5. Factors

Understanding Categorical Variables and Manipulating Them with forcats
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To install and load all packages used in this chapter, run the following code:

```r
for (pkg in c("forcats", "janitor", "patchwork", "tidyverse")) {
  if (!require(pkg, character.only = TRUE)) install.packages(pkg)
}

library(forcats)
library(janitor)
library(patchwork)
library(tidyverse)
```

Introduction

Anyone working with categorical data in R will sooner or later encounter the concept of **factors**. For beginners, they are often confusing: Why does a column suddenly behave differently than expected? Why do the bars in the chart appear in a strange order?

This chapter explains what factors are, when you need them, and how to elegantly manipulate them with the {forcats} package.

Example Data

We again use the `starwars` dataset, filtered to humans:

```r
humans <- starwars %>%
  filter(species == "Human") %>%
  select(name, height, mass, hair_color, eye_color, gender)

humans
```

```
# A tibble: 35 × 6
   name               height  mass hair_color    eye_color gender
   <chr>               <int> <dbl> <chr>         <chr>     <chr>
 1 Luke Skywalker        172    77 blond         blue      masculine
 2 Darth Vader           202   136 none          yellow    masculine
 3 Leia Organa           150    49 brown         brown     feminine
 4 Owen Lars             178   120 brown, grey   blue      masculine
 5 Beru Whitesun Lars    165    75 brown         blue      feminine
 6 Biggs Darklighter     183    84 black         brown     masculine
 7 Obi-Wan Kenobi        182    77 auburn, white blue-gray masculine
 8 Anakin Skywalker      188    84 blond         blue      masculine
 9 Wilhuff Tarkin        180    NA auburn, grey  blue      masculine
10 Han Solo              180    80 brown         brown     masculine
# ℹ 25 more rows
```

Character vs. Factor: The Difference

Character: Simply Text

A character variable is simply text. R treats each value as an independent string:

```r
# eye_color is a character vector
class(humans$eye_color)
```

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

```r
# Unique values (in order of first occurrence)
unique(humans$eye_color)
```

```
[1] "blue"      "yellow"    "brown"     "blue-gray" "hazel"     "dark"
[7] "unknown"
```

When we sort character values, it happens **alphabetically**:

```r
sort(unique(humans$eye_color))
```

```
[1] "blue"      "blue-gray" "brown"     "dark"      "hazel"     "unknown"
[7] "yellow"
```

Factor: Text with Structure

A factor is text **plus additional information**:

1. **Levels**: The possible categories
2. **Order**: The sorting of the levels

```r
# Convert character to factor
eye_factor <- factor(humans$eye_color)

class(eye_factor)
```

```
[1] "factor"
```

```r
levels(eye_factor)  # The stored levels
```

```
[1] "blue"      "blue-gray" "brown"     "dark"      "hazel"     "unknown"
[7] "yellow"
```

The levels are sorted alphabetically by default. But we can define a **custom order**:

```r
eye_custom <- factor(
  humans$eye_color,
  levels = c("blue", "brown", "hazel", "dark", "blue-gray")
)

levels(eye_custom)
```

```
[1] "blue"      "brown"     "hazel"     "dark"      "blue-gray"
```

Why Does This Matter?

The level order affects:

