Tidy Survival Analysis: Applying R's Tidyverse to Survival Data

Module 2. Data Manipulation with Tidyverse

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Overview of Tidyverse

The `tidyverse` Ecosystem

- **Motivation**: tidy data for reproducible analysis
- **Key packages**
  - `dplyr` (filtering, mutating, grouping, summarizing)
  - `tidyr` (pivoting, nesting, reshaping)
  - `tibble` (modern data frames)
  - `readr` / `haven` (importing .csv or .sas7bdat)
  - `lubridate` (handling time variables)
  - `ggplot2` (visualization)

```r
# Load core tidyverse packages
library(tidyverse)
```

Basic Functionalities

- **Data manipulation**: using `dplyr` verbs
  - `mutate()` to create new variables (e.g., age group, log-transformed labs)
  - `filter()` to subset by treatment or age
  - `select()` and `rename()` for variable formatting
  - `arrange()` to sort
  - `group_by()` and `summarize()` for descriptive summaries by arm
- **Data reshaping**: using `tidyr` functions
  - `pivot_longer()` to convert wide to long format
  - `pivot_wider()` to convert long to wide format
  - `nest()` and `unnest()` for hierarchical data

A Simple Example

- **Example dataset**

```r
# Simulated data example
df1 <- tibble(
  id = 1:6,
  trt = c("A", "A", "B", "B", "A", "B"),
  age = c(65, 70, 58, 60, 64, 59),
  time = c(5, 8, 12, 3, 2, 6),
  status = c(1, 0, 1, 1, 0, 0)  # 1 = event, 0 = censored
)
df1
```

```
# A tibble: 6 × 5
     id trt     age  time status
  <int> <chr> <dbl> <dbl>  <dbl>
1     1 A        65     5      1
2     2 A        70     8      0
3     3 B        58    12      1
4     4 B        60     3      1
5     5 A        64     2      0
6     6 B        59     6      0
```

Native Pipe Operator: |>

- **What is |>**
  - Introduced in **R 4.1** (hot key: `Ctrl + Shift + M`)
  - Passes the result of one expression into the first argument of the next
  - Same idea as `%>%`, but **built into base R**
- **Example**

```r
df1 |> # passes tibble data frame df1 to the next function
  mutate(age_group = if_else(age >= 65, "older", "younger")) |> # create age group
  filter(trt == "A") |> # filter for treatment A
  arrange(time) # sort by time
```

```
# A tibble: 3 × 6
     id trt     age  time status age_group
  <int> <chr> <dbl> <dbl>  <dbl> <chr>
1     5 A        64     2      0 younger
2     1 A        65     5      1 older
3     2 A        70     8      0 older
```

Summarizing and Grouping

- Survival-specific summaries (e.g., number of events)
  - `group_by()` and `summarize()` for descriptive summaries by arm

```r
df1 |>
  group_by(trt) |> # group by treatment arm
  summarize( # summarize each group
    n = n(), # count number of rows (subjects)
    events = sum(status), # sum of events (status = 1)
    median_time = median(time) # median survival time
  )
```

```
# A tibble: 2 × 4
  trt         n events median_time
  <chr> <int>  <dbl>       <dbl>
1 A           3      1           5
2 B           3      2           6
```

What Does “Tidy” Mean?

> A dataset is tidy if:
>
> - Each **variable** is a column
> - Each **observation** is a row
> - Each **type of observational unit** is a table
>
> — Hadley Wickham, *Tidy Data* (2014)
> https://www.jstatsoft.org/article/view/v059i10

Why Tidy Data?

- **Tidy data principles**
  - Easy to reshape and transform
  - Compatible with `ggplot2`, `dplyr`, `tidyr`, and modeling tools
  - Encourages modular and reproducible code
- **Messy data challenges:**
  - Time in rows, covariates in columns
  - Multiple data types in one column
  - Separte randomization and event/censoring dates
  - Missing/censored values inconsistently coded

Tidy Survival Data

- **Possible pre-processing steps**
  - Calculate survival time from start to event/censoring
  - Creating the (X, δ) structure expected by `Surv()`
  - Reshaping data to long format in case of multiple events
- **An Example**

