Group 4 Report

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TidyR data setup

The data is composed of two datasets with other lapping patients (see ID), exam.dataset.txt consists of PCR rdts for COVID19 during the 2020 pandemic, data includes information on patients including clinic, gender, test results week of pandemic, and exam_joindata.txt containing endpoint titer data from some of the patients (information can be found in the files codebook_exam_data.html, exam.descr.md). Data files were joined and processed as per conventions of tidyR for later visulization and analysis.

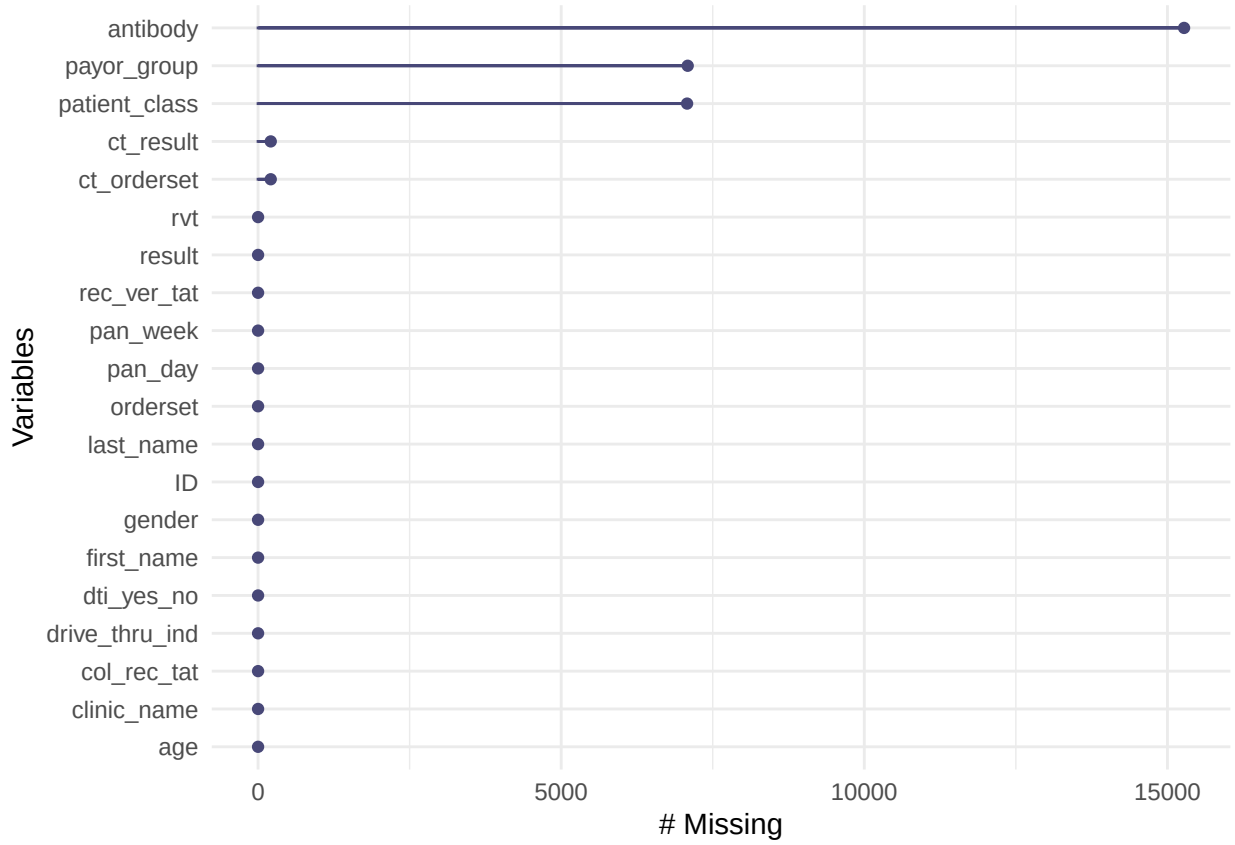
An overview of the data follows

```
summary(complete_data)
```

```
##        ID             age            gender      first_name
##  Min.   :    1   Min.   :  0.00   female:7832   Length:15524
##  1st Qu.: 2330   1st Qu.:  2.00   male  :7692   Class :character
##  Median : 5268   Median :  9.00                 Mode  :character
##  Mean   : 5571   Mean   : 14.19
##  3rd Qu.: 8636   3rd Qu.: 18.00
##  Max.   :12346   Max.   :138.00
##
##   last_name                    clinic_name        result      drive_thru_ind
##  Length:15524       clinical lab     :7500   invalid :  301   0:7537
##  Class :character   emergency dept   :3413   negative:14358   1:7987
##  Mode  :character   oncology day hosp: 533   positive:  865
##                     nicu             : 294
##                     laboratory       : 270
##                     picu             : 261
##                     (Other)          :3253
##    ct_result        orderset                  payor_group
##  Min.   :14.05   Min.   :0.0000   commercial        :3726
##  1st Qu.:45.00   1st Qu.:0.0000   government        :3644
##  Median :45.00   Median :1.0000   unassigned        : 733
##  Mean   :44.12   Mean   :0.6952   self pay          : 216
##  3rd Qu.:45.00   3rd Qu.:1.0000   medical assistance:  84
##  Max.   :45.00   Max.   :1.0000   (Other)           :  34
##  NA's   :209                      NA's              :7087
##               patient_class     pan_day        rec_ver_tat
##  inpatient           :3438   Min.   :  4.00   Min.   :-18.600
##  emergency           :1378   1st Qu.: 38.00   1st Qu.:  4.000
##  not applicable      :1096   Median : 65.00   Median :  5.000
##  outpatient          : 973   Mean   : 63.21   Mean   :  5.639
##  recurring outpatient: 795   3rd Qu.: 87.00   3rd Qu.:  6.200
##  (Other)             : 767   Max.   :107.00   Max.   :218.200
##  NA's                :7077
```

```
##   col_rec_tat          rvt              pan_week       dti_yes_no
##  Min.   :    0.00   Length:15524       Min.   : 0.5714   Length:15524
##  1st Qu.:    0.70   Class :character   1st Qu.: 5.4286   Class :character
##  Median :    1.90   Mode  :character   Median : 9.2857   Mode  :character
##  Mean   :    7.22                      Mean   : 9.0298
##  3rd Qu.:    3.60                      3rd Qu.:12.4286
##  Max.   :61370.20                      Max.   :15.2857
##
##   ct_orderset      antibody
##  Min.   : 0.0   Min.   : 21.48
##  1st Qu.: 0.0   1st Qu.: 63.30
##  Median :45.0   Median :103.52
##  Mean   :30.6   Mean   :109.99
##  3rd Qu.:45.0   3rd Qu.:156.95
##  Max.   :45.0   Max.   :199.89
##  NA's   :209    NA's   :15275
```

```
naniar::gg_miss_var(complete_data)
```