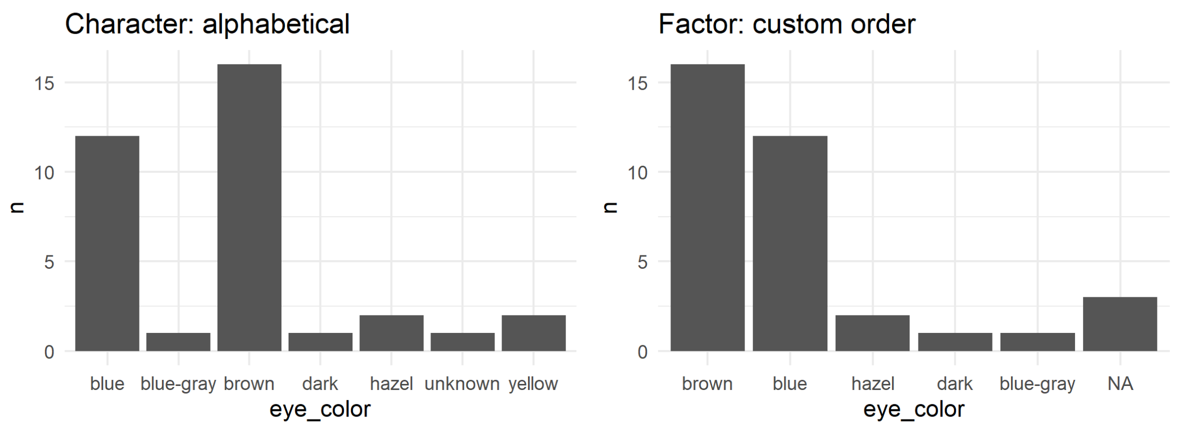
- **Sorting in tables**
- **Order in graphics** (e.g., bar charts)

- **Reference category** in statistical models

```r
# With character: alphabetical order
p1 <- humans %>%
  count(eye_color) %>%
  ggplot(aes(x = eye_color, y = n)) +
  geom_col() +
  labs(title = "Character: alphabetical") +
  theme_minimal()

# With factor: our order
p2 <- humans %>%
  mutate(eye_color = factor(eye_color,
                            levels = c("brown", "blue", "hazel", "dark", "blue-
gray"))) %>%
  count(eye_color) %>%
  ggplot(aes(x = eye_color, y = n)) +
  geom_col() +
  labs(title = "Factor: custom order") +
  theme_minimal()

# Display side by side
p1 + p2
```



Exercise: Character vs. Factor

a) Check with `class()` whether `hair_color` in the `humans` dataset is a character or factor.

b) Convert `hair_color` to a factor and display the levels.

c) Create a factor for `hair_color` with the order: “brown”, “black”, “blond”, “auburn”, then all others.

Solution

```r
# a) Check class
class(humans$hair_color)
```

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

```r
# b) Convert to factor
hair_factor <- factor(humans$hair_color)
levels(hair_factor)
```

```
 [1] "auburn"         "auburn, grey"  "auburn, white" "black"
 [5] "blond"          "brown"         "brown, grey"   "grey"
 [9] "none"           "white"
```

```r
# c) With custom order
hair_custom <- factor(
  humans$hair_color,
  levels = c("brown", "black", "blond", "auburn",
             "auburn, grey", "auburn, white", "grey", "white", "none")
)
levels(hair_custom)
```

```
[1] "brown"         "black"         "blond"         "auburn"
[5] "auburn, grey"  "auburn, white" "grey"          "white"
[9] "none"
```

Creating Factors

factor() vs. as_factor()

There are two main functions for creating factors:

```r
colors <- c("red", "blue", "red", "green", "blue")

# factor(): Levels alphabetical
factor(colors)
```

```
[1] red   blue  red   green blue 
Levels: blue green red
```

```r
# as_factor(): Levels by order of first occurrence
as_factor(colors)
```

```
[1] red   blue  red   green blue 
Levels: red blue green
```

Function	Package	Level Order
`factor()`	base R	Alphabetical
`as_factor()`	forcats	By occurrence in vector

`as_factor()` is often more practical because the order of the data is preserved.

Specifying Levels Explicitly

With the `levels` argument, we can determine the order ourselves:

```r
# Custom order
satisfaction <- c("medium", "high", "low", "high", "medium")

# WRONG: alphabetical
factor(satisfaction)
```

```
[1] medium high   low    high   medium
Levels: high low medium
```

```r
# RIGHT: logical order
factor(satisfaction, levels = c("low", "medium", "high"))
```

```
[1] medium high   low    high   medium
Levels: low medium high
```

forcats: Manipulating Factors

The {forcats} package (part of the tidyverse) provides practical functions for factor manipulation. All functions start with `fct_`.