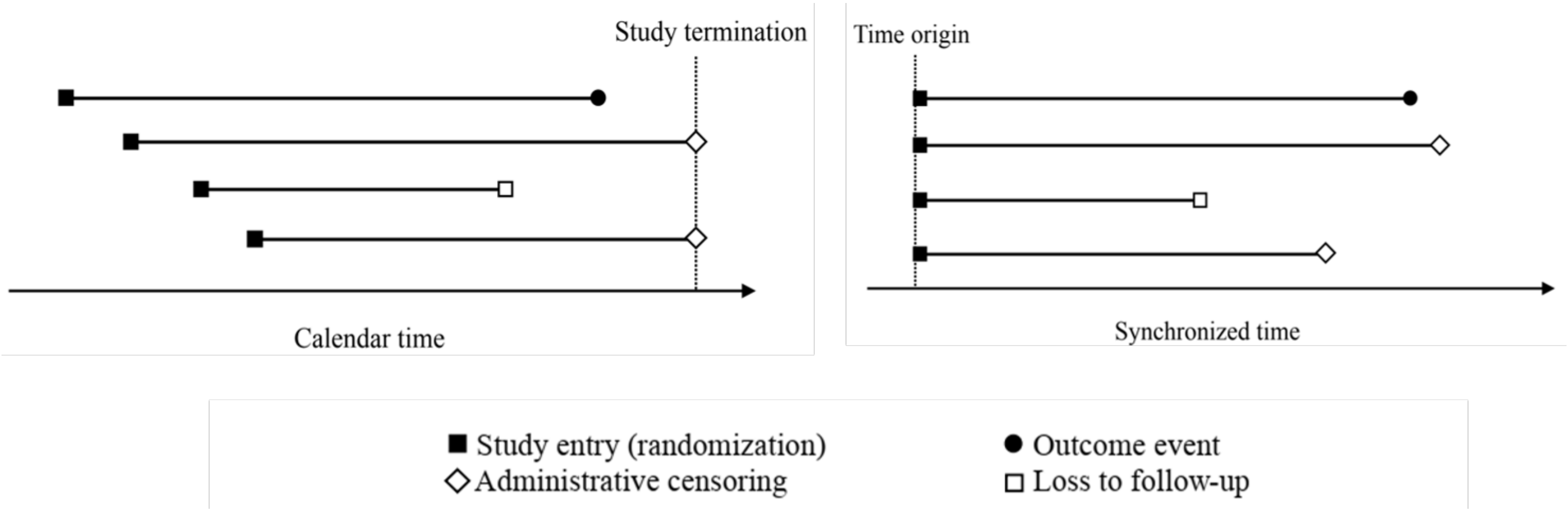
```r
# Load GBC data
gbc <- read.table("data/gbc.txt", header = TRUE)
head(gbc)
```

```
  id     time status hormone age meno size grade nodes prog estrg
1  1 43.83607      1       1  38    1   18     3     5  141   105
2  1 74.81967      0       1  38    1   18     3     5  141   105
3  2 46.55738      1       1  52    1   20     1     1   78    14
4  2 65.77049      0       1  52    1   20     1     1   78    14
5  3 41.93443      1       1  47    1   30     2     1  422    89
6  3 47.73770      2       1  47    1   30     2     1  422    89
```

Tidying Survival Data

Calendar vs. Event Times

- Time from start to event/censoring ()



Dates to Time Difference

- A data example

```r
# Example: raw dates as character strings
df2 <- tibble(
  id = 1:3,
  rand_date = c("2022-01-01", "2022-01-15", "2022-01-20"),
  end_date = c("2022-04-01", "2022-06-01", "2022-03-15"),
  status = c("dead", "censored", "dead")
)
df2
```

```
# A tibble: 3 × 4
     id rand_date  end_date   status
  <int> <chr>      <chr>      <chr>
1     1 2022-01-01 2022-04-01 dead
2     2 2022-01-15 2022-06-01 censored
3     3 2022-01-20 2022-03-15 dead
```

