

Blood Storage

```
library(tidyverse)
```

```
-- Attaching core tidyverse packages ----- tidyverse 2.0.0 --
v dplyr     1.1.4     v readr     2.1.5
v forcats   1.0.0     v stringr   1.5.1
v ggplot2   3.5.2     v tibble    3.3.0
v lubridate  1.9.4     v tidyr    1.3.1
v purrr     1.1.0
-- Conflicts -----
x dplyr::filter() masks stats::filter()
x dplyr::lag()   masks stats::lag()
i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become non-conflicting
```

```
blood <- read.csv("BloodStorage.csv")
```

```
names(blood)
```

```
[1] "RBC.Age.Group"      "Median.RBC.Age"    "Age"          "AA"
[5] "FamHx"              "PVol"            "TVol"         "T.Stage"
[9] "bGS"                "BN."             "OrganConfined" "PreopPSA"
[13] "PreopTherapy"       "Units"           "sGS"          "AnyAdjTherapy"
[17] "AdjRadTherapy"      "Recurrence"      "Censor"       "TimeToRecurrence"
```

```
blood$`RBC.Age.Group` <- factor(blood$`RBC.Age.Group`,
                                    levels = c(1, 2, 3),
                                    labels = c("Younger", "Middle", "Older"))
anova_result <- aov(TimeToRecurrence ~ RBC.Age.Group, data = blood)
summary(anova_result)
```

```
Df Sum Sq Mean Sq F value Pr(>F)
RBC.Age.Group    2     771   385.5   0.471  0.625
Residuals       312 255329   818.4
1 observation deleted due to missingness
```

```
[1] 4
```

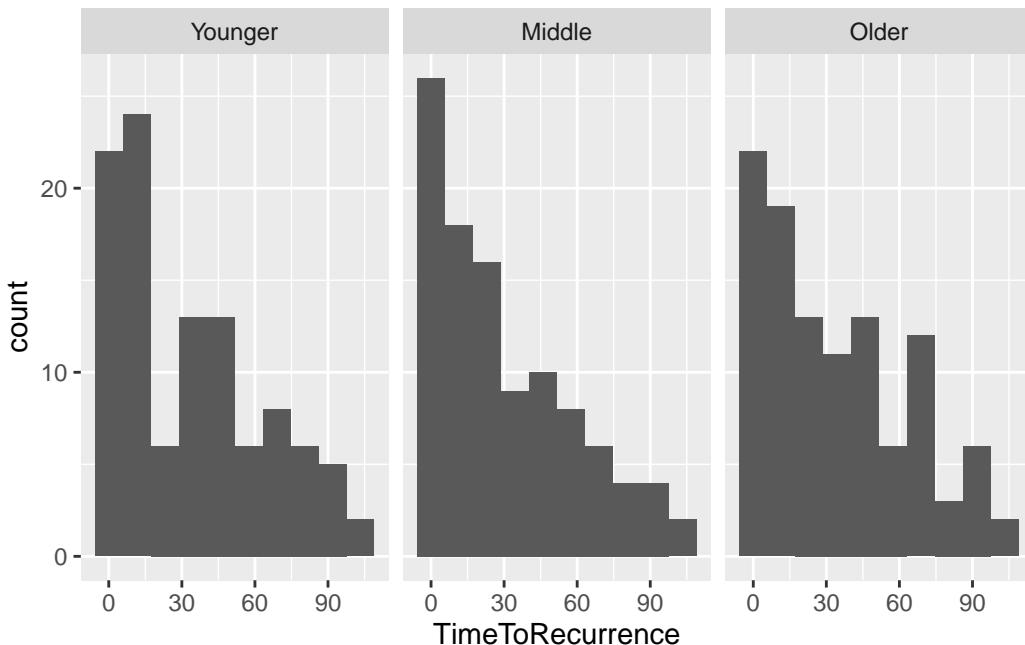
Assumptions 1) The samples are independent.

This assumption is reasonably met by the nature of the data. Each sample represents an independent individual patient. Any conditions for one patient would not impact the conditions of another patient.

2) The variance is the same within all groups

```
library(ggplot2)
ggplot(data = blood, aes(x = TimeToRecurrence)) +
  geom_histogram(bins = 10) +
  facet_grid(~ RBC.Age.Group)
```

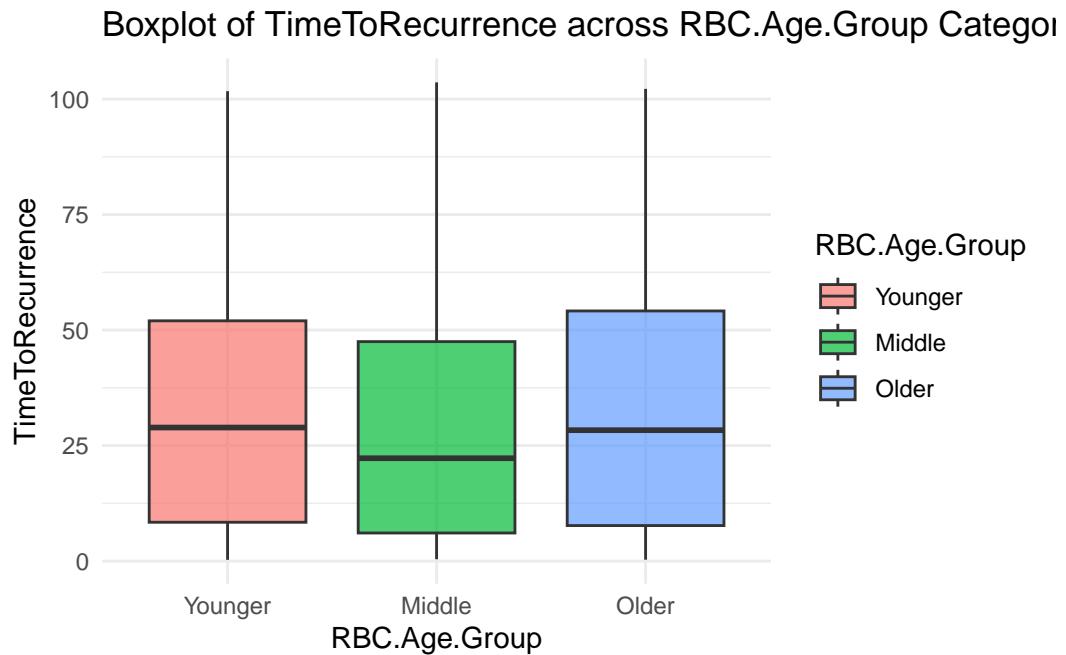
Warning: Removed 1 row containing non-finite outside the scale range
(`stat_bin()`).



This assumption is not met. Outcomes between groups of Blood Age (Younger, Middle, Older) are not normally distributed. Rather, they are right skewed in each group.

- 3) Outcomes within groups are normally distributed

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(`stat_boxplot()`).



This assumption of anova is met. The variance across groups is nearly identical.