Changing Order

fct_relevel() – Manual Reordering

```r
# Original order
humans %>%
  mutate(eye_color = factor(eye_color)) %>%
  pull(eye_color) %>%
  levels()
```

```
[1] "blue"      "blue-gray" "brown"     "dark"      "hazel"     "unknown"  
[7] "yellow"   
```

```r
# Move "brown" to the beginning
humans %>%
  mutate(eye_color = fct_relevel(eye_color, "brown")) %>%
  pull(eye_color) %>%
  levels()
```

```
[1] "brown"     "blue"      "blue-gray" "dark"      "hazel"     "unknown"  
[7] "yellow"   
```

```r
# Multiple levels in specific order
humans %>%
  mutate(eye_color = fct_relevel(eye_color, "brown", "blue", "hazel")) %>%
  pull(eye_color) %>%
  levels()
```

```
[1] "brown"     "blue"      "hazel"     "blue-gray" "dark"      "unknown"  
[7] "yellow"   
```

fct_reorder() – Sort by Another Variable

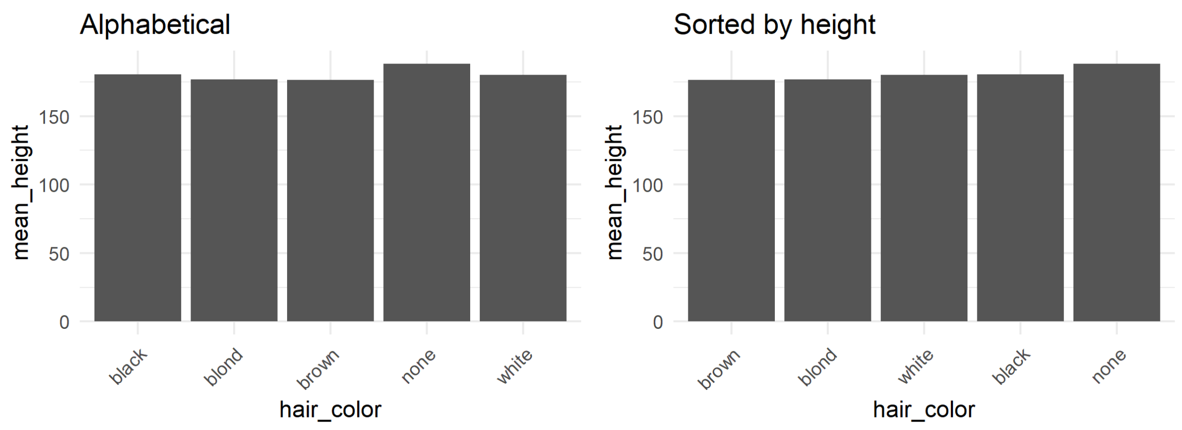
Particularly useful for graphics – sort categories by a numerical value:

```r
# Average height by hair color
hair_height <- humans %>%
  filter(!is.na(hair_color), !is.na(height)) %>%
  group_by(hair_color) %>%
  summarise(mean_height = mean(height), n = n()) %>%
  filter(n >= 2)  # Only groups with at least 2 people

# Without fct_reorder: alphabetical
p1 <- hair_height %>%
  ggplot(aes(x = hair_color, y = mean_height)) +
  geom_col() +
  labs(title = "Alphabetical") +
  theme_minimal() +
  theme(axis.text.x = element_text(angle = 45, hjust = 1))

# With fct_reorder: sorted by height
p2 <- hair_height %>%
  ggplot(aes(x = fct_reorder(hair_color, mean_height), y = mean_height)) +
  geom_col() +
  labs(title = "Sorted by height", x = "hair_color") +
  theme_minimal() +
  theme(axis.text.x = element_text(angle = 45, hjust = 1))
```

```r
p1 + p2
```



fct_infreq() – Sort by Frequency

```r
humans %>%
  mutate(eye_color = fct_infreq(eye_color)) %>%
  pull(eye_color) %>%
  levels()
```

```
[1] "brown"     "blue"      "hazel"     "yellow"    "blue-gray" "dark"
[7] "unknown"
```