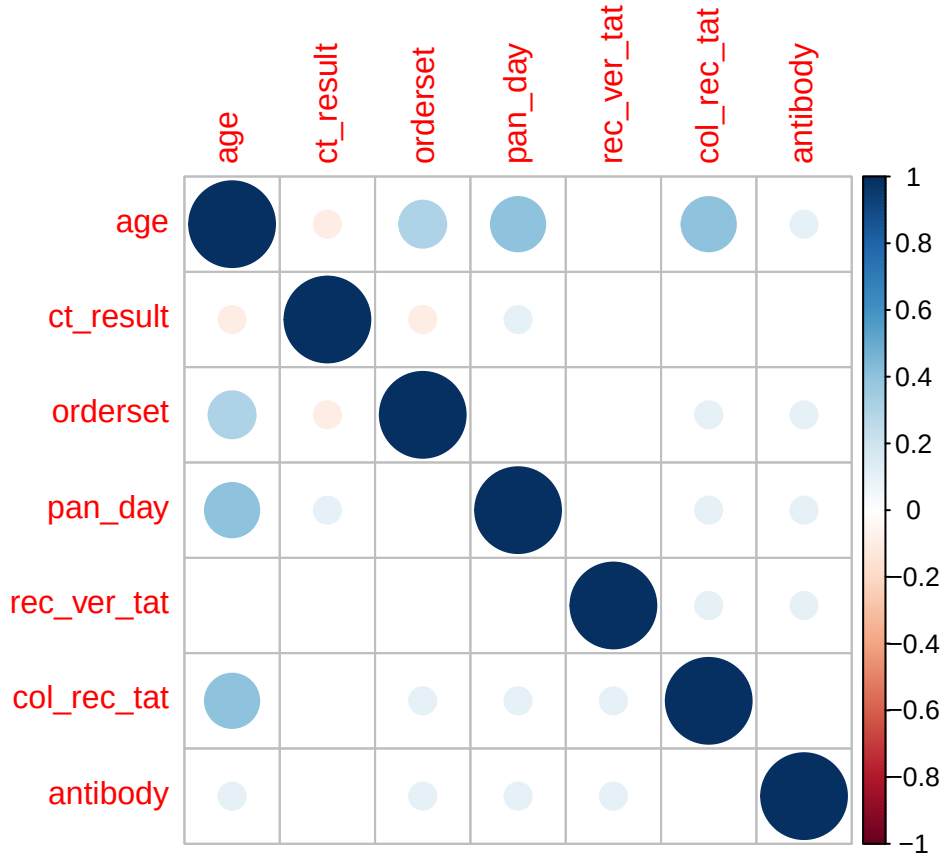


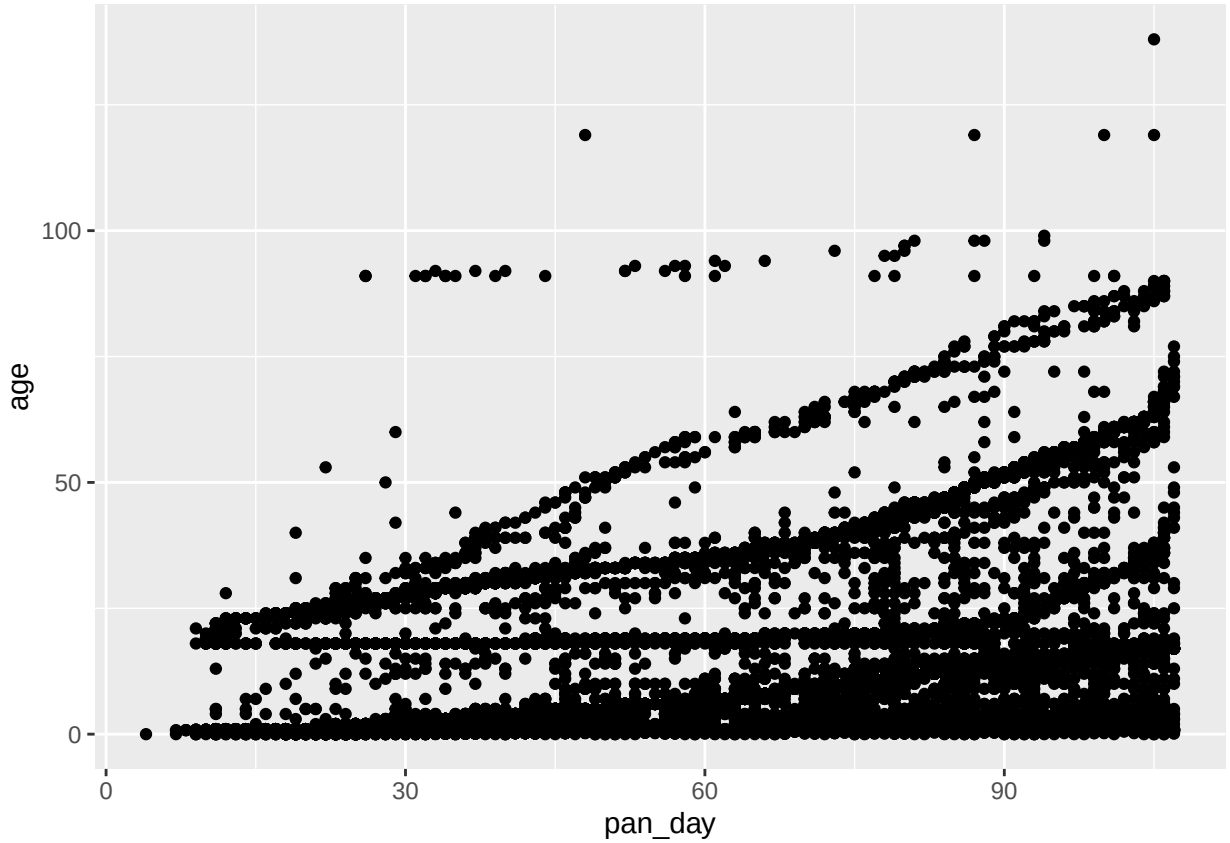
Descriptive plots

Visulization was done using a number of plots. Significant correlations are observiable with age, and orderset and days since the pandemic. Indicating early in the pandemic individuals seen in the clinic were usually young adults and children

```
## # A tibble: 7 x 8
##   rowname          age ct_result  orderset   pan_day rec_ver_tat col_rec_tat
```

```
##   <chr>           <dbl>     <dbl>     <dbl>     <dbl>       <dbl>       <dbl>
## 1 age         0          4.54e-17 9.34e-151 3.95e-323    0.0666      0.844
## 2 ct_result   4.54e- 17  0        3   e- 11 7.86e-  1    0.0829      0.849
## 3 orderset    9.34e-151  3   e-11 0         7.38e-  1    0.000108    0.158
## 4 pan_day     3.95e-323  7.86e- 1 7.38e-  1 0            0.125       0.809
## 5 rec_ver_tat 6.66e-  2  8.29e- 2 1.08e-  4 1.25e-  1    0           0.854
## 6 col_rec_tat 8.44e-  1  8.49e- 1 1.58e-  1 8.09e-  1    0.854       0
## 7 antibody    4.16e-  2  9.53e- 1 2.89e-  1 4.05e-  2    0.0704      0.623
## # i 1 more variable: antibody <dbl>
```

