df = 1, p-value = 0.6152

# Get the expected values
expected_values <- result$expected

# Print the expected values
print(expected_values) ##in order to check the assumption of chi square test:
Each cell in the contingency table should have an expected count of 5 or more
.

##
##           0           1
## IQB3  4.857143 29.14286
## Other 3.142857 18.85714

#The assumptions of that test were met:

#### Sample Size: Each cell in the contingency table has an expected count of
5 or more.
#### Independence: The observations are independent of each other. This mean
s that the selection of one observation should not influence or affect the se
lection of another observation.
#### Random Sampling: The data is a random sample.
#### Categorical Data: Both variables should be categorical (either nominal or
ordinal).
```

Calculate frequency and percentage for CorresAuthor

```
CorresAuthor_summary <- data %>%
  group_by(CorresAuthor) %>%
  summarise(count = n(), .groups = "drop")

# Calculate the overall total
overall_total <- sum(CorresAuthor_summary$count)

# Add a column for the percentage of each category relative to the overall to
tal
CorresAuthor_summary <- CorresAuthor_summary %>%
  mutate(percentage = (count / overall_total) * 100)

print(CorresAuthor_summary)

## # A tibble: 2 × 3
##   CorresAuthor count percentage
##       <int> <int>       <dbl>
## 1         0    21        16.2
## 2         1   109        83.8
```

```
# Frequency and Percentage of the papers with CorresAuthor being 0 or 1
data %>%
```

```
  group_by(Type, CorresAuthor) %>%
  summarise(count = n(), .groups = "drop") %>%
  group_by(Type) %>%
  mutate(total = sum(count),
         percentage = (count/total)*100) %>%
  ungroup() %>%
  arrange(Type, CorresAuthor)
```

```
## # A tibble: 4 × 5
##   Type CorresAuthor count total percentage
##   <chr>      <int> <int> <int>      <dbl>
## 1 IQB3          0     14     80       17.5
## 2 IQB3          1     66     80       82.5
## 3 Other         0      7     50        14
## 4 Other         1     43     50        86
```

```
# Assuming 'data' is your DataFrame and has been loaded correctly
# Transform the CorresAuthor variable
```

```
data <- data %>%
  mutate(CorresAuthorStatus = case_when(
    CorresAuthor == 1 ~ "Group Leader",
    CorresAuthor == 0 ~ "Not Group Leader",
    TRUE ~ as.character(CorresAuthor) # Fallback for unexpected values
  ))
```

```
# Check the class of the new variable
```

```
class(data$CorresAuthorStatus)
```

```
## [1] "character"
```

```
# Convert the new Funding Source Status variable to a factor for plotting
```

```
data <- data %>%
  mutate(CorresAuthorStatus = factor(CorresAuthorStatus, levels = c("Not
Group Leader", "Group Leader")))
```

```
# Calculate frequency and percentage for each 'Complete' score and 'Funding
Source Status'
```

```
CorresAuthor_frequency <- data %>%
  group_by(Complete, CorresAuthorStatus) %>%
  summarise(Frequency = n(), .groups = 'drop') %>%
  mutate(Percentage = (Frequency / sum(Frequency)) * 100)
```

```
# Define specific colors for the Funding Source status
```

```
colors <- c("Not Group Leader" = "#E5696F", "Group Leader" = "#50689B") #
Correct the color names to match factor levels
```

```
# Create the plot
```

```
CorresAuthor_plot <- ggplot(CorresAuthor_frequency, aes(x
```

```

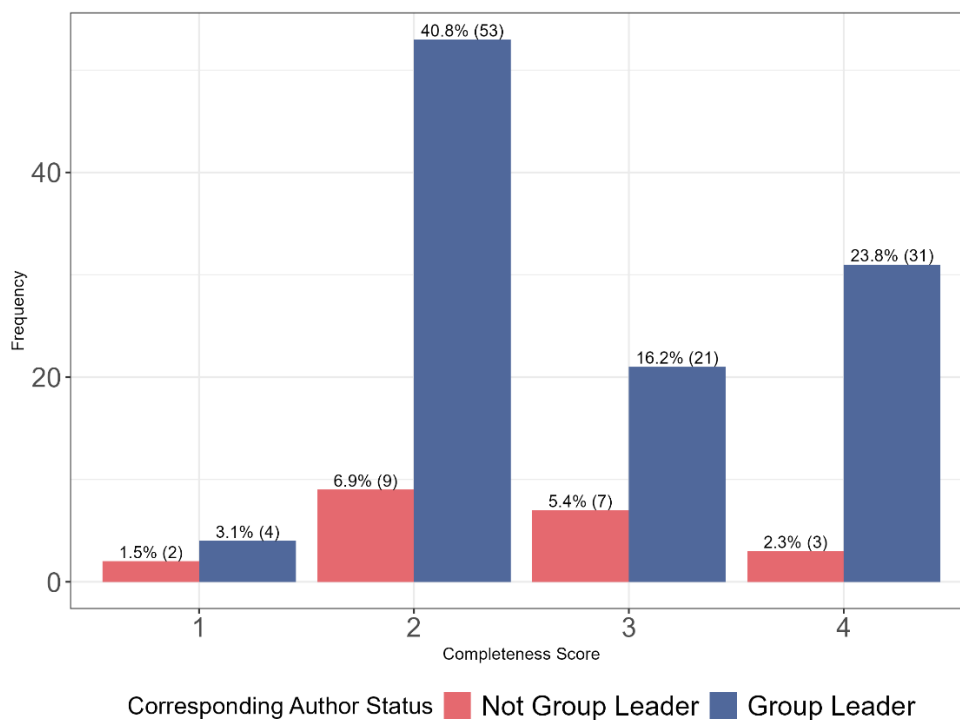
= as.factor(Complete), y = Frequency, fill = CorresAuthorStatus)) +
  geom_bar(stat = "identity", position = "dodge") +
  geom_text(aes(label = paste0(round(Percentage, 1), "% (", Frequency, ")")),
            position = position_dodge(width = 0.9), vjust = -0.25, size
= 3.5) +
  scale_fill_manual(values = colors, name = "Corresponding Author
Status") + # Ensure the name matches the Legend
  theme_bw() +
  theme(
    axis.title = element_text(size = 10),
    axis.text = element_text(size = 16),
    legend.title = element_text(size = 14),
    legend.text = element_text(size = 16),
    legend.position = "bottom"
  ) +
  labs(x = "Completeness Score", y = "Frequency")

```

```

# Print the plot
print(CorresAuthor_plot)

```



```

# Save the plot to a file
ggsave("CorresAuthor_status_distribution_plot.png", CorresAuthor_plot, width
= 8, height = 6, bg = "white")

```


Calculate frequency and percentage for Code Sharing

```
CodeArchived_summary <- data %>%
  group_by(CodeArchived) %>%
  summarise(count = n(), .groups = "drop")

# Calculate the overall total
overall_total <- sum(CodeArchived_summary$count)

# Add a column for the percentage of each Code Archived category relative to
the overall total
CodeArchived_summary <- CodeArchived_summary %>%
  mutate(percentage = (count / overall_total) * 100)

print(CodeArchived_summary)

## # A tibble: 3 × 3
##   CodeArchived count percentage
##       <int> <int>      <dbl>
## 1         0     3        2.31
## 2         1    17       13.1
## 3        NA   110       84.6

# Frequency and Percentage of the papers that shared the code used
data %>%
  group_by(Type, CodeArchived) %>%
  summarise(count = n(), .groups = "drop") %>%
  group_by(Type) %>%
  mutate(total = sum(count),
         percentage = (count/total)*100) %>%
  ungroup() %>%

  arrange(Type, CodeArchived)

## # A tibble: 6 × 5
##   Type CodeArchived count total percentage
##   <chr>      <int> <int> <int>      <dbl>
## 1 IQB3         0     2    80        2.5
## 2 IQB3         1    12    80        15
## 3 IQB3        NA    66    80       82.5
## 4 Other         0     1    50         2
## 5 Other         1     5    50        10
## 6 Other        NA    44    50        88

#Chi square test to assess if there is any difference in Code Sharing between the two types
(IQB3, Other)

# Create a contingency table
table_code <- table(data$Type, data$CodeArchived)
```

```

# Perform the Chi-square test
result <- chisq.test(table_code)

## Warning in chisq.test(table_code): Chi-squared approximation may be incorrect

#Print the chi-square results
print(result)

##
## Pearson's Chi-squared test with Yates' continuity correction
##
## data: table_code
## X-squared = 2.1717e-31, df = 1, p-value = 1

# Get the expected values
expected_values <- result$expected

# Print the expected values
print(expected_values) ##in order to check the assumption of chi square test:
Each cell in the contingency table should have an expected count of 5 or more
.

##
##      0      1
## IQB3 2.1 11.9
## Other 0.9  5.1

#The assumptions of that test were met:

#### Sample Size: Each cell in the contingency table has an expected count of 5 or more.
#### Independence: The observations are independent of each other. This means that the selection of one observation should not influence or affect the selection of another observation.
#### Random Sampling: The data is a random sample.
#### Categorical Data: Both variables should be categorical (either nominal or ordinal).

```

#Plot the 4 scoring criteria for all the papers

```

# Convert all relevant columns to factors first to avoid the error
data <- data %>%
  mutate(across(c(Complete, Reuse, Access, Licence), as.character), .groups = "drop")

# Reshape data to long format
long_data <- data %>%
  pivot_longer(cols = c(Complete, Reuse, Access, Licence), names_to = "Category", values_to = "Value") %>%
  mutate(Value = as.character(Value))

```

```

# Rename and reorder categories
long_data$Category <- recode(long_data$Category,
                             "Complete" = "Completeness",
                             "Reuse" = "Reusability",
                             "Access" = "Accessibility",
                             "Licence" = "Licence")
long_data$Category <- factor(long_data$Category, levels = c("Completeness", "
Reusability", "Accessibility", "Licence"))

# Calculate counts and percentages ensuring percentages do not exceed 100%
long_data <- long_data %>%
  group_by(Category, Value) %>%
  summarise(Count = n(), .groups = "drop") %>%
  ungroup() %>%
  group_by(Category) %>%
  mutate(Total = sum(Count),
         Percentage = pmin(Count / Total * 100, 100)) %>%
  ungroup() %>%
  arrange(Category, desc(Value)) %>%
  group_by(Category) %>%
  mutate(Label = ifelse(Percentage > 5, paste0(round(Percentage, 1), "%"), ""
),
         CumPercentage = pmin(cumsum(Percentage), 100)) %>%
  ungroup()

# Plot
plot_all <- ggplot(long_data, aes(x = Category, y = Percentage, fill = Value)
) +
  geom_bar(stat = "identity", position = "stack") +
  scale_fill_manual(values = c("#E5696F", "#50689B", "#36D0A1", "#D0A136")) +
  labs(y = "Percentage", fill = "Score", title = "Scoring Criteria for Papers
") +
  theme_minimal() +
  geom_text(aes(label = Label, y = pmin(CumPercentage - 0.5 * Percentage, 100
)),
            position = position_stack(vjust = 0.5), size = 6, check_overlap =
TRUE) +
  theme(
    axis.title = element_text(size = 14),
    axis.text = element_text(size = 18),
    legend.title = element_text(size = 12),
    legend.text = element_text(size = 14)
  ) +
  ylim(0, 100)

# Ensure the values are factored in reverse order so that 4 is at the top of
the stack
long_data$Value <- factor(long_data$Value, levels = c("4", "3", "2", "1"))

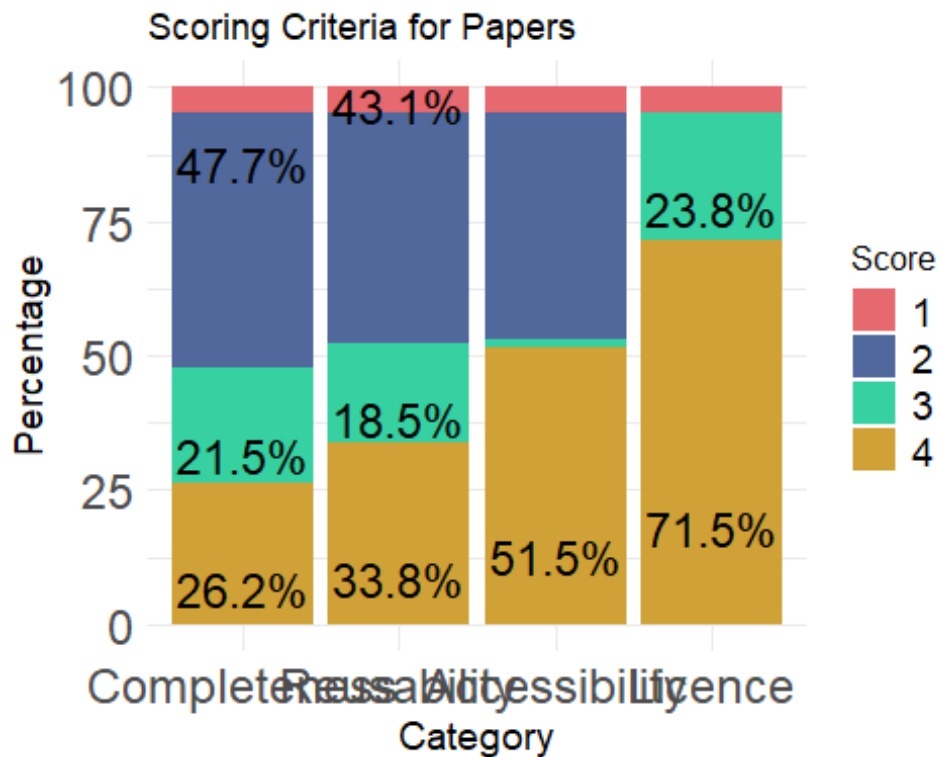
```

```
# Show the plot
```

```
print(plot_all)
```

```
## Warning: Removed 5 rows containing missing values or values outside the scale range
```

```
## (`geom_text()`).
```



```
# Save the plot
```

```
ggsave("plotall.png", plot_all, width = 10, height = 8, dpi = 300, bg="white")
```

```
## Warning: Removed 5 rows containing missing values or values outside the scale range
```

```
## (`geom_text()`).
```

```
#Cluster bar chart fro the completeness criteria by the Type of the study
```

```
library(ggplot2)
```

```
library(dplyr)
```

```
# Reorder the Levels of variables
```

```
data$Complete <- factor(data$Complete, levels = c("4", "3", "2", "1"))
```

```
# Summarize data
```

```
summarized_data <- data %>%
```

```
  group_by(Type, Complete) %>%
```

```

summarise(Count = n(), .groups = "drop") %>%
left_join(data %>% group_by(Type) %>% summarise(Total = n(), .groups = "drop"), by = "Type") %>%
mutate(Percentage = Count/Total * 100)

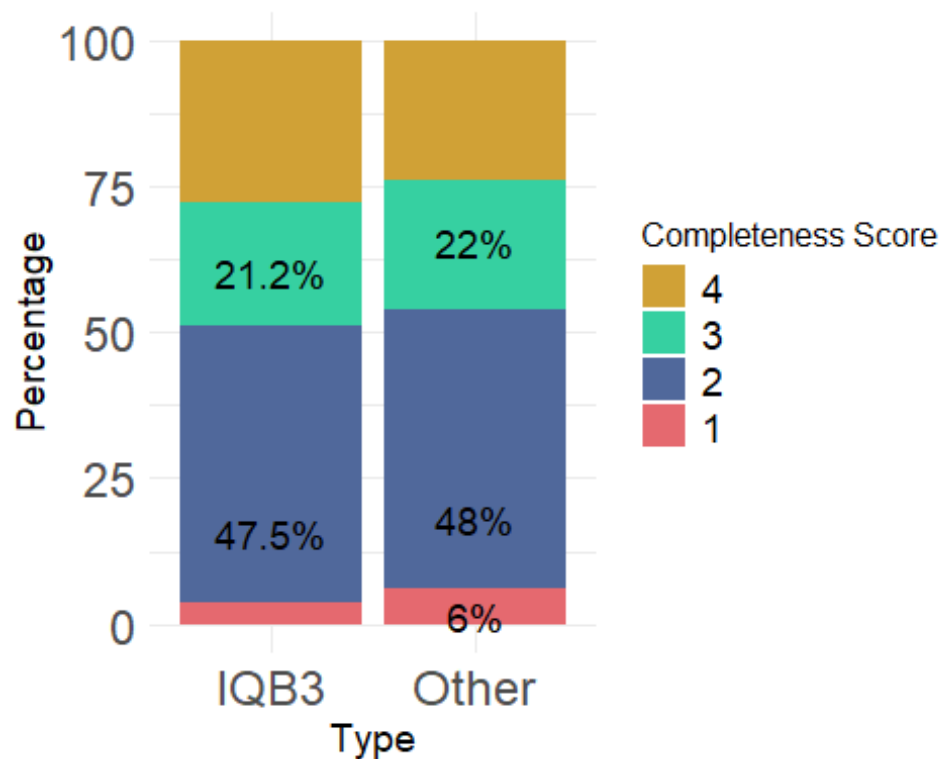
# For cumulative percentages
summarized_data <- summarized_data %>%
  arrange(Type, desc(Complete)) %>%
  group_by(Type) %>%
  mutate(CumPercentage = cumsum(Percentage))

# Create the stacked bar chart for Completeness with colors and annotations
gcomp <- ggplot(summarized_data, aes(x = Type, y = Percentage, fill = as.factor(Complete))) +
  geom_bar(stat = "identity", position = "stack") +
  scale_fill_manual(values = c("#D0A136", "#36D0A1", "#50689B", "#E5696F")) +
  labs(x = "Type", y = "Percentage", fill = "Completeness Score") +
  theme_minimal() +
  geom_text(aes(label = ifelse(Percentage > 5, paste0(round(Percentage, 1), "%"), ""),
    y = pmin(pmax(ifelse(Complete == 1, Percentage / 2, CumPercentage - (0.5 * Percentage)), 0), 100)),
    position = position_stack(vjust = 0.5), color = "Black", size = 5) +
  theme(
    axis.title = element_text(size = 14), # Increase axis titles
    axis.text = element_text(size = 18), # Increase axis text
    legend.title = element_text(size = 12), # Increase legend title
    legend.text = element_text(size = 14) # Increase legend text
  ) +
  ylim(0, 100)

print(gcomp)

## Warning: Removed 2 rows containing missing values or values outside the scale range
## (`geom_text()`).

```



```
ggsave("gcomp.png", gcomp, width = 10, height = 8, dpi = 300)
```

```
## Warning: Removed 2 rows containing missing values or values outside the scale range
## (`geom_text()`).
```

```
` ##Cluster bar chart for the Reuse criteria by the Type of the study
```

```
# Reorder the levels of variables
```

```
data$Reuse <- factor(data$Reuse, levels = c("4", "3", "2", "1"))
```

```
summarized_data_Reuse <- data %>%
```

```
  group_by(Type, Reuse) %>%
```

```
  summarise(Count = n(), .groups = "drop") %>%
```

```
  left_join(data %>% group_by(Type) %>% summarise(Total = n(), .groups = "drop"), by = "Type") %>%
```

```
  mutate(Percentage = Count/Total * 100)
```

```
summarized_data_Reuse <- summarized_data_Reuse %>%
```

```
  arrange(Type, desc(Reuse)) %>%
```

```
  group_by(Type) %>%
```

```
  mutate(CumPercentage = cumsum(Percentage))
```

```
print(summarized_data_Reuse)
```

```
## # A tibble: 8 × 6
```

```
## # Groups:   Type [2]
```

```
##   Type  Reuse Count Total Percentage CumPercentage
```

```
##   <chr> <fct> <int> <int>      <dbl>      <dbl>
## 1 IQB3  1      3      80      3.75      3.75
## 2 IQB3  2     37      80     46.2      50
## 3 IQB3  3     10      80     12.5     62.5
## 4 IQB3  4     30      80     37.5     100
## 5 Other 1      3     50      6         6
## 6 Other 2     19     50     38        44
## 7 Other 3     14     50     28        72
## 8 Other 4     14     50     28       100
```

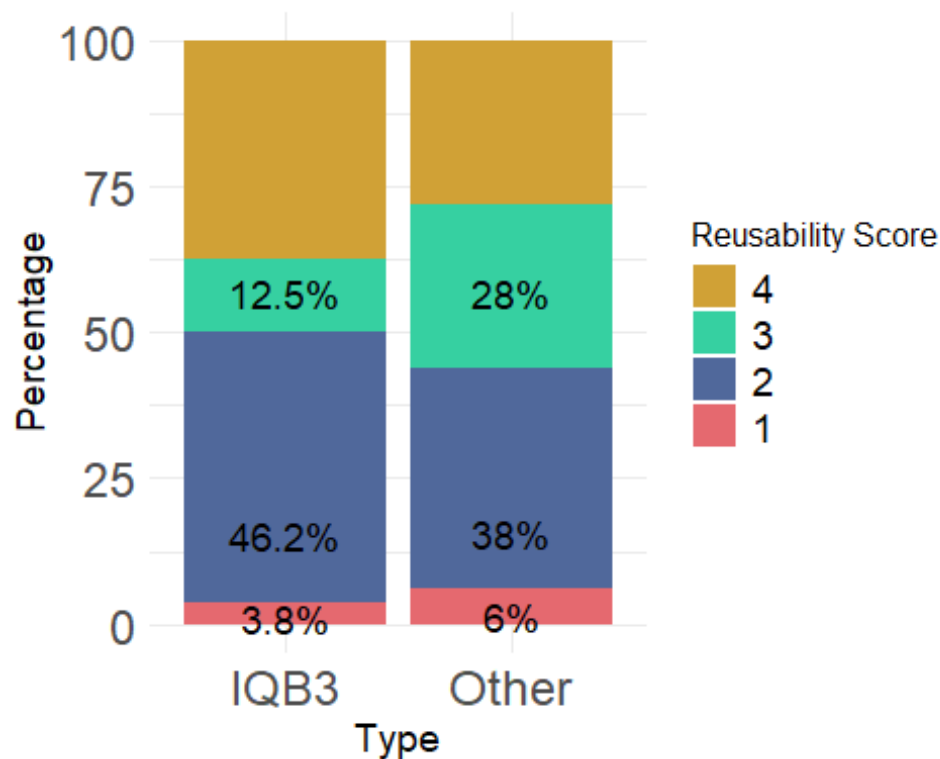
```
colors <- c("#D0A136", "#36D0A1", "#50689B", "#E5696F")
```

```
# Visualization
```

```
gReuse <- ggplot(summarized_data_Reuse, aes(x = Type, y = Percentage, fill =
as.factor(Reuse))) +
  geom_bar(stat = "identity", position = "stack") +
  scale_fill_manual(values = colors) +
  labs(x = "Type", y = "Percentage", fill = "Reusability Score") +
  theme_minimal() +
  geom_text(aes(label = paste0(round(Percentage, 1), "%"),
                    y = CumPercentage - (0.5 * Percentage)),
            position = position_stack(vjust = 0.5), color = "Black", size = 5
) +
  theme(
    axis.title = element_text(size = 14), # Increase axis titles
    axis.text = element_text(size = 18), # Increase axis text
    legend.title = element_text(size = 12), # Increase Legend title
    legend.text = element_text(size = 14) # Increase Legend text
  ) +
  ylim(0, 100)

print(gReuse)

## Warning: Removed 2 rows containing missing values or values outside the scale range
## (`geom_text()`).
```



```
ggsave("gReuse.png", gReuse, width = 10, height = 8, dpi = 300)
```

```
## Warning: Removed 2 rows containing missing values or values outside the scale range
## (`geom_text()`).
```

#bar chart for the Accessibility criteria by the Type of the study

```
# Reorder the levels of variables
```

```
data$Access <- factor(data$Access, levels = c("4", "3", "2", "1"))
```

```
summarized_data_Access <- data %>%
  group_by(Type, Access) %>%
  summarise(Count = n(), .groups = "drop") %>%
  left_join(data %>% group_by(Type) %>% summarise(Total = n(), .groups = "drop"),
    by = "Type") %>%
  mutate(Percentage = Count/Total * 100)
```

```
summarized_data_Access <- summarized_data_Access %>%
  arrange(Type, desc(Access)) %>%
  group_by(Type) %>%
  mutate(CumPercentage = cumsum(Percentage))
print(summarized_data_Access)
```

```
## # A tibble: 8 × 6
```

```
## # Groups:   Type [2]
```

```
##   Type Access Count Total Percentage CumPercentage
```



```
##   <chr> <fct>   <int> <int>      <dbl>      <dbl>
## 1 IQB3  1         3     80       3.75       3.75
## 2 IQB3  2        34    80       42.5       46.2
## 3 IQB3  3         1    80        1.25       47.5
## 4 IQB3  4        42    80       52.5      100
## 5 Other 1         3    50         6         6
## 6 Other 2        21    50        42        48
## 7 Other 3         1    50         2        50
## 8 Other 4        25    50        50       100
```

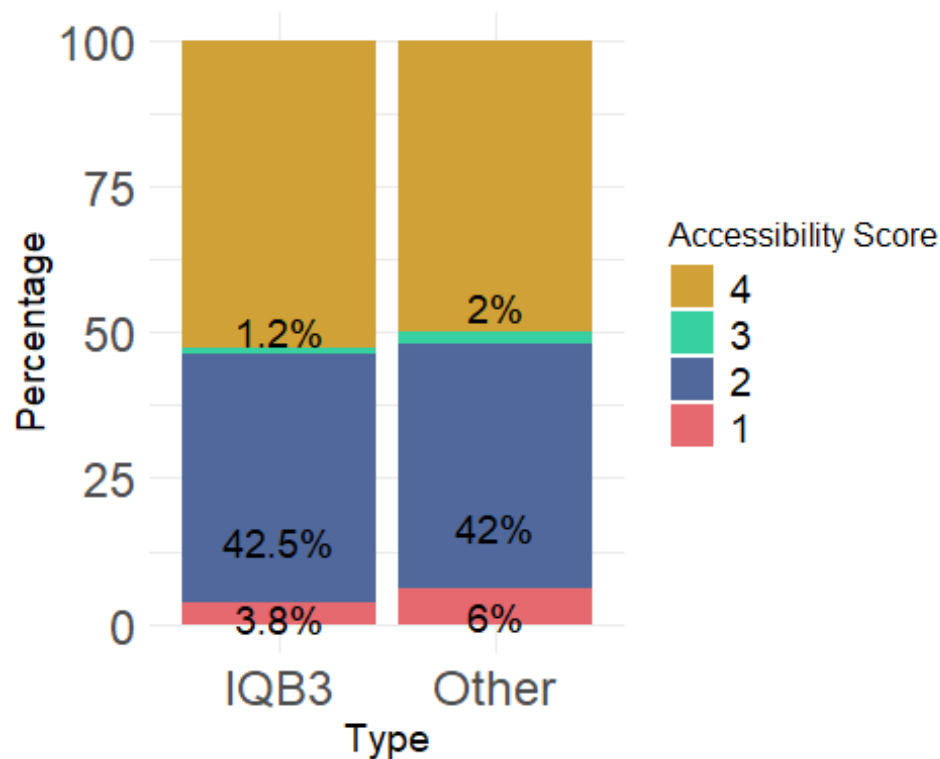
```
colors <- c("#D0A136", "#36D0A1", "#50689B", "#E5696F")
```

```
# Visualization
```

```
gaccess <- ggplot(summarized_data_Access, aes(x = Type, y = Percentage, fill
= as.factor(Access))) +
  geom_bar(stat = "identity", position = "stack") +
  scale_fill_manual(values = colors) +
  labs(x = "Type", y = "Percentage", fill = "Accessibility Score") +
  theme_minimal() +
  geom_text(aes(label = paste0(round(Percentage, 1), "%"),
    y = CumPercentage - (0.5 * Percentage)),
    position = position_stack(vjust = 0.5), color = "Black", size = 5
) +
  theme(
    axis.title = element_text(size = 14), # Increase axis titles
    axis.text = element_text(size = 18), # Increase axis text
    legend.title = element_text(size = 12), # Increase Legend title
    legend.text = element_text(size = 14) # Increase Legend text
  ) +
  ylim(0, 100)

print(gaccess)

## Warning: Removed 2 rows containing missing values or values outside the scale range
## (`geom_text()`).
```



```
ggsave("gaccess.png", gaccess, width = 10, height = 8, dpi = 300)
```

```
## Warning: Removed 2 rows containing missing values or values outside the scale range
## (`geom_text()`).
```

#bar chart for the Licence criteria by the Type of the study

```
# Reorder the levels of variables
```

```
data$Licence <- factor(data$Licence, levels = c("4", "3", "2", "1"))
```

```
summarized_data_Licence <- data %>%
```

```
  group_by(Type, Licence) %>%
```

```
  summarise(Count = n(), .groups = "drop") %>%
```

```
  left_join(data %>% group_by(Type) %>% summarise(Total = n(), .groups = "drop"), by = "Type") %>%
```

```
  mutate(Percentage = Count/Total * 100)
```

```
summarized_data_Licence <- summarized_data_Licence %>%
```

```
  arrange(Type, desc(Licence)) %>%
```

```
  group_by(Type) %>%
```

```
  mutate(CumPercentage = cumsum(Percentage))
```

```
print(summarized_data_Licence)
```

```
## # A tibble: 6 × 6
```

```
## # Groups:   Type [2]
```

```
##   Type Licence Count Total Percentage CumPercentage
```

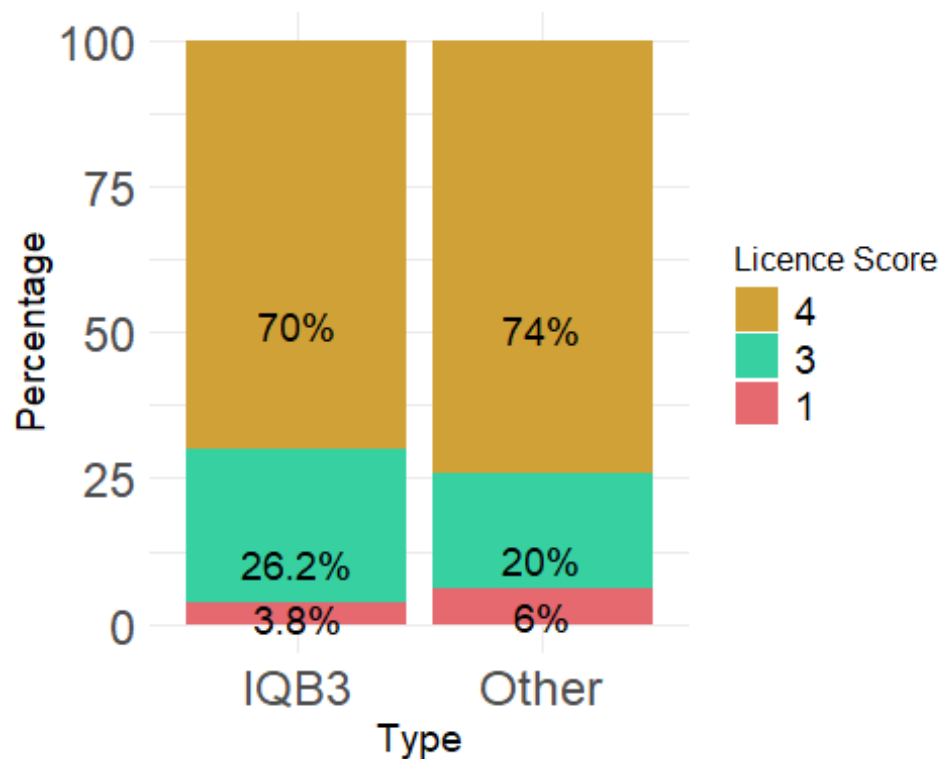
##	<chr>	<fct>	<int>	<int>	<dbl>	<dbl>
## 1	IQB3	1	3	80	3.75	3.75
## 2	IQB3	3	21	80	26.2	30
## 3	IQB3	4	56	80	70	100
## 4	Other	1	3	50	6	6
## 5	Other	3	10	50	20	26
## 6	Other	4	37	50	74	100

```
colors <- c("#D0A136", "#36D0A1", "#E5696F")
```

```
# Visualization
```

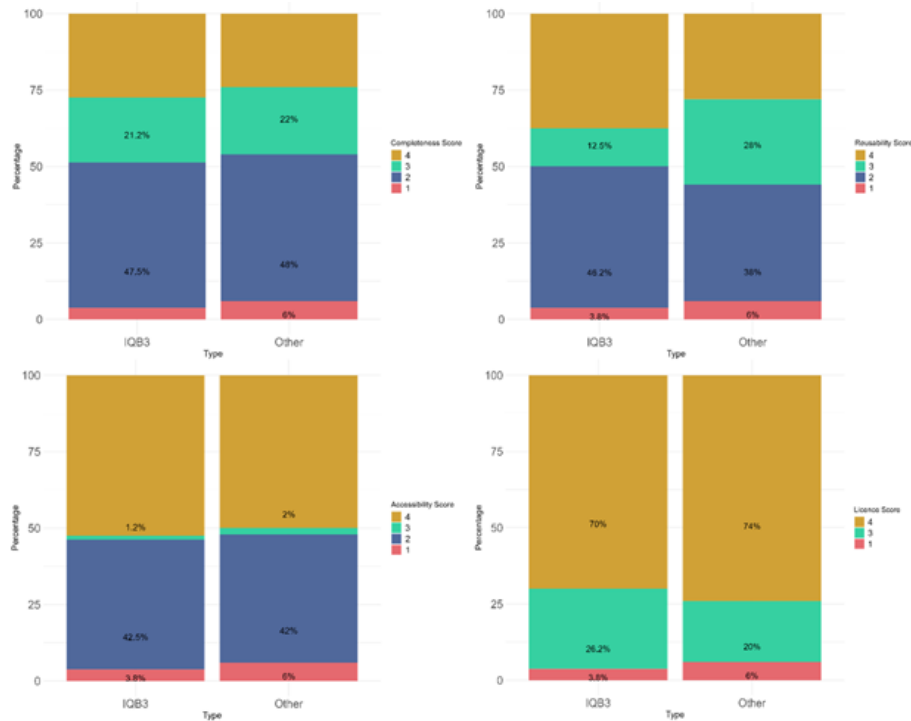
```
glicence <- ggplot(summarized_data_Licence, aes(x = Type, y = Percentage, fill = as.factor(Licence))) +
  geom_bar(stat = "identity", position = "stack") +
  scale_fill_manual(values = colors) +
  labs(x = "Type", y = "Percentage", fill = "Licence Score") +
  theme_minimal() +
  geom_text(aes(label = paste0(round(Percentage, 1), "%"),
    y = CumPercentage - (0.5 * Percentage)),
    position = position_stack(vjust = 0.5), color = "Black", size = 5)
) +
  theme(
    axis.title = element_text(size = 14), # Increase axis titles
    axis.text = element_text(size = 18), # Increase axis text
    legend.title = element_text(size = 12), # Increase Legend title
    legend.text = element_text(size = 14) # Increase Legend text
  ) +
  ylim(0, 100)

print(glicence)
```



```
ggsave("glicence.png", gllicence, width = 10, height = 8, dpi = 300)

## Warning: Removed 2 rows containing missing values or values outside the
## scale range
## (`geom_text()`).
library(patchwork)
## Warning: package 'patchwork' was built under R version 4.3.3
##
## Attaching package: 'patchwork'
## The following object is masked from 'package:MASS':
##
##      area
combinedplot <- gcomp + greuse + gaccess + gllicence +
  plot_layout(
    ncol = 2, heights = c(10, 10), widths = c(10, 10)
  )
print(combinedplot)
```



##Calculate the frequency and percentage for each 'Complete' score within each 'Year'

```
long_data <- data %>%
  count(Year, Complete) %>%
  group_by(Year) %>%
  mutate(Percentage = n / sum(n) * 100) %>%
  mutate(Label = ifelse(Percentage > 5, paste0(round(Percentage, 1), "%"), "")) %>%
  mutate(Cumulative_Percentage = cumsum(Percentage) - (0.5 * Percentage)) %>%
  ungroup()
```

Custom colors