Parsing Dates and Calculating Time

- Using `lubridate` to parse dates
  - `ymd()` for “year-month-day” format
  - `mdy()` for “month-day-year” format

```r
# Parse dates and calculate time/status
df2 |>
  mutate(
    rand_date = ymd(rand_date), # convert character to Date
    end_date = ymd(end_date), # convert character to Date
    time = as.numeric(end_date - rand_date), # calculate time in days
    status = if_else(status == "dead", 1, 0) # convert status to 1/0
  )
```

```
# A tibble: 3 × 5
     id rand_date  end_date   status  time
  <int> <date>     <date>      <dbl> <dbl>
1     1 2022-01-01 2022-04-01      1    90
2     2 2022-01-15 2022-06-01      0   137
3     3 2022-01-20 2022-03-15      1    54
```

Exercise: Calculate Survival Time (I)

- Calculate `time` and `status` variables for `df3`:

```r
# create a df3 with dates in the form of month-day-year
df3 <- tibble(
  id = 1:3,
  rand_date = c("Jan-01-2022", "01-15-2022", "01-20-2022"),
  end_date = c("04-01-2022", "Jun-01-2022", "03-15-2022"),
  status = c("dead", "censored", "dead")
)
df3
```

```
# A tibble: 3 × 4
     id rand_date   end_date    status
  <int> <chr>       <chr>       <chr>
1     1 Jan-01-2022 04-01-2022  dead
2     2 01-15-2022  Jun-01-2022 censored
3     3 01-20-2022  03-15-2022  dead
```

Exercise: Calculate Survival Time (II)

- **Hint**: use `mdy()` to parse dates

▶ Solution

- More about manipulating dates
  - lubridate official documentation
  - R for Data Science: Dates and times

Parsing Censored Observations

- **Alternative formats for censored times**
  - `"32+"`, `">17"`, etc
  - `parse_number()` for get `time`; `str_detect()` for `status`

```r
# Example data: relapse times with "+" indicating censoring
MP <- c(10,  "32+", 23, "25+")
# Convert to (time, status) format
df4 <- tibble(
  MP = MP,                                 # Original data
  time = parse_number(MP),                 # Extract numeric part
  status = 1 - str_detect(MP, "\\+")      # Censored if "+" detected
)
df4
```

```
# A tibble: 4 × 3
  MP     time status
  <chr> <dbl>  <dbl>
1 10       10      1
2 32+      32      0
3 23       23      1
4 25+      25      0
```

Exercise: Parse Censored Times

- **Task**: Parse `MP` in `df5` to create `time` and `status`

```r
df5 <- tibble(
  MP = c(10, "32+", 23, ">25")
)
```

▶ Solution

- More on string operation
  - stringr official documentation
  - R for Data Science: Strings

Reshaping Data

- **Why reshape?**
  - Multiple events per subject
  - Wide format (multiple columns) long format (one row per event)

```r
# Example: wide format with multiple events
df6 <- tibble(
  id = 1:3,
  prog_time = c(10, 20, 30),
  prog_status = c(1, 0, 1), # 1 = progression, 0 = censored
  death_time = c(15, 20, 35),
  death_status = c(0, 1, 1) # 1 = dead, 0 = censored
)
# 1: progression at 10, censored at 15
# 2: dead at 20 without progression
# 3: progression at 30, dead at 35
df6
```

```
# A tibble: 3 × 5
     id prog_time prog_status death_time death_status
  <int>     <dbl>       <dbl>      <dbl>        <dbl>
1     1        10           1         15            0
2     2        20           0         20            1
3     3        30           1         35            1
```

Wide to Long

- Using `pivot_longer()`
  - Convert wide format to long format
  - Specify `names_to` and `values_to` for new columns

```r
df7 <- df6 |>
  pivot_longer(
    cols = c(prog_time, prog_status, death_time, death_status), # columns to reshape
    names_to = c("event", ".value"), # .value keeps the variable name, event is the new column
    names_pattern = "(.*)_(.*)" # split by underscore
  )
df7
```

```
# A tibble: 6 × 4
     id event  time status
  <int> <chr> <dbl>  <dbl>
1     1 prog     10      1
2     1 death    15      0
3     2 prog     20      0
4     2 death    20      1
5     3 prog     30      1
6     3 death    35      1
```

Exercise: Clean Up

- **Task**: Clean up `df7` to create a tidy survival dataset
  - Remove rows with `event = prog` and `status = 0` (non-terminal event)
  - Recode `status = 2` for death events