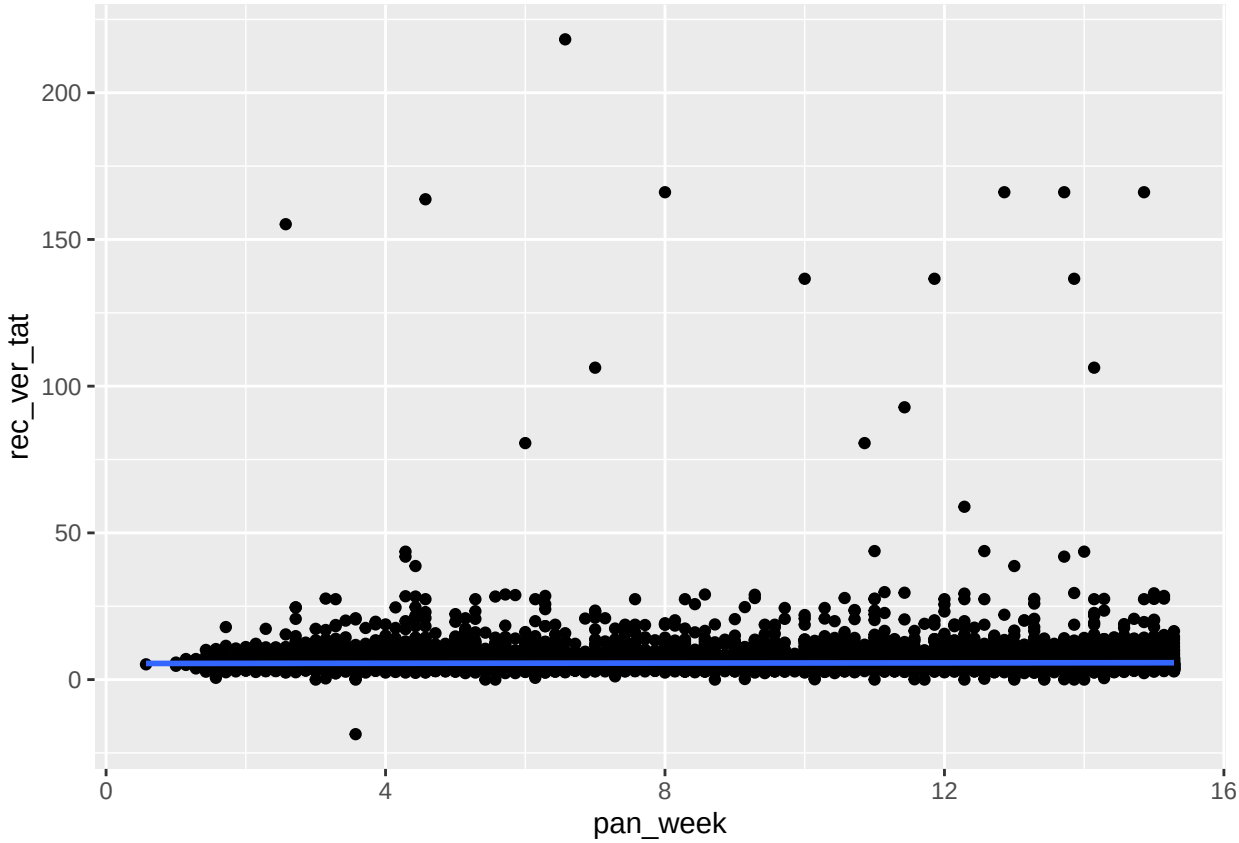




Suprisingly over the course of the pandemic there was no indication that the wait time from collection of patient sample to PCR test result was reduced.

```
## # A tibble: 15 x 4
##    pan_week mean_value   std `median(rec_ver_tat)`
##       <dbl>      <dbl> <dbl>                 <dbl>
##  1        1       5.51  1.57                   5.3
##  2        2       5.27  2.00                   4.8
##  3        3       5.62  5.44                   5
##  4        4       5.50  3.19                   5
##  5        5       5.57  5.07                   5
##  6        6       5.69  3.61                   5.1
##  7        7       5.73  7.81                   4.9
##  8        8       5.66  5.97                   4.9
##  9        9       5.48  2.59                   4.9
## 10       10       5.65  4.68                   5
## 11       11       5.73  4.17                   5
## 12       12       5.57  4.73                   4.9
## 13       13       5.59  5.22                   4.9
## 14       14       5.82  6.88                   5
## 15       15       5.81  5.62                   5
```

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



We observe that there are slightly more females than males in the cleaned data set. The bar plot below indicates that more people from both genders took the test at the drive-through than those who did not. However, from