```
colors <- c("#D0A136", "#36D0A1", "#50689B", "#E5696F")
```

Creating the stacked bar chart with percentage labels

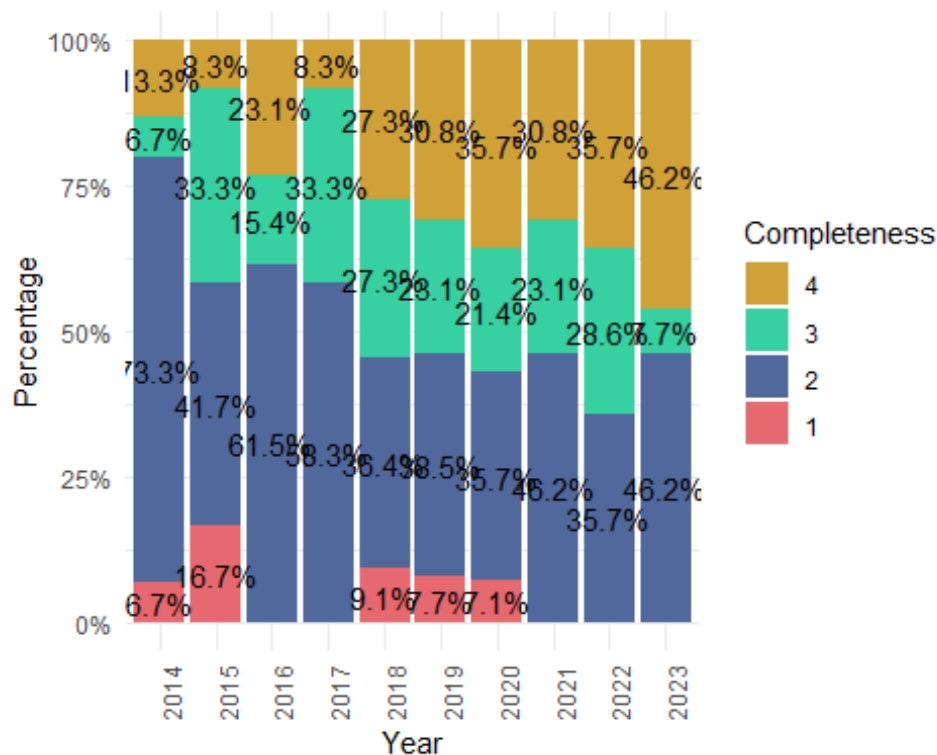
```
Compyear <- ggplot(long_data, aes(x = as.factor(Year), y = n, fill = as.factor(Complete))) +
  geom_bar(stat = "identity", position = "fill") + # Scale the bar heights to proportions
  scale_y_continuous(labels = percent_format()) + # Convert the y-axis to percentage
  geom_text(
    aes(label = Label, y = Percentage),
    size = 4,
    color = "black",
    position = position_fill(vjust = 0.5)
  ) +
  scale_fill_manual(values = colors) +
```

```

labs(x = "Year",
     y = "Percentage",
     fill = "Completeness") +
theme(
  axis.title = element_text(size = 14), # Increase axis titles
  axis.text = element_text(size = 20), # Increase axis text
  legend.title = element_text(size = 18), # Increase Legend title
  legend.text = element_text(size = 20) # Increase Legend text
) +
theme_minimal() +
scale_x_discrete(name = "Year", labels = unique(long_data$Year)) +
theme(axis.text.x = element_text(angle = 90, hjust = 1)) # Adjust text angle for readability

# Print the plot
print(Compyear)

```



```

ggsave("Compyear.png", Compyear, width = 15, height = 10, units = "in", bg = "white")

# Calculate the frequency and percentage for each 'Reuse' score within each 'Year'
long_data <- data %>%
  count(Year, Reuse) %>%
  group_by(Year) %>%
  mutate(Percentage = n / sum(n) * 100) %>%
  mutate(Label = ifelse(Percentage > 5, paste0(round(Percentage, 1), "%"), ""))

```

```

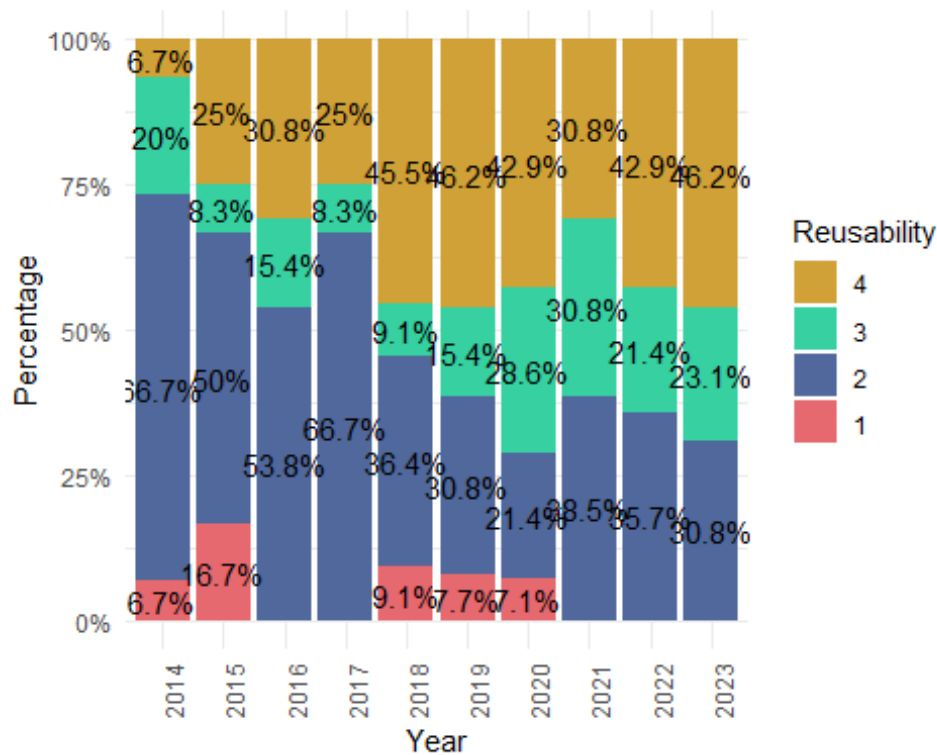
)) %>%
  mutate(Cumulative_Percentage = cumsum(Percentage) - (0.5 * Percentage)) %>%
  ungroup()

# Custom colors
colors <- c("#D0A136", "#36D0A1", "#50689B", "#E5696F")

# Creating the stacked bar chart with percentage labels
Reuseyear <- ggplot(long_data, aes(x = as.factor(Year), y = n, fill = as.factor(Reuse))) +
  geom_bar(stat = "identity", position = "fill") + # Scale the bar heights to proportions
  scale_y_continuous(labels = percent_format()) + # Convert the y-axis to percentage
  geom_text(
    aes(label = Label, y = Percentage),
    size = 4,
    color = "black",
    position = position_fill(vjust = 0.5)
  ) +
  scale_fill_manual(values = colors) +
  labs(x = "Year",
       y = "Percentage",
       fill = "Reusability") +
  theme(
    axis.title = element_text(size = 14), # Increase axis titles
    axis.text = element_text(size = 20), # Increase axis text
    legend.title = element_text(size = 18), # Increase legend title
    legend.text = element_text(size = 20) # Increase legend text
  ) +
  theme_minimal() +
  scale_x_discrete(name = "Year", labels = unique(long_data$Year)) +
  theme(axis.text.x = element_text(angle = 90, hjust = 1)) # Adjust text angle for readability

# Print the plot
print(Reuseyear)

```



```

ggsave("Reuseyear.png", Reuseyear, width = 15, height = 10, units = "in", bg
= "white")

# Calculate the frequency and percentage for each 'Access' score within each
'Year'
long_data <- data %>%
  count(Year, Access) %>%
  group_by(Year) %>%
  mutate(Percentage = n / sum(n) * 100) %>%
  mutate(Label = ifelse(Percentage > 5, paste0(round(Percentage, 1), "%"), ""
)) %>%
  mutate(Cumulative_Percentage = cumsum(Percentage) - (0.5 * Percentage)) %>%
  ungroup()

# Custom colors
colors <- c("#D0A136", "#36D0A1", "#50689B", "#E5696F")

# Creating the stacked bar chart with percentage labels
accessyear <- ggplot(long_data, aes(x = as.factor(Year), y = n, fill = as.fac
tor(Access))) +
  geom_bar(stat = "identity", position = "fill") + # Scale the bar heights t
o proportions
  scale_y_continuous(labels = percent_format()) + # Convert the y-axis to pe
rcentage
  geom_text(
    aes(label = Label, y = Percentage),
    size = 4,

```

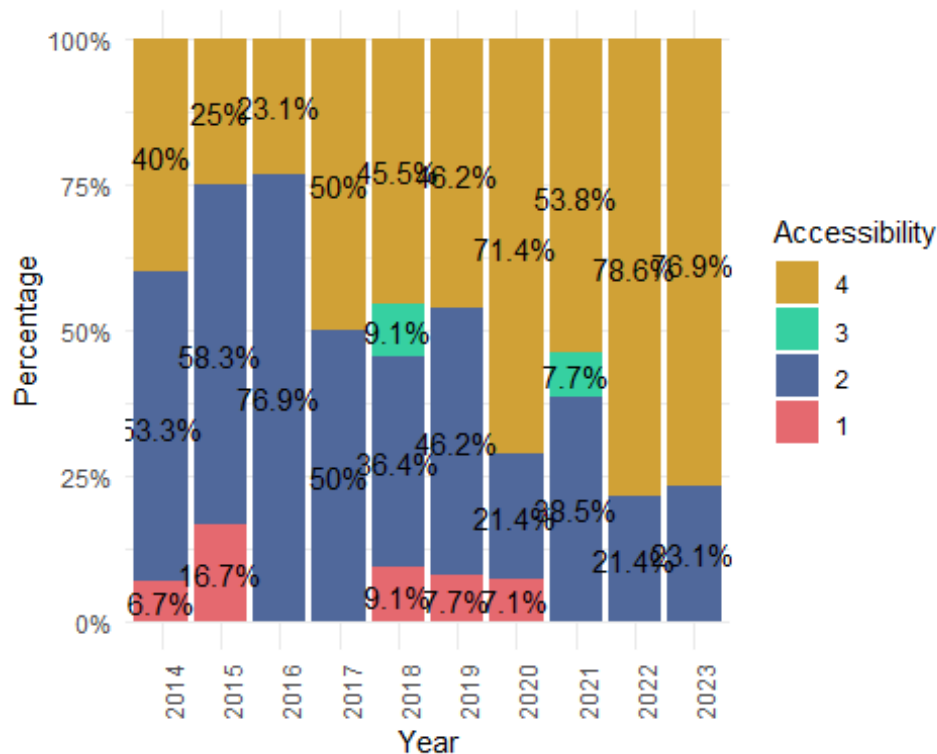


```

    color = "black",
    position = position_fill(vjust = 0.5)
  ) +
  scale_fill_manual(values = colors) +
  labs(x = "Year",
       y = "Percentage",
       fill = "Accessibility") +
  theme(
    axis.title = element_text(size = 14), # Increase axis titles
    axis.text = element_text(size = 20), # Increase axis text
    legend.title = element_text(size = 18), # Increase Legend title
    legend.text = element_text(size = 20) # Increase Legend text
  ) +
  theme_minimal() +
  scale_x_discrete(name = "Year", labels = unique(long_data$Year)) +
  theme(axis.text.x = element_text(angle = 90, hjust = 1)) # Adjust text angle for readability

# Print the plot
print(accessyear)

```



```

ggsave("accessyear.png", accessyear, width = 15, height = 10, units = "in", bg = "white")

# Calculate the frequency and percentage for each 'Licence' score within each 'Year'
long_data <- data %>%

```

```

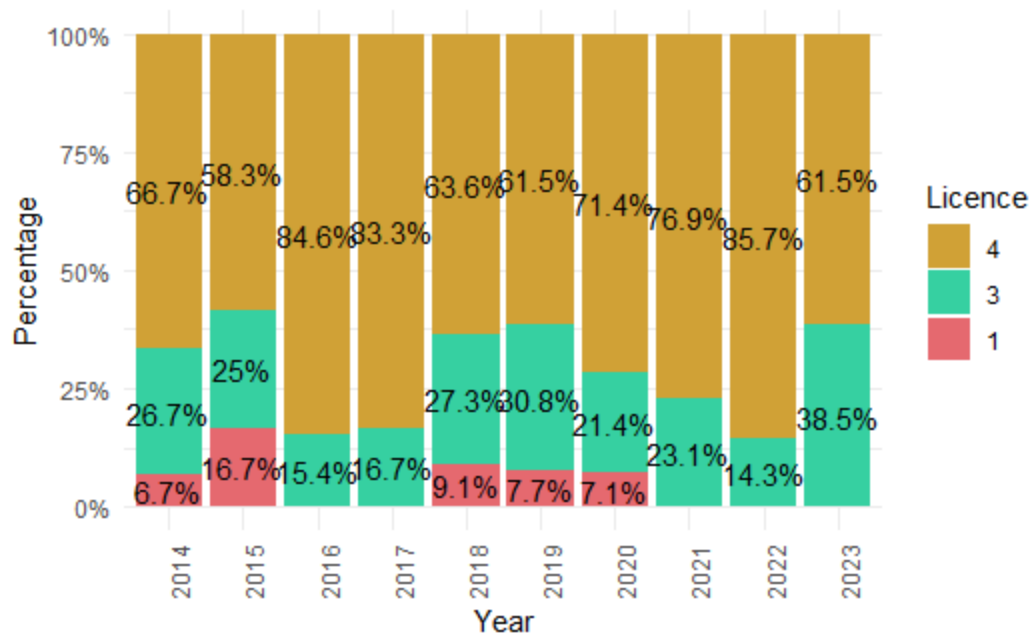
count(Year, Licence) %>%
group_by(Year) %>%
mutate(Percentage = n / sum(n) * 100) %>%
mutate(Label = ifelse(Percentage > 5, paste0(round(Percentage, 1), "%"), ""
)) %>%
mutate(Cumulative_Percentage = cumsum(Percentage) - (0.5 * Percentage)) %>%
ungroup()

# Custom colors
colors <- c("#D0A136", "#36D0A1", "#50689B", "#E5696F")

# Creating the stacked bar chart with percentage labels
licenceyear <- ggplot(long_data, aes(x = as.factor(Year), y = n, fill = as.factor(Licence))) +
  geom_bar(stat = "identity", position = "fill") + # Scale the bar heights to proportions
  scale_y_continuous(labels = percent_format()) + # Convert the y-axis to percentage
  geom_text(
    aes(label = Label, y = Percentage),
    size = 4,
    color = "black",
    position = position_fill(vjust = 0.5)
  ) +
  scale_fill_manual(values = colors) +
  labs(x = "Year",
    y = "Percentage",
    fill = "Licence") +
  theme(
    axis.title = element_text(size = 14), # Increase axis titles
    axis.text = element_text(size = 20), # Increase axis text
    legend.title = element_text(size = 18), # Increase legend title
    legend.text = element_text(size = 20) # Increase legend text
  ) +
  theme_minimal() +
  scale_x_discrete(name = "Year", labels = unique(long_data$Year)) +
  theme(axis.text.x = element_text(angle = 90, hjust = 1)) # Adjust text angle for readability

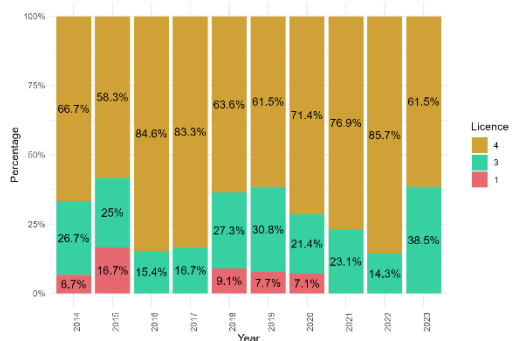
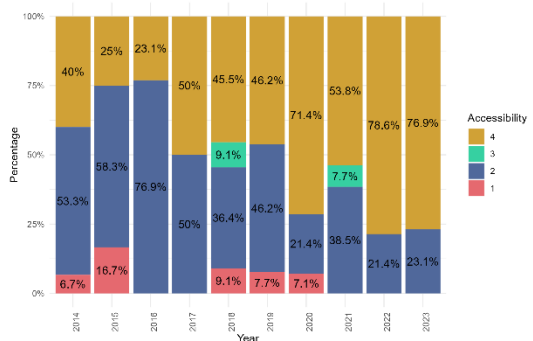
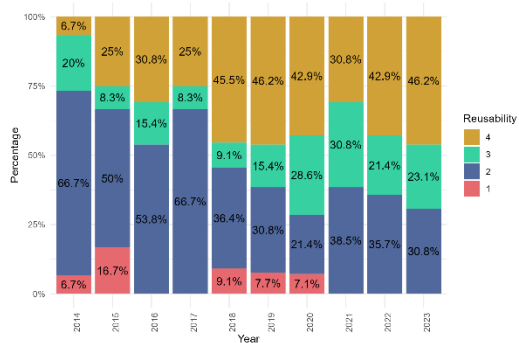
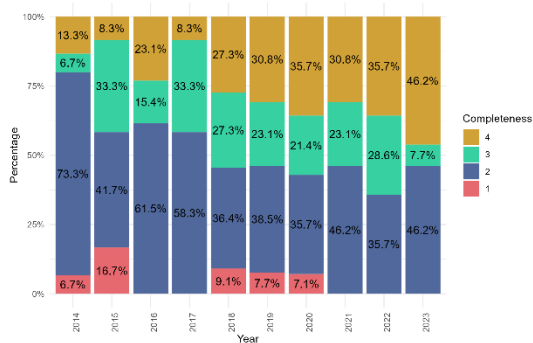
# Print the plot
print(licenceyear)

```



```
ggsave("licenceyear.png", licenceyear, width = 15, height = 10, units = "in",
bg = "white")
```

```
plotyear <- Compyear + reuseyear + accessyear + licenceyear +
  plot_layout(
    ncol = 2, heights = c(10, 10), widths = c(10, 10)
  )
print(plotyear)
```



#study the significant difference between two type of the research for each scoring criteria

Convert scoring criteria to numeric (if not already)

```
data <- data %>%  
  mutate(across(c(Complete, Reuse, Access, Licence),  
    ~as.numeric(as.character(.))))
```

Assumption checks for each criterion

```
for (criterion in c("Complete", "Reuse", "Access", "Licence")) {  
  # Create and display a box plot to check the distribution shape and spread  
  print(ggplot(data, aes_string(x = "Type", y = criterion, fill = "Type")) +  
    geom_boxplot() +  
    ggtitle(paste("Boxplot for", criterion)))
```

Print the median for a basic comparison

```
cat(paste("Median of", criterion, "by Type:\n"))  
print(aggregate(. ~ Type, data[c("Type", criterion)], median))
```

```
cat("\n")
```

```
}
```

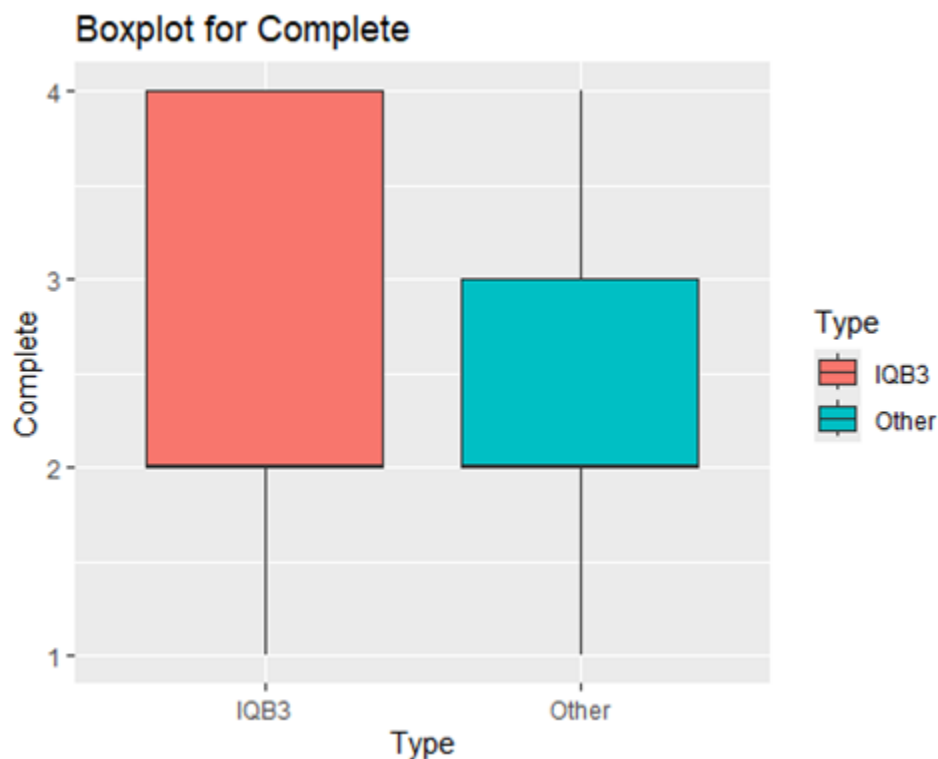
Warning: `aes_string()` was deprecated in ggplot2 3.0.0.

[i] Please use tidy evaluation idioms with `aes()`.

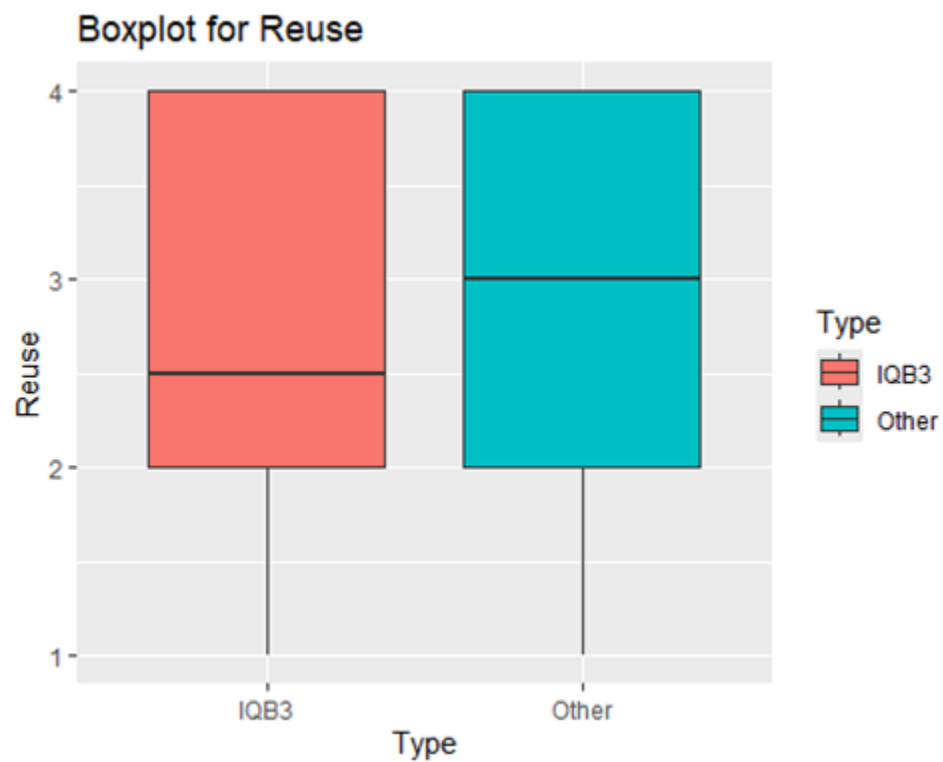
[i] See also `vignette("ggplot2-in-packages")` for more information.

This warning is displayed once every 8 hours.

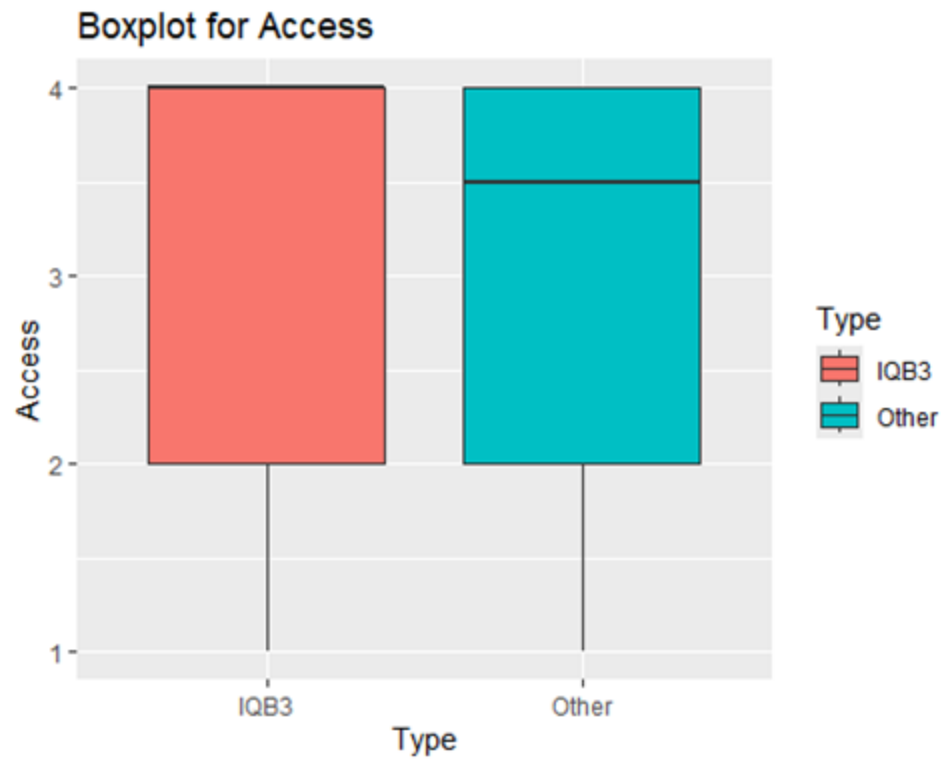
Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
generated.



```
## Median of Complete by Type:  
##   Type Complete  
## 1  IQB3         2  
## 2 Other         2
```



```
## Median of Reuse by Type:  
##   Type Reuse  
## 1  IQB3    2.5  
## 2 Other    3.0
```

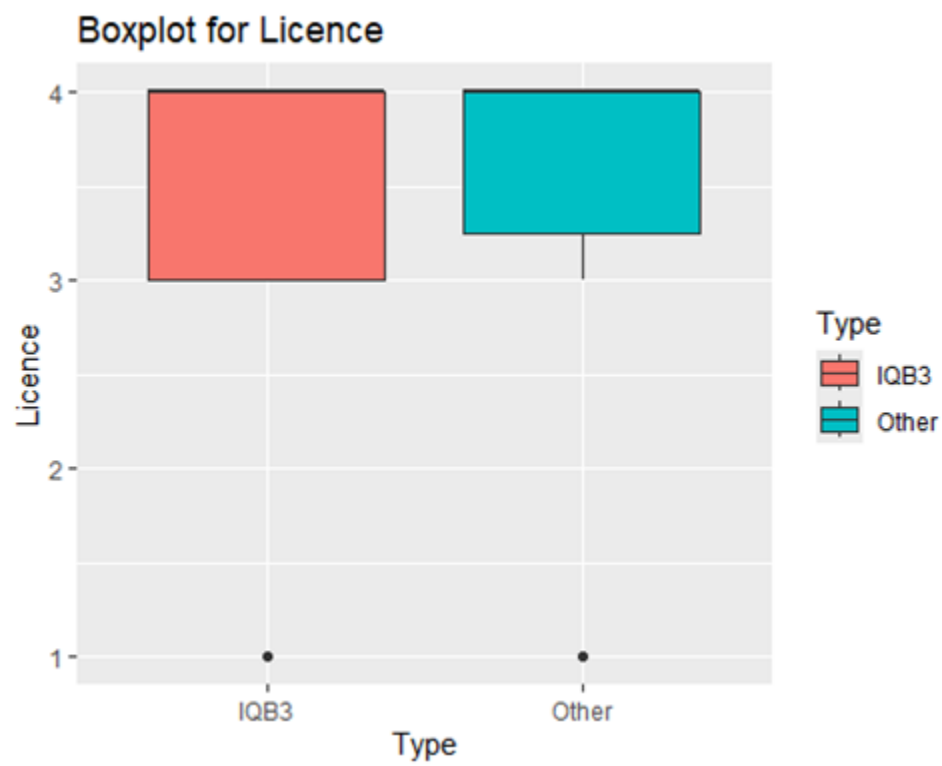


```
## Median of Access by Type:
```

```
##   Type Access
```

```
## 1  IQB3    4.0
```

```
## 2  Other    3.5
```



```

## Median of Licence by Type:
##   Type Licence
## 1  IQB3      4
## 2 Other      4
# Function to perform Mann-Whitney U test
perform_mann_whitney <- function(data, criterion) {
  test_result <- wilcox.test(
    reformulate("Type", response = criterion),
    data = data,
    exact = FALSE
  )
  list(criterion = criterion, p.value = test_result$p.value)
}

# Perform the test for each criterion
mw_results <- lapply(c("Complete", "Reuse", "Access", "Licence"),
function(criterion) {
  perform_mann_whitney(data, criterion)
})

# Convert the list of results to a dataframe
mw_results_df <- do.call(rbind, mw_results)

print(mw_results_df)
##      criterion p.value
## [1,] "Complete" 0.6265178
## [2,] "Reuse"    0.8119625
## [3,] "Access"   0.7360586
## [4,] "Licence"  0.7018642
#The assumptions of the test were met:
### Ordinal Data Check: The scoring criteria are ordinal variables
### Similar Distribution Shapes: For each criterion, it creates a box plot to
visually inspect the distribution shapes. This is crucial to check if the
distributions are similar across groups.
### Independence of Observations:the variables are independence
observations.

```

#Create variables for FAIR principles in 2016 and COVID-19 in 2020

```

data <- data %>%
  mutate(Period2020 = ifelse(Year <= 2020, "Before 2020", "After 2020")) %>%
  mutate(Period2016 = ifelse(Year <= 2016, "Before 2016", "After 2016"))#

```

#Study the significant difference before and afterCovid-19 2020 using Median and Mann Whitney U test

```

# Ensure the scoring criteria are numeric
data <- data %>%
  mutate(across(c(Complete, Reuse, Access, Licence), ~as.numeric(as.character(
    .))))

```

```

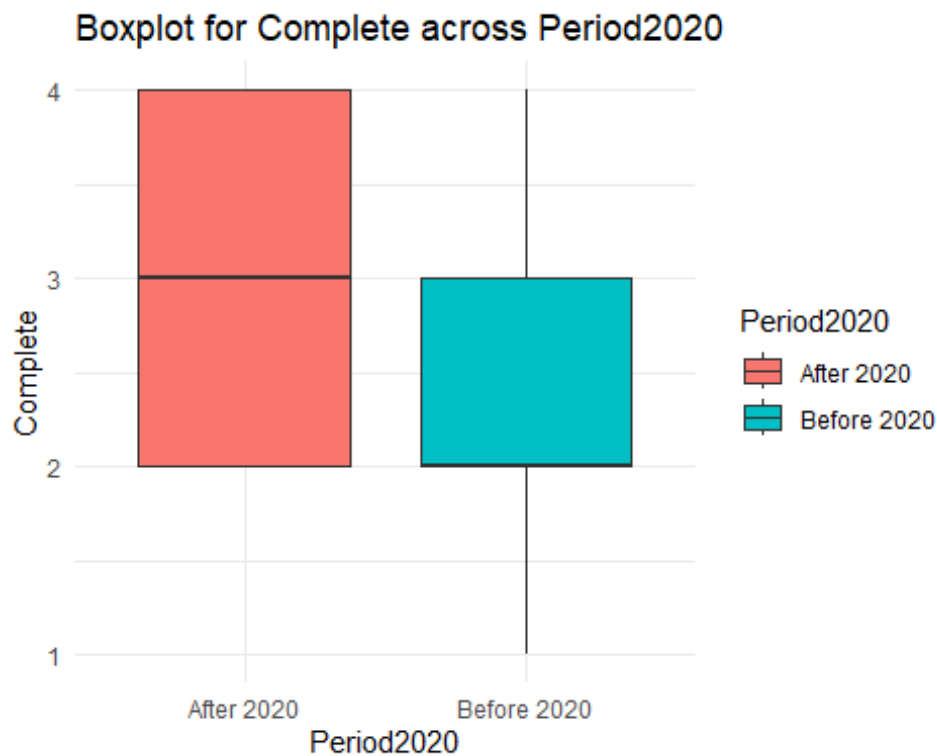
# Function to generate box plots for distribution checks
generate_boxplot <- function(data, score_var, period_var) {
  ggplot(data, aes_string(x = period_var, y = score_var, fill = period_var))
+
  geom_boxplot() +
  labs(title = paste("Boxplot for", score_var, "across", period_var),
       x = period_var,
       y = score_var) +
  theme_minimal()
}

# Generate and display box plots for each score with Period2020
lapply(c("Complete", "Reuse", "Access", "Licence"), function(score_var) {
  generate_boxplot(data, score_var, "Period2020")
}))

## Warning: `aes_string()` was deprecated in ggplot2 3.0.0.
## [i] Please use tidy evaluation idioms with `aes()`.
## [i] See also `vignette("ggplot2-in-packages")` for more information.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.