The most frequent categories come first – ideal for bar charts.

fct_rev() – Reverse Order

```r
# Most frequent first, then reverse (least frequent first)
humans %>%
  mutate(eye_color = fct_rev(fct_infreq(eye_color))) %>%
  pull(eye_color) %>%
  levels()
```

```
[1] "unknown"   "dark"      "blue-gray" "yellow"    "hazel"     "blue"
[7] "brown"
```

Combining Levels

fct_lump_n() – Combine Rare into "Other"

```r
# Keep only the 3 most frequent, rest becomes "Other"
humans %>%
  mutate(eye_color = fct_lump_n(eye_color, n = 3)) %>%
  tabyl(eye_color)
```

```
 eye_color  n    percent
      blue 12 0.34285714
     brown 16 0.45714286
     hazel  2 0.05714286
    yellow  2 0.05714286
     Other  3 0.08571429
```

```r
# With custom label
humans %>%
  mutate(eye_color = fct_lump_n(eye_color, n = 3, other_level = "Misc")) %>%
  tabyl(eye_color)
```

```
 eye_color  n    percent
      blue 12 0.34285714
     brown 16 0.45714286
     hazel  2 0.05714286
    yellow  2 0.05714286
      Misc  3 0.08571429
```

Related functions:

- `fct_lump_min()` – Combine if fewer than n occurrences
- `fct_lump_prop()` – Combine if proportion below x%

fct_collapse() – Combine Multiple Levels

```
humans %>%
  mutate(
    eye_group = fct_collapse(
      eye_color,
      "light" = c("blue", "blue-gray", "hazel"),
      "dark" = c("brown", "dark")
    )
  ) %>%
  tabyl(eye_group)
```

```
 eye_group  n    percent
     light 15 0.42857143
      dark 17 0.48571429
   unknown  1 0.02857143
    yellow  2 0.05714286
```

Renaming Levels

fct_recode()

```
humans %>%
  mutate(
    eye_color_full = fct_recode(
      eye_color,
      "Blue" = "blue",
      "Brown" = "brown",
      "Dark" = "dark",
      "Hazel" = "hazel",
      "Blue-Gray" = "blue-gray"
    )
  ) %>%
  tabyl(eye_color_full)
```

```
 eye_color_full  n    percent
           Blue 12 0.34285714
      Blue-Gray  1 0.02857143
          Brown 16 0.45714286
           Dark  1 0.02857143
          Hazel  2 0.05714286
        unknown  1 0.02857143
         yellow  2 0.05714286
```

Exercise: forcats

Work with the `humans` dataset:

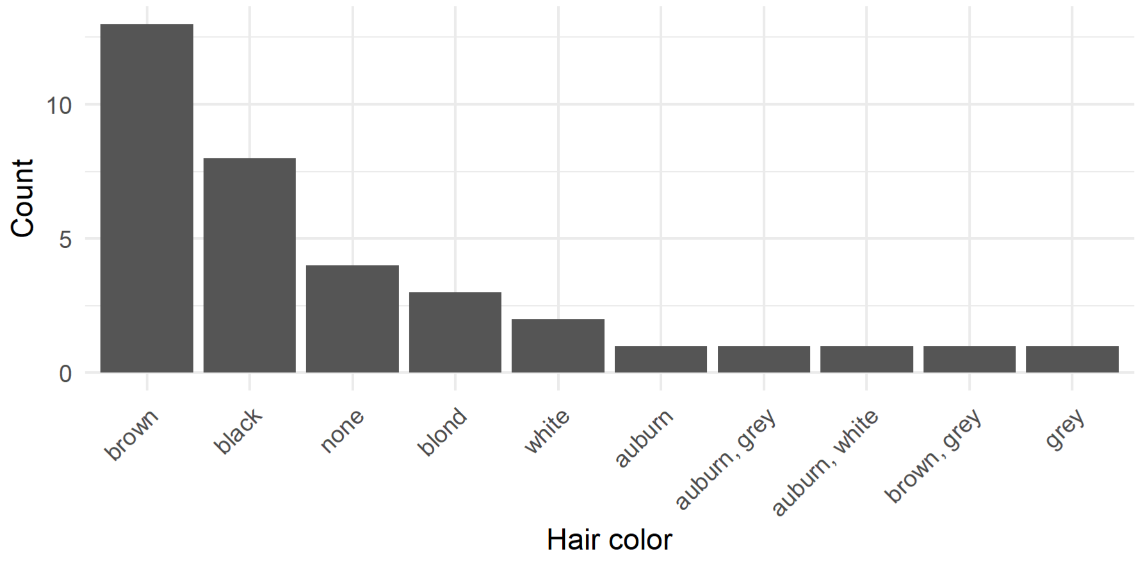
a) Create a bar chart of `hair_color` where the bars are sorted by frequency (most frequent on the left).