observation, the difference between genders is slightly larger among those who took the test at the drive-through compared to those who did not. To examine the relationship between gender and drive-through test participation, we conducted a Chi-squared test. With a p-value of 0.8728, we fail to reject the null hypothesis, suggesting that there is no significant association between gender and drive-through test participation in this data set.

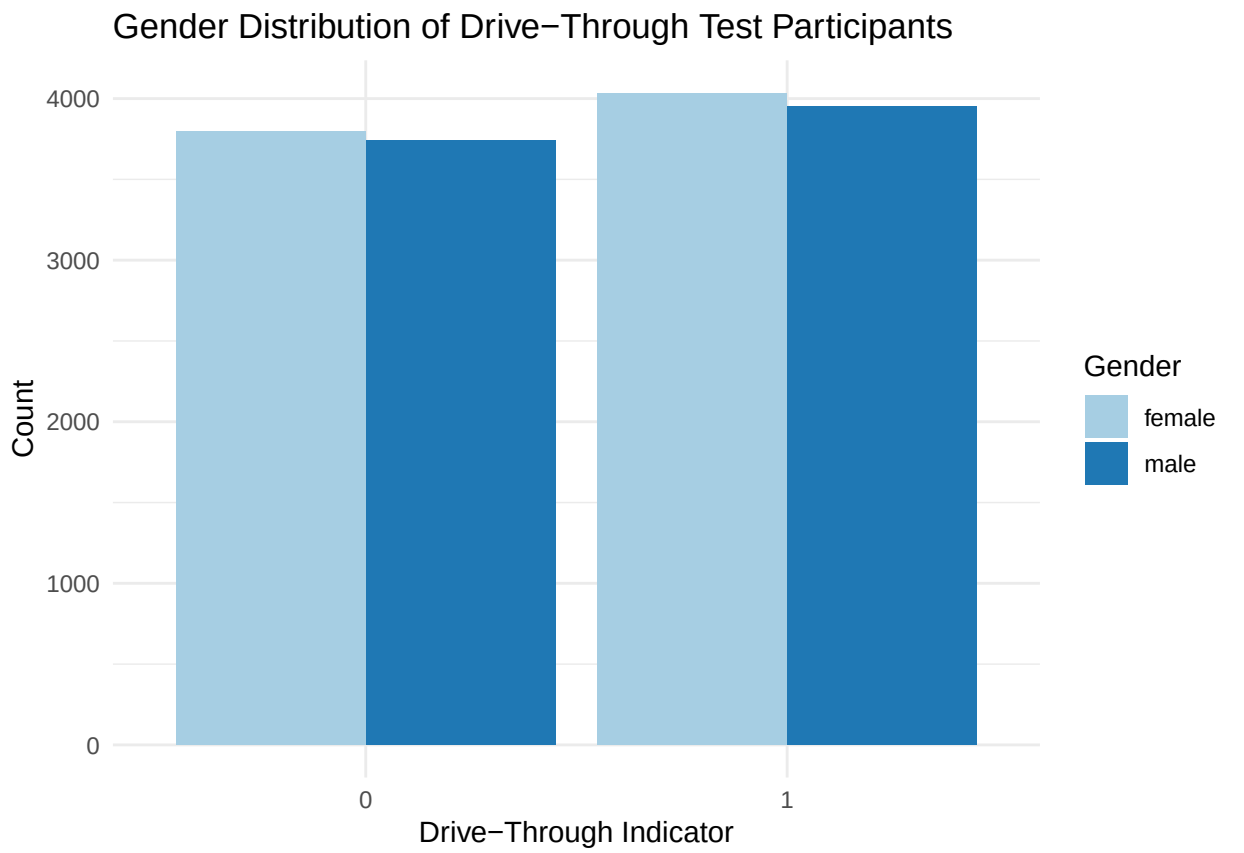
```
dt_and_gender <- table(complete_data$gender, complete_data$drive_thru_ind)
# Create dt_and_gender as a data frame from the table
dt_and_gender_df <- as.data.frame(dt_and_gender)
print(chisq.test(dt_and_gender))
```

```
##
##  Pearson's Chi-squared test with Yates' continuity correction
##
## data:  dt_and_gender
## X-squared = 0.02564, df = 1, p-value = 0.8728
```

```
# Rename columns for clarity (since table() creates V1, V2, and Freq by default)
colnames(dt_and_gender_df) <- c("Gender", "Drive_Through", "Count")

# Now use ggplot2 to plot
ggplot(dt_and_gender_df, aes(x = Drive_Through, y = Count, fill = Gender)) +
  geom_bar(stat = "identity", position = "dodge") +
  labs(title = "Gender Distribution of Drive-Through Test Participants",
       x = "Drive-Through Indicator",
```

```
       y = "Count") +
  scale_fill_manual(values = c("#a6cee3", "#1f78b4")) +  # Custom colors
  theme_minimal()
```