## [[1]]

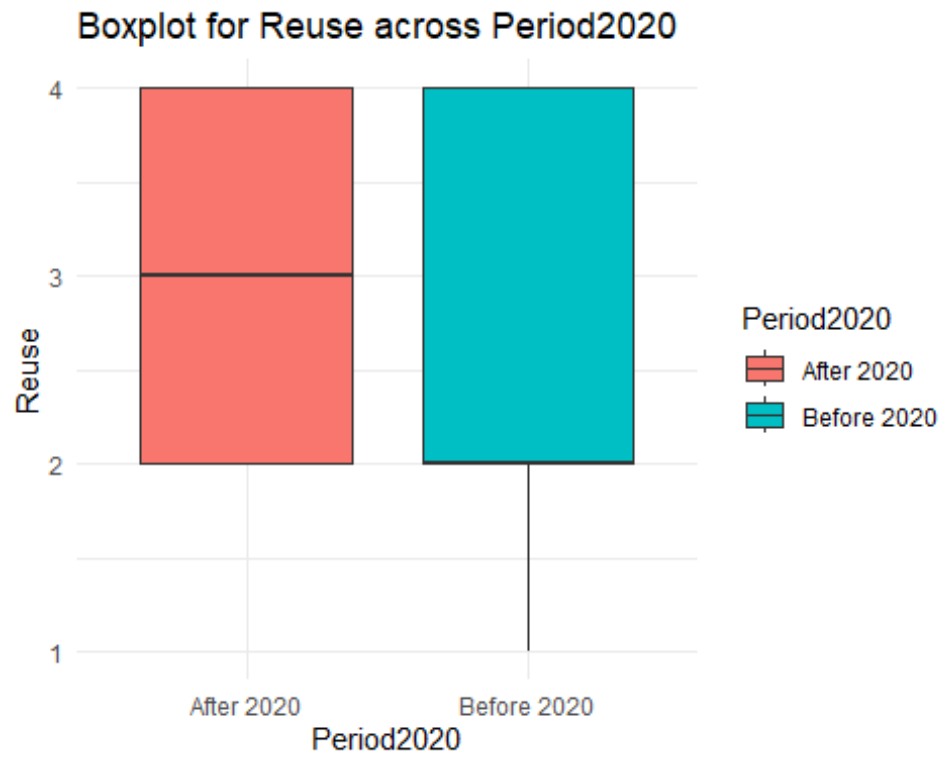
```



```

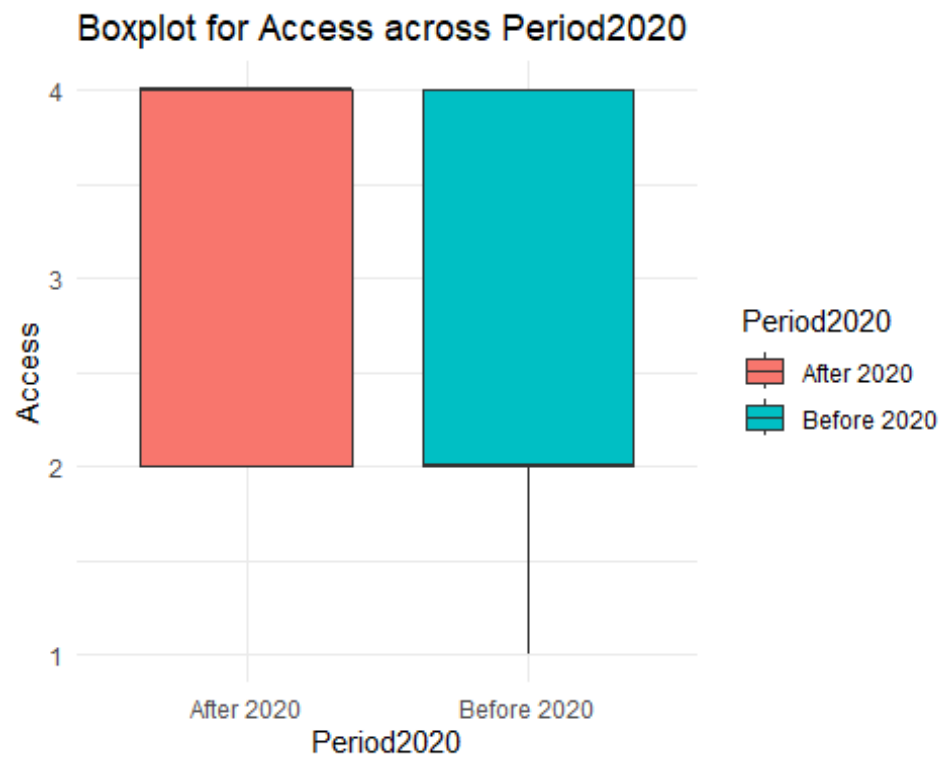
##
## [[2]]

```

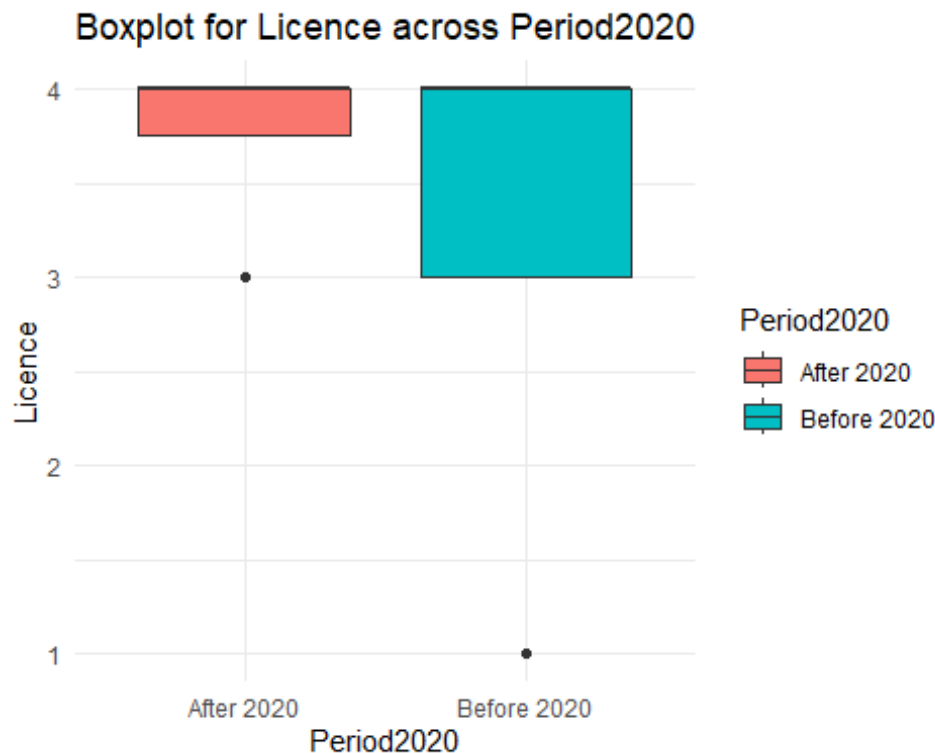



```
##
```

```
## [[3]]
```



```
##
## [[4]]
```



```
# Function to perform the Mann-Whitney test and calculate medians
perform_analysis <- function(data, score_var, period_var) {
  test_result <- wilcox.test(reformulate(period_var, score_var), data = data,
    exact = FALSE)

  medians <- data %>%
    group_by(!sym(period_var)) %>%
    summarise(median = median(!sym(score_var), na.rm = TRUE), .groups = 'dro
p')

  list(median = medians, p.value = test_result$p.value)
}

# Analysis for each score for 2020
results_complete_2020 <- perform_analysis(data, "Complete", "Period2020")
results_reuse_2020 <- perform_analysis(data, "Reuse", "Period2020")
results_access_2020 <- perform_analysis(data, "Access", "Period2020")
results_licence_2020 <- perform_analysis(data, "Licence", "Period2020")

# Print results
print(results_complete_2020)

## $median
## # A tibble: 2 × 2
```

```
##   Period2020  median
##   <chr>      <dbl>
## 1 After 2020      3
## 2 Before 2020     2
##
## $p.value
## [1] 0.0394013
```

```
print(results_Reuse_2020)
```

```
## $median
## # A tibble: 2 × 2
##   Period2020  median
##   <chr>      <dbl>
## 1 After 2020      3
## 2 Before 2020     2
##
## $p.value
## [1] 0.0639665
```

```
print(results_access_2020)
```

```
## $median
## # A tibble: 2 × 2
##   Period2020  median
##   <chr>      <dbl>
## 1 After 2020      4
## 2 Before 2020     2
##
## $p.value
## [1] 0.002491228
```

```
print(results_licence_2020)
```

```
## $median
## # A tibble: 2 × 2
##   Period2020  median
##   <chr>      <dbl>
## 1 After 2020      4
## 2 Before 2020     4
##
## $p.value
## [1] 0.4440382
```

#The assumptions of the test were met:

Ordinal Data Check: The scoring criteria are ordinal variables

Similar Distribution Shapes: For each criterion, it creates a box plot to visually inspect the distribution shapes. This is crucial to check if the distributions are similar across groups.

Independence of Observations: the variables are independence observations.

#Study the significant difference before and afterCovid-19 2020 using Median and Mann Whitney U test for the IQB3 Papers

```
data_IQB3 <- data %>%
  filter(Type == "IQB3")

perform_analysis <- function(data_IQB3, score_var, period_var) {
  test_result <- wilcox.test(reformulate(period_var, score_var), data = data_IQB3, exact = FALSE)

  medians <- data_IQB3 %>%
    group_by(!sym(period_var)) %>%
    summarise(median = median(!sym(score_var), na.rm = TRUE), .groups = 'drop')

  list(median = medians, p.value = test_result$p.value)
}

# Analysis for each score for 2020
results_complete_2020_IQB3 <- perform_analysis(data_IQB3, "Complete", "Period2020")
results_Reuse_2020_IQB3 <- perform_analysis(data_IQB3, "Reuse", "Period2020")
results_access_2020_IQB3 <- perform_analysis(data_IQB3, "Access", "Period2020")
results_licence_2020_IQB3 <- perform_analysis(data_IQB3, "Licence", "Period2020")

# Print results
results_complete_2020_IQB3

## $median
## # A tibble: 2 × 2
##   Period2020 median
##   <chr>         <dbl>
## 1 After 2020      3
## 2 Before 2020    2
##
## $p.value
## [1] 0.3644481

results_Reuse_2020_IQB3

## $median
## # A tibble: 2 × 2
##   Period2020 median
##   <chr>         <dbl>
## 1 After 2020      3
## 2 Before 2020    2
##
```

```
## $p.value
## [1] 0.268142

results_access_2020_IQB3

## $median
## # A tibble: 2 × 2
##   Period2020 median
##   <chr>      <dbl>
## 1 After 2020      4
## 2 Before 2020     2
##
## $p.value
## [1] 0.01209852

results_licence_2020_IQB3

## $median
## # A tibble: 2 × 2
##   Period2020 median
##   <chr>      <dbl>
## 1 After 2020      4
## 2 Before 2020     4
##
## $p.value
## [1] 0.7285709
```

#Study the significant difference before and after Covid-19 2020 using Median and Mann Whitney U test for the Other Papers

```
data_Other <- data %>%
  filter(Type == "Other")

perform_analysis <- function(data_Other, score_var, period_var) {
  test_result <- wilcox.test(reformulate(period_var, score_var), data = data_
Other, exact = FALSE)

  medians <- data_Other %>%
    group_by(!sym(period_var)) %>%
    summarise(median = median(!sym(score_var), na.rm = TRUE), .groups = 'dro
p')

  list(median = medians, p.value = test_result$p.value)
}

# Analysis for each score for 2020
results_complete_2020_Other <- perform_analysis(data_Other, "Complete", "Peri
od2020")
results_Reuse_2020_Other <- perform_analysis(data_Other, "Reuse", "Period2020
")
```

```

results_access_2020_Other <- perform_analysis(data_Other, "Access", "Period20
20")
results_licence_2020_Other <- perform_analysis(data_Other, "Licence", "Period
2020")

# Print results
results_complete_2020_Other

## $median
## # A tibble: 2 × 2
##   Period2020 median
##   <chr>         <dbl>
## 1 After 2020    3.5
## 2 Before 2020   2
##
## $p.value
## [1] 0.03066192

results_Reuse_2020_Other

## $median
## # A tibble: 2 × 2
##   Period2020 median
##   <chr>         <dbl>
## 1 After 2020    3
## 2 Before 2020  2.5
##
## $p.value
## [1] 0.1037424

results_access_2020_Other

## $median
## # A tibble: 2 × 2
##   Period2020 median
##   <chr>         <dbl>
## 1 After 2020    4
## 2 Before 2020   2
##
## $p.value
## [1] 0.1016182

results_licence_2020_Other

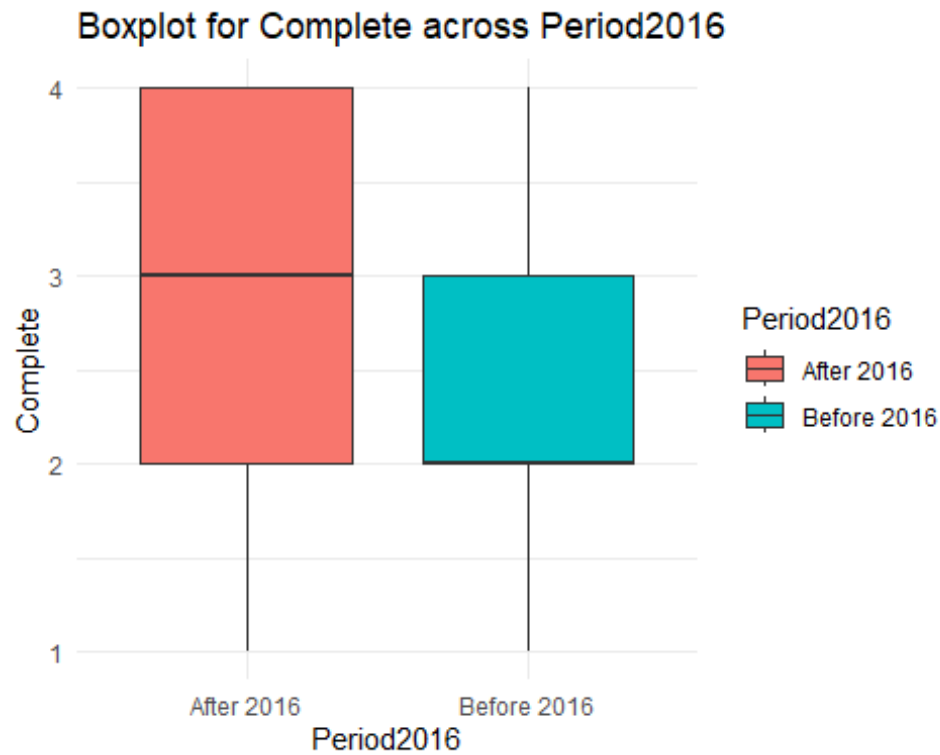
## $median
## # A tibble: 2 × 2
##   Period2020 median
##   <chr>         <dbl>
## 1 After 2020    4
## 2 Before 2020   4
##

```

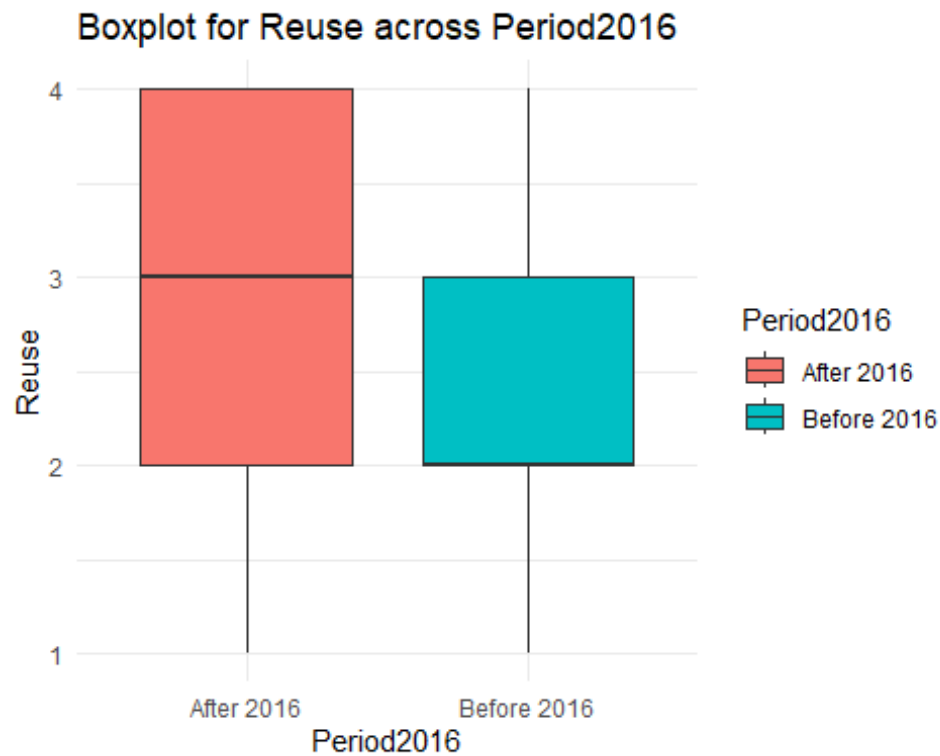
```
## $p.value  
## [1] 0.365762
```

#Study the significant difference before and after Fair 2016 using Median and Mann Whitney U for all the papers

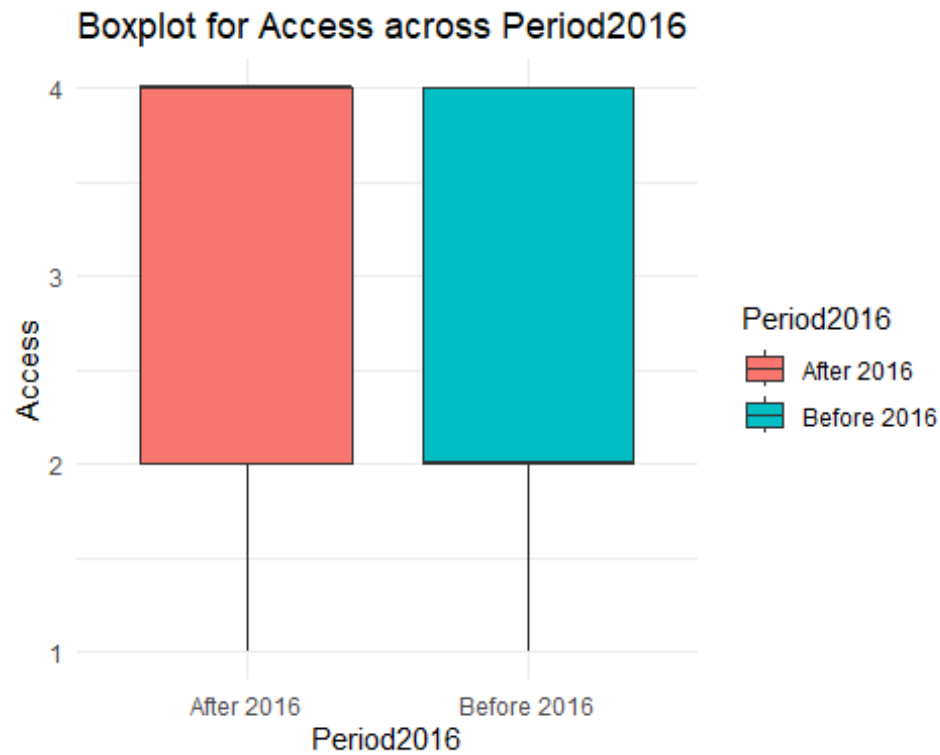
```
data <- data %>%  
  mutate(Period2016 = ifelse(Year <= 2016, "Before 2016", "After 2016"))  
  
# Function to perform the Mann-Whitney test, calculate medians, and generate box plots  
perform_analysis <- function(data, score_var, period_var) {  
  test_result <- wilcox.test(reformulate(period_var, score_var), data = data,  
    exact = FALSE)  
  
  medians <- data %>%  
    group_by(!sym(period_var)) %>%  
    summarise(median = median(!sym(score_var), na.rm = TRUE), .groups = 'drop')  
  
  # Generate a box plot  
  box_plot <- ggplot(data, aes_string(x = period_var, y = score_var, fill = period_var)) +  
    geom_boxplot() +  
    labs(title = paste("Boxplot for", score_var, "across", period_var),  
      x = period_var,  
      y = score_var) +  
    theme_minimal()  
  
  # Print the box plot  
  print(box_plot)  
  
  list(median = medians, p.value = test_result$p.value, plot = box_plot)  
}  
  
# Analysis for each score for 2016  
results_complete_2016 <- perform_analysis(data, "Complete", "Period2016")
```



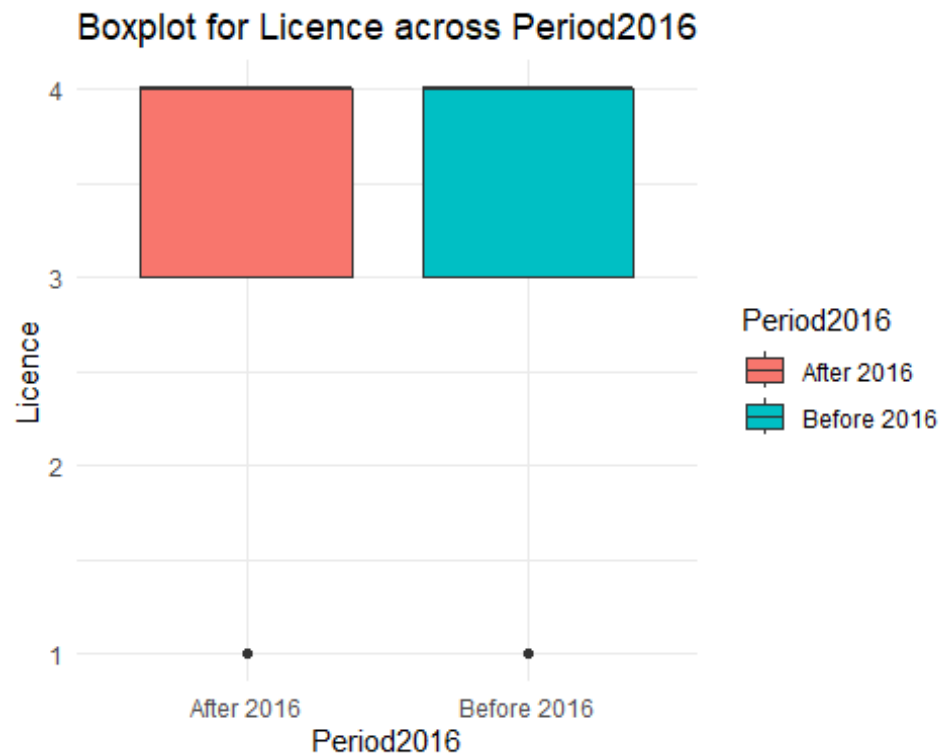
```
results_Reuse_2016 <- perform_analysis(data, "Reuse", "Period2016")
```



```
results_access_2016 <- perform_analysis(data, "Access", "Period2016")
```

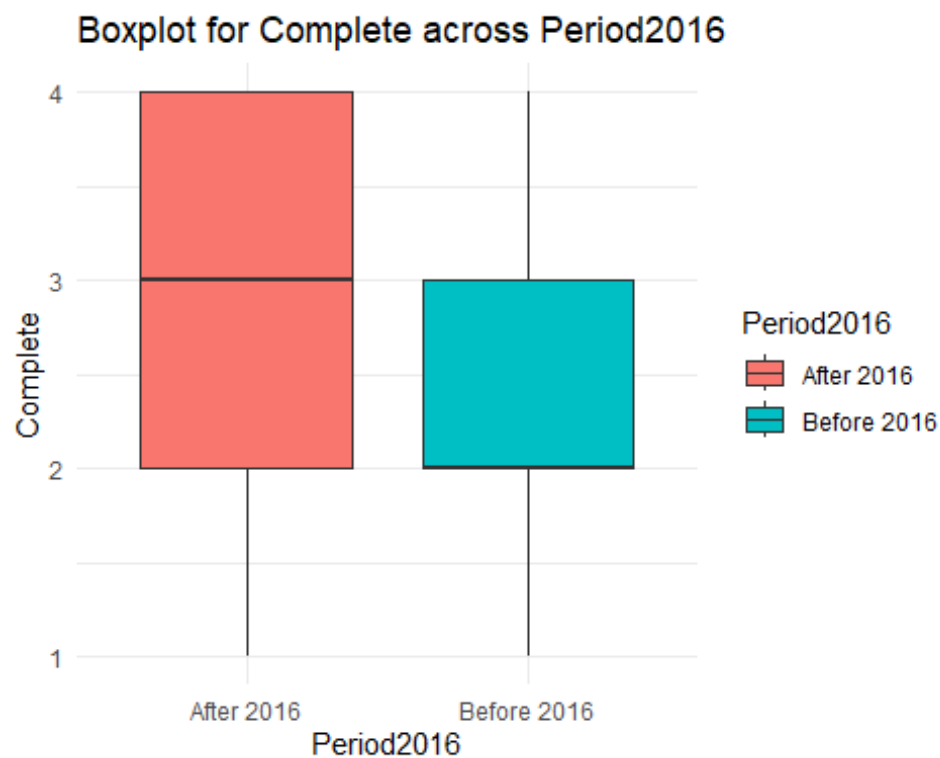



```
results_licence_2016 <- perform_analysis(data, "Licence", "Period2016")
```



```
# Print results
results_complete_2016

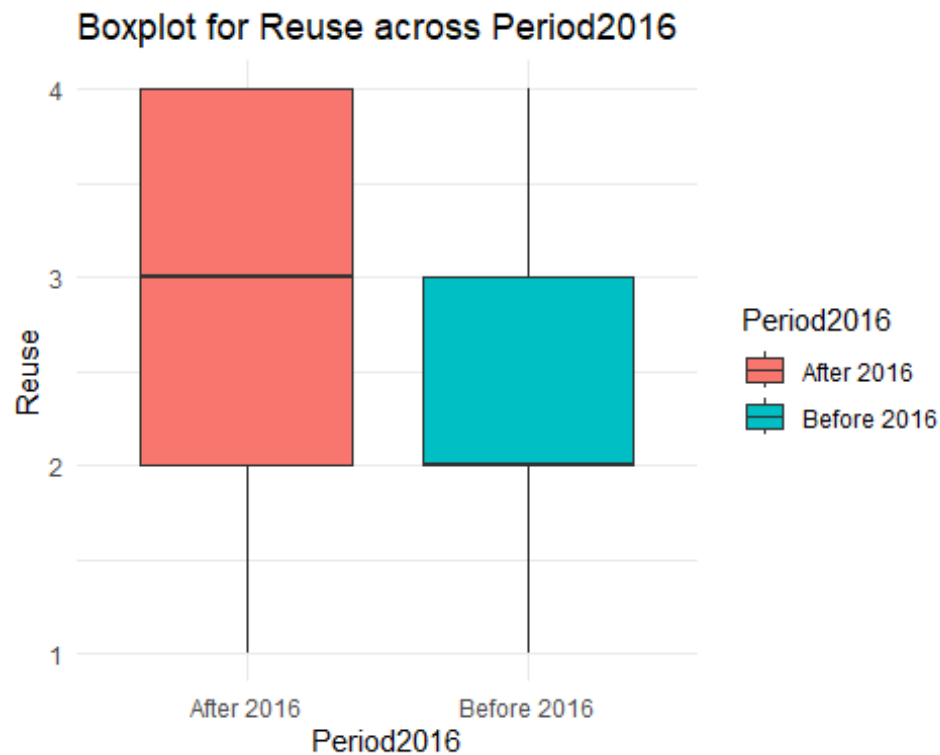
## $median
## # A tibble: 2 × 2
##   Period2016 median
##   <chr>         <dbl>
## 1 After 2016     3
## 2 Before 2016    2
##
## $p.value
## [1] 0.01447046
##
## $plot
```



```
results_Reuse_2016

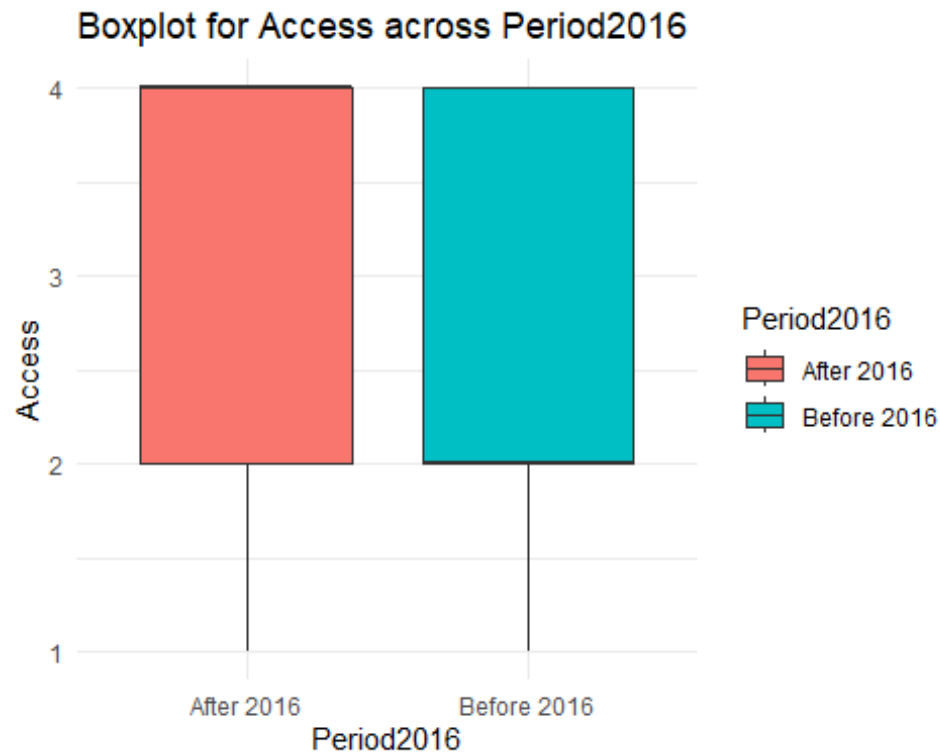
## $median
## # A tibble: 2 × 2
##   Period2016 median
##   <chr>         <dbl>
## 1 After 2016     3
## 2 Before 2016    2
##
## $p.value
## [1] 0.006953216
```

```
##  
## $plot
```



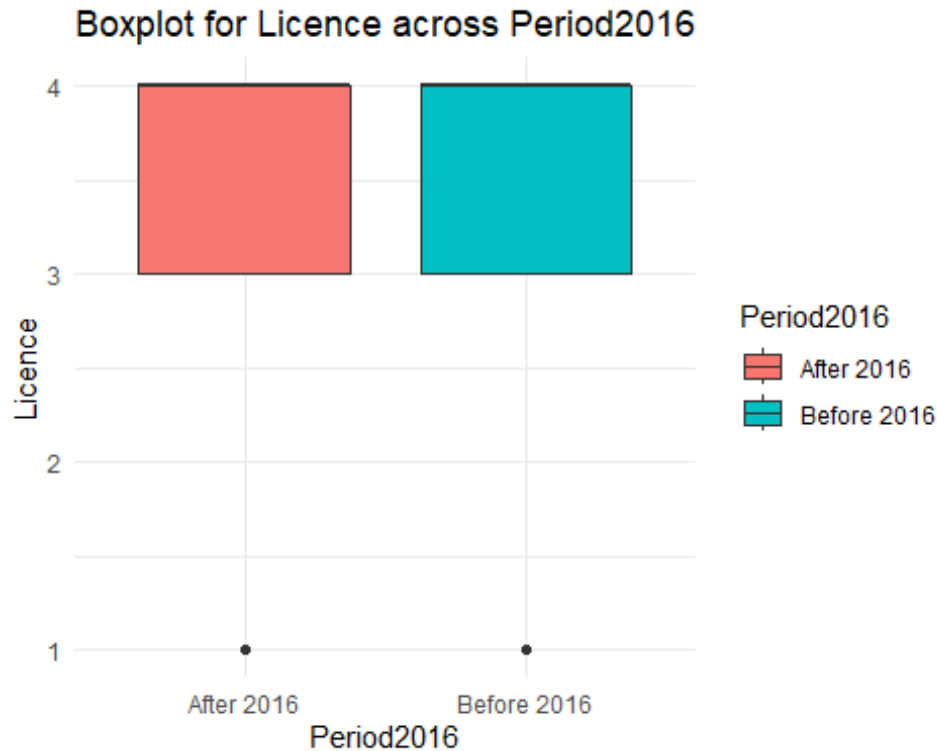
```
results_access_2016
```

```
## $median  
## # A tibble: 2 × 2  
##   Period2016 median  
##   <chr>      <dbl>  
## 1 After 2016      4  
## 2 Before 2016     2  
##  
## $p.value  
## [1] 0.0007181409  
##  
## $plot
```



```
results_licence_2016
```

```
## $median
## # A tibble: 2 × 2
##   Period2016 median
##   <chr>      <dbl>
## 1 After 2016      4
## 2 Before 2016     4
##
## $p.value
## [1] 0.7055106
##
## $plot
```



#Study the significant difference before and after Fair 2016 using Median and Mann Whitney U test for the IQB3 Papers

```
perform_analysis <- function(data_IQB3, score_var, period_var) {
  test_result <- wilcox.test(reformulate(period_var, score_var), data = data_
  IQB3, exact = FALSE)

  medians <- data_IQB3 %>%
    group_by(!sym(period_var)) %>%
    summarise(median = median(!sym(score_var), na.rm = TRUE), .groups = 'dro
    p')

  list(median = medians, p.value = test_result$p.value)
}
# Analysis for each score for 2016
results_complete_2016_IQB3 <- perform_analysis(data_IQB3, "Complete", "Period
2016")
results_Reuse_2016_IQB3 <- perform_analysis(data_IQB3, "Reuse", "Period2016")
results_access_2016_IQB3 <- perform_analysis(data_IQB3, "Access", "Period2016
")
results_licence_2016_IQB3 <- perform_analysis(data_IQB3, "Licence", "Period20
16")

# Print results
results_complete_2016_IQB3
```

```
## $median
## # A tibble: 2 × 2
##   Period2016 median
##   <chr>      <dbl>
## 1 After 2016      3
## 2 Before 2016     2
##
## $p.value
## [1] 0.3265723
```

```
results_Reuse_2016_IQB3
```

```
## $median
## # A tibble: 2 × 2
##   Period2016 median
##   <chr>      <dbl>
## 1 After 2016      3
## 2 Before 2016     2
##
## $p.value
## [1] 0.1311435
```

```
results_access_2016_IQB3
```

```
## $median
## # A tibble: 2 × 2
##   Period2016 median
##   <chr>      <dbl>
## 1 After 2016      4
## 2 Before 2016     2
##
## $p.value
## [1] 0.004984167
```

```
results_licence_2016_IQB3
```

```
## $median
## # A tibble: 2 × 2
##   Period2016 median
##   <chr>      <dbl>
## 1 After 2016      4
## 2 Before 2016     4
##
## $p.value
## [1] 0.5687401
```

#Study the significant difference before and after Fair 2016 using Median and Mann Whitney U test for the Other Papers

Analysis for each score for 2016

```
results_complete_2016_Other <- perform_analysis(data_Other, "Complete", "Peri
```

```

od2016")
results_Reuse_2016_Other <- perform_analysis(data_Other, "Reuse", "Period2016
")
results_access_2016_Other <- perform_analysis(data_Other, "Access", "Period20
16")
results_licence_2016_Other <- perform_analysis(data_Other, "Licence", "Period
2016")

# Print results
results_complete_2016_Other

## $median
## # A tibble: 2 × 2
##   Period2016 median
##   <chr>         <dbl>
## 1 After 2016      3
## 2 Before 2016     2
##
## $p.value
## [1] 0.01351854

results_Reuse_2016_Other

## $median
## # A tibble: 2 × 2
##   Period2016 median
##   <chr>         <dbl>
## 1 After 2016      3
## 2 Before 2016     2
##
## $p.value
## [1] 0.01741414

results_access_2016_Other

## $median
## # A tibble: 2 × 2
##   Period2016 median
##   <chr>         <dbl>
## 1 After 2016      4
## 2 Before 2016     2
##
## $p.value
## [1] 0.05851632

results_licence_2016_Other

## $median
## # A tibble: 2 × 2
##   Period2016 median
##   <chr>         <dbl>

```

```
## 1 After 2016      4
## 2 Before 2016     4
##
## $p.value
## [1] 1
```

#plot the distribution of DAS for each completeness score

```
# Transform the DAS variable
data <- data %>%
  mutate(NewDAS = case_when(
    is.na(DAS) ~ "Not present",
    DAS == 1 ~ "Shared",
    DAS == 0 ~ "Not shared",
    TRUE ~ as.character(DAS))) # This line is just a fallback to handle unexpected values

class(data$NewDAS)

## [1] "character"

# Convert the new DAS variable to a factor for plotting
data$NewDAS <- factor(data$NewDAS, levels = c("Not present", "Not shared", "Shared"))

# Calculate frequency and percentage for each combination of 'Complete' score and 'NewDAS' status
das_frequency <- data %>%
  group_by(Complete, NewDAS) %>%
  summarise(Frequency = n(), .groups = 'drop') %>%
  mutate(Percentage = (Frequency / sum(Frequency)) * 100)

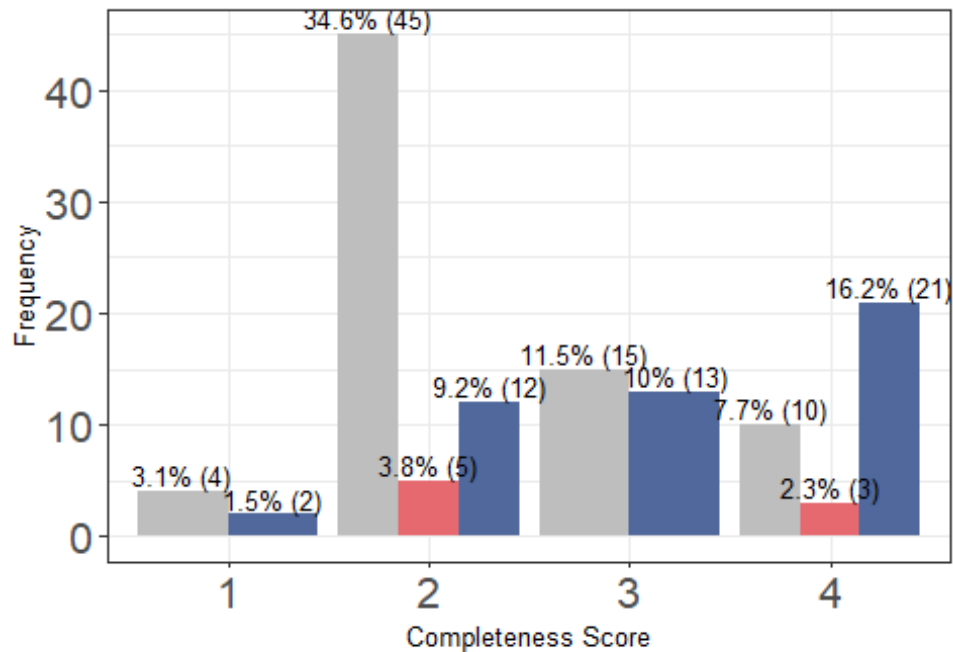
# Define specific colors for the new DAS values
colors <- c("Not present" = "gray", "Not shared" = "#E5696F", "Shared" = "#50689B")