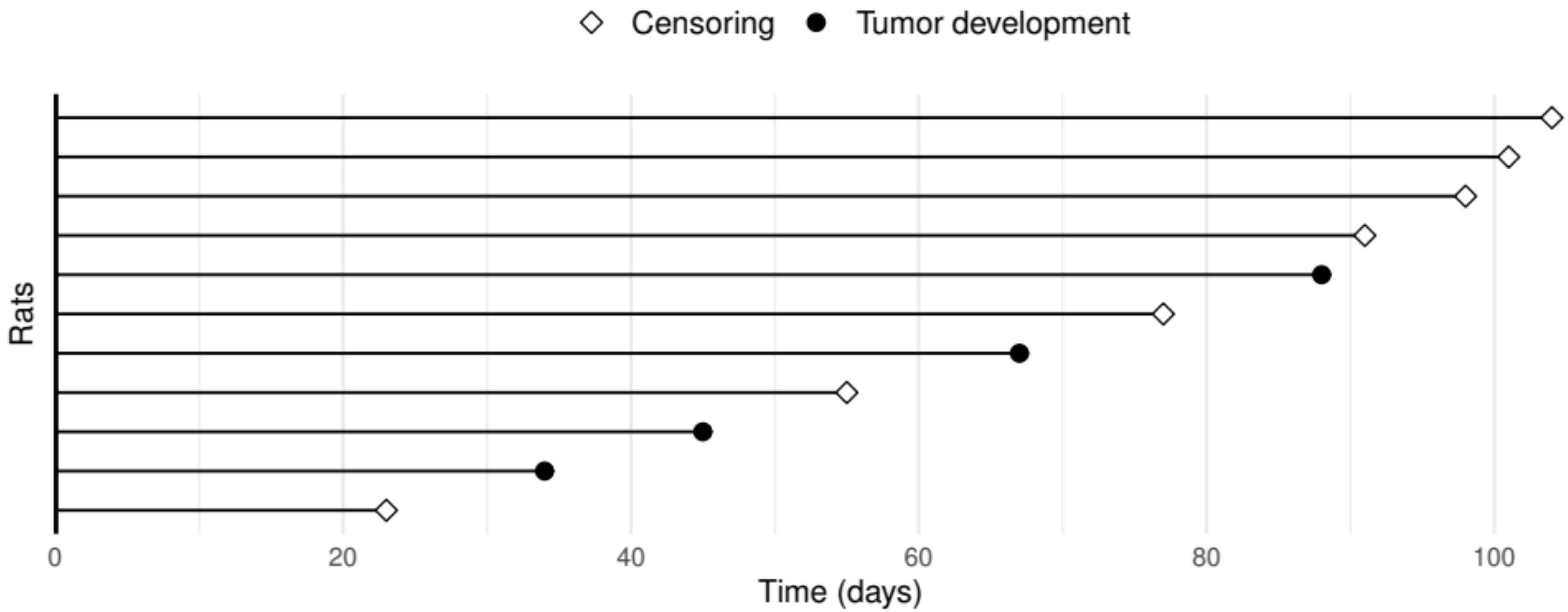
▶ Solution

- More on reshaping data
  - tidyr official documentation
  - R for Data Science: Data tidying

Visualizing Subject Follow-Up

Swimmer Plot

- **What is a swimmer plot?**
  - Visualizes subject follow-up
  - Each row represents a subject
  - Horizontal lines show time to event/censoring



Swimmer Plot Basics

- Using `ggplot2`
  - `geom_linerange()` for horizontal lines
  - `geom_point()` for events
  - `facet_wrap()` for treatment arms (optional)
- A data example

```r
# Example data: rat survival times
df8 <- tibble(
  time = c(101, 55, 67, 23, 45, 98, 34, 77, 91, 104, 88),
  status = c(0, 0, 1, 0, 1, 0, 1, 0, 0, 0, 1),
  group = c("A", "A", "A", "B", "B", "B", "A", "B", "B", "A", "B")
) |>
  mutate(
    id = row_number(), # create id column using row number
    .before = 1 # place id before time
  )
```