A comparison of cycle threshold values between men and women shows a similar distribution in the number of reaction cycles. However, males showed the lowest cycle threshold value compared to females. Despite this, the majority of threshold values exceeded 40 cycles for both genders. The p-value of 0.272 from the one-way ANOVA test means that we fail to reject the null hypothesis, suggesting that gender does not significantly affect the cycle threshold value.

```
ct_result_cat <- cut(complete_data$ct_result, c(10, 20, 30, 40, 50))
summary(ct_result_cat)
```

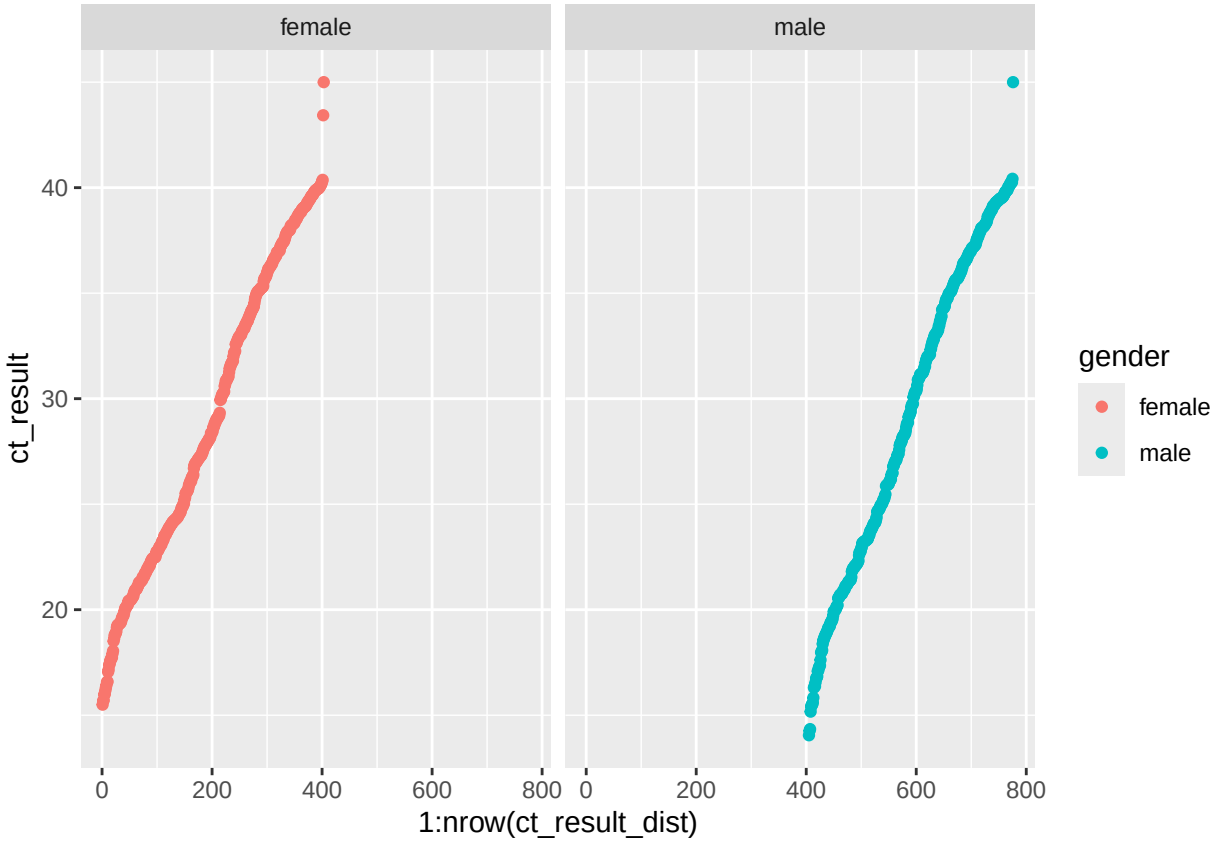
```
## (10,20] (20,30] (30,40] (40,50]    NA's
##      92     346     415   14462     209
```

```
ct_result_dist <- complete_data %>%
  group_by(gender) %>%
  count(ct_result)

ggplot(ct_result_dist,
       aes(
         x = 1:nrow(ct_result_dist),
         y = ct_result,
         group = gender,
         color = gender)
) +
```

```
  geom_point() +
  facet_wrap(vars(gender))
```

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




```
ct_result_gender_anova <- aov(complete_data$ct_result ~ complete_data$gender, data = complete_data)
summary(ct_result_gender_anova)
```

```
##                          Df Sum Sq Mean Sq F value Pr(>F)
## complete_data$gender      1     19   19.11   1.206  0.272
## Residuals             15313 242691   15.85
## 209 observations deleted due to missingness
```