# Create the plot
das_plot <- ggplot(das_frequency, aes(x = as.factor(Complete), y = Frequency, fill = NewDAS)) +
  geom_bar(stat = "identity", position = "dodge") +
  geom_text(aes(label = paste0(round(Percentage, 1), "% (", Frequency, ")")),
    position = position_dodge(width = 0.9), vjust = -0.25, size = 3.5
  ) +
  scale_fill_manual(values = colors, name = "DAS Status") +
  theme_bw() + # Use theme_bw for a white background
  theme(
    axis.title = element_text(size = 10), # Increase axis titles
    axis.text = element_text(size = 16), # Increase axis text
    legend.title = element_text(size = 14), # Increase legend title
    legend.text = element_text(size = 16) # Increase legend text
```



```
) +
  labs(x = "Completeness Score", y = "Frequency") +
  theme(legend.position = "bottom")

# Print and save the plot
print(das_plot)
```



DAS Status ■ Not present ■ Not shared ■ Shared

```
ggsave("new_das_distribution_plot.png", das_plot, width = 8, height = 6, bg
= "white")

# Calculate the total count per year
yearly_totals <- data %>%
  group_by(Year) %>%
  summarise(Total = n(), .groups = 'drop')

# Join the totals back to the original data and calculate proportions
proportion_data <- data %>%
  left_join(yearly_totals, by = "Year") %>%
  group_by(Year, NewDAS) %>%
  summarise(Count = n(), .groups = 'drop') %>%
  mutate(Proportion = Count / n())

# Get all unique years for the x-axis
all_years <- sort(unique(proportion_data$Year))

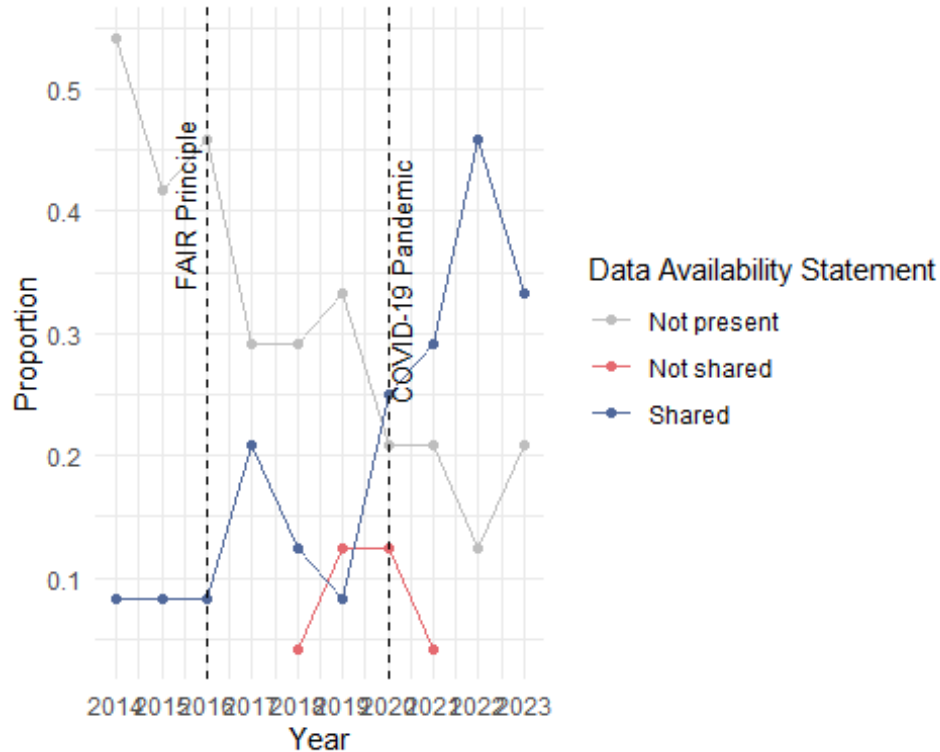
colors <- c("Not present" = "gray", "Not shared" = "#E5696F", "Shared" = "#50
689B")
```

```

# Plot with every year on the x-axis
DASyear <- ggplot(proportion_data, aes(x = Year, y = Proportion, color = NewDAS, group = NewDAS)) +
  geom_line() +
  geom_point() +
  geom_vline(xintercept = 2016, linetype = "dashed", color = "black") +
  geom_vline(xintercept = 2020, linetype = "dashed", color = "black") +
  annotate("text", x = 2016, y = max(proportion_data$Proportion), label = "FAIR Principle", angle = 90, hjust = 1.5, vjust = -0.5, size = 3.5) +
  annotate("text", x = 2020, y = max(proportion_data$Proportion), label = "COVID-19 Pandemic", angle = 90, hjust = 1.5, vjust = 1, size = 3.5) +
  scale_x_continuous(breaks = all_years) +
  labs(x = "Year", y = "Proportion", color = "Data Availability Statement") +
  theme(
    axis.title = element_text(size = 10), # Increase axis titles
    axis.text = element_text(size = 16), # Increase axis text
    legend.title = element_text(size = 14), # Increase legend title
    legend.text = element_text(size = 16) # Increase legend text
  ) +
  theme_minimal() +
  scale_color_manual(values = colors)

print(DASyear)

```



```

ggsave("DASyear.png", DASyear, width = 8, height = 6, bg = "white")

```

```

#Convert the Preprint numeric values to factor levels 'Yes' and 'No'
data$Preprint <- factor(ifelse(data$Preprint == 1, "Yes", "No"))

# Calculate the total count per year and proportion for Preprint
proportion_data <- data %>%
  group_by(Year) %>%
  count(Preprint) %>%
  mutate(Total = sum(n),
         Proportion = n / Total)

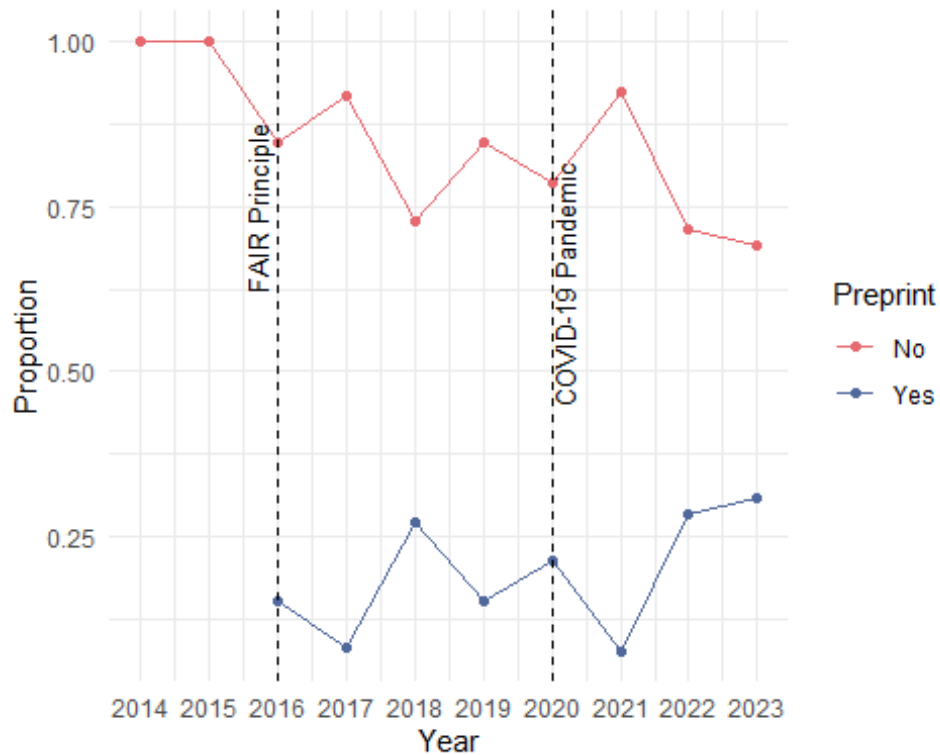
# Get all unique years for the x-axis
all_years <- sort(unique(proportion_data$Year))

# Define colors for 'Yes' and 'No'
colors <- c("No" = "#E5696F", "Yes" = "#50689B")

# Plot with every year on the x-axis for Preprint
PreprintYear <- ggplot(proportion_data, aes(x = Year, y = Proportion, color =
Preprint, group = Preprint)) +
  geom_line() +
  geom_point() +
  geom_vline(xintercept = 2016, linetype = "dashed", color = "black") +
  geom_vline(xintercept = 2020, linetype = "dashed", color = "black") +
  annotate("text", x = 2016, y = max(proportion_data$Proportion), label = "FA
IR Principle", angle = 90, hjust = 1.5, vjust = -0.5, size = 3.5) +
  annotate("text", x = 2020, y = max(proportion_data$Proportion), label = "CO
VID-19 Pandemic", angle = 90, hjust = 1.5, vjust = 1, size = 3.5) +
  scale_x_continuous(breaks = all_years) +
  labs(x = "Year", y = "Proportion", color = "Preprint") +
  theme(
    axis.title = element_text(size = 10), # Increase axis titles
    axis.text = element_text(size = 16), # Increase axis text
    legend.title = element_text(size = 14), # Increase Legend title
    legend.text = element_text(size = 16) # Increase Legend text
  ) +
  theme_minimal() +
  scale_color_manual(values = colors)

print(PreprintYear)

```



```
# Save the plot for Preprint
ggsave("PreprintYear.png", PreprintYear, width = 8, height = 6, bg = "white")
```

#study if FAIR implementation and Covid19 have an effect on DAS and Preprint # 1- Fair implementataion

```
total_by_period <- data %>%
  group_by(Period2016) %>%
  summarise(Total = n(), .groups = "drop")
```

Join this total with the DAS and Preprint summaries and calculate the percentage

```
Preprint_summary <- data %>%
  group_by(Period2016, Preprint) %>%
  summarise(Frequency = n(), .groups = "drop") %>%
  left_join(total_by_period, by = "Period2016") %>%
  mutate(Percentage = (Frequency / Total) * 100)
```

Print the Preprint summary table

```
print(Preprint_summary)
```

```
## # A tibble: 4 × 5
##   Period2016 Preprint Frequency Total Percentage
##   <chr>      <fct>      <int> <int>      <dbl>
## 1 After 2016 No          72    90         80
## 2 After 2016 Yes         18    90         20
```

```
## 3 Before 2016 No          38    40          95
## 4 Before 2016 Yes         2    40          5

Preprint_table <- table(data$Preprint, data$Period2016)

# Perform the Chi-square test
result <- chisq.test(Preprint_table)

#Print the chi-square results
print(result)

##
## Pearson's Chi-squared test with Yates' continuity correction
##
## data: Preprint_table
## X-squared = 3.7034, df = 1, p-value = 0.0543

# Get the expected values
expected_values <- result$expected

# Print the expected values
print(expected_values) ##in order to check the assumption of chi square test:
Each cell in the contingency table should have an expected count of 5 or more
.

##
##      After 2016 Before 2016
## No      76.15385   33.846154
## Yes     13.84615    6.153846

#The assumptions of that test were met:

#### Sample Size: Each cell in the contingency table has an expected count of 5 or more.
#### Independence: The observations are independent of each other. This means that the selection of one observation should not influence or affect the selection of another observation.
#### Random Sampling: The data is a random sample.
#### Categorical Data: Both variables should be categorical (either nominal or ordinal).

total_by_period <- data %>%
  group_by(Period2016) %>%
  summarise(Total = n(), .groups = "drop")

# Join this total with the NewDAS and Preprint summaries and calculate the percentage
das_summary <- data %>%
  group_by(Period2016, NewDAS)%>%
  summarise(Frequency = n(), .groups = "drop") %>%
  left_join(total_by_period, by = "Period2016") %>%
```

```

mutate(Percentage = (Frequency / Total) * 100)

# Print the DAS summary table
print(das_summary)

## # A tibble: 5 × 5
##   Period2016 NewDAS      Frequency Total Percentage
##   <chr>      <fct>      <int> <int>      <dbl>
## 1 After 2016 Not present      40     90      44.4
## 2 After 2016 Not shared       8     90       8.89
## 3 After 2016 Shared         42     90      46.7
## 4 Before 2016 Not present     34     40      85
## 5 Before 2016 Shared         6     40      15

das_table <- table(data$NewDAS, data$Period2016)

# Perform the Chi-square test
result <- chisq.test(das_table)

## Warning in chisq.test(das_table): Chi-squared approximation may be incorrect

#Print the chi-square results
print(result)

##
## Pearson's Chi-squared test
##
## data:  das_table
## X-squared = 19.078, df = 2, p-value = 7.199e-05

# Get the expected values
expected_values <- result$expected

# Print the expected values
print(expected_values) ##in order to check the assumption of chi square test:
Each cell in the contingency table should have an expected count of 5 or more
.

##
##           After 2016 Before 2016
## Not present  51.230769  22.769231
## Not shared   5.538462   2.461538
## Shared       33.230769  14.769231

#The assumptions of that test were met:

#### Sample Size: Each cell in the contingency table has an expected count of 5 or more.
#### Independence: The observations are independent of each other. This means that the selection of one observation should not influence or affect the se

```

Lection of another observation.

Random Sampling: The data is a random sample.

Categorical Data: Both variables should be categorical (either nominal or ordinal).

#2- Covid 19 # the impact of COVID-19 on Preprint

```
total_by_period <- data %>%
  group_by(Period2020)%>%
  summarise(Total = n(), .groups = "drop")

# Join this total with the DAS and Preprint summaries and calculate the percentage
Preprint_summary <- data %>%
  group_by(Period2020, Preprint) %>%
  summarise(Frequency = n(), .groups = "drop") %>%
  left_join(total_by_period, by = "Period2020") %>%
  mutate(Percentage = (Frequency / Total) * 100)

# Print the Preprint summary table
print(Preprint_summary)

## # A tibble: 4 × 5
##   Period2020 Preprint Frequency Total Percentage
##   <chr>      <fct>      <int> <int>      <dbl>
## 1 After 2020 No          31    40        77.5
## 2 After 2020 Yes         9    40        22.5
## 3 Before 2020 No         79    90        87.8
## 4 Before 2020 Yes        11    90        12.2

Preprint_table <- table(data$Preprint, data$Period2020)

# Perform the Chi-square test
result <- chisq.test(Preprint_table)

#Print the chi-square results
print(result)

##
## Pearson's Chi-squared test with Yates' continuity correction
##
## data: Preprint_table
## X-squared = 1.5269, df = 1, p-value = 0.2166

# Get the expected values
expected_values <- result$expected

# Print the expected values
print(expected_values) ##in order to check the assumption of chi square test:
Each cell in the contingency table should have an expected count of 5 or more
.
```

```
##
##      After 2020 Before 2020
## No   33.846154   76.15385
## Yes   6.153846   13.84615

#The assumptions of that test were met:

#### Sample Size: Each cell in the contingency table has an expected count of
5 or more.
#### Independence: The observations are independent of each other. This mean
s that the selection of one observation should not influence or affect the se
lection of another observation.
#### Random Sampling: The data is a random sample.
#### Categorical Data: Both variables should be categorical (either nominal or
ordinal)

# the impact of COVID-19 on DAS

total_by_period <- data %>%
  group_by(Period2020) %>%
  summarise(Total = n(), .groups = "drop")

# Join this total with the NewDAS and Preprint summaries and calculate the pe
rcentage
das_summary <- data %>%
  group_by(Period2020, NewDAS)%>%
  summarise(Frequency = n(), .groups = "drop") %>%
  left_join(total_by_period, by = "Period2020") %>%
  mutate(Percentage = (Frequency / Total) * 100)

# Print the DAS summary table
print(das_summary)

## # A tibble: 6 × 5
##   Period2020 NewDAS      Frequency Total Percentage
##   <chr>      <fct>      <int> <int>      <dbl>
## 1 After 2020 Not present      13    40      32.5
## 2 After 2020 Not shared       1    40       2.5
## 3 After 2020 Shared          26    40      65
## 4 Before 2020 Not present      61    90     67.8
## 5 Before 2020 Not shared       7    90      7.78
## 6 Before 2020 Shared          22    90     24.4

das_table <- table(data$NewDAS, data$Period2016)

# Perform the Chi-square test
result <- chisq.test(das_table)

## Warning in chisq.test(das_table): Chi-squared approximation may be incorre
ct
```



```

#Print the chi-square results
print(result)

##
## Pearson's Chi-squared test
##
## data:  das_table
## X-squared = 19.078, df = 2, p-value = 7.199e-05

# Get the expected values
expected_values <- result$expected

# Print the expected values
print(expected_values) ##in order to check the assumption of chi square test:
Each cell in the contingency table should have an expected count of 5 or more
.

##
##           After 2016 Before 2016
## Not present  51.230769  22.769231
## Not shared   5.538462   2.461538
## Shared       33.230769  14.769231

#The assumptions of that test were met:

#### Sample Size: Each cell in the contingency table has an expected count of
5 or more.
#### Independence: The observations are independent of each other. This mean
s that the selection of one observation should not influence or affect the se
lection of another observation.
### Random Sampling: The data is a random sample.
### Categorical Data: Both variables should be categorical (either nominal or
ordinal)

Image_summary <- data %>%
  group_by(Image) %>%
  summarise(count = n(), .groups = "drop")

# Calculate the overall total
overall_total <- sum(Image_summary$count)

# Add a column for the percentage of each DAS category relative to the overal
l total
Image_summary <- Image_summary %>%
  mutate(percentage = (count / overall_total) * 100)

print(Image_summary)

## # A tibble: 3 × 3
##   Image count percentage
##   <int> <int>      <dbl>

```

```
## 1      0      57      43.8
## 2      1      11      8.46
## 3     NA      62      47.7
```

```
data$DAS <- as.factor(data$DAS)
```

```
# Frequency and Percentage of the papers with DAS in the publications
```

```
data %>%
  group_by(Type, Image) %>%
  summarise(count = n(), .groups = "drop") %>%
  group_by(Type) %>%
  mutate(total = sum(count),
         percentage = (count/total)*100) %>%
  ungroup() %>%
  arrange(Type, Image)
```

```
## # A tibble: 6 × 5
##   Type  Image count total percentage
##   <chr> <int> <int> <int>      <dbl>
## 1 IQB3      0     32     80        40
## 2 IQB3      1      2     80         2.5
## 3 IQB3     NA     46     80        57.5
## 4 Other      0     25     50         50
## 5 Other      1      9     50         18
## 6 Other     NA     16     50         32
```

```
#plot the distribution of Image for each completeness score
```

```
# Transform the Image variable
```

```
data <- data %>%
  mutate(NewImage = case_when(
    is.na(Image) ~ "Not used",
    Image == 1 ~ "Shared",
    Image == 0 ~ "Not shared",
    TRUE ~ as.character(Image))) # This line is just a fallback to handle un
expected values
```

```
class(data$NewImage)
```

```
## [1] "character"
```

```
# Convert the new DAS variable to a factor for plotting
```

```
data$NewImage <- factor(data$NewImage, levels = c("Not used", "Not shared", "
Shared"))
```

```
# Calculate frequency and percentage for each combination of 'Complete' score
and 'NewImage' status
```

```
Image_frequency <- data %>%
  group_by(Complete, NewImage) %>%
  summarise(Frequency = n(), .groups = 'drop') %>%
  mutate(Percentage = (Frequency / sum(Frequency)) * 100)
```

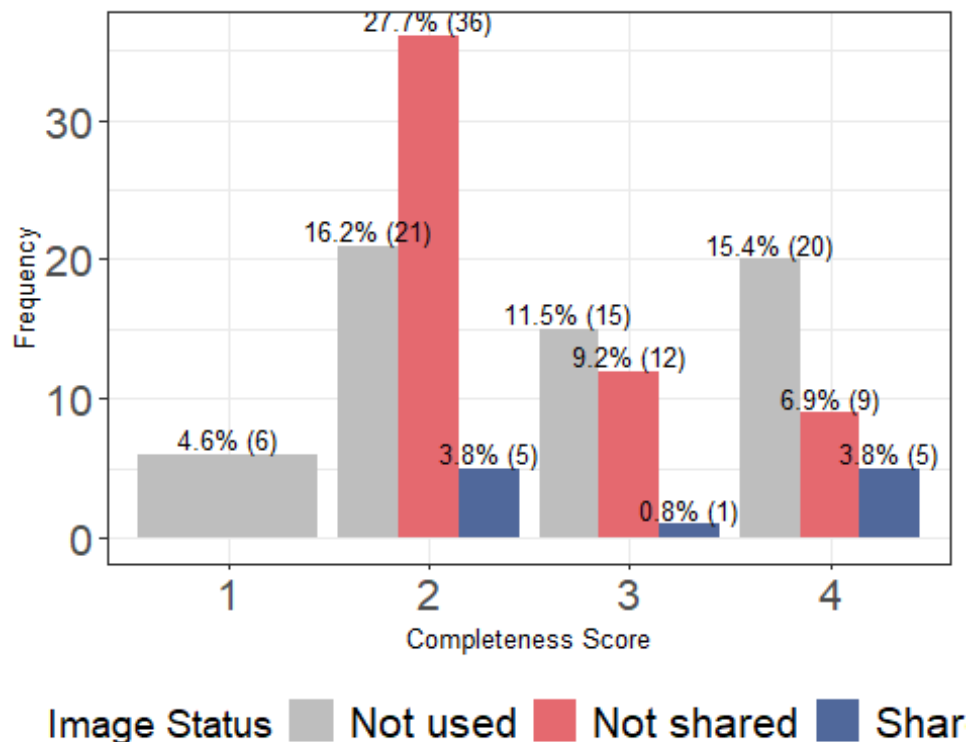
```

# Define specific colors for the new Image values
colors <- c("Not used" = "gray", "Not shared" = "#E5696F", "Shared" = "#50689B")

# Create the plot
Image_plot <- ggplot(Image_frequency, aes(x = as.factor(Complete), y = Frequency, fill = NewImage)) +
  geom_bar(stat = "identity", position = "dodge") +
  geom_text(aes(label = paste0(round(Percentage, 1), "% (", Frequency, ")")),
            position = position_dodge(width = 0.9), vjust = -0.25, size = 3.5) +
  scale_fill_manual(values = colors, name = "Image Status") +
  theme_bw() + # Use theme_bw for a white background
  theme(
    axis.title = element_text(size = 10), # Increase axis titles
    axis.text = element_text(size = 16), # Increase axis text
    legend.title = element_text(size = 14), # Increase Legend title
    legend.text = element_text(size = 16) # Increase Legend text
  ) +
  labs(x = "Completeness Score", y = "Frequency") +
  theme(legend.position = "bottom")

# Print and save the plot
print(Image_plot)

```



```

ggsave("new_Image_distribution_plot.png", Image_plot, width = 8, height = 6,
bg = "white")

# Calculate the total count per year
yearly_totals <- data %>%
  group_by(Year) %>%
  summarise(Total = n(), .groups = 'drop')

# Join the totals back to the original data and calculate proportions
proportion_data <- data %>%
  left_join(yearly_totals, by = "Year") %>%
  group_by(Year, NewImage) %>%
  summarise(Count = n(), .groups = 'drop') %>%
  mutate(Proportion = Count / n())

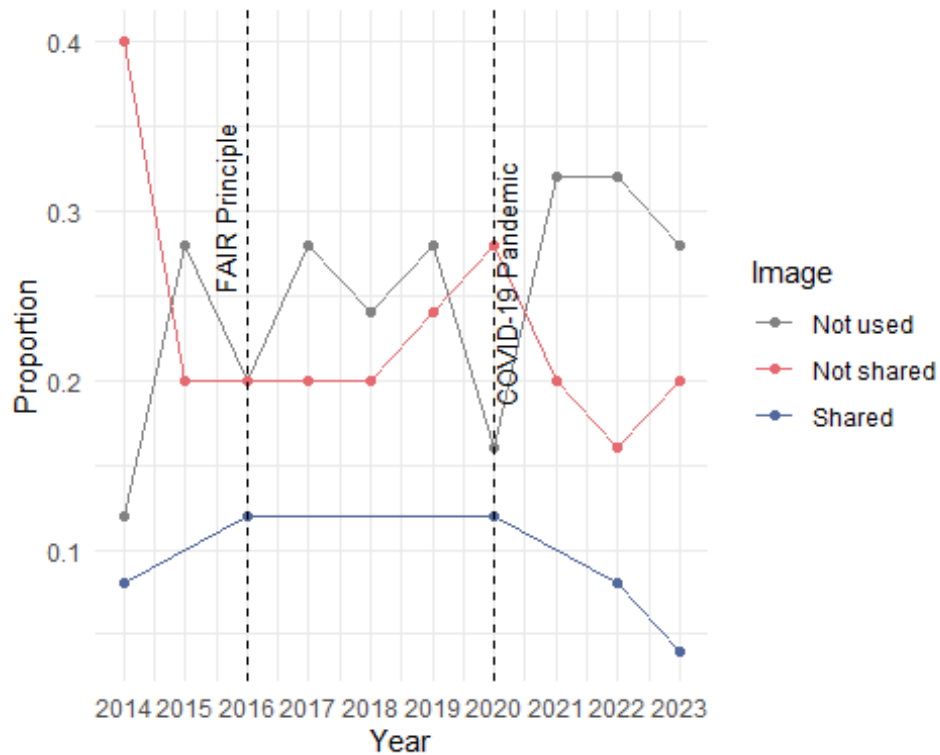
# Get all unique years for the x-axis
all_years <- sort(unique(proportion_data$Year))

colors <- c("Not used" = "#828282", "Not shared" = "#E5696F", "Shared" = "#50
689B")

# Plot with every year on the x-axis
Imageyear <- ggplot(proportion_data, aes(x = Year, y = Proportion, color = Ne
wImage, group = NewImage)) +
  geom_line() +
  geom_point() +
  geom_vline(xintercept = 2016, linetype = "dashed", color = "black") +
  geom_vline(xintercept = 2020, linetype = "dashed", color = "black") +
  annotate("text", x = 2016, y = max(proportion_data$Proportion), label = "FA
IR Principle", angle = 90, hjust = 1.5, vjust = -0.5, size = 3.5) +
  annotate("text", x = 2020, y = max(proportion_data$Proportion), label = "CO
VID-19 Pandemic", angle = 90, hjust = 1.5, vjust = 1, size = 3.5) +
  scale_x_continuous(breaks = all_years) +
  labs(x = "Year", y = "Proportion", color = "Image") +
  theme(
    axis.title = element_text(size = 10), # Increase axis titles
    axis.text = element_text(size = 16), # Increase axis text
    legend.title = element_text(size = 14), # Increase legend title
    legend.text = element_text(size = 16) # Increase legend text
  ) +
  theme_minimal() +
  scale_color_manual(values = colors)

print(Imageyear)

```



```
ggsave("Imageyear.png", Imageyear, width = 8, height = 6, bg = "white")
```

#Chi square test to assess if there is any difference in Image between the two types (IQB3, Other)

```
# Create a contingency table
```

```
table_Image <- table(data$Type, data$Image)
```

```
# Perform the Chi-square test
```

```
result <- chisq.test(table_Image)
```

```
#Print the chi-square results
```

```
print(result)
```

```
##
```

```
## Pearson's Chi-squared test with Yates' continuity correction
```

```
##
```

```
## data: table_Image
```

```
## X-squared = 3.9043, df = 1, p-value = 0.04816
```

```
# Get the expected values
```

```
expected_values <- result$expected
```

```
# Print the expected values
```

```
print(expected_values) ##in order to check the assumption of chi square test:
Each cell in the contingency table should have an expected count of 5 or more
```

```
.
```

```
##
##           0    1
## IQB3  28.5 5.5
## Other 28.5 5.5
```

#The assumptions of that test were met:

Sample Size: Each cell in the contingency table has an expected count of 5 or more.

Independence: The observations are independent of each other. This means that the selection of one observation should not influence or affect the selection of another observation.

Random Sampling: The data is a random sample.

Categorical Data: Both variables should be categorical (either nominal or ordinal).

```
Genomics_summary <- data %>%
  group_by(Genomics) %>%
  summarise(count = n(), .groups = "drop")
```

Calculate the overall total

```
overall_total <- sum(Genomics_summary$count)
```

Add a column for the percentage of each Genomics category relative to the overall total

```
Genomics_summary <- Genomics_summary %>%
  mutate(percentage = (count / overall_total) * 100)
```

```
print(Genomics_summary)
```

```
## # A tibble: 3 × 3
##   Genomics count percentage
##   <int> <int>      <dbl>
## 1      0    27      20.8
## 2      1    27      20.8
## 3     NA    76      58.5
```

```
data$Genomics <- as.factor(data$Genomics)
```

Frequency and Percentage of the papers with Genomics in the publications

```
data %>%
  group_by(Type, Genomics) %>%
  summarise(count = n(), .groups = "drop") %>%
  group_by(Type) %>%
  mutate(total = sum(count),
         percentage = (count/total)*100) %>%
  ungroup() %>%
  arrange(Type, Genomics)
```

```
## # A tibble: 6 × 5
##   Type Genomics count total percentage
##   <chr> <fct>   <int> <int>   <dbl>
## 1 IQB3  0         17    80    21.2
## 2 IQB3  1         15    80    18.8
## 3 IQB3  <NA>      48    80     60
## 4 Other 0         10    50     20
## 5 Other 1         12    50     24
## 6 Other <NA>      28    50     56
```

#plot the distribution of Genomics for each completeness score

```
# Transform the Genomics variable
data <- data %>%
  mutate(NewGenomics = case_when(
    is.na(Genomics) ~ "Not used",
    Genomics == 1 ~ "Shared",
    Genomics == 0 ~ "Not shared",
    TRUE ~ as.character(Genomics))) # This line is just a fallback to handle
unexpected values

class(data$NewGenomics)

## [1] "character"

# Convert the new Genomic variable to a factor for plotting
data$NewGenomics <- factor(data$NewGenomics, levels = c("Not used", "Not shar
ed", "Shared"))

# Calculate frequency and percentage for each combination of 'Complete' score
and 'NewGenomics' status
Genomics_frequency <- data %>%
  group_by(Complete, NewGenomics) %>%
  summarise(Frequency = n(), .groups = 'drop') %>%
  mutate(Percentage = (Frequency / sum(Frequency)) * 100)

# Define specific colors for the new Genomics values
colors <- c("Not used" = "gray", "Not shared" = "#E5696F", "Shared" = "#50689
B")

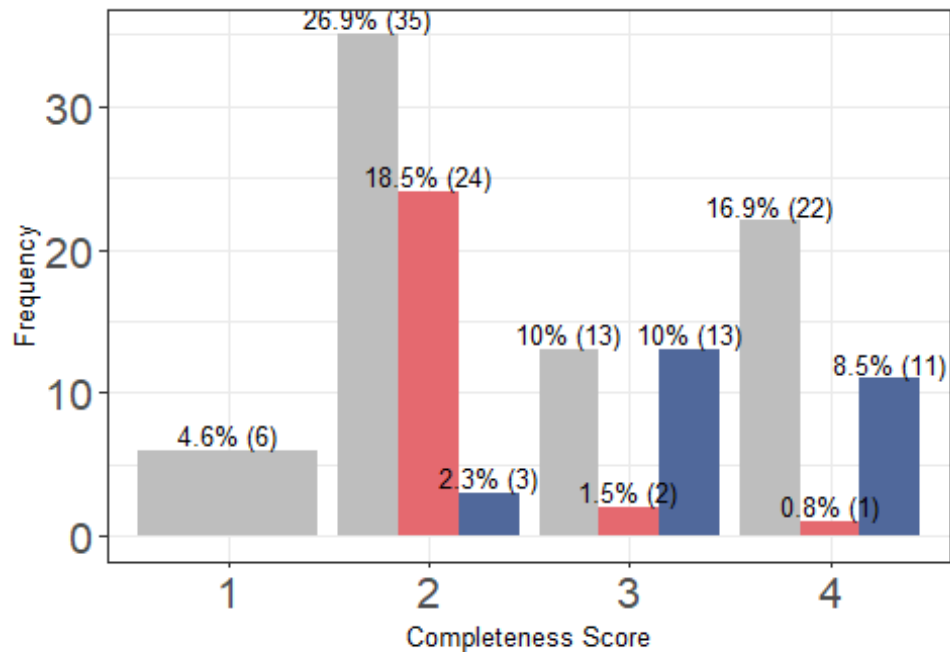
# Create the plot
Genomics_plot <- ggplot(Genomics_frequency, aes(x = as.factor(Complete), y =
Frequency, fill = NewGenomics)) +
  geom_bar(stat = "identity", position = "dodge") +
  geom_text(aes(label = paste0(round(Percentage, 1), "% (", Frequency, ")")),
    position = position_dodge(width = 0.9), vjust = -0.25, size = 3.5
) +
  scale_fill_manual(values = colors, name = "Genomics Status") +
  theme_bw() + # Use theme_bw for a white background
  theme(
```

```

axis.title = element_text(size = 10), # Increase axis titles
axis.text = element_text(size = 16), # Increase axis text
legend.title = element_text(size = 14), # Increase legend title
legend.text = element_text(size = 16) # Increase legend text
) +
labs(x = "Completeness Score", y = "Frequency") +
theme(legend.position = "bottom")

# Print and save the plot
print(Genomics_plot)

```



Genomics Status Not used Not shared Shared

```

ggsave("new_Genomics_distribution_plot.png", Image_plot, width = 8, height = 6,
bg = "white")

# Calculate the total count per year
yearly_totals <- data %>%
  group_by(Year) %>%
  summarise(Total = n(), .groups = 'drop')

# Join the totals back to the original data and calculate proportions
proportion_data <- data %>%
  left_join(yearly_totals, by = "Year") %>%
  group_by(Year, NewGenomics) %>%
  summarise(Count = n(), .groups = 'drop') %>%
  mutate(Proportion = Count / n())

# Get all unique years for the x-axis

```



```

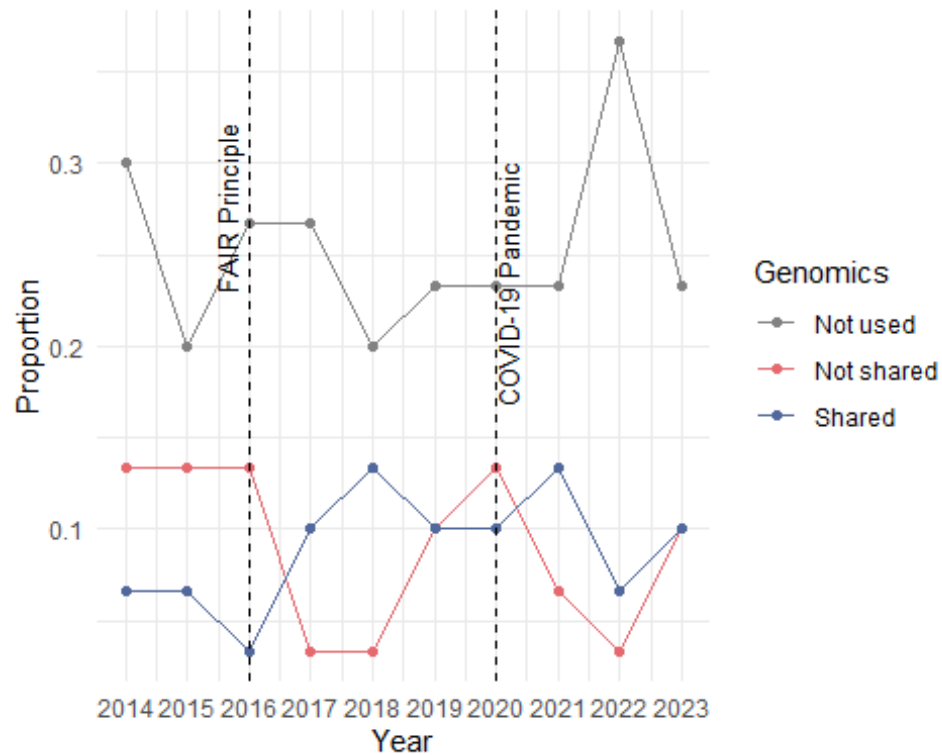
all_years <- sort(unique(proportion_data$Year))

colors <- c("Not used" = "#828282", "Not shared" = "#E5696F", "Shared" = "#50
689B")

# Plot with every year on the x-axis
Genomicsyear <- ggplot(proportion_data, aes(x = Year, y = Proportion, color =
NewGenomics, group = NewGenomics)) +
  geom_line() +
  geom_point() +
  geom_vline(xintercept = 2016, linetype = "dashed", color = "black") +
  geom_vline(xintercept = 2020, linetype = "dashed", color = "black") +
  annotate("text", x = 2016, y = max(proportion_data$Proportion), label = "FA
IR Principle", angle = 90, hjust = 1.5, vjust = -0.5, size = 3.5) +
  annotate("text", x = 2020, y = max(proportion_data$Proportion), label = "CO
VID-19 Pandemic", angle = 90, hjust = 1.5, vjust = 1, size = 3.5) +
  scale_x_continuous(breaks = all_years) +
  labs(x = "Year", y = "Proportion", color = "Genomics") +
  theme(
    axis.title = element_text(size = 10), # Increase axis titles
    axis.text = element_text(size = 16), # Increase axis text
    legend.title = element_text(size = 14), # Increase Legend title
    legend.text = element_text(size = 16) # Increase Legend text
  ) +
  theme_minimal() +
  scale_color_manual(values = colors)

print(Genomicsyear)

```



```
ggsave("Genomicsyear.png", Genomicsyear, width = 8, height = 6, bg = "white")
```

```
# Create a contingency table
```

```
table_Genomics <- table(data$Type, data$Genomics)
```

```
# Perform the Chi-square test
```

```
result <- chisq.test(table_Genomics)
```

```
#Print the chi-square results
```

```
print(result)
```

```
##
```

```
## Pearson's Chi-squared test with Yates' continuity correction
```

```
##
```

```
## data: table_Genomics
```

```
## X-squared = 0.076705, df = 1, p-value = 0.7818
```

```
# Get the expected values
```

```
expected_values <- result$expected
```

```
# Print the expected values
```

```
print(expected_values) ##in order to check the assumption of chi square test:
```

```
Each cell in the contingency table should have an expected count of 5 or more
```

```
.
```

```
##
##           0  1
## IQB3    16 16
## Other   11 11
```

#The assumptions of that test were met:

Sample Size: Each cell in the contingency table has an expected count of 5 or more.

Independence: The observations are independent of each other. This means that the selection of one observation should not influence or affect the selection of another observation.

Random Sampling: The data is a random sample.

Categorical Data: Both variables should be categorical (either nominal or ordinal).