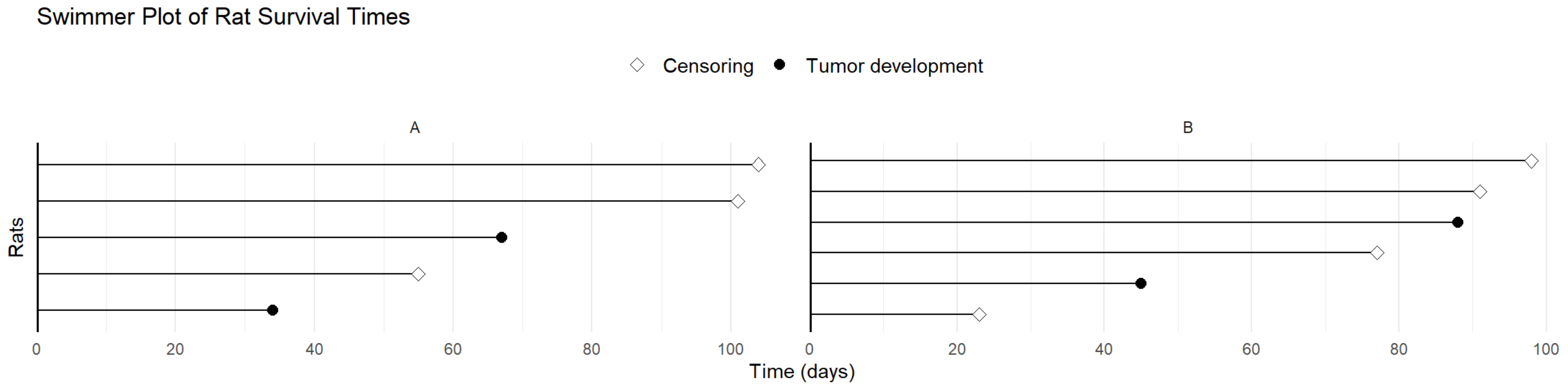
Creating a Swimmer Plot

- Code to reproduce previous plot

```r
# Specify the plot
fig8 <- df8 |>
  # Set-up: id on the y-axis, time on the x-axis
  ggplot(aes(x = time, y = reorder(id, time))) + # reorder id by time
  # Add geometric objects
  geom_linerange(aes(xmin = 0, xmax = time)) + # horizontal lines from 0 to time
  # Add points for events/censoring, distinguish by status
  geom_point(aes(shape = factor(status)), size = 2.5, fill = "white") +
  # Add vertical line at x = 0
  geom_vline(xintercept = 0, linewidth = 1) +
  theme_minimal() + # use minimal theme
  # Format y axis
  scale_y_discrete(name = "Rats") + # y-axis label
  # Format x axis (label, breaks, no expansion on left, 0.05 expansion on right)
  scale_x_continuous(name = "Time (days)", breaks = seq(0, 100, by = 20),
                     expand = expansion(c(0, 0.05))) +
  # Format point shape (pch = 23 for censoring, pch = 19 for event; label shape)
  scale_shape_manual(values = c(23, 19), labels = c("Censoring", "Tumor development")) +
  # Further formatting using theme()
  theme(
    legend.position = "top", # place legend at the top
    legend.title = element_blank(), # no legend title
```

Exercise: Swimmer Plot by Group

- **Task**: Create a swimmer plot for `df8` by `group`
  - Use `facet_wrap()` to create separate panels for each group
  - Add a title "Swimmer Plot of Rat Survival Times"



▶ Solution

Creating “Table 1”

Descriptive Statistics

- **Importance of Table 1**
  - Summarizes baseline characteristics
  - Provides context for formal analysis
- **Using `gtsummary`**
  - `tbl_summary()` for descriptive statistics
  - `add_p()` for p-values comparing groups (not recommended for randomized trials)
  - `add_overall` to add overall summary
  - `modify_header()` to customize table headers

Basic Syntax of `tbl_summary()`

- **Common arguments**
  - `by = "group"` to summarize by group
  - `include = c("variable1", "variable2")` to include specific variables
  - `label = list(variable = "Label")` to customize variable labels
  - `statistic = list(variable ~ "statistic")` to specify statistics
    - `statistic = list(all_continuous() ~ "{mean} ({sd})")` for mean and SD
  - `digits = list(variable ~ 2)` to set decimal places