b) Combine all hair colors except the 3 most frequent under “Other” and create a frequency table with `tabyl()`.

c) Rename the levels of `gender`: “feminine” → “female”, “masculine” → “male”.

i Solution

```
# a) Bar chart by frequency
humans %>%
  filter(!is.na(hair_color)) %>%
  ggplot(aes(x = fct_infreq(hair_color))) +
  geom_bar() +
  labs(x = "Hair color", y = "Count") +
  theme_minimal() +
  theme(axis.text.x = element_text(angle = 45, hjust = 1))
```



```
# b) Lump and tabyl
humans %>%
  mutate(hair_color = fct_lump_n(hair_color, n = 3, other_level = "Other")) %>%
  tabyl(hair_color, show_na = FALSE)
```

```
 hair_color  n   percent
      black  8 0.2285714
      brown 13 0.3714286
       none  4 0.1142857
      Other 10 0.2857143
```

```
# c) Rename gender
humans %>%
  mutate(
    gender_renamed = fct_recode(
      gender,
      "female" = "feminine",
      "male" = "masculine"
    )
  ) %>%
  tabyl(gender_renamed)
```

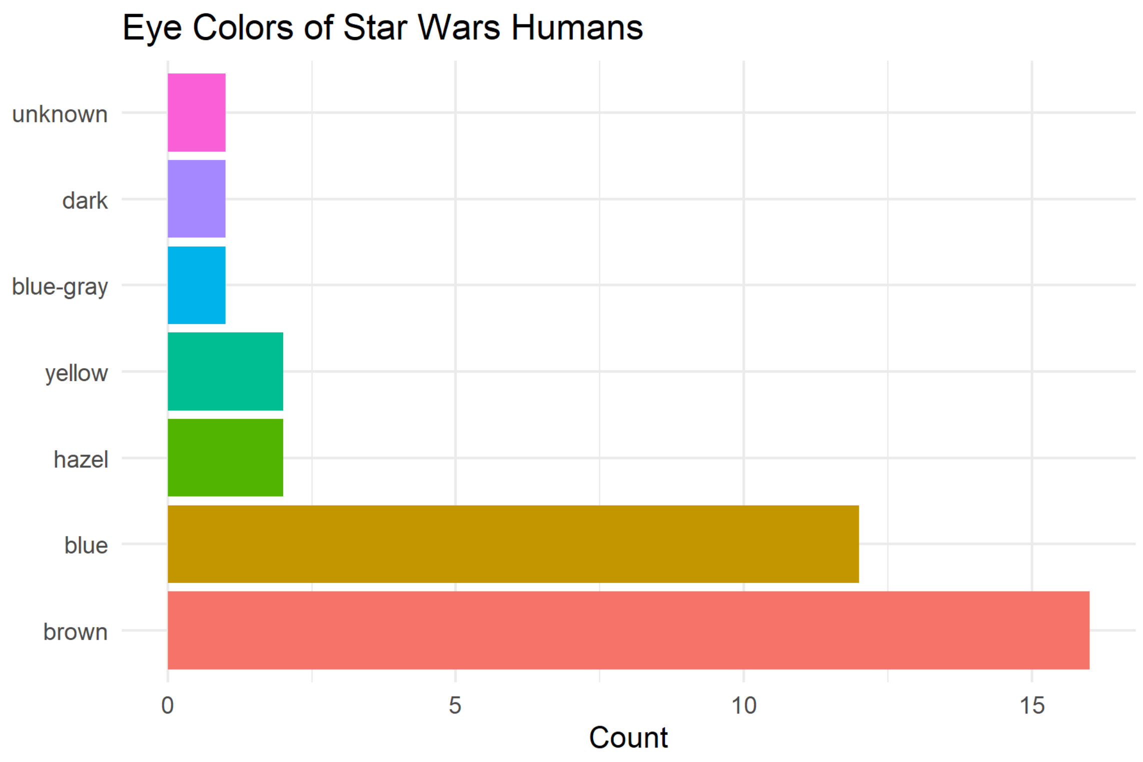
```
 gender_renamed  n   percent
         female  9 0.2571429
           male 26 0.7428571
```