```
Proteometabolomic_summary <- data %>%
  group_by(Proteometabolomic) %>%
  summarise(count = n(), .groups = "drop")
```

Calculate the overall total

```
overall_total <- sum(Proteometabolomic_summary$count)
```

Add a column for the percentage of each Proteometabolomic category relative to the overall total

```
Proteometabolomic_summary <- Proteometabolomic_summary %>%
  mutate(percentage = (count / overall_total) * 100)
```

```
print(Proteometabolomic_summary)
```

```
## # A tibble: 3 × 3
##   Proteometabolomic count percentage
##           <int> <int>         <dbl>
## 1             0    34          26.2
## 2             1    10           7.69
## 3            NA    86          66.2
```

```
data$Proteometabolomic <- as.factor(data$Proteometabolomic)
```

Frequency and Percentage of the papers with Proteometabolomic in the publications

```
data %>%
  group_by(Type, Proteometabolomic) %>%
  summarise(count = n(), .groups = "drop") %>%
  group_by(Type) %>%
  mutate(total = sum(count),
         percentage = (count/total)*100) %>%
  ungroup() %>%
  arrange(Type, Proteometabolomic)
```

```
## # A tibble: 6 × 5
##   Type Proteometabolomic count total percentage
##   <chr> <fct>           <int> <int>      <dbl>
## 1 IQB3  0                25    80      31.2
## 2 IQB3  1                 8    80       10
## 3 IQB3  <NA>          47    80      58.8
## 4 Other 0                 9    50       18
## 5 Other 1                 2    50        4
## 6 Other <NA>         39    50       78
```

#plot the distribution of Proteometabolomic for each completeness score

```
library(dplyr)
library(ggplot2)

# Transform the Proteometabolomic variable
data <- data %>%
  mutate(NewProteometabolomic = case_when(
    is.na(Proteometabolomic) ~ "Not used",
    Proteometabolomic == 1 ~ "Shared",
    Proteometabolomic == 0 ~ "Not shared",
    TRUE ~ as.character(Proteometabolomic)))

# Convert the new New Proteometabolomic variable to a factor for plotting
data$NewProteometabolomic <- factor(data$NewProteometabolomic, levels = c("Not used", "Not shared", "Shared"))

# Calculate frequency and percentage for each combination of 'Complete' score and 'NewProteometabolomic' status
Proteometabolomic_frequency <- data %>%
  count(Complete, NewProteometabolomic) %>%
  group_by(Complete) %>%
  mutate(Percentage = (n / sum(n)) * 100) %>%
  ungroup()

# Define specific colors for the Proteometabolomic values
colors <- c("Not used" = "gray", "Not shared" = "#E5696F", "Shared" = "#50689B")

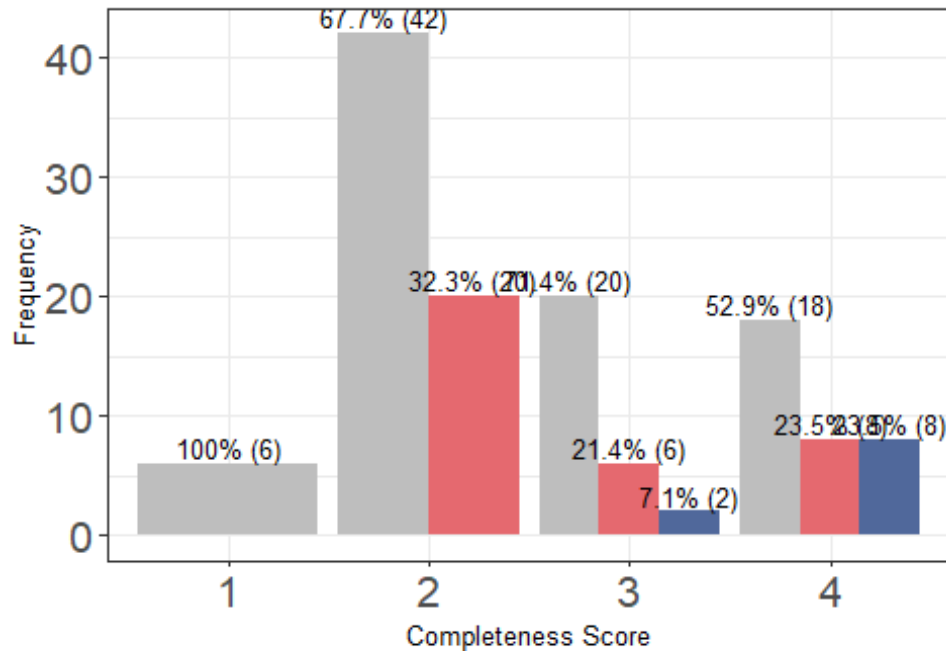
# Create the plot
Proteometabolomic_plot <- ggplot(Proteometabolomic_frequency, aes(x = as.factor(Complete), y = n, fill = NewProteometabolomic)) +
  geom_bar(stat = "identity", position = "dodge") +
  geom_text(aes(label = paste0(round(Percentage, 1), "% (", n, ")")),
            position = position_dodge(width = 0.9), vjust = -0.25, size = 3.5) +
  scale_fill_manual(values = colors, name = "Proteometabolomic Status") +
  theme_bw() +
  theme(
    axis.title = element_text(size = 10),
```

```

axis.text = element_text(size = 16),
legend.title = element_text(size = 14),
legend.text = element_text(size = 16)
) +
labs(x = "Completeness Score", y = "Frequency") +
theme(legend.position = "bottom")

# Print and save the plot
print(Proteometabolomic_plot)

```



teometabolomic Status Not used Not shared

```

ggsave("new_Proteometabolomic_distribution_plot.png", Proteometabolomic_plot,
width = 8, height = 6, bg = "white")

# Calculate the total count per year
yearly_totals <- data %>%
  group_by(Year) %>%
  summarise(Total = n(), .groups = 'drop')

# Join the totals back to the original data and calculate proportions
proportion_data <- data %>%
  left_join(yearly_totals, by = "Year") %>%
  group_by(Year, NewProteometabolomic) %>%
  summarise(Count = n(), .groups = 'drop') %>%
  mutate(Proportion = Count / n())

# Get all unique years for the x-axis
all_years <- sort(unique(proportion_data$Year))

```

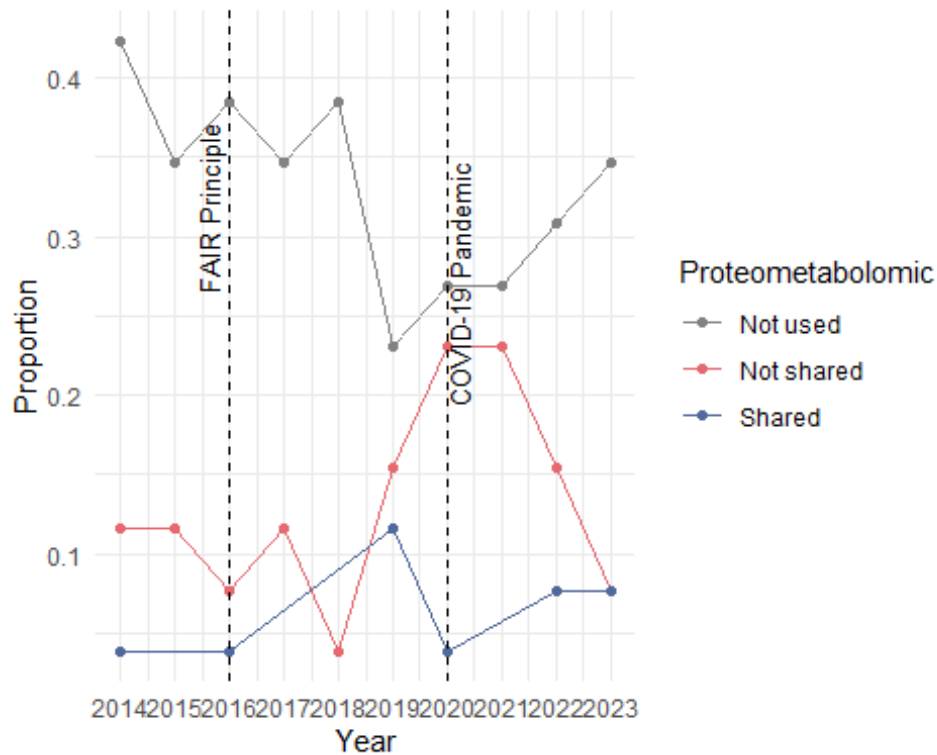
```

colors <- c("Not used" = "#828282", "Not shared" = "#E5696F", "Shared" = "#50
689B")

# Plot with every year on the x-axis
Proteometabolomicyear <- ggplot(proportion_data, aes(x = Year, y = Proportion
, color = NewProteometabolomic, group = NewProteometabolomic)) +
  geom_line() +
  geom_point() +
  geom_vline(xintercept = 2016, linetype = "dashed", color = "black") +
  geom_vline(xintercept = 2020, linetype = "dashed", color = "black") +
  annotate("text", x = 2016, y = max(proportion_data$Proportion), label = "FA
IR Principle", angle = 90, hjust = 1.5, vjust = -0.5, size = 3.5) +
  annotate("text", x = 2020, y = max(proportion_data$Proportion), label = "CO
VID-19 Pandemic", angle = 90, hjust = 1.5, vjust = 1, size = 3.5) +
  scale_x_continuous(breaks = all_years) +
  labs(x = "Year", y = "Proportion", color = "Proteometabolomic") +
  theme(
    axis.title = element_text(size = 10), # Increase axis titles
    axis.text = element_text(size = 16), # Increase axis text
    legend.title = element_text(size = 14), # Increase legend title
    legend.text = element_text(size = 16) # Increase legend text
  ) +
  theme_minimal() +
  scale_color_manual(values = colors)

print(Proteometabolomicyear)

```



```
ggsave("Proteometabolomicyear.png", Proteometabolomicyear, width = 8, height = 6, bg = "white")
```

```
# Create a contingency table
```

```
table_Proteometabolomic <- table(data$Type, data$Proteometabolomic)
```

```
# Perform the Chi-square test
```

```
result <- chisq.test(table_Proteometabolomic)
```

```
## Warning in chisq.test(table_Proteometabolomic): Chi-squared approximation may be incorrect
```

```
#Print the chi-square results
```

```
print(result)
```

```
##
```

```
## Pearson's Chi-squared test with Yates' continuity correction
```

```
##
```

```
## data: table_Proteometabolomic
```

```
## X-squared = 0, df = 1, p-value = 1
```

```
# Get the expected values
```

```
expected_values <- result$expected
```

```
# Print the expected values
```

```
print(expected_values) ##in order to check the assumption of chi square test:
```

Each cell in the contingency table should have an expected count of 5 or more .

```
##  
##           0    1  
## IQB3    25.5 7.5  
## Other    8.5 2.5
```

#The assumptions of that test were met:

Sample Size: Each cell in the contingency table has an expected count of 5 or more.

Independence: The observations are independent of each other. This means that the selection of one observation should not influence or affect the selection of another observation.

Random Sampling: The data is a random sample.

Categorical Data: Both variables should be categorical (either nominal or ordinal).

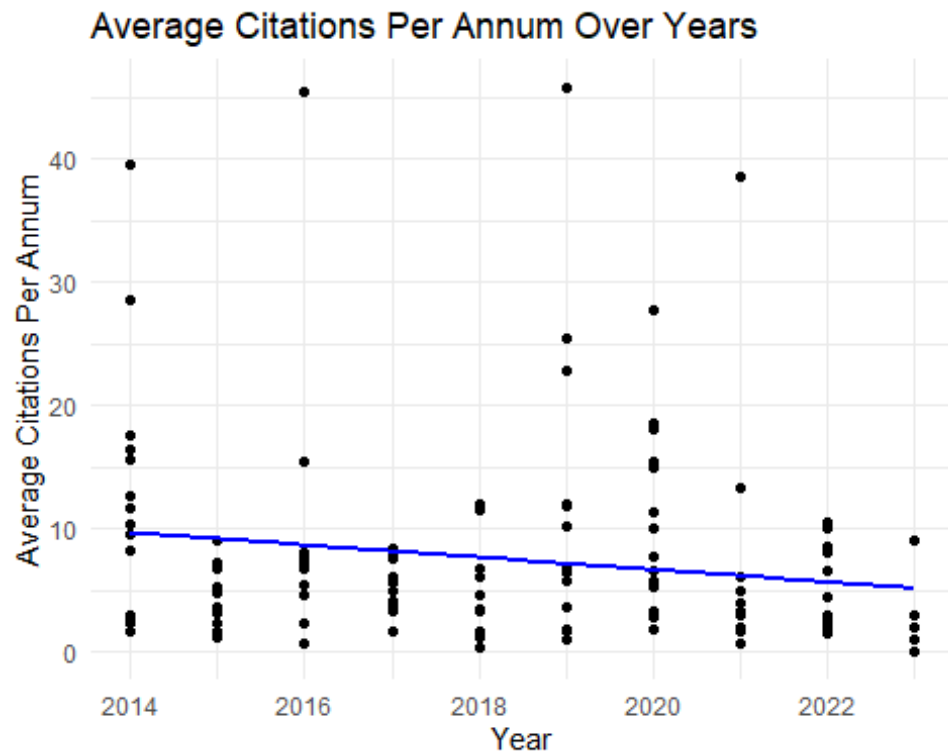
Load the data

```
data <- read.csv("datarecord.csv")
```

Plot using ggplot2

```
ggplot(data, aes(x = Year, y = CitationsPA)) +  
  geom_point() + # Add points  
  geom_smooth(method = "lm", se = FALSE, color = "blue") + # Add a Linear trend line without confidence interval  
  labs(title = "Average Citations Per Annum Over Years",  
        x = "Year",  
        y = "Average Citations Per Annum") +  
  theme_minimal()
```

```
## `geom_smooth()` using formula = 'y ~ x'
```

#add the difference

between high and low completeness score

```
df <- read.csv("datarecord.csv")

# Ensure the 'Complete' and 'CitationsPA' columns are correctly formatted
# 'Complete' should be numeric or integer, and 'CitationsPA' should be numeric.
# If not, you might need to convert them, for example:
# df$Complete <- as.numeric(df$Complete)
# df$CitationsPA <- as.numeric(df$CitationsPA)

# Step 1: Split the data into two groups based on 'Complete' scores
group1 <- df$CitationsPA[df$Complete %in% c(1,2)]
group2 <- df$CitationsPA[df$Complete %in% c(3,4)]

# Ensure that there are no NA values that could affect the t-test
# This step is optional but recommended
group1 <- na.omit(group1)
group2 <- na.omit(group2)

# Step 2: Conduct a T-test to compare the mean citation counts between the two groups
t_test_result <- t.test(group1, group2)

# Display the t-test results
print(t_test_result)
```

```

##
## Welch Two Sample t-test
##
## data: group1 and group2
## t = -0.22511, df = 127.94, p-value = 0.8223
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -3.232464 2.572094
## sample estimates:
## mean of x mean of y
## 7.229044 7.559229

# Additional: Display mean citations for insight
mean_group1 <- mean(group1)
mean_group2 <- mean(group2)

cat("Mean citation counts for Completeness 1-2:", mean_group1, "\n")

## Mean citation counts for Completeness 1-2: 7.229044

cat("Mean citation counts for Completeness 3-4:", mean_group2, "\n")

## Mean citation counts for Completeness 3-4: 7.559229

# Assuming 'data' is your DataFrame and has been loaded correctly
# Transform the PI Group Leader variable
data <- data %>%
  mutate(PIGroupLeaderStatus = case_when(
    PIGroupLeader == 1 ~ "Leader",
    PIGroupLeader == 0 ~ "Not leader",
    TRUE ~ as.character(PIGroupLeader))) # Fallback for unexpected values

# Check the class of the new variable
class(data$PIGroupLeaderStatus)

## [1] "character"

# Convert the new PI Group Leader variable to a factor for plotting
data <- data %>%
  mutate(PIGroupLeaderStatus = factor(PIGroupLeaderStatus, levels = c("Not leader", "Leader")))

# Calculate frequency and percentage for each 'Complete' score and 'PIGroupLeaderStatus'
pi_group_frequency <- data %>%
  group_by(Complete, PIGroupLeaderStatus) %>%
  summarise(Frequency = n(), .groups = 'drop') %>%
  mutate(Percentage = (Frequency / sum(Frequency)) * 100)

# Define specific colors for the PI Group Leader status
colors <- c("Not leader" = "#E5696F", "Leader" = "#50689B")

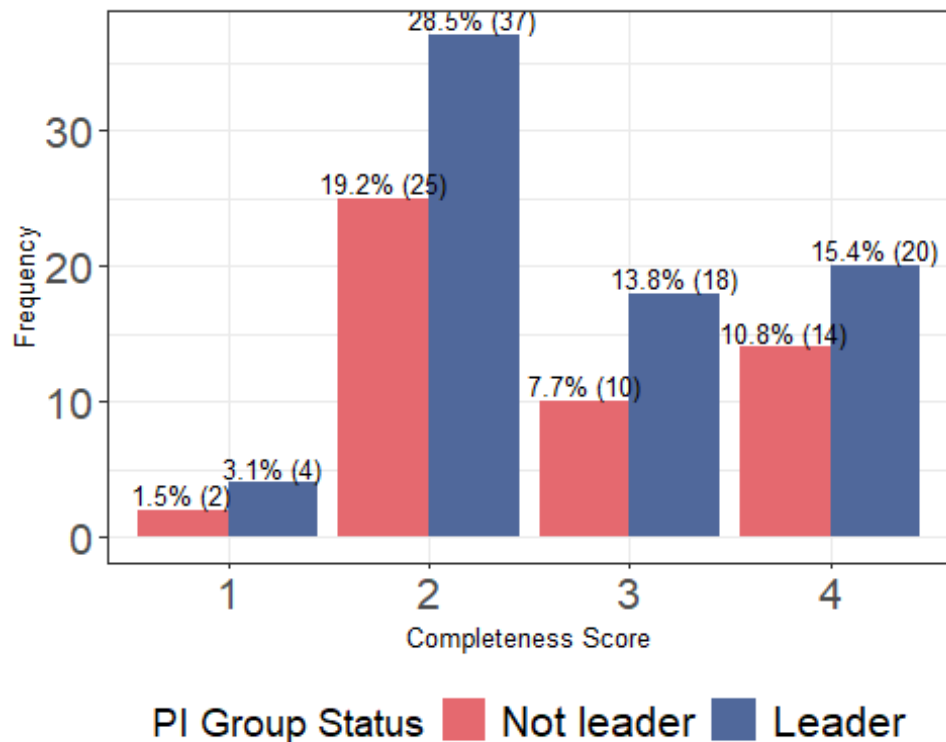
```

```

# Create the plot
pi_group_plot <- ggplot(pi_group_frequency, aes(x = as.factor(Complete), y =
Frequency, fill = PIGroupLeaderStatus)) +
  geom_bar(stat = "identity", position = "dodge") +
  geom_text(aes(label = paste0(round(Percentage, 1), "% (", Frequency, ")")),
            position = position_dodge(width = 0.9), vjust = -0.25, size = 3.5
) +
  scale_fill_manual(values = colors, name = "PI Group Status") +
  theme_bw() +
  theme(
    axis.title = element_text(size = 10),
    axis.text = element_text(size = 16),
    legend.title = element_text(size = 14),
    legend.text = element_text(size = 16)
  ) +
  labs(x = "Completeness Score", y = "Frequency") +
  theme(legend.position = "bottom")

# Print the plot
print(pi_group_plot)

```



```

# Save the plot to a file
ggsave("pi_group_status_distribution_plot.png", pi_group_plot, width = 8, height = 6, bg = "white")

```

```

#Convert the PIGroupLeader numeric values to factor levels 'Yes' and 'No'
data$PIGroupLeader <- factor(ifelse(data$PIGroupLeader == 1, "Yes", "No"))

# Calculate the total count per year and proportion for PIGroupLeader
proportion_data <- data %>%
  group_by(Year) %>%
  count(PIGroupLeader) %>%
  mutate(Total = sum(n),
         Proportion = n / Total)

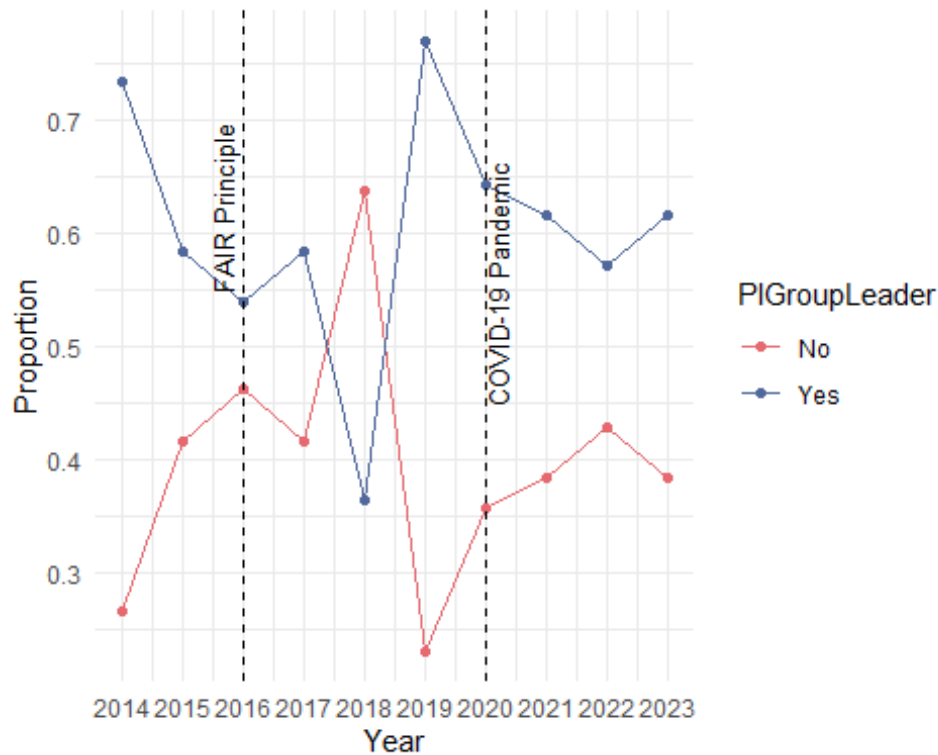
# Get all unique years for the x-axis
all_years <- sort(unique(proportion_data$Year))

# Define colors for 'Yes' and 'No'
colors <- c("No" = "#E5696F", "Yes" = "#50689B")

# Plot with every year on the x-axis for PIGroupLeader
PIGroupLeaderYear <- ggplot(proportion_data, aes(x = Year, y = Proportion, color = PIGroupLeader, group = PIGroupLeader)) +
  geom_line() +
  geom_point() +
  geom_vline(xintercept = 2016, linetype = "dashed", color = "black") +
  geom_vline(xintercept = 2020, linetype = "dashed", color = "black") +
  annotate("text", x = 2016, y = max(proportion_data$Proportion), label = "FA
IR Principle", angle = 90, hjust = 1.5, vjust = -0.5, size = 3.5) +
  annotate("text", x = 2020, y = max(proportion_data$Proportion), label = "CO
VID-19 Pandemic", angle = 90, hjust = 1.5, vjust = 1, size = 3.5) +
  scale_x_continuous(breaks = all_years) +
  labs(x = "Year", y = "Proportion", color = "PIGroupLeader") +
  theme(
    axis.title = element_text(size = 10), # Increase axis titles
    axis.text = element_text(size = 16), # Increase axis text
    legend.title = element_text(size = 14), # Increase legend title
    legend.text = element_text(size = 16) # Increase legend text
  ) +
  theme_minimal() +
  scale_color_manual(values = colors)

print(PIGroupLeaderYear)

```



```
# Save the plot for PIGroupLeader
ggsave("PIGroupLeader.png", PIGroupLeaderYear, width = 8, height = 6, bg = "white")

# Assuming 'data' is your DataFrame and has been loaded correctly
# Transform the completeness score into a binary variable (high vs. low)
data <- data %>%
  mutate(CompletenessCategory = case_when(
    Complete %in% 3:4 ~ "High",
    Complete %in% 1:2 ~ "Low",
    TRUE ~ NA_character_ # Handle potential unexpected values
  ))

# Drop rows with NA in CompletenessCategory if any exist due to unexpected values
data <- data %>% filter(!is.na(CompletenessCategory))

# Create a contingency table
contingency_table <- table(data$PIGroupLeader, data$CompletenessCategory)

# Conduct a Chi-square test of independence
chi_square_result <- chisq.test(contingency_table)

# Print the result of the Chi-square test
print(chi_square_result)
```

```
##  
## Pearson's Chi-squared test with Yates' continuity correction  
##  
## data: contingency_table  
## X-squared = 6.4044e-31, df = 1, p-value = 1
```

#2 - Ordinal regression models (Scoring Criteria and year)

```
library(ordinal) # ordinal logistic regression: cumulative link mixed models,  
clm function is in this package; For a detailed explanation of the package and  
the functions available see: https://cran.r-project.org/web/packages/ordinal/vignettes/clm\_article.pdf
```

```
## Warning: package 'ordinal' was built under R version 4.2.3
```

```
##  
## Attaching package: 'ordinal'  
  
## The following object is masked from 'package:dplyr':  
##  
## slice
```

```
library(VGAM) # more ordinal regression
```

```
## Warning: package 'VGAM' was built under R version 4.2.3
```

```
## Loading required package: stats4
```

```
## Loading required package: splines
```

```
##  
## Attaching package: 'VGAM'
```

```
## The following objects are masked from 'package:ordinal':  
##  
## dgumbel, dlgamma, pgumbel, plgamma, qgumbel, rgumbel, wine
```

```
library(dplyr) # Data manipulation  
library(chisq.posthoc.test) # If needed
```

```
## Warning: package 'chisq.posthoc.test' was built under R version 4.2.3
```

```
library(gmodels) # For SPSS style chi-sq/ contingency tables
```

```
## Warning: package 'gmodels' was built under R version 4.2.3
```

```
library(emmeans)
```

```
## Warning: package 'emmeans' was built under R version 4.2.3
```

```
library(sure)
```

```
## Warning: package 'sure' was built under R version 4.2.3
```

```

data$Complete <- factor(data$Complete, ordered = TRUE)
data$Reuse <- factor(data$Reuse, ordered = TRUE)
data$Access <- factor(data$Access, ordered = TRUE)
data$Licence <- factor(data$Licence, ordered = TRUE)
data$Year <- as.numeric(data$Year)

```

#Ordinal regression model for the Completeness by year

```

m1a <- clm(Complete ~ Year, data = data)

## Warning in x$code == 0L || action == "silent": 'length(x) = 2 > 1' in coercion
## to 'logical(1)'

## Warning: (2) Model is nearly unidentifiable: very large eigenvalue
## - Rescale variables?
## In addition: Absolute and relative convergence criteria were met

summary_m1a <- summary(m1a)

# Extract coefficients and standard errors
coefs <- summary(m1a)$coefficients
OR <- exp(coefs[,1])
lower_ci <- exp(coefs[,1] - 1.96 * coefs[,2])
upper_ci <- exp(coefs[,1] + 1.96 * coefs[,2])

# Calculate z-values and p-values
z_values <- coefs[,1] / coefs[,2]
p_values <- 2 * (1 - pnorm(abs(z_values)))

# Combine everything into a data frame for easy viewing
results <- data.frame(OR = OR, LowerCI = lower_ci, UpperCI = upper_ci, p_value = p_values)
print(results)

##              OR      LowerCI      UpperCI      p_value
## 1|2  1.622844e+151  2.282840e+50  1.153661e+252  0.003296030
## 2|3  4.125302e+152  5.138138e+51  3.312117e+253  0.003032294
## 3|4  1.117896e+153  1.334844e+52  9.362075e+253  0.002955632
## Year  1.190114e+00  1.060719e+00  1.335293e+00  0.003038852

#Check the Assumptions
nominal_test(m1a) # This is a test of the proportional odds assumption, odds
are proportional in this case.

## Tests of nominal effects
##
## formula: Complete ~ Year
##      Df  logLik    AIC  LRT Pr(>Chi)
## <none>   -148.39  304.78
## Year

```

```
scale_test(m1a) # scale test checks for equal variance/ scale across year, as
sumptions are not violated here because  $p = 0.8386$ . If  $p$  is less than 0.05 then
assumptions are violated
```

```
## Warning: (-1) Model failed to converge with max|grad| = 154.368 (tol = 1e-
06)
```

```
## In addition: iteration limit reached
```

```
## Tests of scale effects
```

```
##
```

```
## formula: Complete ~ Year
```

```
##      Df  logLik   AIC  LRT Pr(>Chi)
```

```
## <none>    -148.39 304.78
```

```
## Year
```

```
convergence(m1a) # This is another way to assess the model
```

```
##  nobs logLik  niter max.grad cond.H  logLik.Error
```

```
##  130  -148.39 7(0)  6.62e-10 6.3e+12 <1e-10
```

```
##
```

```
##      Estimate  Std.Err  Gradient      Error Cor.Dec Sig.Dig
```

```
## 1|2   348.175 118.47952 -8.05e-14 -9.96e-11      9      12
```

```
## 2|3   351.410 118.54160  4.79e-13 -9.97e-11      9      12
```

```
## 3|4   352.407 118.56313 -7.34e-13 -9.97e-11      9      12
```

```
## Year    0.174   0.05873  6.62e-10 -4.94e-14     13     13
```

```
##
```

```
## Eigen values of Hessian:
```

```
## 1.484e+08 6.886e+01 8.253e+00 2.371e-05
```

```
##
```

```
## Convergence message from clm:
```

```
## (2) Model is nearly unidentifiable: very large eigenvalue
```

```
## - Rescale variables?
```

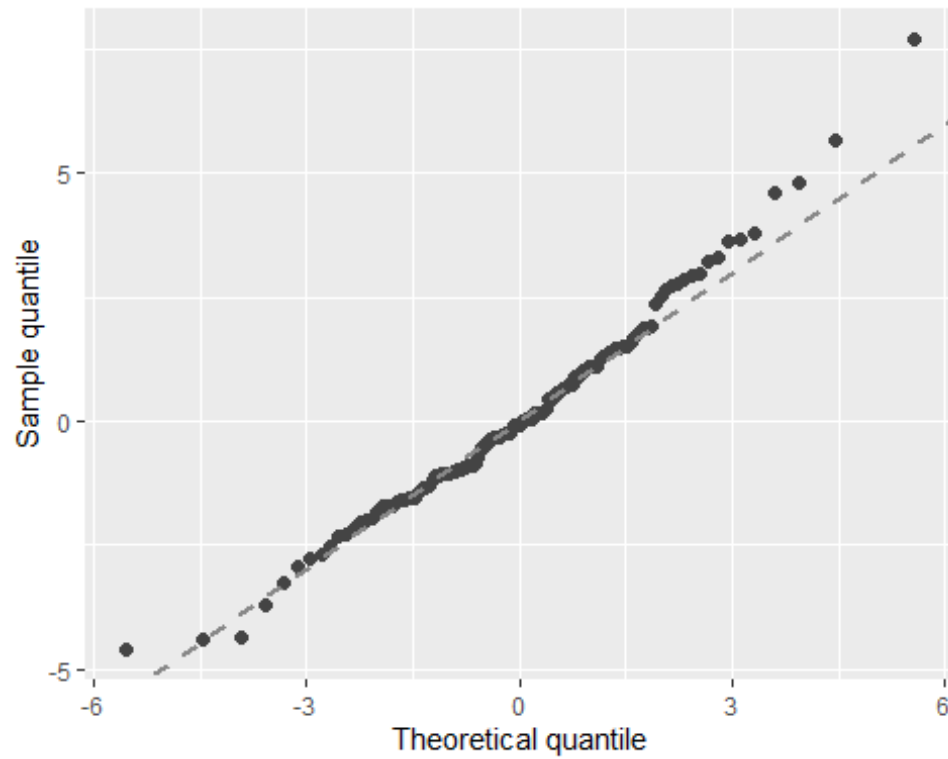
```
## (3) Model is nearly unidentifiable: large eigenvalue ratio
```

```
## - Rescale variables?
```

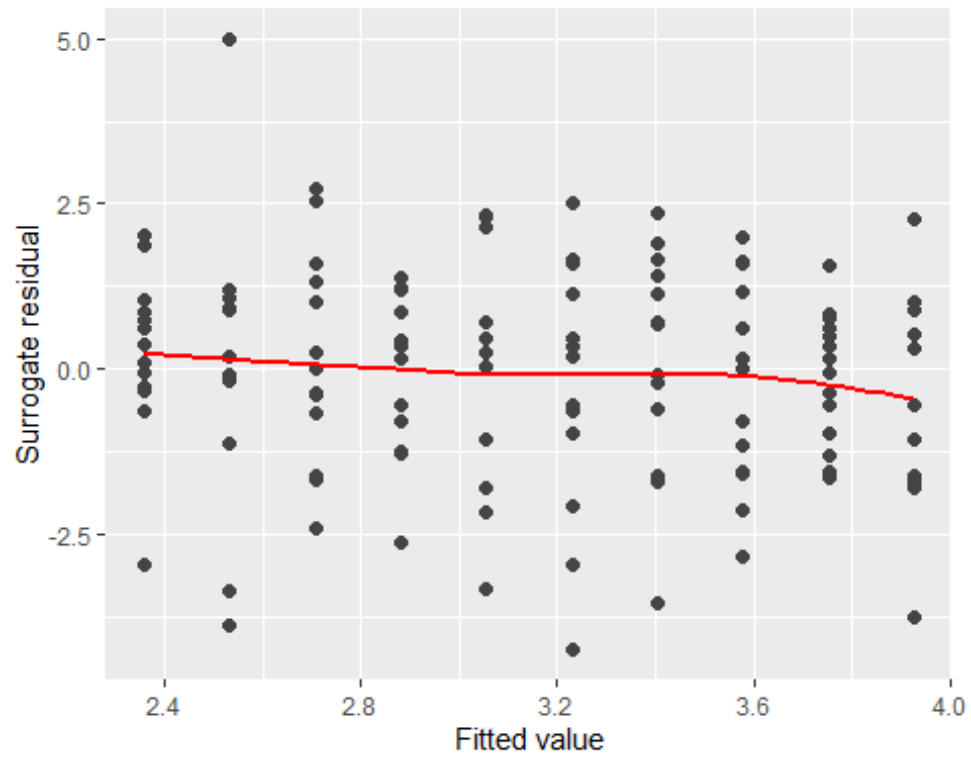
```
## In addition: Absolute and relative convergence criteria were met
```