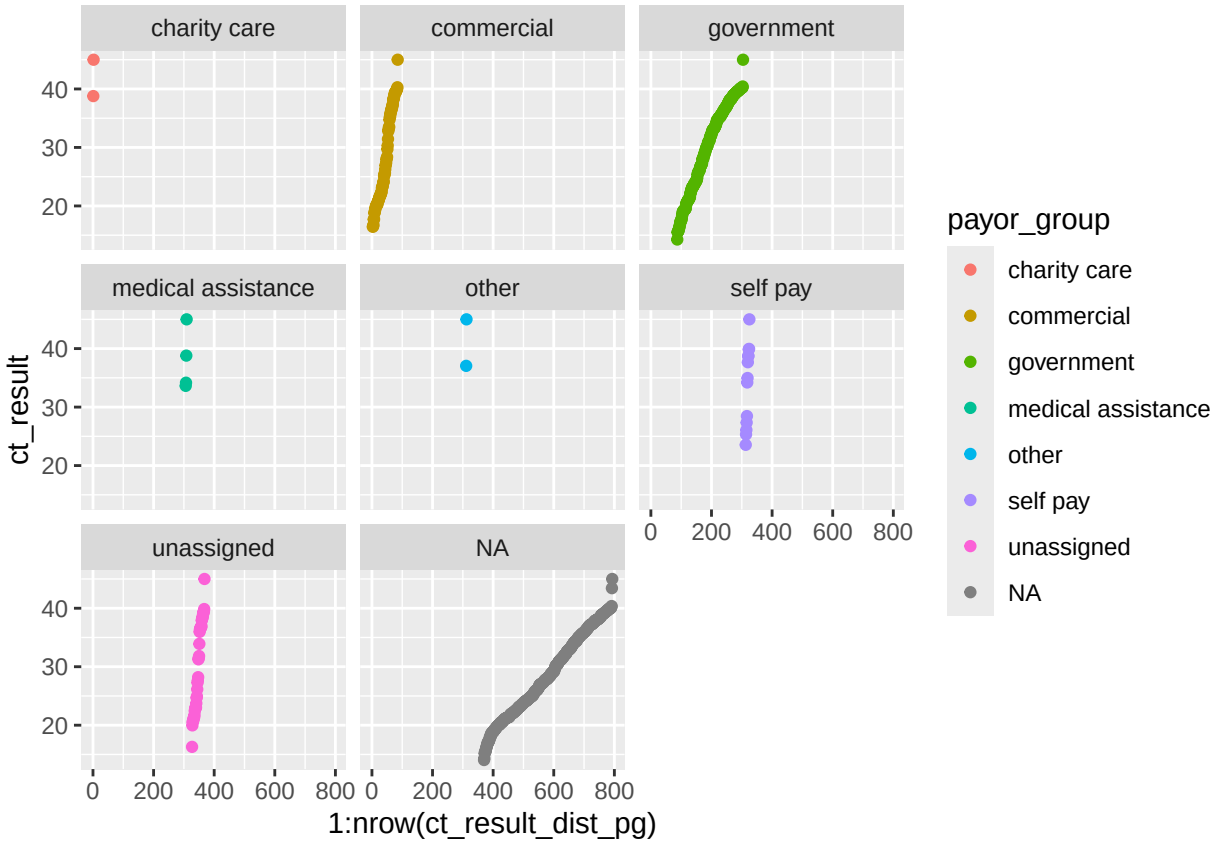
The distribution of patients by payor group shows that the most common groups were commercial and government, with a significant proportion of patients listed as NA or unassigned. Despite this, a similar pattern was observed between government and commercial patients, while for charity care, medical assistance, other, and self-pay patients the minimum cycle threshold value was higher compared to the former groups. The one-way ANOVA test result is highly significant, indicating that the cycle threshold value is influenced by the payor group.

```
ct_result_dist_pg <- complete_data %>%
  group_by(payor_group) %>%
  count(ct_result)

ggplot(
  ct_result_dist_pg,
```

```
  aes(
    x = 1:nrow(ct_result_dist_pg),
    y = ct_result,
    group = payor_group,
    color = payor_group
    )
  ) +
  geom_point() +
  facet_wrap(vars(payor_group))
```

```
## Warning: Removed 6 rows containing missing values or values outside the scale range
## (‘geom_point()‘).
```




```
ct_result_pg_anova <- aov(complete_data$ct_result ~ complete_data$payor_group, data = complete_data)
summary(ct_result_pg_anova)
```

```
##                              Df Sum Sq Mean Sq F value   Pr(>F)
## complete_data$payor_group     6    672   111.9     9.1 6.03e-10 ***
## Residuals                  8296 102040    12.3
## ---
## Signif. codes:  0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1 ’ ’ 1
## 7221 observations deleted due to missingness
```

The distribution of results by gender shows a similar pattern for both, with women comprising a slightly larger proportion in each result category except for the invalid category. The chi-square test yielded a p-value of 0.5481, meaning that we fail to reject the null hypothesis, suggesting that gender does not have a significant influence on the test result.