A Simple Example

- **Example dataset**

```r
# Example data: 10 subjects with treatment, age, and sex
df9 <- tibble(
  id = 1:10,
  time = c(101, 55, 67, 23, 45, 98, 34, 77, 91, 104),
  status = c(0, 1, 1, 0, 1, 0, 1, 0, 1, 0), # 0 = censored, 1 = event
  trt = c("A", "A", "B", "B", "A", "B", "A", "B", "A", "B"),
  sex = c("M", "F", "M", "F", "M", "F", "M", "F", "M", "F"),
  age = c(65, 70, 58, 60, 64, 59, 66, 62, 68, 61)
)
head(df9)
```

```
# A tibble: 6 × 6
     id  time status trt   sex     age
  <int> <dbl>  <dbl> <chr> <chr> <dbl>
1     1   101      0 A     M        65
2     2    55      1 A     F        70
3     3    67      1 B     M        58
4     4    23      0 B     F        60
5     5    45      1 A     M        64
6     6    98      0 B     F        59
```

Creating a Summary Table

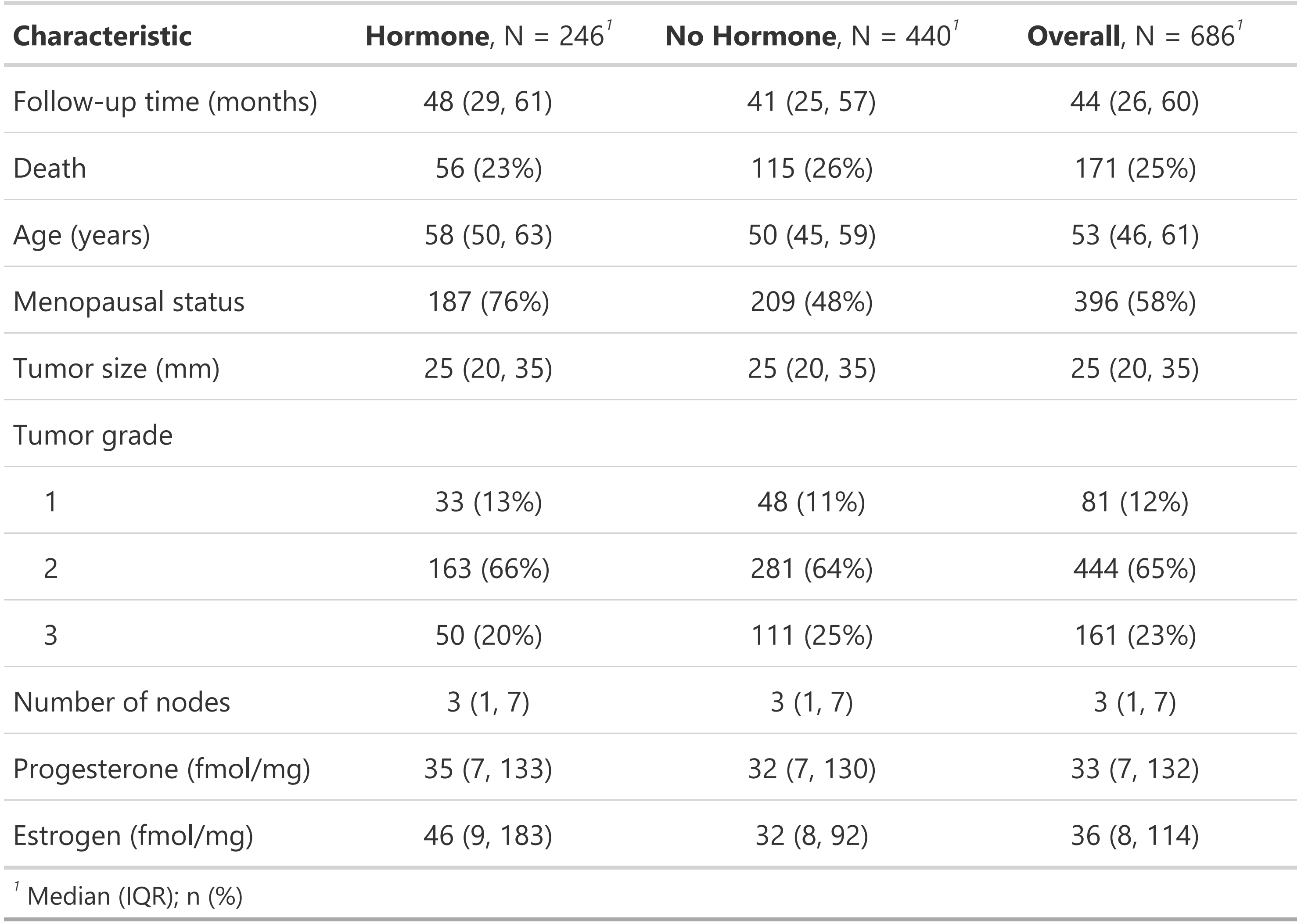
```r
library(gtsummary) # load package
df9 |>
  tbl_summary(
    by = trt,                             # summarize by treatment arm
    include = c(sex, age, time, status), # include specific variables
    label = list(                         # label variables
      time = "Follow-up time (months)",
      status = "Events"
    )
  )
```