```
##### Graphically validate proportional odds using the sure package #####
#
```

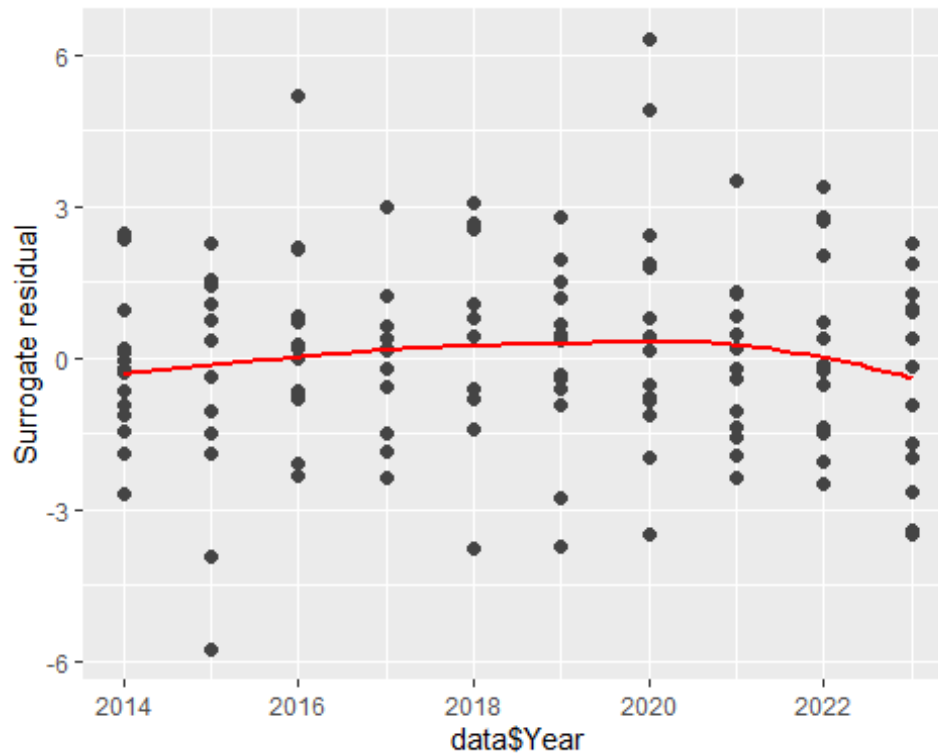
```
autoplot.clm(m1a, what = c("qq")) # most of the points fall along the line, s
o no violation of linearity
```

```
autoplot.clm(m1a, what = c("fitted")) # the residuals do not show a clear pattern or trend  
## `geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```



```
autoplot.clm(m1a, what = c("covariate"), x = data$Year) # scale test indicate
d no variance issues. This residual, covariate plots seems acceptable as well
## `geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```



N.B. - Interpreting residual plots is largely subjective!

####plotting the model

Predict probabilities for each level of 'Complete'

```
new_data <- data.frame(Year = sort(unique(data$Year)))
pred_probs <- predict(m1a, newdata = new_data, type = "prob")
```

Add the 'Year' column to the predicted probabilities dataframe

```
pred_probs_df <- cbind(new_data, as.data.frame(pred_probs))
```

Convert the predicted probabilities to a long format for ggplot

```
library(reshape2)
```

```
## Warning: package 'reshape2' was built under R version 4.2.3
```

```
##
```

```
## Attaching package: 'reshape2'
```

```
##
```

```
## The following object is masked from 'package:tidyr':
```

```
##
```

```
## smiths
```

```
pred_probs_long <- melt(pred_probs_df, id.vars = 'Year', variable.name = 'CompleteLevel', value.name = 'PredictedProbability')
```

Set the colors

```
my_colors <- c("#E5696F", "#50689B", "#36D0A1", "#D0A136")
```

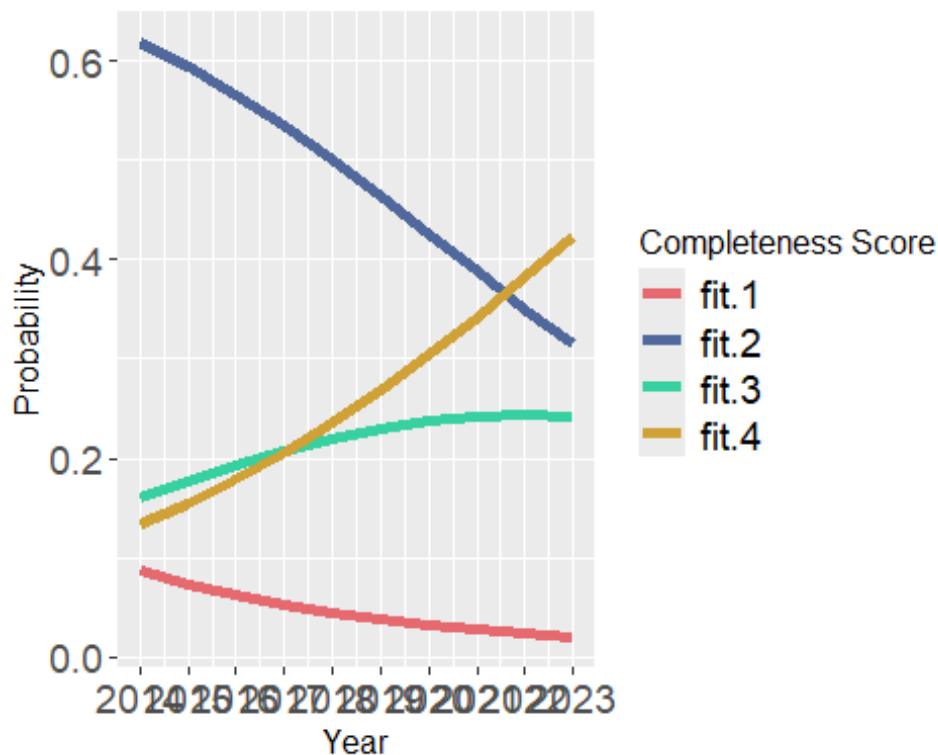
```

# Modify ggplot command
og1 <- ggplot(pred_probs_long, aes(x = Year, y = PredictedProbability, group
= CompleteLevel, color = CompleteLevel)) +
  geom_line(size = 2) + # Set size of the lines to make them thicker
  scale_color_manual(values = my_colors) +
  scale_x_continuous(breaks = unique(pred_probs_long$Year)) + # Show all years on x-axis
  labs(x = "Year", y = "Probability", color = "Completeness Score") +
  theme(
    axis.title = element_text(size = 12), # Increase axis titles
    axis.text = element_text(size = 14), # Increase axis text
    legend.title = element_text(size = 12), # Increase Legend title
    legend.text = element_text(size = 14) # Increase Legend text
  )

## Warning: Using `size` aesthetic for lines was deprecated in ggplot2 3.4.0.
## [i] Please use `linewidth` instead.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.

print(og1)

```



```

ggsave("og1.png", og1, width = 15, height = 10, units = "in", bg = "white")

```

#Ordinal regression model for the Reusability by year

```

m1a <- clm(Reuse ~ Year, data = data)

## Warning in x$code == 0L || action == "silent": 'length(x) = 2 > 1' in coercion
## to 'logical(1)'

## Warning: (2) Model is nearly unidentifiable: very large eigenvalue
## - Rescale variables?
## In addition: Absolute and relative convergence criteria were met

summary_m1a <- summary(m1a)

# Extract coefficients and standard errors
coefs <- summary(m1a)$coefficients
OR <- exp(coefs[,1])
lower_ci <- exp(coefs[,1] - 1.96 * coefs[,2])
upper_ci <- exp(coefs[,1] + 1.96 * coefs[,2])

# Calculate z-values and p-values
z_values <- coefs[,1] / coefs[,2]
p_values <- 2 * (1 - pnorm(abs(z_values)))

# Combine everything into a data frame for easy viewing
results <- data.frame(OR = OR, LowerCI = lower_ci, UpperCI = upper_ci, p_value = p_values)
print(results)

##              OR      LowerCI      UpperCI      p_value
## 1|2  1.068091e+156  2.411247e+57  4.731236e+254  0.001934390
## 2|3  2.302380e+157  4.592835e+58  1.154179e+256  0.001778537
## 3|4  5.188970e+157  9.966839e+58  2.701500e+256  0.001739712
## Year  1.196679e+00  1.069257e+00  1.339285e+00  0.001773416

#Check the Assumptions
nominal_test(m1a) # This is a test of the proportional odds assumption, odds
are proportional in this case.

## Tests of nominal effects
##
## formula: Reuse ~ Year
##      Df  logLik    AIC LRT Pr(>Chi)
## <none>   -148.73  305.47
## Year

scale_test(m1a) # scale test checks for equal variance/ scale across year, as
sumptions are not violated here

## Warning: (-1) Model failed to converge with max|grad| = 124.904 (tol = 1e-
06)
## In addition: iteration limit reached

```

```

## Tests of scale effects
##
## formula: Reuse ~ Year
##      Df  logLik    AIC LRT Pr(>Chi)
## <none>   -148.73 305.47
## Year

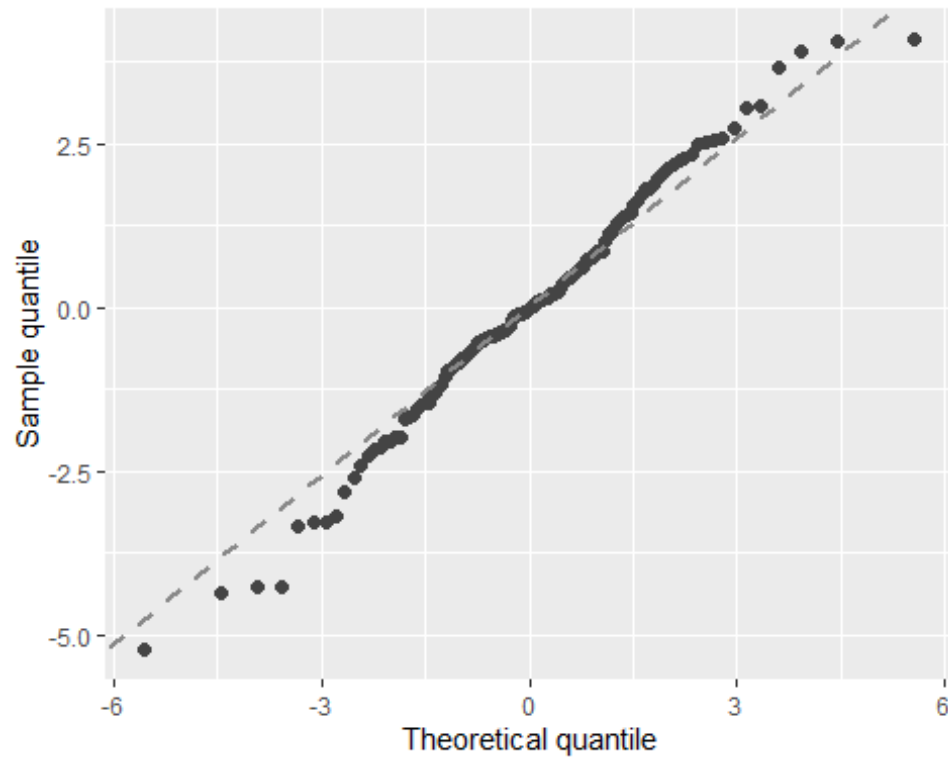
convergence(m1a) # This is another way to assess the model

## nobs logLik  niter max.grad cond.H  logLik.Error
## 130  -148.73 7(0)  6.29e-10 6.0e+12 <1e-10
##
##      Estimate  Std.Err  Gradient    Error Cor.Dec Sig.Dig
## 1|2  359.2691 115.88860 -1.73e-13 1.13e-11     10     13
## 2|3  362.3398 115.95172  1.92e-12 1.13e-11     10     13
## 3|4  363.1524 115.97102 -2.06e-12 1.13e-11     10     13
## Year    0.1796    0.05744 6.29e-10 5.60e-15     13     13
##
## Eigen values of Hessian:
## 1.496e+08 8.699e+01 8.406e+00 2.480e-05
##
## Convergence message from clm:
## (2) Model is nearly unidentifiable: very large eigenvalue
## - Rescale variables?
## (3) Model is nearly unidentifiable: large eigenvalue ratio
## - Rescale variables?
## In addition: Absolute and relative convergence criteria were met

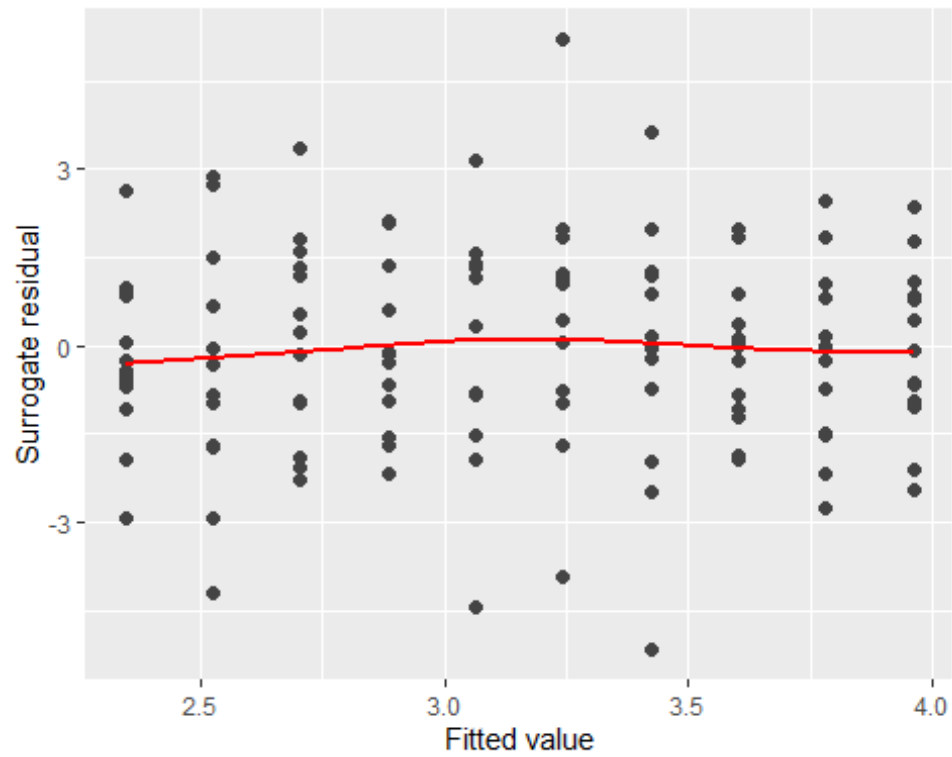
##### Graphically validate proportional odds using the sure package #####
#

autoplot.clm(m1a, what = c("qq")) # most of the points fall along the line, s
o no violation of linearity

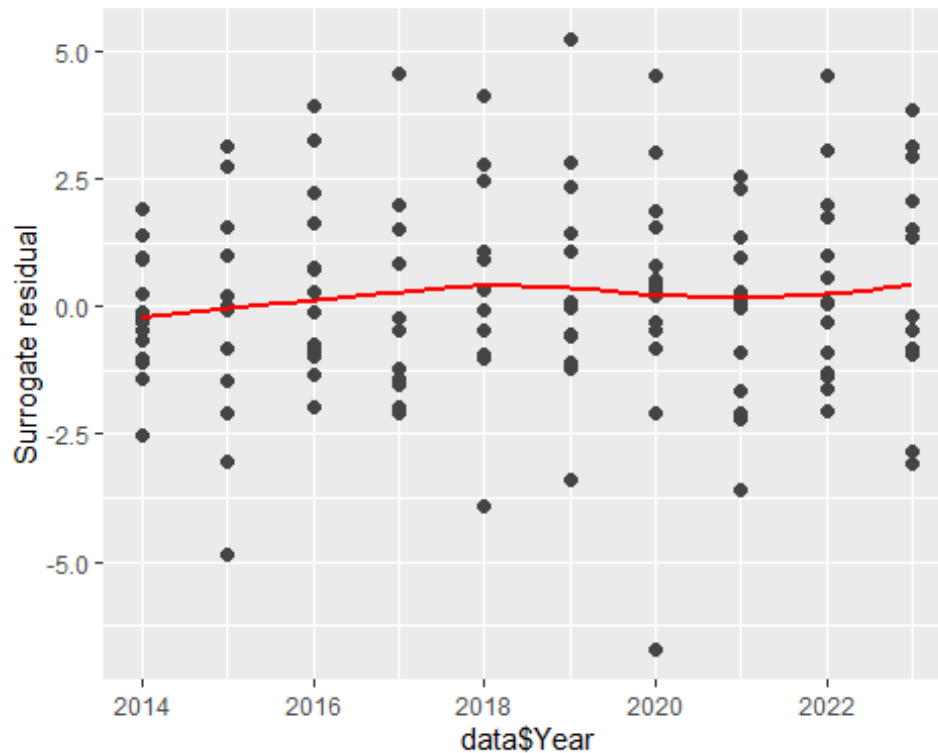
```



```
autoplot.clm(m1a, what = c("fitted")) # the residuals do not show a clear pattern or trend  
## `geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```



```
autoplot.clm(m1a, what = c("covariate"), x = data$Year) # scale test indicate
d no variance issues. This residual, covariate plots seems acceptable as well
## `geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```

N.B. - Interpreting residual plots is largely subjective!

####plotting the model

Predict probabilities for each level of 'Complete'

```
new_data <- data.frame(Year = sort(unique(data$Year)))
pred_probs <- predict(m1a, newdata = new_data, type = "prob")
```

Add the 'Year' column to the predicted probabilities dataframe

```
pred_probs_df <- cbind(new_data, as.data.frame(pred_probs))
```

Convert the predicted probabilities to a long format for ggplot

```
library(reshape2)
pred_probs_long <- melt(pred_probs_df, id.vars = 'Year', variable.name = 'Reuselevel', value.name = 'PredictedProbability')
```

Set the colors

```
my_colors <- c("#E5696F", "#50689B", "#36D0A1", "#D0A136")
```

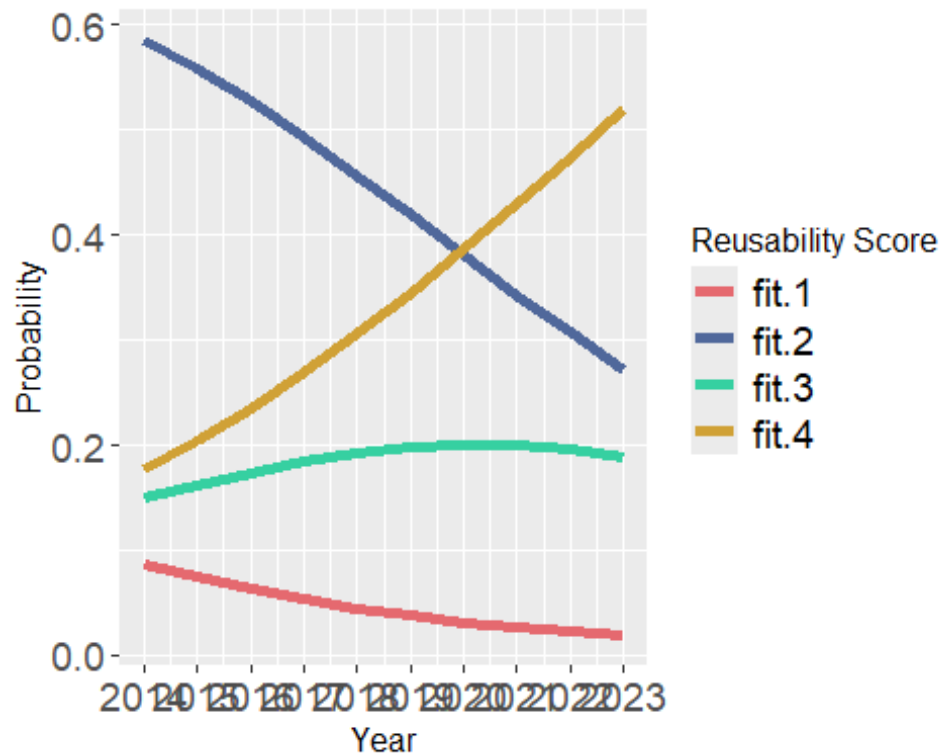
Modify ggplot command

```
og2 <- ggplot(pred_probs_long, aes(x = Year, y = PredictedProbability, group = Reuselevel, color = Reuselevel)) +
  geom_line(size = 2) + # Set size of the lines to make them thicker
  scale_color_manual(values = my_colors) + # Use colors
  scale_x_continuous(breaks = unique(pred_probs_long$Year)) + # Show all years on x-axis
  labs(x = "Year", y = "Probability", color = "Reusability Score") +
```

```

theme(
  axis.title = element_text(size = 12), # Increase axis titles
  axis.text = element_text(size = 14), # Increase axis text
  legend.title = element_text(size = 12), # Increase legend title
  legend.text = element_text(size = 14) # Increase legend text
)
print(og2)

```



```

ggsave("og2.png", og2, width = 15, height = 10, units = "in", bg = "white")

m1a <- clm(Access ~ Year, data = data)

## Warning in x$code == 0L || action == "silent": 'length(x) = 2 > 1' in coercion
## to 'logical(1)'

## Warning: (2) Model is nearly unidentifiable: very large eigenvalue
## - Rescale variables?
## In addition: Absolute and relative convergence criteria were met

summary_m1a <- summary(m1a)

# Extract coefficients and standard errors
coefs <- summary_m1a$coefficients[, 1] # Coefficients
se_coefs <- summary_m1a$coefficients[, 2] # Standard errors

```

```

# Extract coefficients and standard errors
coefs <- summary(m1a)$coefficients
OR <- exp(coefs[,1])
lower_ci <- exp(coefs[,1] - 1.96 * coefs[,2])
upper_ci <- exp(coefs[,1] + 1.96 * coefs[,2])

# Calculate z-values and p-values
z_values <- coefs[,1] / coefs[,2]
p_values <- 2 * (1 - pnorm(abs(z_values)))

# Combine everything into a data frame for easy viewing
results <- data.frame(OR = OR, LowerCI = lower_ci, UpperCI = upper_ci, p_value = p_values)
print(results)

##              OR      LowerCI  UpperCI      p_value
## 1|2  2.193927e+208  1.045919e+98      Inf  0.0002143828
## 2|3  4.895981e+209  2.007751e+99      Inf  0.0001967226
## 3|4  5.246755e+209  2.142653e+99      Inf  0.0001963546
## Year  1.270317e+00  1.120009e+00  1.440796  0.0001960819

#Check the Assumptions
nominal_test(m1a) # This is a test of the proportional odds assumption, odds
are proportional in this case.

## Tests of nominal effects
##
## formula: Access ~ Year
##           Df  logLik   AIC  LRT Pr(>Chi)
## <none>      -110.95  229.9
## Year

scale_test(m1a) # scale test checks for equal variance/ scale across year, as
assumptions are not violated here

## Warning: (-1) Model failed to converge with max|grad| = 301.489 (tol = 1e-
06)
## In addition: iteration limit reached

## Tests of scale effects
##
## formula: Access ~ Year
##           Df  logLik   AIC  LRT Pr(>Chi)
## <none>      -110.95  229.9
## Year

convergence(m1a) # This is another way to assess the model

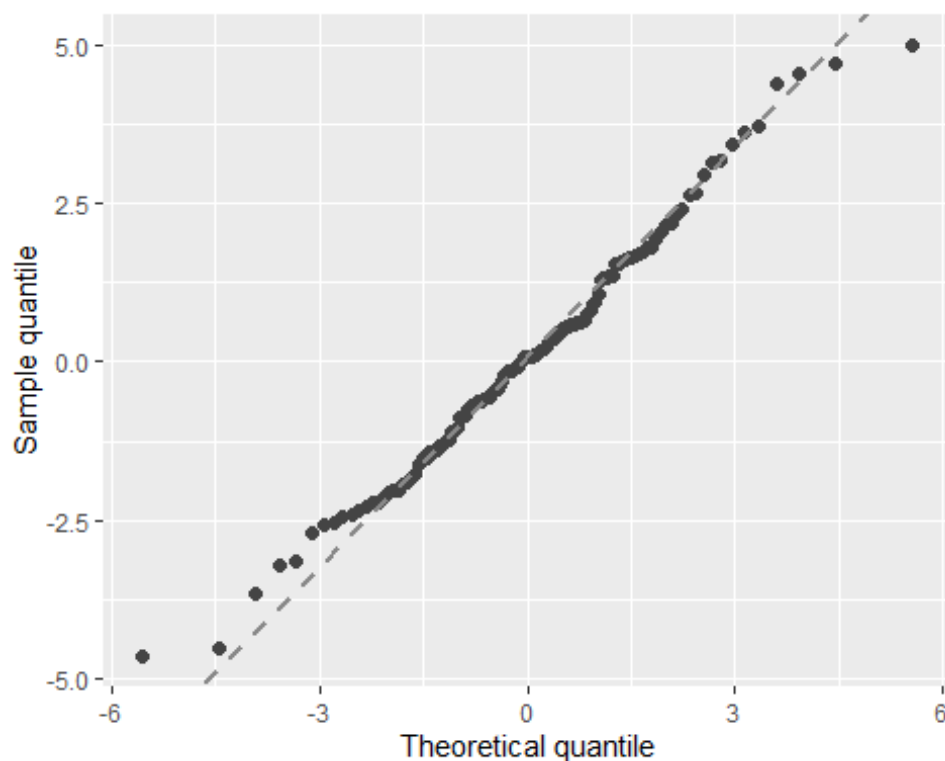
##  nobs logLik  niter max.grad cond.H  logLik.Error
##  130  -110.95  8(2)  1.15e-09  6.4e+12 <1e-10
##

```

```
##      Estimate   Std.Err   Gradient   Error Cor.Dec Sig.Dig
## 1|2  479.7234  129.60467 -2.94e-13  2.78e-11     10     13
## 2|3  482.8287  129.68151  9.06e-12  2.79e-11     10     13
## 3|4  482.8979  129.68364 -9.34e-12  2.79e-11     10     13
## Year    0.2393    0.06425  1.15e-09  1.38e-14     13     13
##
## Eigen values of Hessian:
## 1.276e+08 8.504e+02 8.325e+00 1.983e-05
##
## Convergence message from clm:
## (2) Model is nearly unidentifiable: very large eigenvalue
## - Rescale variables?
## (3) Model is nearly unidentifiable: large eigenvalue ratio
## - Rescale variables?
## In addition: Absolute and relative convergence criteria were met
```

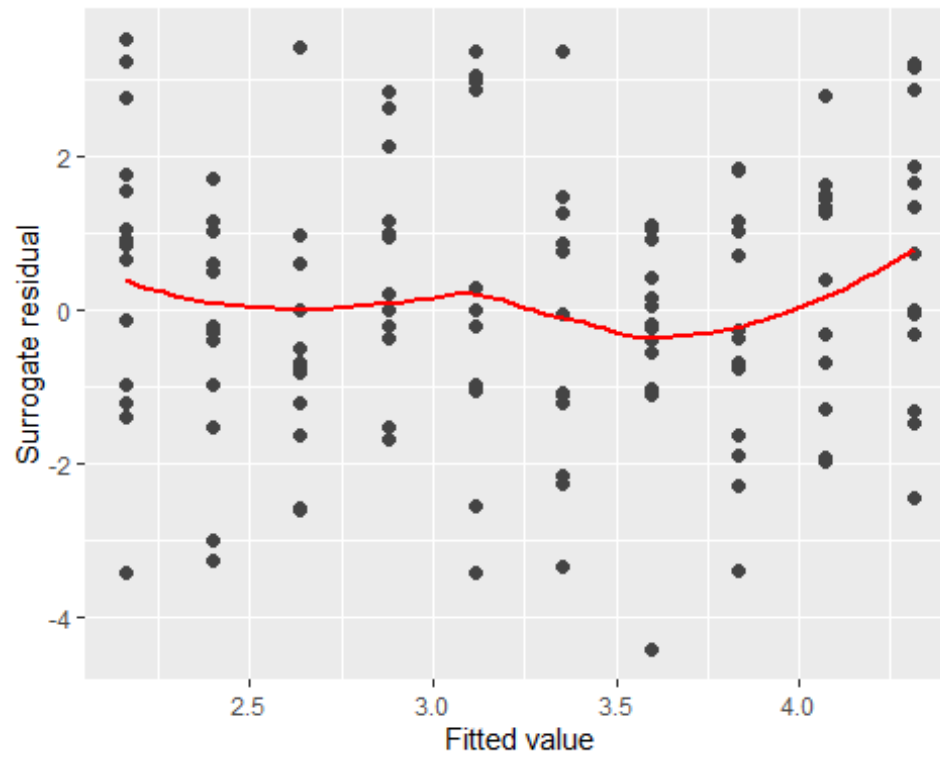
Graphically validate proportional odds using the sure package
#

`autoplot.clm(m1a, what = c("qq"))` # most of the points fall along the line, so no violation of linearity

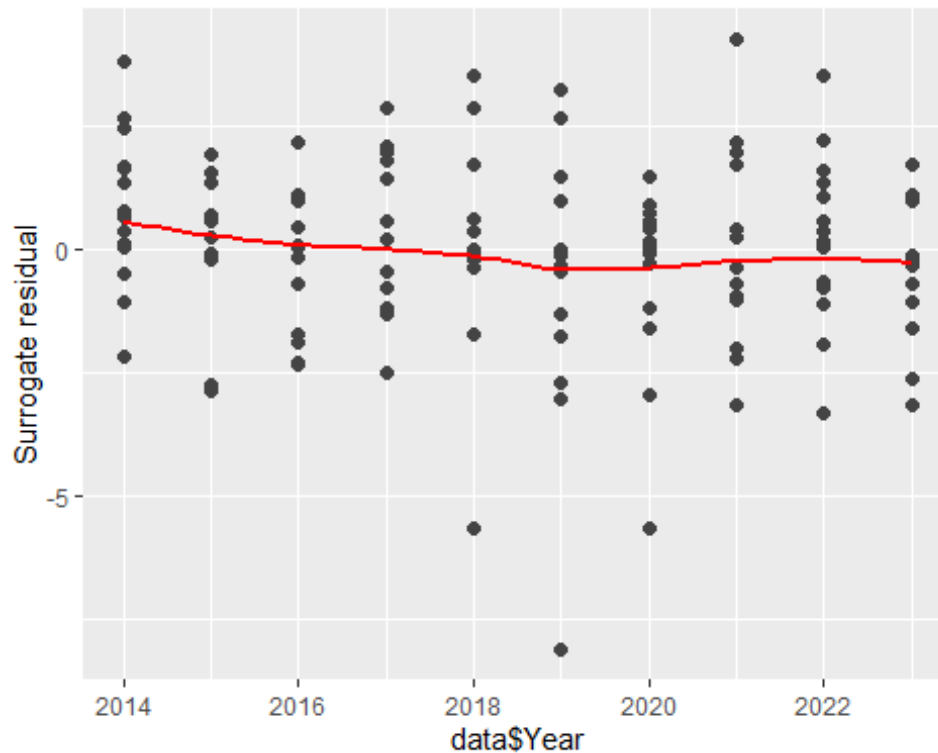


`autoplot.clm(m1a, what = c("fitted"))` # the residuals do not show a clear pattern or trend

``geom_smooth()`` using method = 'loess' and formula = 'y ~ x'



```
autoplot.clm(m1a, what = c("covariate"), x = data$Year) # scale test indicate
d no variance issues. This residual, covariate plots seems acceptable as well
## `geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```



N.B. - Interpreting residual plots is largely subjective!