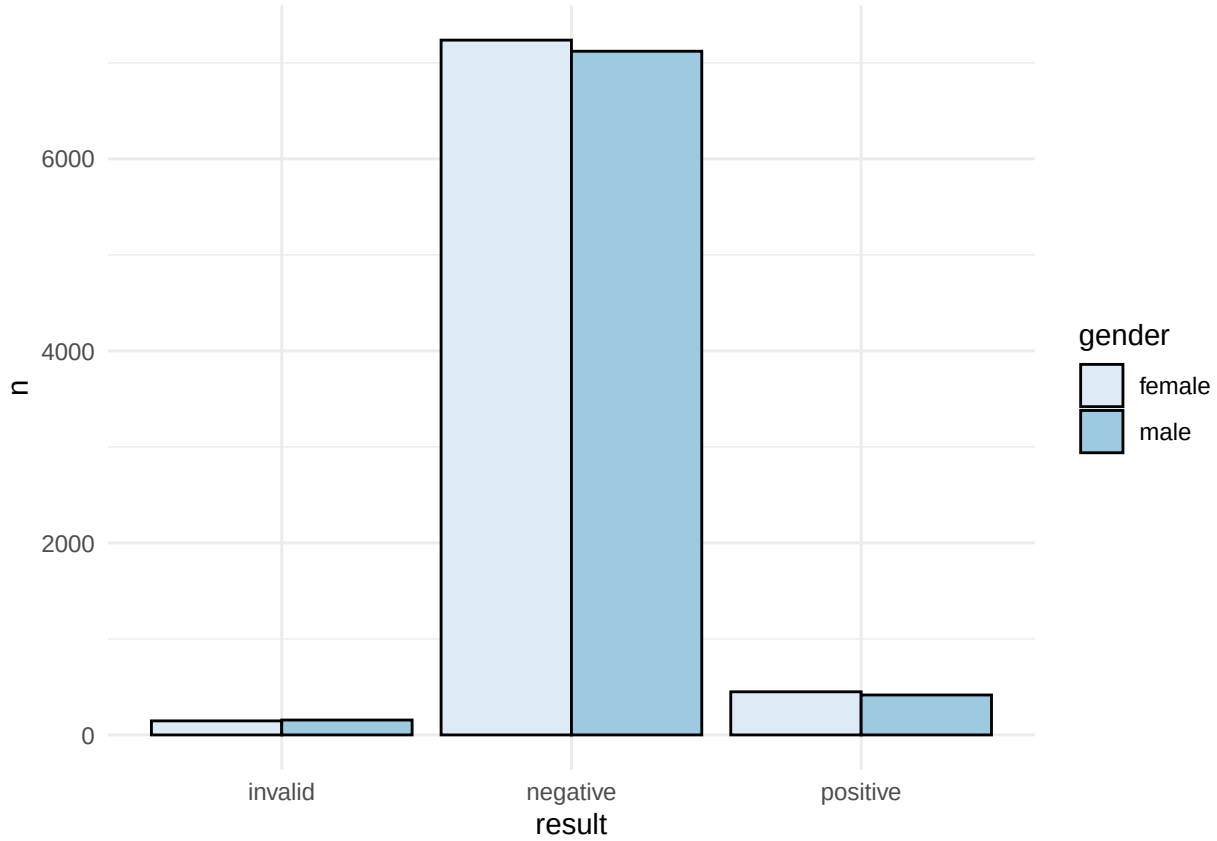
```
tests_by_gender <- complete_data %>%
  group_by(gender) %>%
  count(result)

tests_by_gender
```

```
## # A tibble: 6 x 3
## # Groups:   gender [2]
##   gender result       n
##   <fct>  <fct>    <int>
## 1 female invalid    146
## 2 female negative  7237
## 3 female positive   449
## 4 male   invalid    155
## 5 male   negative  7121
## 6 male   positive   416
```

```
ggplot(data = tests_by_gender, aes(x = result, y = n, fill = gender)) +
  geom_bar(stat = "identity", color="black", position=position_dodge())+
  theme_minimal() +
  scale_fill_manual(values=c('#999999','#E69F00')) +
# Use brewer color palettes
  scale_fill_brewer(palette="Blues")
```

```
## Scale for fill is already present.
## Adding another scale for fill, which will replace the existing scale.
```



```r
test_and_gender <- table(complete_data$gender, complete_data$result)
test_and_gender
```

```
##
##          invalid negative positive
##   female     146     7237      449
##   male       155     7121      416
```

```r
#chi-square test
test_and_gender_df <- as.data.frame(test_and_gender)
print(chisq.test(test_and_gender))
```

```
##
##  Pearson's Chi-squared test
##
## data:  test_and_gender
## X-squared = 1.2028, df = 2, p-value = 0.5481
```

Statistics

wilcox test indicated that the more tests from a single patient does not associate with increase positive test, in fact the opposite trend was noted.

```
## # A tibble: 1 x 4
##   statistic  p.value method                                          alternative
##       <dbl>    <dbl> <chr>                                           <chr>
## 1   4979785 8.14e-11 Wilcoxon rank sum test with continuity correct~ two.sided
```

While drive-through use was associated with an increase in positive tests

```
##
##  Pearson's Chi-squared test with simulated p-value (based on 2000
##  replicates)
##
## data:  positive_visits$n and positive_visits$positive
## X-squared = 44.749, df = NA, p-value = 0.01199
```