Characteristic	**A**, N = 5[1]	**B**, N = 5[1]
sex		
F	1 (20%)	4 (80%)
M	4 (80%)	1 (20%)
age	66.0 (65.0, 68.0)	60.0 (59.0, 61.0)
Follow-up time (months)	55 (45, 91)	77 (67, 98)
Events	4 (80%)	1 (20%)

[1] n (%); Median (IQR)

Exercise: Summarize GBC Data (I)

- **Task**: Summarize the GBC mortality data (`gbc_mort.txt`) like below



Characteristic	**Hormone**, N = 246[1]	**No Hormone**, N = 440[1]	**Overall**, N = 686[1]
Follow-up time (months)	48 (29, 61)	41 (25, 57)	44 (26, 60)
Death	56 (23%)	115 (26%)	171 (25%)
Age (years)	58 (50, 63)	50 (45, 59)	53 (46, 61)
Menopausal status	187 (76%)	209 (48%)	396 (58%)
Tumor size (mm)	25 (20, 35)	25 (20, 35)	25 (20, 35)
Tumor grade			
1	33 (13%)	48 (11%)	81 (12%)
2	163 (66%)	281 (64%)	444 (65%)
3	50 (20%)	111 (25%)	161 (23%)
Number of nodes	3 (1, 7)	3 (1, 7)	3 (1, 7)
Progesterone (fmol/mg)	35 (7, 133)	32 (7, 130)	33 (7, 132)
Estrogen (fmol/mg)	46 (9, 183)	32 (8, 92)	36 (8, 114)

[1] Median (IQR); n (%)

Exercise: Summarize GBC Data (II)

- **Points to note**
  - Summarize by hormone therapy (`hormone`)
  - Include variables: `time`, `status`, `age`, `meno`, `size`, `grade`, `nodes`, `prog`, `estrg`
  - Label variables appropriately
  - Add overall summary column at the end

Exercise: Summarize GBC Data (III)

▶ Solution

Exercise: Summarize GBC Data (IV)

- **Task**: summarize *relapse* and death data from `gbc.txt`
  - Hint: `group_by(id)` and `summarize()`

Characteristic	**Hormone**, N = 246[1]	**No Hormone**, N = 440[1]	**Overall**, N = 686[1]
Relapse	94 (38%)	205 (47%)	299 (44%)
Death	56 (23%)	115 (26%)	171 (25%)
Composite	94 (38%)	205 (47%)	299 (44%)
Relapse then death	56 (23%)	115 (26%)	171 (25%)

[1] n (%)

Exercise: Summarize GBC Data (V)

▶ Solution

Summary

Key Takeaways

- **Tidyverse** provides powerful tools for data manipulation and visualization
- **Tidy data** principles simplify analysis and visualization
- **Survival data** may require pre-processing steps (`dplyr`, `tidyr`,`lubridate`)
- **Swimmer plots** effectively visualize subject follow-up (`ggplot2`)
- **Descriptive statistics** can be easily summarized using `gtsummary::tbl_summary()`

Next Steps

- Format analysis results from the `survival` package:
  - **Nonparametric estimates** with `survfit()`
  - **Regression models** with `coxph()`
- Explore advanced visualization techniques:
  - Kaplan–Meier curves with `ggsurvfit` or `survminer`
  - Layered plots using `ggplot2`
  - Annotated plots for publications