###plotting the model

Predict probabilities for each level of 'Complete'

```
new_data <- data.frame(Year = sort(unique(data$Year)))
pred_probs <- predict(m1a, newdata = new_data, type = "prob")
```

Add the 'Year' column to the predicted probabilities dataframe

```
pred_probs_df <- cbind(new_data, as.data.frame(pred_probs))
```

Convert the predicted probabilities to a long format for ggplot

```
library(reshape2)
pred_probs_long <- melt(pred_probs_df, id.vars = 'Year', variable.name = 'AccessLevel', value.name = 'PredictedProbability')
```

Set the colors

```
my_colors <- c("#E5696F", "#50689B", "#36D0A1", "#D0A136")
```

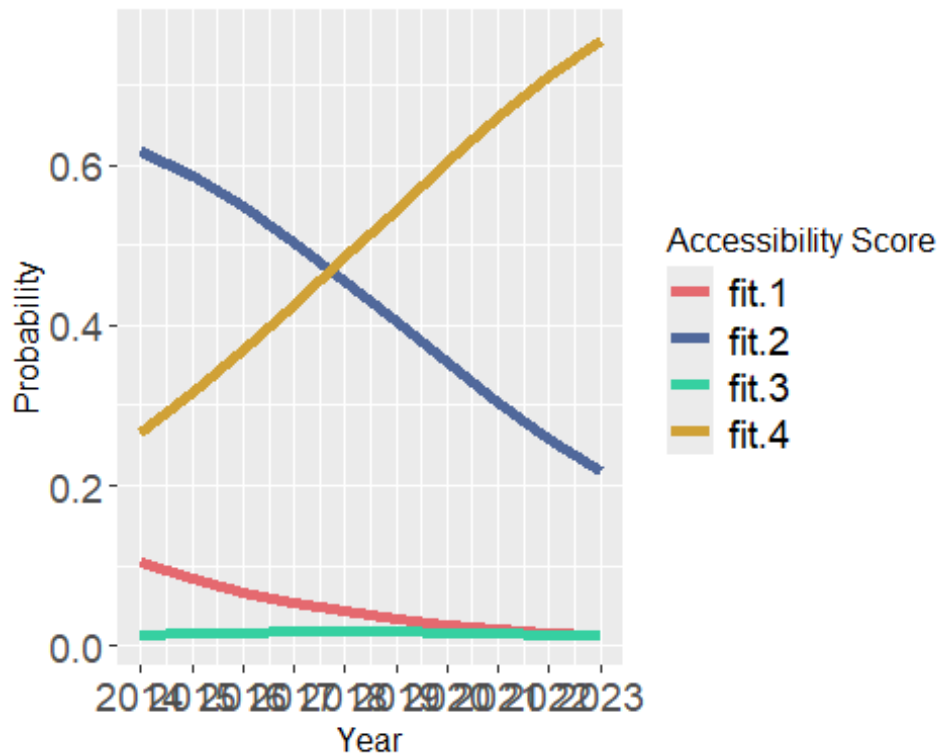
Modify ggplot command

```
og3 <- ggplot(pred_probs_long, aes(x = Year, y = PredictedProbability, group = AccessLevel, color = AccessLevel)) +
  geom_line(size = 2) + # Set size of the lines to make them thicker
  scale_color_manual(values = my_colors) + # Use colors
  scale_x_continuous(breaks = unique(pred_probs_long$Year)) + # Show all years on x-axis
  labs(x = "Year", y = "Probability", color = "Accessibility Score") +
```

```

theme(
  axis.title = element_text(size = 12), # Increase axis titles
  axis.text = element_text(size = 14), # Increase axis text
  legend.title = element_text(size = 12), # Increase legend title
  legend.text = element_text(size = 14) # Increase legend text
)
print(og3)

```



```

ggsave("og3.png", og3, width = 15, height = 10, units = "in", bg = "white")

m1a <- clm(Licence ~ Year, data = data)

## Warning in x$code == 0L || action == "silent": 'length(x) = 2 > 1' in coercion
## to 'logical(1)'

## Warning: (2) Model is nearly unidentifiable: very large eigenvalue
## - Rescale variables?
## In addition: Absolute and relative convergence criteria were met

summary_m1a <- summary(m1a)

# Extract coefficients and standard errors
coefs <- summary_m1a$coefficients[, 1] # Coefficients
se_coefs <- summary_m1a$coefficients[, 2] # Standard errors

```

```

# Extract coefficients and standard errors
coefs <- summary(m1a)$coefficients
OR <- exp(coefs[,1])
lower_ci <- exp(coefs[,1] - 1.96 * coefs[,2])
upper_ci <- exp(coefs[,1] + 1.96 * coefs[,2])

# Calculate z-values and p-values
z_values <- coefs[,1] / coefs[,2]
p_values <- 2 * (1 - pnorm(abs(z_values)))

# Combine everything into a data frame for easy viewing
results <- data.frame(OR = OR, LowerCI = lower_ci, UpperCI = upper_ci, p_value = p_values)
print(results)

##              OR      LowerCI      UpperCI    p_value
## 1|3  7.570575e+27  7.413337e-86  7.731148e+140  0.6287208
## 3|4  6.239265e+28  6.046581e-85  6.438089e+141  0.6175010
## Year  1.033865e+00  9.088113e-01  1.176126e+00  0.6126309

#Check the Assumptions
nominal_test(m1a) # This is a test of the proportional odds assumption, odds
are proportional in this case.

## Tests of nominal effects
##
## formula: Licence ~ Year
##          Df  logLik    AIC LRT Pr(>Chi)
## <none>      -93.915 193.83
## Year

scale_test(m1a) # scale test checks for equal variance/ scale across year, as
assumptions are not violated here

## Warning: (-1) Model failed to converge with max|grad| = 33798.1 (tol = 1e-
06)
## In addition: iteration limit reached

## Tests of scale effects
##
## formula: Licence ~ Year
##          Df  logLik    AIC LRT Pr(>Chi)
## <none>      -93.915 193.83
## Year

convergence(m1a) # This is another way to assess the model

##  nobs logLik niter max.grad cond.H  logLik.Error
##  130  -93.92  6(0)  3.37e-10 3.9e+12 <1e-10
##
##      Estimate   Std.Err  Gradient    Error Cor.Dec Sig.Dig

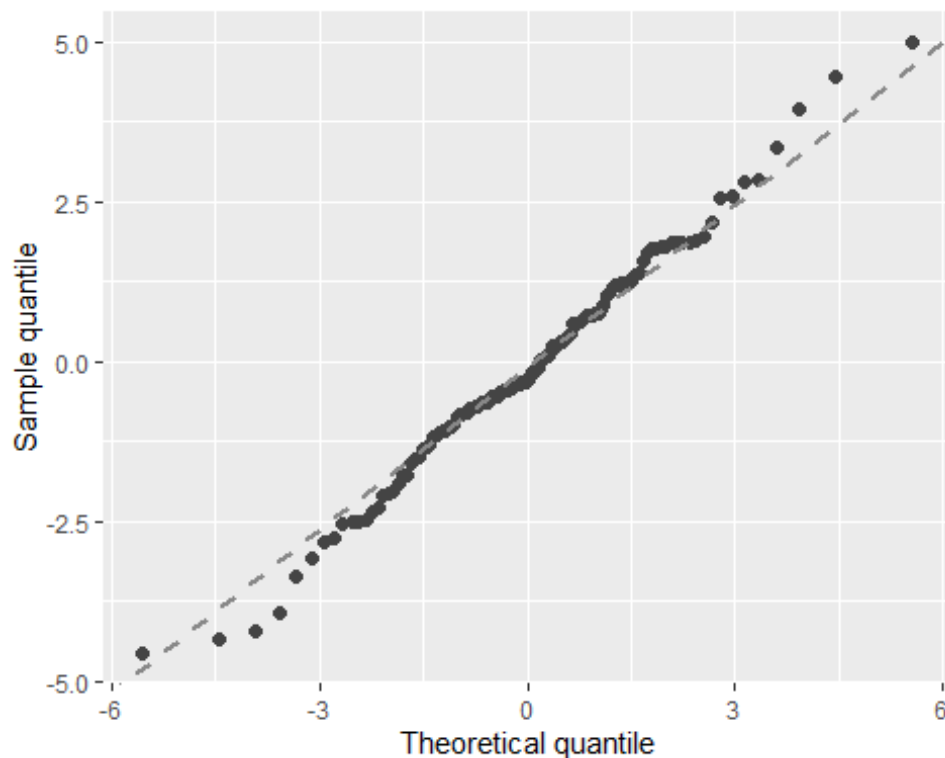
```



```
## 1|3 64.1941 132.76179 3.93e-14 -7.29e-12 10 12
## 3|4 66.3032 132.76708 1.27e-13 -7.29e-12 10 12
## Year 0.0333 0.06578 -3.37e-10 -3.62e-15 14 13
##
## Eigen values of Hessian:
## 1.093e+08 1.282e+01 2.837e-05
##
## Convergence message from clm:
## (2) Model is nearly unidentifiable: very large eigenvalue
## - Rescale variables?
## (3) Model is nearly unidentifiable: large eigenvalue ratio
## - Rescale variables?
## In addition: Absolute and relative convergence criteria were met
```

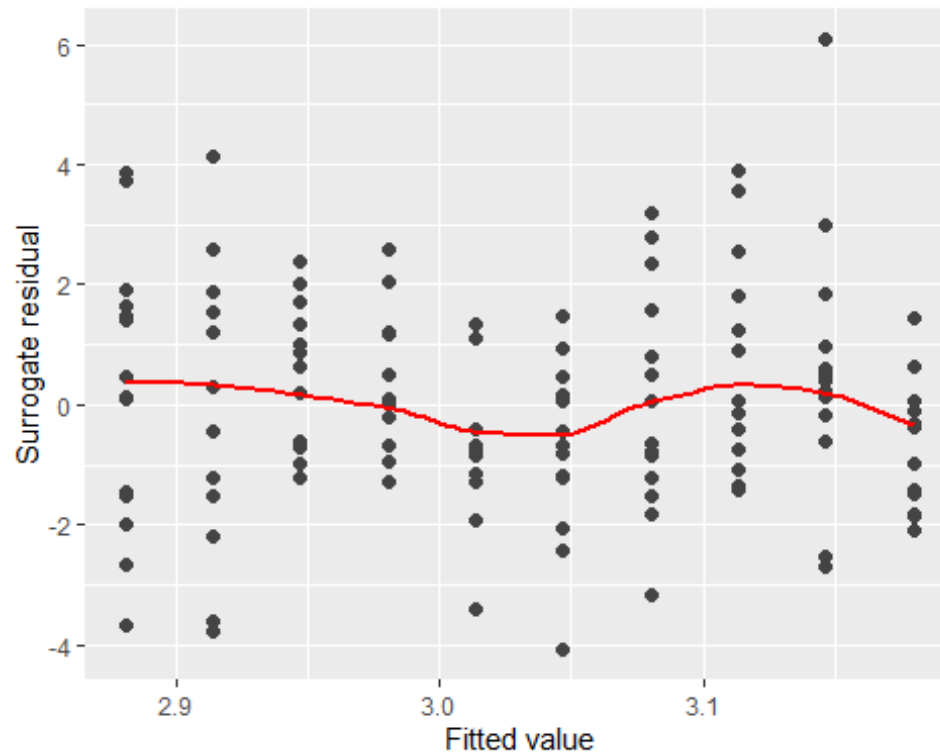
Graphically validate proportional odds using the sure package
#

```
autoplot.clm(m1a, what = c("qq")) # most of the points fall along the line, so no violation of linearity
```

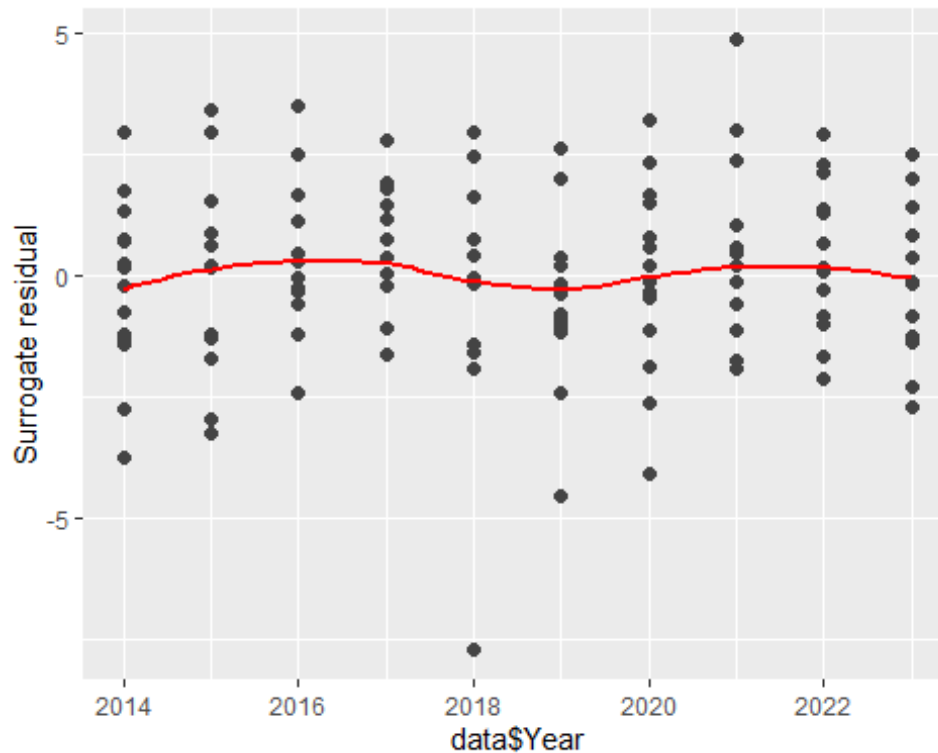


```
autoplot.clm(m1a, what = c("fitted")) # the residuals do not show a clear pattern or trend
```

```
## `geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```



```
autoplot.clm(m1a, what = c("covariate"), x = data$Year) # scale test indicate
d no variance issues. This residual, covariate plots seems acceptable as well
## `geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```



N.B. - Interpreting residual plots is largely subjective!

###plotting the model

Predict probabilities for each level of 'Complete'

```
new_data <- data.frame(Year = sort(unique(data$Year)))
pred_probs <- predict(m1a, newdata = new_data, type = "prob")
```

Add the 'Year' column to the predicted probabilities dataframe

```
pred_probs_df <- cbind(new_data, as.data.frame(pred_probs))
```

Convert the predicted probabilities to a long format for ggplot

```
library(reshape2)
pred_probs_long <- melt(pred_probs_df, id.vars = 'Year', variable.name = 'Licencelevel', value.name = 'PredictedProbability')
```

Set the colors

```
my_colors <- c("#E5696F", "#36D0A1", "#D0A136")
```

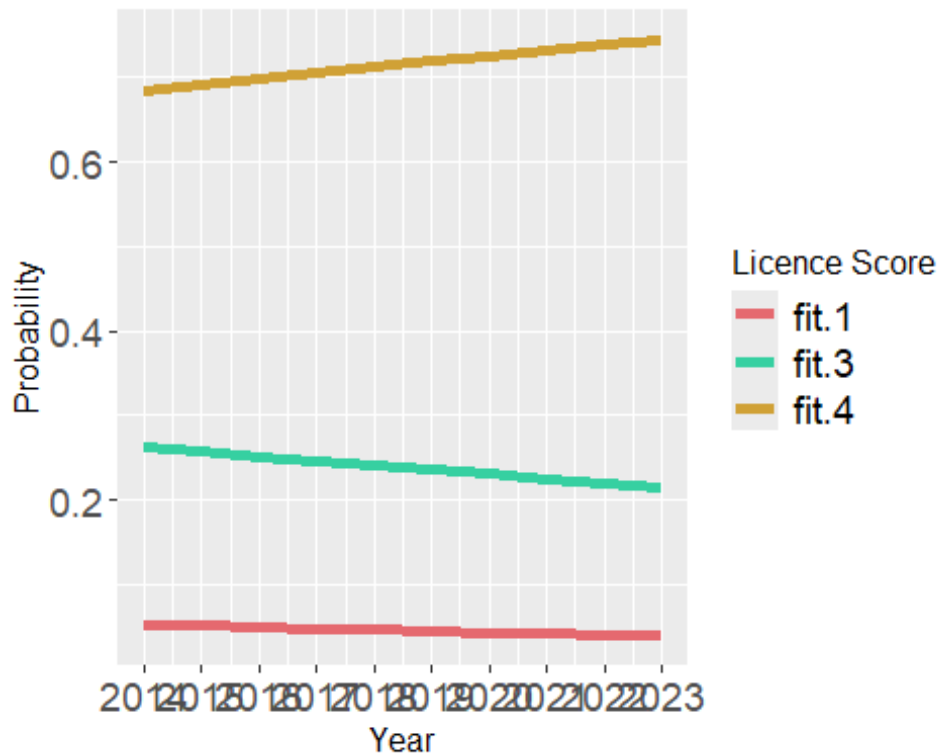
Modify ggplot command

```
og4 <- ggplot(pred_probs_long, aes(x = Year, y = PredictedProbability, group = Licencelevel, color = Licencelevel)) +
  geom_line(size = 2) + # Set size of the lines to make them thicker
  scale_color_manual(values = my_colors) + # Use colors
  scale_x_continuous(breaks = unique(pred_probs_long$Year)) + # Show all years on x-axis
  labs(x = "Year", y = "Probability", color = "Licence Score") +
```

```

theme(
  axis.title = element_text(size = 12), # Increase axis titles
  axis.text = element_text(size = 14), # Increase axis text
  legend.title = element_text(size = 12), # Increase legend title
  legend.text = element_text(size = 14) # Increase legend text
)
print(og4)

```



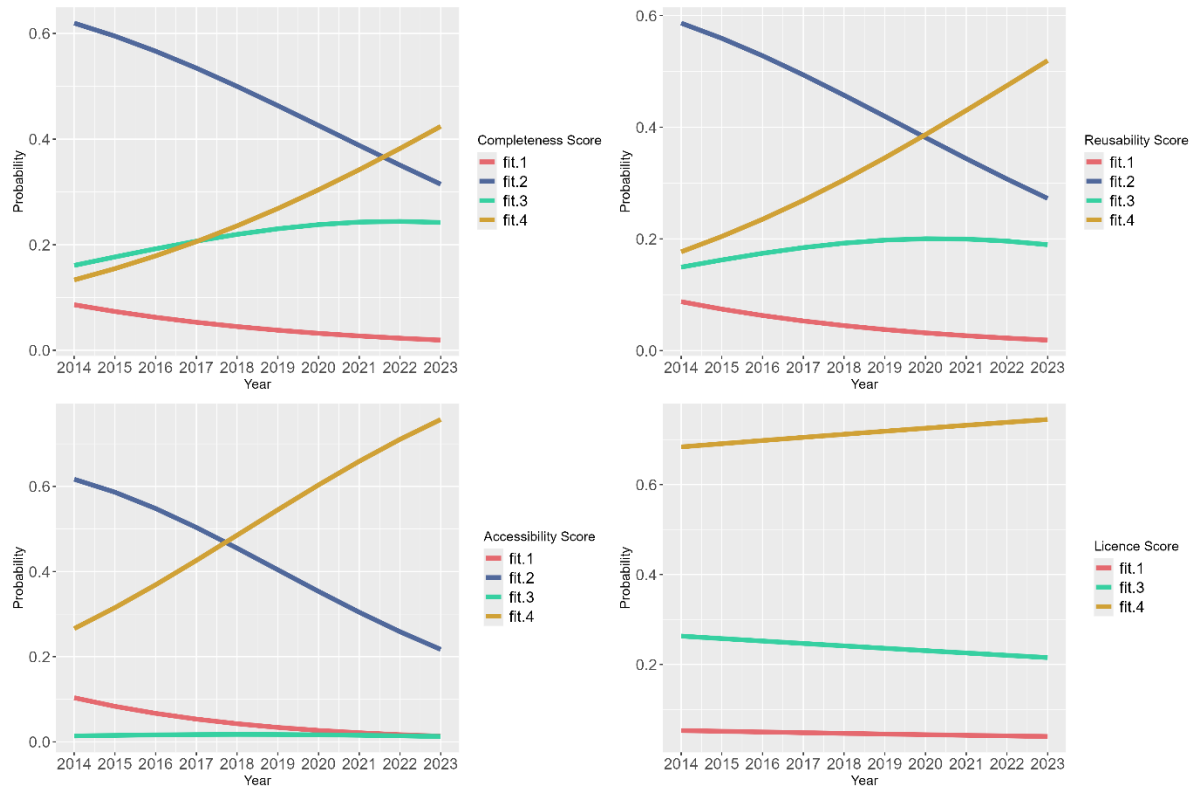
```

ggsave("og4.png", og4, width = 15, height = 10, units = "in", bg = "white")
install.packages("patchwork")
## Installing package into 'M:/R/Win-Library/4.2'
## (as 'lib' is unspecified)
## package 'patchwork' successfully unpacked and MD5 sums checked
##
## The downloaded binary packages are in
## C:\Users\s2146807\AppData\Local\Temp\RtmpGEDx57\downloaded_packages
library(patchwork)
## Warning: package 'patchwork' was built under R version 4.2.3
##
## Attaching package: 'patchwork'

```

```
## The following object is masked from 'package:MASS':
##
##      area
```

```
ordinalplot <- og1 + og2 + og3 + og4 +
  plot_layout(
    ncol = 2, heights = c(10, 10), widths = c(10, 10)
  )
print(ordinalplot)
```



```
ggsave("ordinalplot.png", ordinalplot, width = 15, height = 10, units = "in",
bg="white")
```

#Ordinal Regression models depending on the sharing projects

```
m1a <- clm(Complete ~ NewDAS + Preprint, data = data)
summary_m1a <- summary(m1a)
```

```
# Extract coefficients and standard errors
coefs <- summary_m1a$coefficients[, 1] # Coefficients
se_coefs <- summary_m1a$coefficients[, 2] # Standard errors
```

```
# Extract coefficients and standard errors
coefs <- summary(m1a)$coefficients
OR <- exp(coefs[,1])
lower_ci <- exp(coefs[,1] - 1.96 * coefs[,2])
upper_ci <- exp(coefs[,1] + 1.96 * coefs[,2])
```

```

# Calculate z-values and p-values
z_values <- coefs[,1] / coefs[,2]
p_values <- 2 * (1 - pnorm(abs(z_values)))

# Combine everything into a data frame for easy viewing
results <- data.frame(OR = OR, LowerCI = lower_ci, UpperCI = upper_ci, p_value = p_values)
print(results)

##              OR      LowerCI      UpperCI      p_value
## 1|2          0.08040527 0.03446409 0.1875867 5.481457e-09
## 2|3          2.30928285 1.40274308 3.8016850 9.996808e-04
## 3|4          6.98540751 3.86569749 12.6227979 1.201850e-10
## NewDASNot shared 2.22062795 0.50650870 9.7356443 2.900738e-01
## NewDASShared    4.43200155 2.15464581 9.1164115 5.207790e-05
## Preprint        3.11203452 1.21055487 8.0002642 1.844070e-02

#Check the Assumptions
nominal_test(m1a) # This is a test of the proportional odds assumption, odds
are proportional in this case.

## Tests of nominal effects
##
## formula: Complete ~ NewDAS + Preprint
##           Df logLik   AIC   LRT Pr(>Chi)
## <none>      -141.46 294.91
## NewDAS
## Preprint   2 -140.60 297.20 1.706   0.4261

scale_test(m1a) # scale test checks for equal variance/ scale across year, as
sumptions are not violated here because p = 0.8386. If p is less than 0.05 th
en assumptions are violated

## Tests of scale effects
##
## formula: Complete ~ NewDAS + Preprint
##           Df logLik   AIC   LRT Pr(>Chi)
## <none>      -141.46 294.91
## NewDAS     2 -141.06 298.12 0.78479   0.6754
## Preprint   1 -141.39 296.78 0.12885   0.7196

convergence(m1a) # This is another way to assess the model

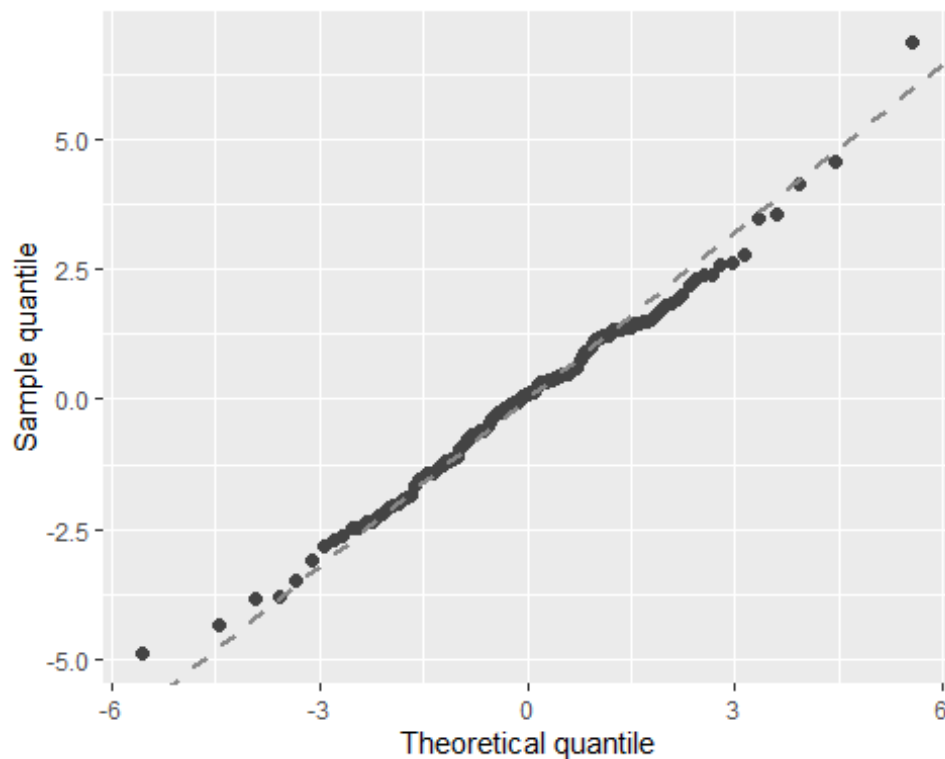
## nobs logLik  niter max.grad cond.H logLik.Error
## 130 -141.45 6(0) 2.36e-08 3.6e+01 <1e-10
##
##           Estimate Std.Err Gradient Error Cor.Dec Sig.Dig
## 1|2          -2.5207 0.4322 2.36e-08 4.00e-09      8      9
## 2|3           0.8369 0.2543 -1.09e-08 -1.02e-10     9      9
## 3|4           1.9438 0.3019 -5.49e-12 -9.47e-11     9     10

```

```
## NewDASNot shared    0.7978  0.7541 -6.88e-10 -9.85e-11      9      9
## NewDASShared        1.4889  0.3680 -9.83e-10 -9.04e-11      9     10
## Preprint            1.1353  0.4817 -6.26e-10 -6.25e-11      9     10
##
## Eigen values of Hessian:
## 58.846 25.507  6.644  5.242  3.748  1.627
##
## Convergence message from clm:
## (0) successful convergence
## In addition: Absolute and relative convergence criteria were met
```

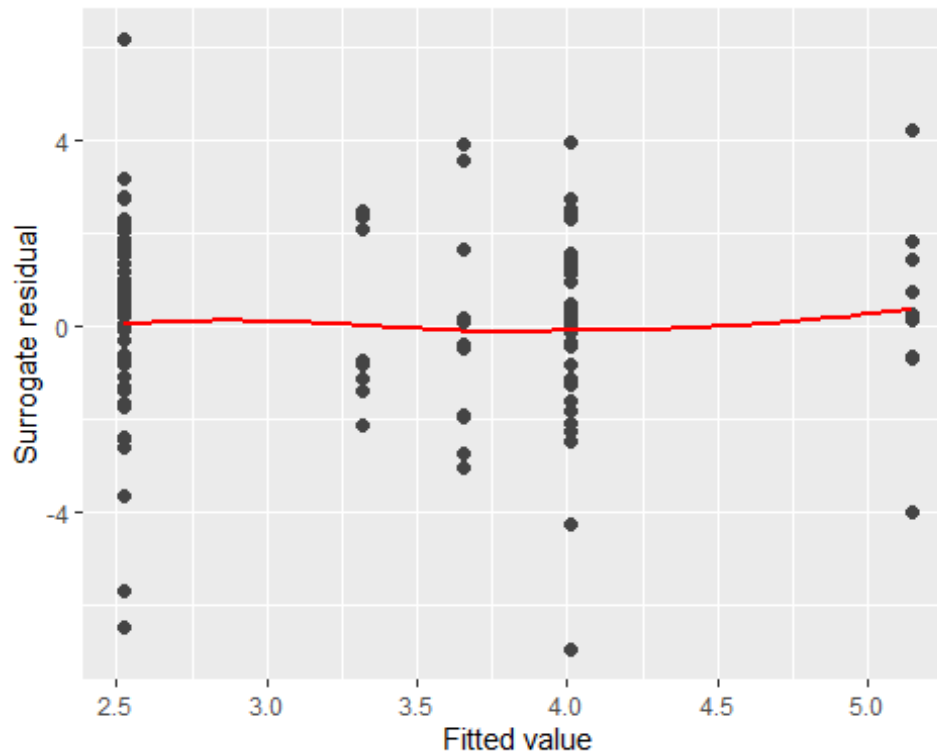
Graphically validate proportional odds using the sure package
#

```
autoplot.clm(m1a, what = c("qq")) # most of the points fall along the line, s
o no violation of linearity
```



```
autoplot.clm(m1a, what = c("fitted")) # the residuals do not show a clear pat
tern or trend
```

```
## `geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```



```
autoplot.clm(m1a, what = c("covariate"), x = data$NewDAS) # scale test indicated no variance issues. This residual, covariate plots seems acceptable as we ll
```

```
## Warning: The `<scale>` argument of `guides()` cannot be `FALSE`. Use "none" instead as
```

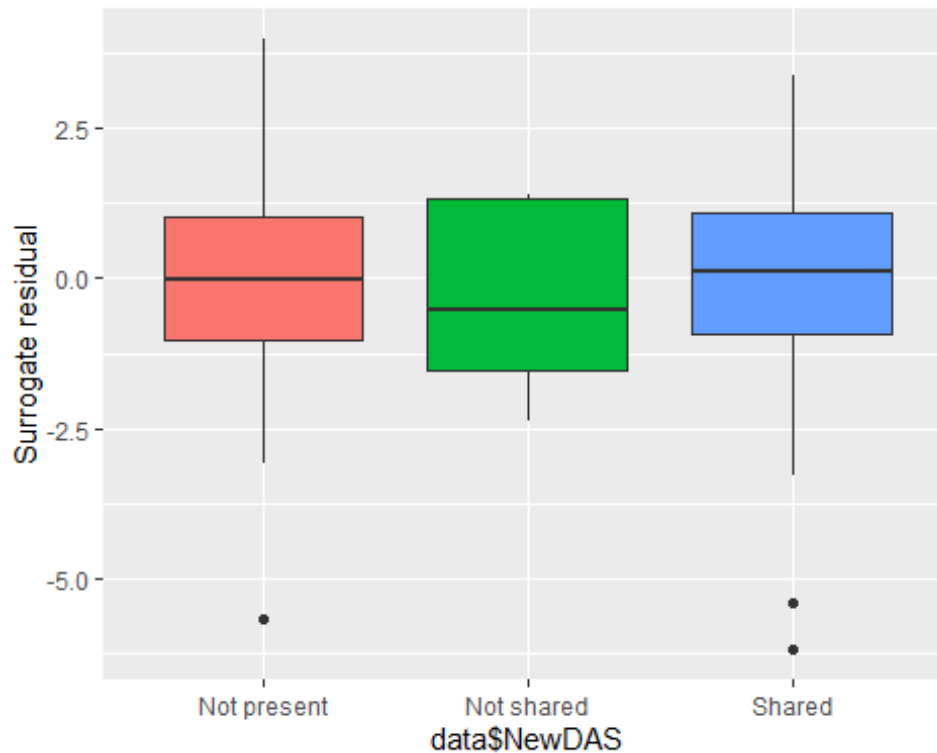
```
## of ggplot2 3.3.4.
```

```
## [i] The deprecated feature was likely used in the sure package.
```

```
## Please report the issue at <]8;;https://github.com/AFIT-R/sure/issueshttps://github.com/AFIT-R/sure/issues]8;;>.
```

```
## This warning is displayed once every 8 hours.
```

```
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was generated.
```

```

autoplot.clm(m1a, what = c("covariate"), x = data$Preprint)

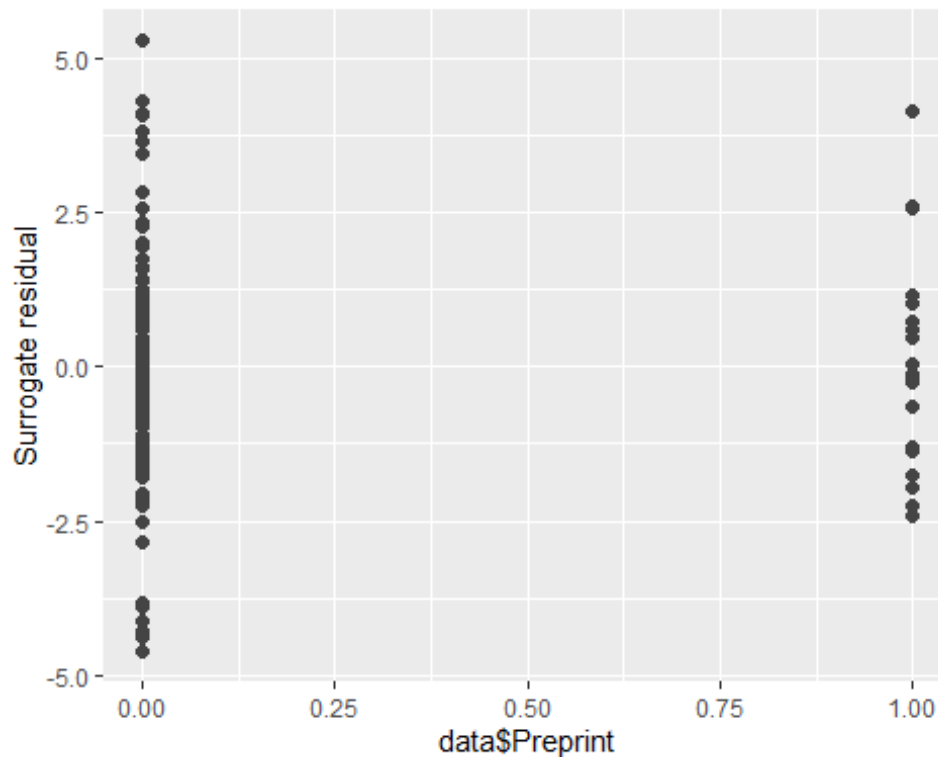
## `geom_smooth()` using method = 'loess' and formula = 'y ~ x'
## Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric,
## : at -0.005
## Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric,
## : radius 2.5e-05
## Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric,
## : all data on boundary of neighborhood. make span bigger
## Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric,
## : pseudoinverse used at -0.005
## Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric,
## : neighborhood radius 0.005
## Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric,
## : reciprocal condition number 1

```

```
## Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric,
## : There are other near singularities as well. 1.01

## Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric,
## : zero-width neighborhood. make span bigger

## Warning: Failed to fit group -1.
## Caused by error in `predLoess()`:
## ! NA/NaN/Inf in foreign function call (arg 5)
```



```
# N.B. - Interpreting residual plots is largely subjective!

m1a <- clm(Reuse ~ NewDAS + Preprint, data = data)
summary_m1a <- summary(m1a)

# Extract coefficients and standard errors
coefs <- summary_m1a$coefficients[, 1] # Coefficients
se_coefs <- summary_m1a$coefficients[, 2] # Standard errors

# Extract coefficients and standard errors
coefs <- summary(m1a)$coefficients
OR <- exp(coefs[,1])
lower_ci <- exp(coefs[,1] - 1.96 * coefs[,2])
upper_ci <- exp(coefs[,1] + 1.96 * coefs[,2])
```

```

# Calculate z-values and p-values
z_values <- coefs[,1] / coefs[,2]
p_values <- 2 * (1 - pnorm(abs(z_values)))

# Combine everything into a data frame for easy viewing
results <- data.frame(OR = OR, LowerCI = lower_ci, UpperCI = upper_ci, p_value = p_values)
print(results)

##              OR      LowerCI      UpperCI      p_value
## 1|2          0.08030323 0.03449122 0.1869638 4.945615e-09
## 2|3          1.94089488 1.19689021 3.1473839 7.173334e-03
## 3|4          4.95212549 2.84354848 8.6242760 1.584018e-08
## NewDASNot shared 3.19798580 0.83340049 12.2715469 9.019262e-02
## NewDASShared    6.37209386 3.00525060 13.5108800 1.367981e-06
## Preprint       1.64953102 0.65229017 4.1713837 2.903525e-01

#Check the Assumptions
nominal_test(m1a) # This is a test of the proportional odds assumption, odds
are proportional in this case.