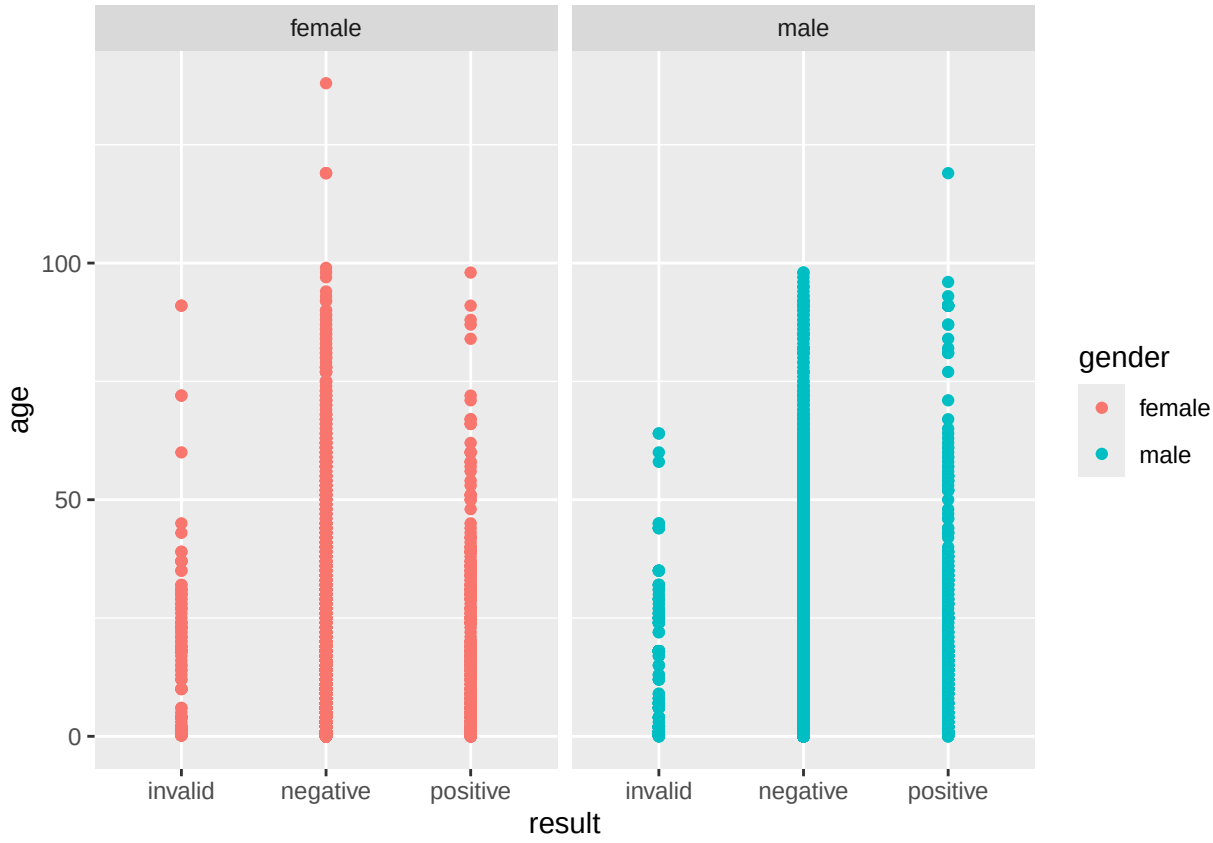
A visual inspection of the distribution suggests that age may be associated with the test result, as there appears to be a positive correlation between age distribution and test outcomes. However, the dataset is skewed toward younger individuals, so the correlation may be due to the age structure. To determine whether this association holds statistically, we performed an ANOVA test. The results showed a significant p-value, indicating that we cannot rule out the possibility of an association between age and test result.

```r
complete_data$age_cat <- cut(complete_data$age,
                             breaks = c(0, 9, 19, 29, 39, 49, 59, 69, 79, 89, 99, Inf),
                             labels = c("0-9", "10-19", "20-29", "30-39",
                                        "40-49", "50-59", "60-69", "70-79",
                                        "80-89", "90-99", "100+"))
by(complete_data$age_cat, complete_data$result, summary)
```

```
## complete_data$result: invalid
##   0-9 10-19 20-29 30-39 40-49 50-59 60-69 70-79 80-89 90-99  100+  NA's
##   143    60    49    29     8     1     4     2     0     2     0     3
## ------------------------------------------------------------
## complete_data$result: negative
##   0-9 10-19 20-29 30-39 40-49 50-59 60-69 70-79 80-89 90-99  100+  NA's
##  7325  3675   935   968   489   370   183    73    56    32     4   248
```

```
## ------------------------------------------------------------
## complete_data$result: positive
##   0-9 10-19 20-29 30-39 40-49 50-59 60-69 70-79 80-89 90-99  100+  NA's
##   296   278    85    99    22    30    16     4     9    13     1    12
```

```
ggplot(complete_data,
       aes(
         x = result,
         y = age,
         group = gender,
         color = gender)
) +
  geom_point() +
  facet_wrap(vars(gender))
```




```
# ANOVA
result_age_aov <- aov(age ~ result, data = complete_data)
result_age_aov
```

```
## Call:
##    aov(formula = age ~ result, data = complete_data)
##
## Terms:
##                   result Residuals
## Sum of Squares     22781   4189232
## Deg. of Freedom        2     15521
##
```

```
## Residual standard error: 16.42886
## Estimated effects may be unbalanced
```

```
summary(result_age_aov)
```

```
##                Df  Sum Sq Mean Sq F value Pr(>F)
## result          2   22781   11391    42.2 <2e-16 ***
## Residuals   15521 4189232     270
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The table below shows the distribution of cycle threshold (Ct) results and test outcomes. As seen earlier, the majority of individuals in this dataset have a Ct value between 40 and 50. Interestingly, this range also has the lowest number of positive test results compared to those with lower Ct values. Additionally, the ANOVA test shows a significant result, suggesting a difference in the distribution of Ct values across different result outcome groups.

```
result_ct_table <- complete_data %>%
  mutate(ct_result_cat = cut(ct_result, breaks = c(10, 20, 30, 40, 50))) %>%
  count(result, ct_result_cat) %>%
  pivot_wider(names_from = ct_result_cat, values_from = n, values_fill = 0)

# View the table
print(result_ct_table)
```

```
## # A tibble: 3 x 6
##   result   `(40,50]`  `NA` `(30,40]` `(10,20]` `(20,30]`
##   <fct>        <int> <int>     <int>     <int>     <int>
## 1 invalid        229    72         0         0         0
## 2 negative     14213   132        13         0         0
## 3 positive        20     5       402        92       346
```

```
ct_result_ct_anova <- aov(complete_data$ct_result ~ complete_data$result, data = complete_data)
summary(ct_result_ct_anova)
```

```
##                         Df Sum Sq Mean Sq F value Pr(>F)
## complete_data$result     2 195741   97870   31905 <2e-16 ***
## Residuals            15312  46970       3
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 209 observations deleted due to missingness
```