Practical Applications

Factors in ggplot2

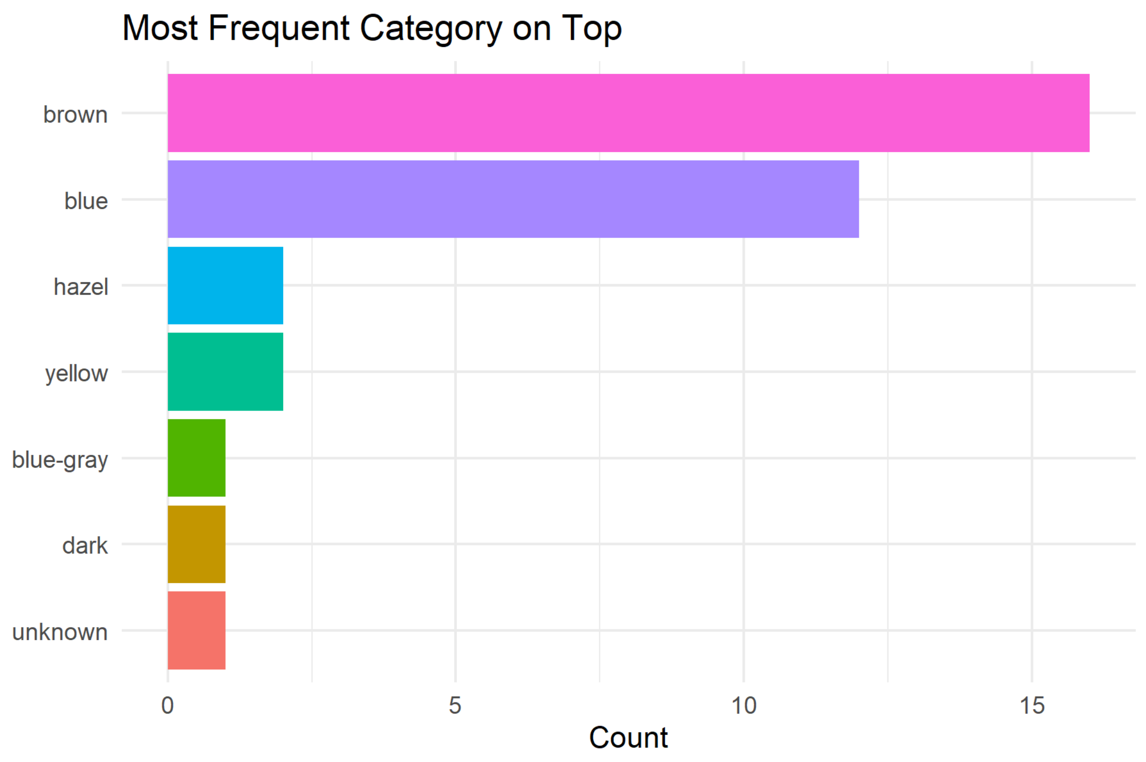
The level order determines the arrangement in graphics:

```
# Sensible order for bar chart
humans %>%
  filter(!is.na(eye_color)) %>%
  mutate(eye_color = fct_infreq(eye_color)) %>%  # By frequency
  ggplot(aes(x = eye_color, fill = eye_color)) +
  geom_bar() +
  coord_flip() +  # Horizontal bars
  labs(
    title = "Eye Colors of Star Wars Humans",
    x = NULL,
    y = "Count"
  ) +
  theme_minimal() +
  theme(legend.position = "none")
```