## Tests of nominal effects
##
## formula: Reuse ~ NewDAS + Preprint
##           Df logLik   AIC    LRT Pr(>Chi)
## <none>      -139.92 291.85
## NewDAS     4 -138.18 296.36 3.4880  0.4797
## Preprint   2 -139.22 294.43 1.4187  0.4920

scale_test(m1a) # scale test checks for equal variance/ scale across year, as
assumptions are not violated here because p = 0.8386. If p is less than 0.05 then
assumptions are violated

## Tests of scale effects
##
## formula: Reuse ~ NewDAS + Preprint
##           Df logLik   AIC    LRT Pr(>Chi)
## <none>      -139.92 291.85
## NewDAS     2 -138.55 293.11 2.7396  0.2542
## Preprint   1 -139.28 292.57 1.2817  0.2576

convergence(m1a) # This is another way to assess the model

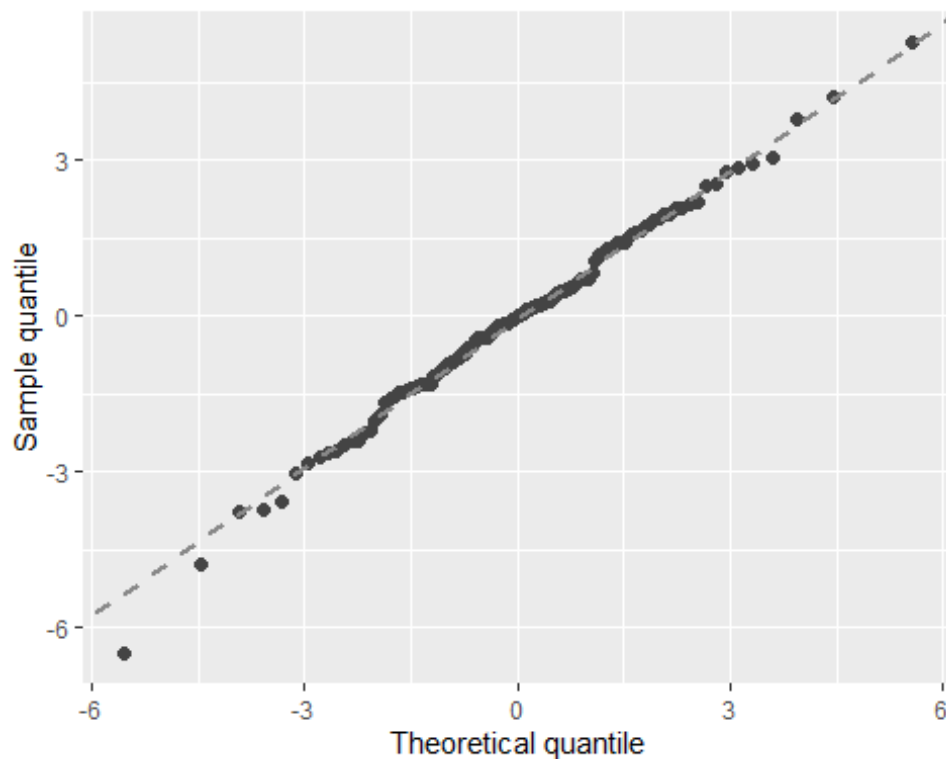
## nobs logLik  niter max.grad cond.H logLik.Error
## 130 -139.92 6(0) 4.40e-09 3.6e+01 <1e-10
##
##           Estimate Std.Err Gradient      Error Cor.Dec Sig.Dig
## 1|2          -2.5219  0.4312 4.40e-09 7.42e-10      8      9
## 2|3           0.6631  0.2466 -2.20e-09 -1.84e-11     10     10
## 3|4           1.5998  0.2830 -1.29e-12 -1.65e-11     10     11
## NewDASNot shared 1.1625  0.6861 -5.46e-11 -1.75e-11     10     11

```

```
## NewDASShared      1.8519  0.3835 -1.05e-10 -1.57e-11      10      11
## Preprint          0.5005  0.4733 -2.18e-10 -7.40e-12      10      10
##
## Eigen values of Hessian:
## 68.197 24.184  6.638  5.094  4.107  1.915
##
## Convergence message from clm:
## (0) successful convergence
## In addition: Absolute and relative convergence criteria were met

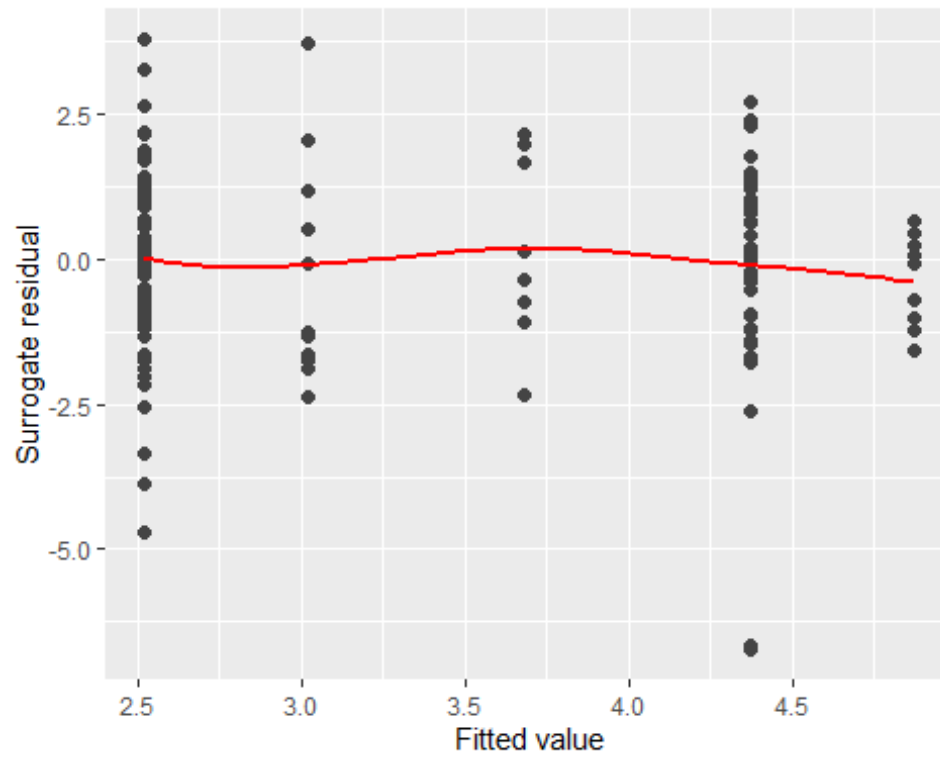
##### Graphically validate proportional odds using the sure package #####
#

autoplot.clm(m1a, what = c("qq")) # most of the points fall along the line, s
o no violation of linearity
```

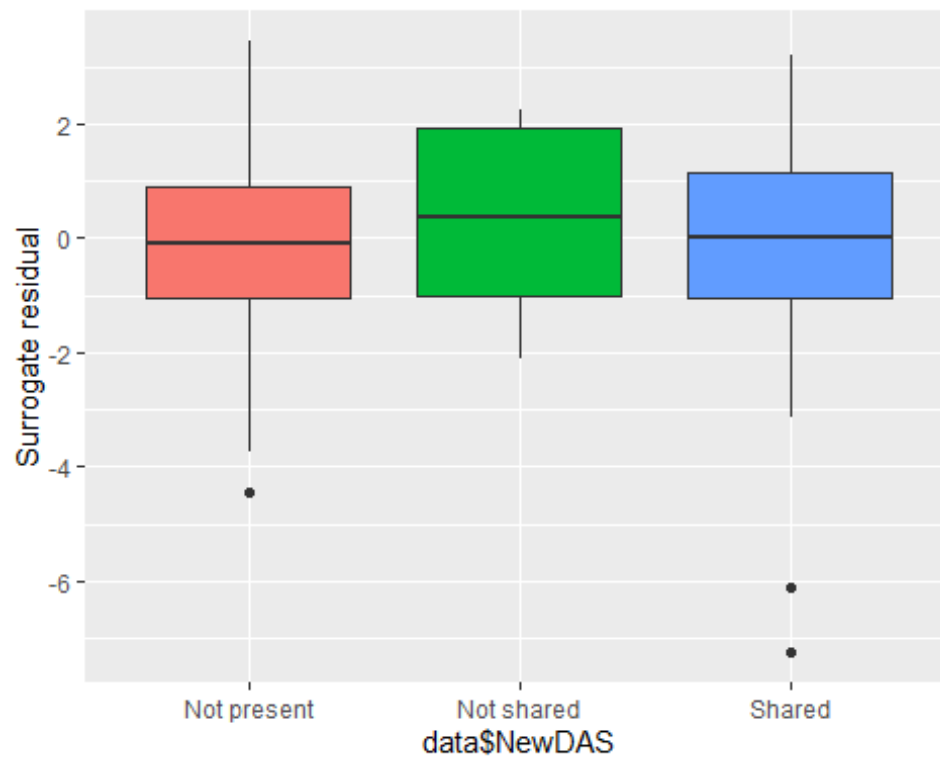


```
autoplot.clm(m1a, what = c("fitted")) # the residuals do not show a clear pat
tern or trend

## `geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```



```
autoplot.clm(m1a, what = c("covariate"), x = data$NewDAS) # scale test indicated no variance issues. This residual, covariate plots seems acceptable as we ll
```



```

autoplot.clm(m1a, what = c("covariate"), x = data$Preprint)

## `geom_smooth()` using method = 'loess' and formula = 'y ~ x'

## Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric,
## : at -0.005

## Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric,
## : radius 2.5e-05

## Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric,
## : all data on boundary of neighborhood. make span bigger

## Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric,
## : pseudoinverse used at -0.005

## Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric,
## : neighborhood radius 0.005

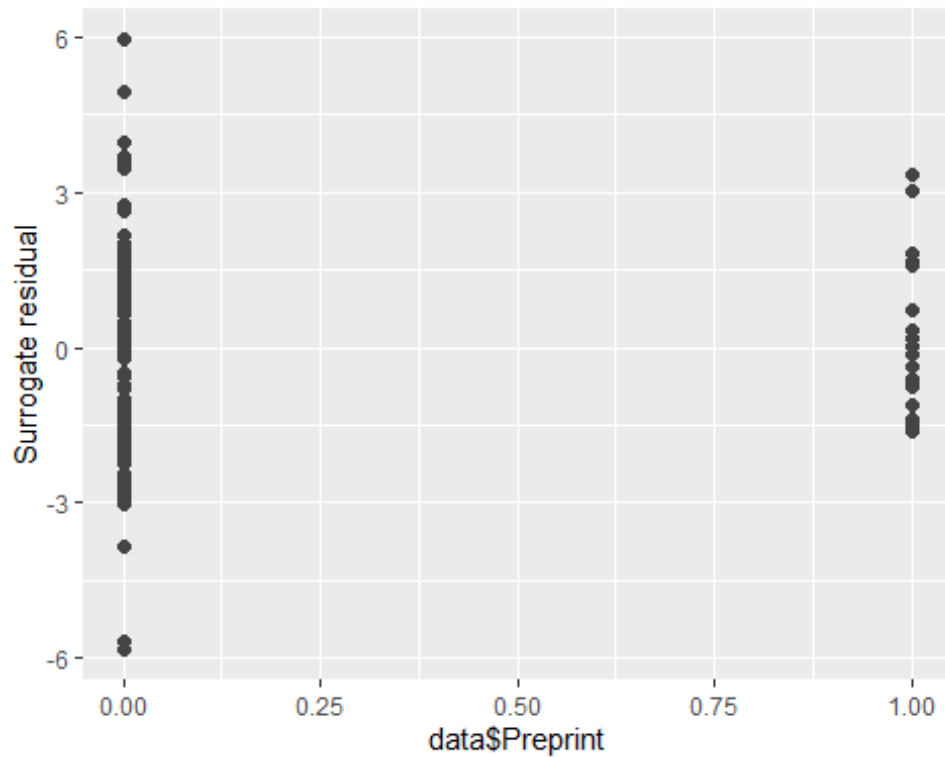
## Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric,
## : reciprocal condition number 1

## Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric,
## : There are other near singularities as well. 1.01

## Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric,
## : zero-width neighborhood. make span bigger

## Warning: Failed to fit group -1.
## Caused by error in `predLoess()`:
## ! NA/NaN/Inf in foreign function call (arg 5)

```



N.B. - Interpreting residual plots is largely subjective!

```
m1a <- clm(Access ~ NewDAS + Preprint, data = data)
summary_m1a <- summary(m1a)
```

Extract coefficients and standard errors

```
coefs <- summary_m1a$coefficients[, 1] # Coefficients
se_coefs <- summary_m1a$coefficients[, 2] # Standard errors
```

Extract coefficients and standard errors

```
coefs <- summary(m1a)$coefficients
OR <- exp(coefs[,1])
lower_ci <- exp(coefs[,1] - 1.96 * coefs[,2])
upper_ci <- exp(coefs[,1] + 1.96 * coefs[,2])
```

Calculate z-values and p-values

```
z_values <- coefs[,1] / coefs[,2]
p_values <- 2 * (1 - pnorm(abs(z_values)))
```

Combine everything into a data frame for easy viewing

```
results <- data.frame(OR = OR, LowerCI = lower_ci, UpperCI = upper_ci, p_value = p_values)
print(results)
```

	OR	LowerCI	UpperCI	p_value
## 1 2	0.08293078	0.03554014	0.193514	8.458039e-09
## 2 3	2.17869399	1.30603472	3.634442	2.857815e-03

```

## 3|4          2.37186800 1.41398150  3.978664 1.065660e-03
## NewDASNot shared 1.94745782 0.49961942  7.590962 3.369174e-01
## NewDASShared    11.85644530 4.63730330 30.314018 2.428559e-07
## Preprint        1.94425820 0.64398445  5.869924 2.382481e-01

#Check the Assumptions
nominal_test(m1a) # This is a test of the proportional odds assumption, odds
are proportional in this case.

## Tests of nominal effects
##
## formula: Access ~ NewDAS + Preprint
##          Df   logLik   AIC    LRT  Pr(>Chi)
## <none>      -100.310 212.62
## NewDAS
## Preprint  2   -88.681 193.36 23.258 8.903e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

scale_test(m1a) # scale test checks for equal variance/ scale across year, as
assumptions are not violated here because p = 0.8386. If p is less than 0.05 th
en assumptions are violated

## Tests of scale effects
##
## formula: Access ~ NewDAS + Preprint
##          Df   logLik   AIC    LRT  Pr(>Chi)
## <none>      -100.310 212.62
## NewDAS      2   -96.004 208.01 8.6128  0.01348 *
## Preprint    1  -100.232 214.46 0.1562  0.69268
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

convergence(m1a) # This is another way to assess the model

## nobs logLik niter max.grad cond.H logLik.Error
## 130 -100.31 7(2) 6.61e-08 3.2e+02 <1e-10
##
##          Estimate Std.Err Gradient Error Cor.Dec Sig.Dig
## 1|2          -2.4897  0.4323  6.61e-08  1.12e-08      7      8
## 2|3           0.7787  0.2611 -3.06e-08 -3.35e-10      9      9
## 3|4           0.8637  0.2639 -3.75e-11 -3.30e-10      9      9
## NewDASNot shared  0.6665  0.6941 -1.80e-09 -3.29e-10      9      9
## NewDASShared     2.4729  0.4789 -5.62e-10 -3.04e-10      9     10
## Preprint         0.6649  0.5638 -2.73e-09 -2.63e-10      9      9
##
## Eigen values of Hessian:
## 566.901 15.759 5.927 4.135 3.161 1.781
##
## Convergence message from clm:

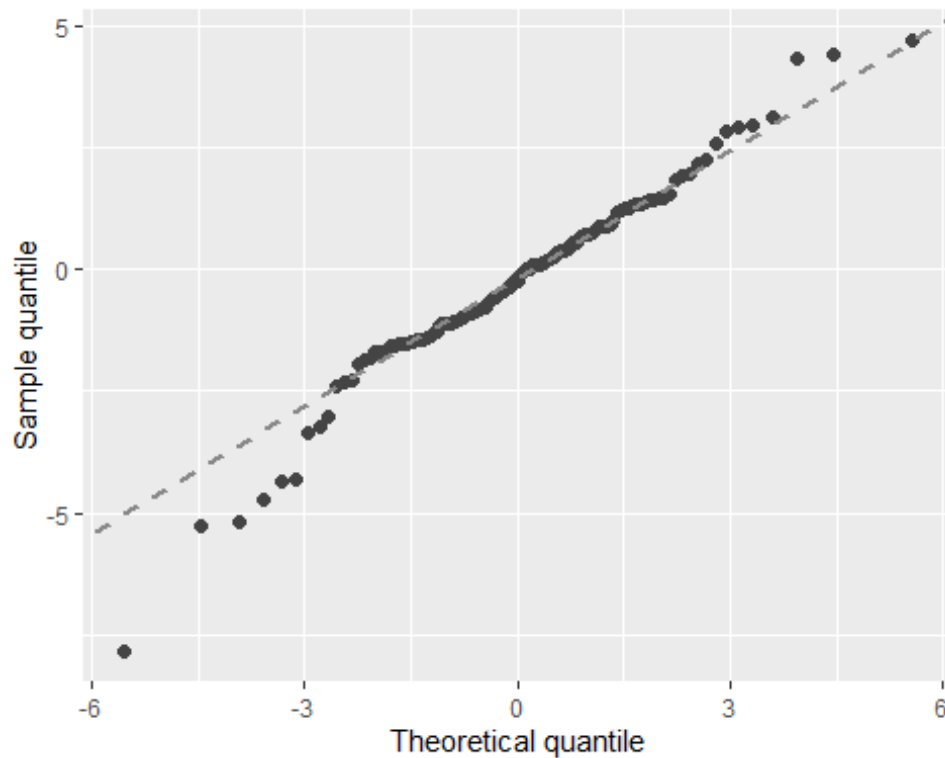
```



```
## (0) successful convergence
## In addition: Absolute and relative convergence criteria were met

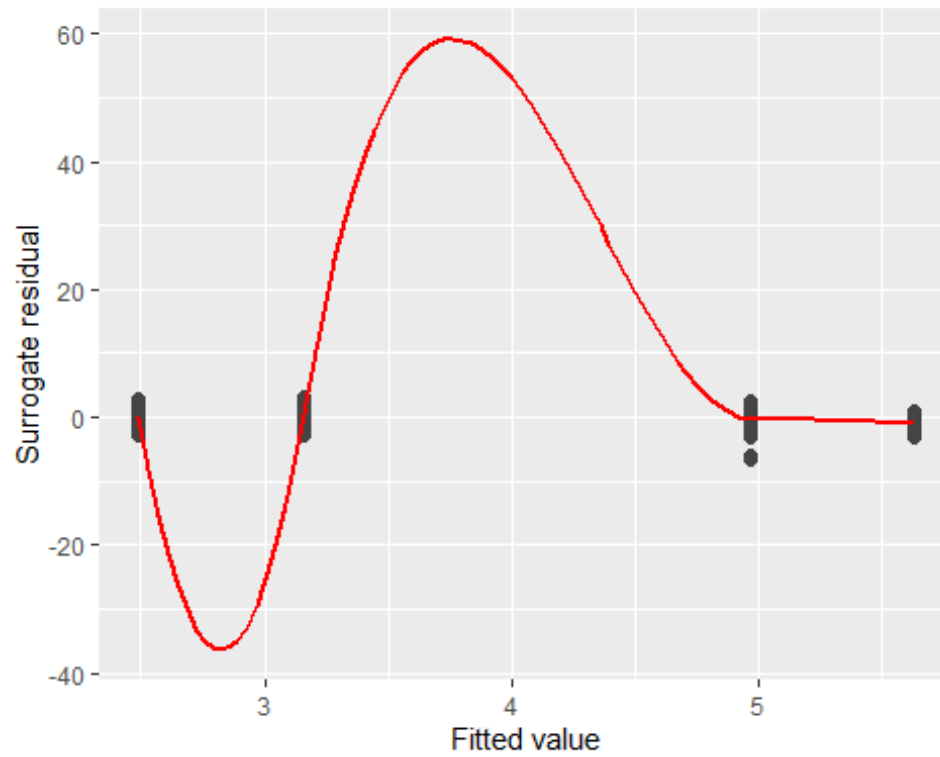
##### Graphically validate proportional odds using the sure package #####
#

autoplot.clm(m1a, what = c("qq")) # most of the points fall along the line, s
o no violation of linearity
```

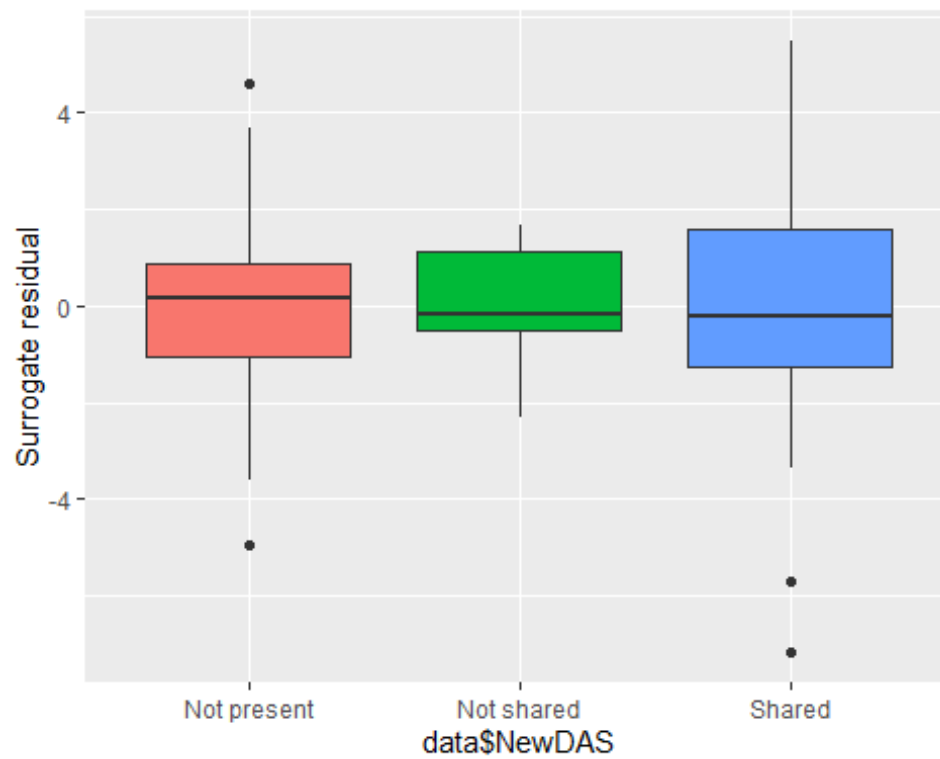


```
autoplot.clm(m1a, what = c("fitted")) # the residuals do not show a clear pat
tern or trend

## `geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```



```
autoplot.clm(m1a, what = c("covariate"), x = data$NewDAS) # scale test indicated no variance issues. This residual, covariate plots seems acceptable as we ll
```



```
autoplot.clm(m1a, what = c("covariate"), x = data$Preprint)

## `geom_smooth()` using method = 'loess' and formula = 'y ~ x'

## Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric,
## : at -0.005

## Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric,
## : radius 2.5e-05

## Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric,
## : all data on boundary of neighborhood. make span bigger

## Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric,
## : pseudoinverse used at -0.005

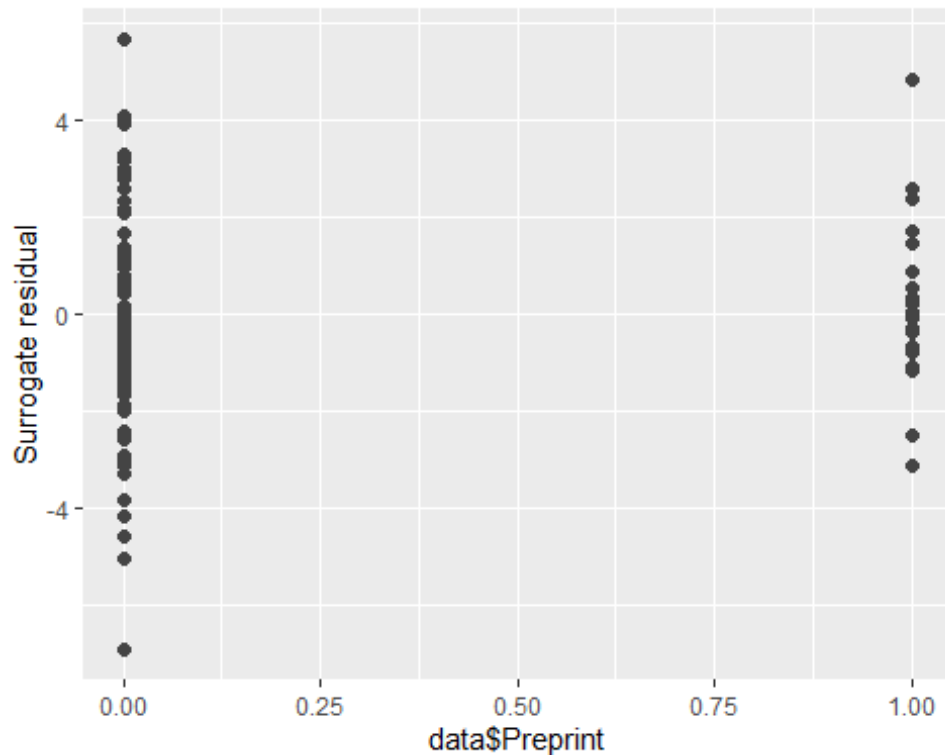
## Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric,
## : neighborhood radius 0.005

## Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric,
## : reciprocal condition number 1

## Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric,
## : There are other near singularities as well. 1.01

## Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric,
## : zero-width neighborhood. make span bigger

## Warning: Failed to fit group -1.
## Caused by error in `predLoess()`:
## ! NA/NaN/Inf in foreign function call (arg 5)
```



N.B. - Interpreting residual plots is largely subjective!

```
m1a <- clm(Licence ~ NewDAS + Preprint, data = data)
summary_m1a <- summary(m1a)
```

Extract coefficients and standard errors

```
coefs <- summary_m1a$coefficients[, 1] # Coefficients
se_coefs <- summary_m1a$coefficients[, 2] # Standard errors
```

Extract coefficients and standard errors

```
coefs <- summary(m1a)$coefficients
OR <- exp(coefs[,1])
lower_ci <- exp(coefs[,1] - 1.96 * coefs[,2])
upper_ci <- exp(coefs[,1] + 1.96 * coefs[,2])
```

Calculate z-values and p-values

```
z_values <- coefs[,1] / coefs[,2]
p_values <- 2 * (1 - pnorm(abs(z_values)))
```

Combine everything into a data frame for easy viewing

```
results <- data.frame(OR = OR, LowerCI = lower_ci, UpperCI = upper_ci, p_value = p_values)
print(results)
```

##		OR	LowerCI	UpperCI	p_value
## 1 3		0.06281708	0.02618925	0.1506720	5.641767e-10
## 3 4		0.56911004	0.34534082	0.9378742	2.699035e-02

```

## NewDASNot shared 1.78733704 0.33990304 9.3984853 4.928701e-01
## NewDASShared      4.46125540 1.67179567 11.9050432 2.824748e-03
## Preprint          0.54460152 0.19750155 1.5017138 2.402780e-01

#Check the Assumptions
nominal_test(m1a) # This is a test of the proportional odds assumption, odds
are proportional in this case.

## Tests of nominal effects
##
## formula: Licence ~ NewDAS + Preprint
##           Df logLik   AIC   LRT Pr(>Chi)
## <none>      -88.207 186.41
## NewDAS      2 -86.914 187.83 2.5854 0.27453
## Preprint    1 -86.238 184.48 3.9372 0.04723 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

scale_test(m1a) # scale test checks for equal variance/ scale across year, as
assumptions are not violated here because p = 0.8386. If p is less than 0.05 th
en assumptions are violated

## Warning: (-1) Model failed to converge with max|grad| = 2.6247e-05 (tol =
1e-06)
## In addition: iteration limit reached

## Tests of scale effects
##
## formula: Licence ~ NewDAS + Preprint
##           Df logLik   AIC   LRT Pr(>Chi)
## <none>      -88.207 186.41
## NewDAS
## Preprint    1 -87.174 186.35 2.0665 0.1506

convergence(m1a) # This is another way to assess the model

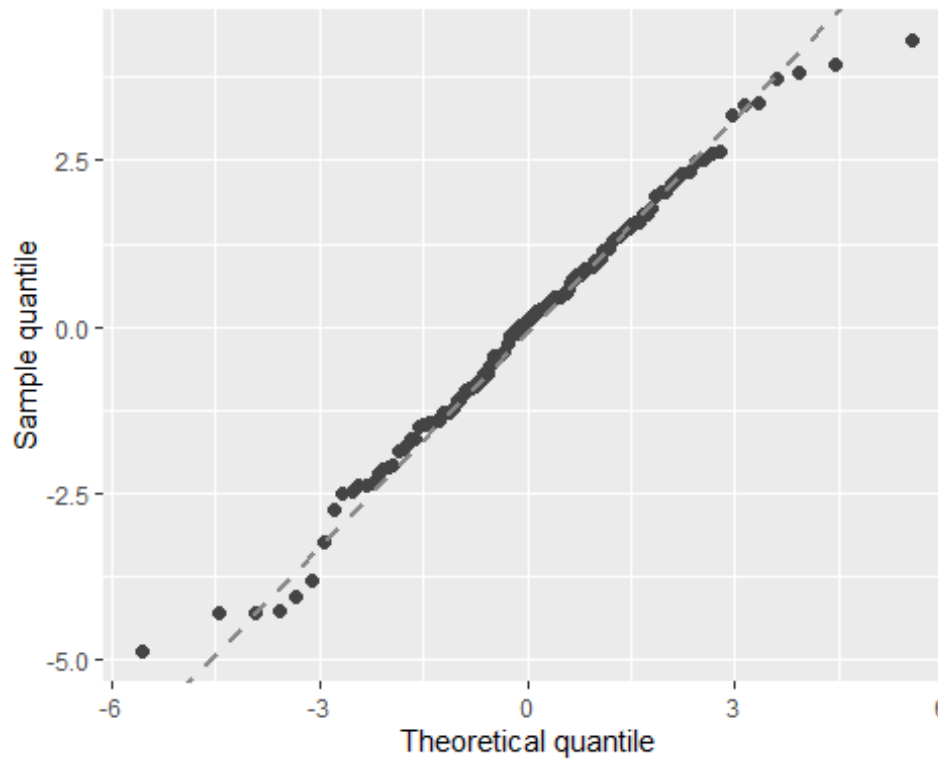
## nobs logLik niter max.grad cond.H logLik.Error
## 130 -88.21 5(0) 4.39e-08 2.2e+01 <1e-10
##
##           Estimate Std.Err Gradient Error Cor.Dec Sig.Dig
## 1|3          -2.7675 0.4464 4.39e-08 6.85e-09 7 8
## 3|4          -0.5637 0.2549 -3.38e-08 -1.62e-10 9 9
## NewDASNot shared 0.5807 0.8468 -3.77e-10 -1.08e-10 9 9
## NewDASShared    1.4954 0.5008 -6.23e-10 -2.03e-10 9 10
## Preprint        -0.6077 0.5175 -2.72e-09 2.21e-10 9 9
##
## Eigen values of Hessian:
## 29.924 6.834 3.658 3.311 1.343
##
## Convergence message from clm:

```

```
## (0) successful convergence
## In addition: Absolute and relative convergence criteria were met

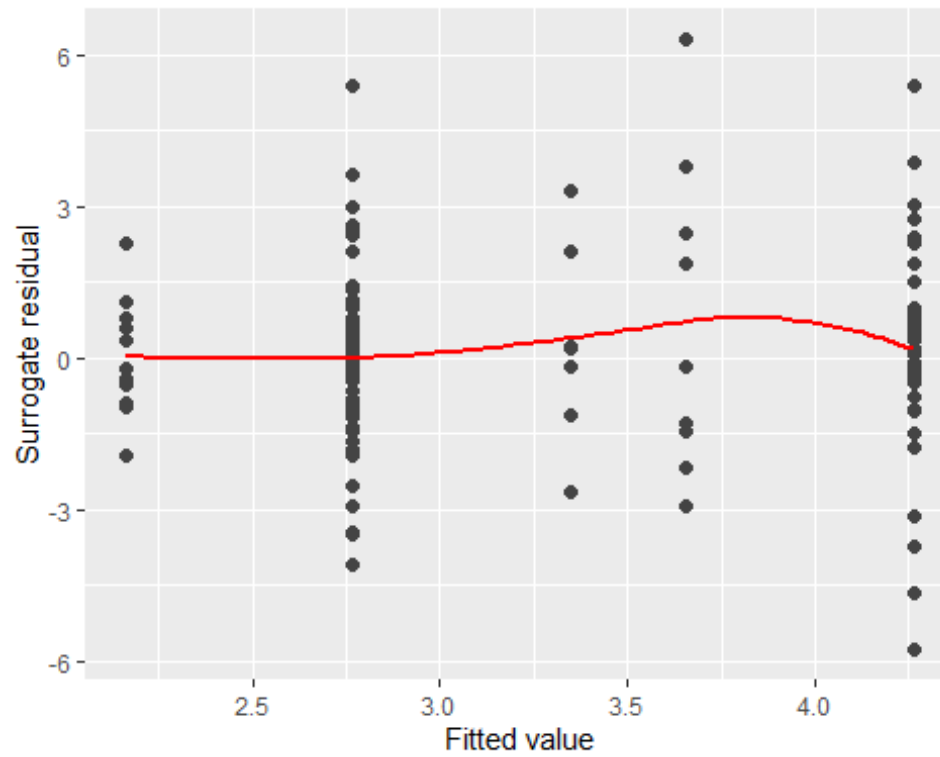
##### Graphically validate proportional odds using the sure package #####
#

autoplot.clm(m1a, what = c("qq")) # most of the points fall along the line, s
o no violation of linearity
```

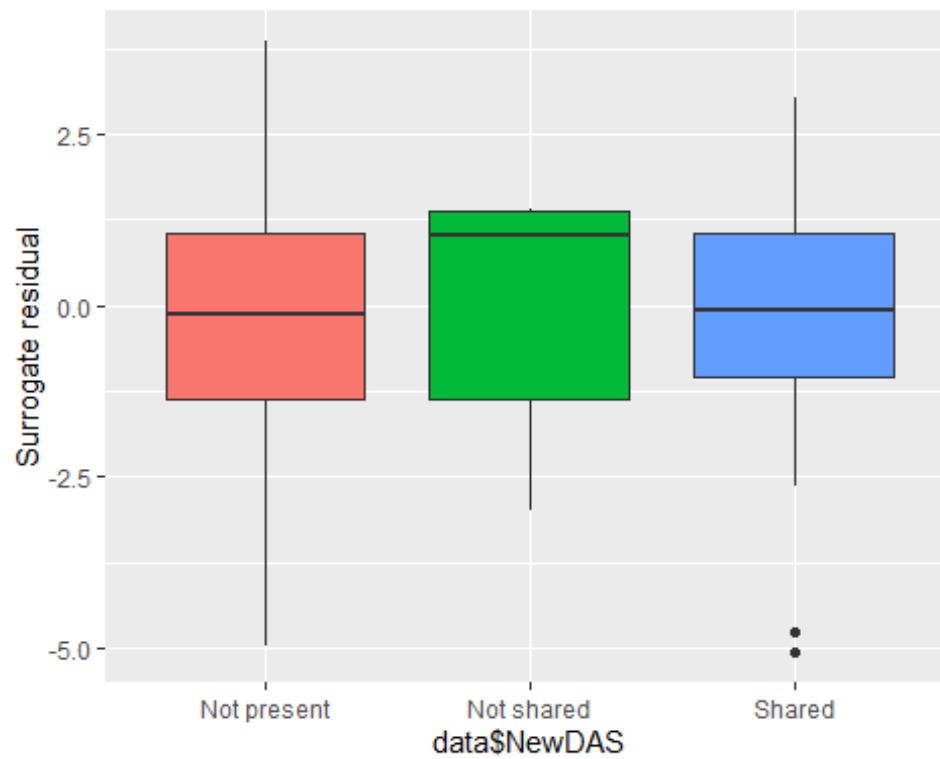


```
autoplot.clm(m1a, what = c("fitted")) # the residuals do not show a clear pat
tern or trend

## `geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```



```
autoplot.clm(m1a, what = c("covariate"), x = data$NewDAS) # scale test indicated no variance issues. This residual, covariate plots seems acceptable as we ll
```



```

autoplot.clm(m1a, what = c("covariate"), x = data$Preprint)

## `geom_smooth()` using method = 'loess' and formula = 'y ~ x'

## Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric,
## : at -0.005

## Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric,
## : radius 2.5e-05

## Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric,
## : all data on boundary of neighborhood. make span bigger

## Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric,
## : pseudoinverse used at -0.005

## Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric,
## : neighborhood radius 0.005

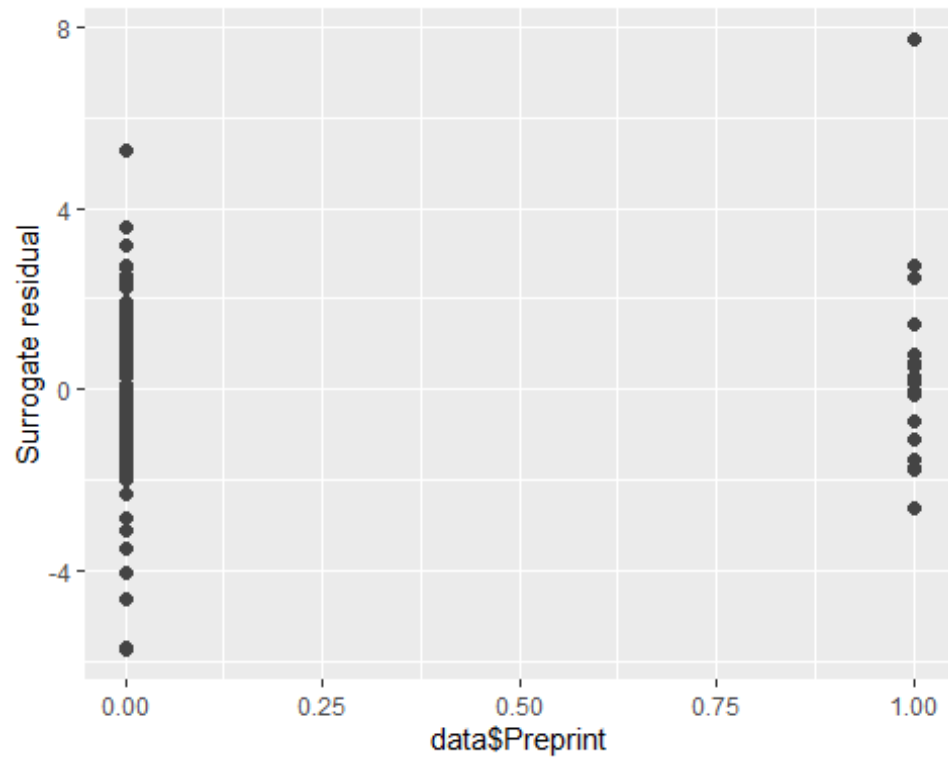
## Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric,
## : reciprocal condition number 1

## Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric,
## : There are other near singularities as well. 1.01

## Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric,
## : zero-width neighborhood. make span bigger

## Warning: Failed to fit group -1.
## Caused by error in `predLoess()`:
## ! NA/NaN/Inf in foreign function call (arg 5)

```

N.B. - Interpreting residual plots is largely subjective