With horizontal bar charts, you often want the most frequent category at the top. For this, combine `fct_infreq()` with `fct_rev()`:

```
humans %>%
  filter(!is.na(eye_color)) %>%
  mutate(eye_color = fct_rev(fct_infreq(eye_color))) %>%  # Reversed
  ggplot(aes(x = eye_color, fill = eye_color)) +
  geom_bar() +
  coord_flip() +
  labs(
    title = "Most Frequent Category on Top",
    x = NULL,
    y = "Count"
  ) +
  theme_minimal() +
  theme(legend.position = "none")
```



Factors in tabyl()

`tabyl()` also respects the level order:

```r
# Without factor: alphabetical
humans %>%
  tabyl(eye_color)
```

```
 eye_color  n    percent
      blue 12 0.34285714
 blue-gray  1 0.02857143
     brown 16 0.45714286
      dark  1 0.02857143
     hazel  2 0.05714286
   unknown  1 0.02857143
    yellow  2 0.05714286
```

```r
# With factor: by our order
humans %>%
  mutate(eye_color = fct_relevel(eye_color, "brown", "blue")) %>%
  tabyl(eye_color)
```

```
 eye_color  n    percent
     brown 16 0.45714286
      blue 12 0.34285714
 blue-gray  1 0.02857143
      dark  1 0.02857143
     hazel  2 0.05714286
   unknown  1 0.02857143
    yellow  2 0.05714286
```

```r
# By frequency
humans %>%
  mutate(eye_color = fct_infreq(eye_color)) %>%
  tabyl(eye_color)
```

```
 eye_color  n    percent
     brown 16 0.45714286
      blue 12 0.34285714
     hazel  2 0.05714286
    yellow  2 0.05714286
 blue-gray  1 0.02857143
      dark  1 0.02857143
   unknown  1 0.02857143
```

This is particularly useful for reports where the order of categories should have a substantive meaning (e.g., “excellent”, “good”, “satisfactory”, “poor”).

Summary

Factors are more powerful than simple character variables because they store a defined set of categories with a specific order.

i Key Takeaways

Character vs. Factor:

Aspect	Character	Factor
Stores	Only text	Text + levels + order
Sorting	Alphabetical	By level order
Unknown values	Allowed	Become NA (if not in levels)
Use case	Free text	Categories with fixed values

When Character, When Factor?

- **Character**: Free text, names, IDs, comments
- **Factor**: Categories with defined values (gender, Likert scales, regions)

Key forcats Functions:

Function	Purpose
`fct_relevel()`	Manually reorder levels
`fct_reorder()`	Sort by numerical variable
`fct_infreq()`	Sort by frequency
`fct_rev()`	Reverse order
`fct_lump_n()`	Combine rare into "Other"
`fct_collapse()`	Combine multiple levels
`fct_recode()`	Rename levels

Typical Workflow for Graphics:

```r
data %>%
  mutate(category = fct_infreq(category)) %>%  # By frequency
  ggplot(aes(x = category)) +
  geom_bar()
```

Further Resources:

- forcats Documentation
- R for Data Science: Factors

Bibliography