R Module 2: Factors and Reshaping Data

BMSC 620 | R Workflow Series

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What We’re Learning Today

By the end of this module, you will be able to:

1. Understand the difference between **characters** and **factors** in R
2. Use **forcats** functions to reorder and relabel factor levels
3. Recognize when data is in **wide** vs. **long** format
4. Use `pivot_longer()` and `pivot_wider()` to reshape data

Note

These skills come up constantly — every time you make a plot with categories or need to restructure data for analysis.

Two Problems You've Probably Already Hit

Problem 1: You make a bar chart and the categories are in alphabetical order instead of a meaningful order.

Problem 2: You have data with multiple columns that should really be rows (or vice versa) and your `ggplot()` code won't cooperate.

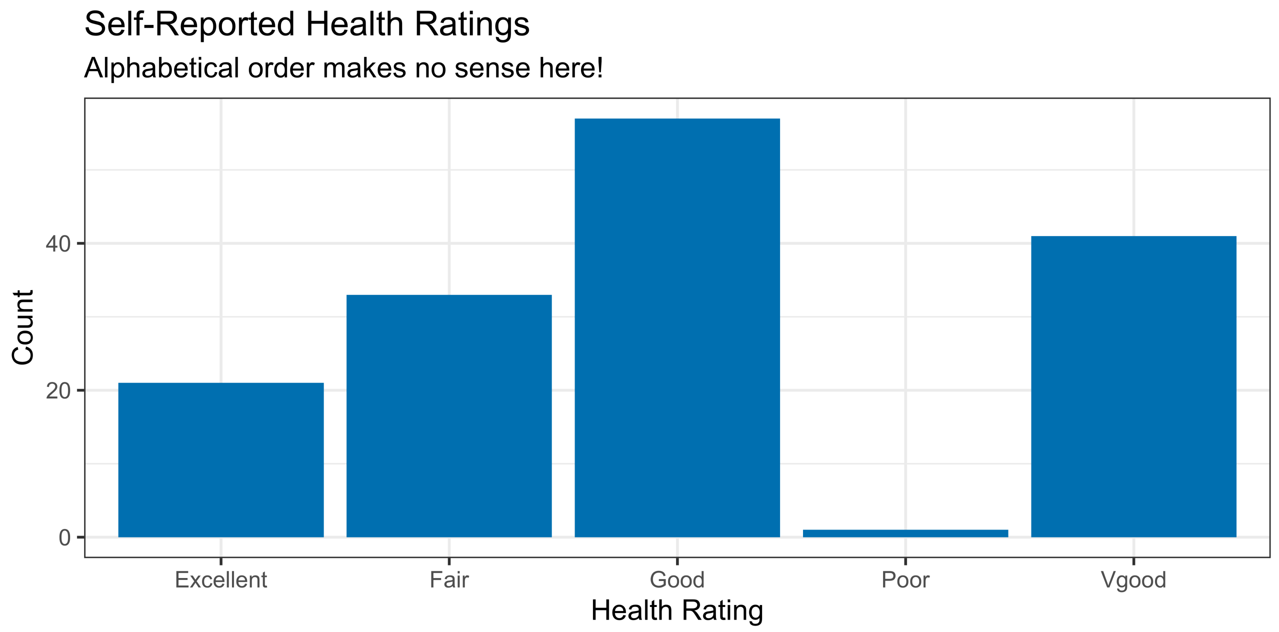
Both problems have the same root cause: R doesn't know what you know about the **structure** of your data.

Today we fix that.

Part 1: What Is a Factor?

The Motivating Bug

```r
nhanes.samp %>%
  filter(!is.na(HealthGen)) %>%
  ggplot(aes(x = HealthGen)) +
  geom_bar(fill = "#0072B2") +
  labs(title = "Self-Reported Health Ratings",
       subtitle = "Alphabetical order makes no sense here!",
       x = "Health Rating",
       y = "Count") +
  theme_bw(base_size = 16)
```



The categories are in **alphabetical order**. That’s not what we want.

Character vs. Factor

Character

- Just text — R treats it like any string
- No inherent order
- Plotted alphabetically by default

```r
class(nhanes.samp$HealthGen)
```

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

Factor

- A categorical variable with a **defined set of levels**
- Levels have an **order** (even if it's arbitrary)
- You control the order

```r
health_factor <- factor(nhanes.samp$HealthG
class(health_factor)
```

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

```r
levels(health_factor)
```

```
[1] "Excellent" "Fair"      "Good"      "Poor"
"Vgood"
```

When R converts a character to a factor automatically, it uses **alphabetical order** — which is almost never what you want.

Creating Factors with `factor()`

You can specify the exact order of levels:

```r
nhanes.samp <- nhanes.samp %>%
  mutate(
    HealthGen = factor(HealthGen,
                       levels = c("Excellent",
                                  "Vgood",
                                  "Good",
                                  "Fair",
                                  "Poor")))

levels(nhanes.samp$HealthGen)
```

```
[1] "Excellent" "Vgood"     "Good"      "Fair"      "Poor"
```

Tip

The `levels` argument defines the order. Categories not listed are set to `NA`.

Cleaning Up Labels with base R

"Vgood" isn't great for a plot or a report. We can rename it:

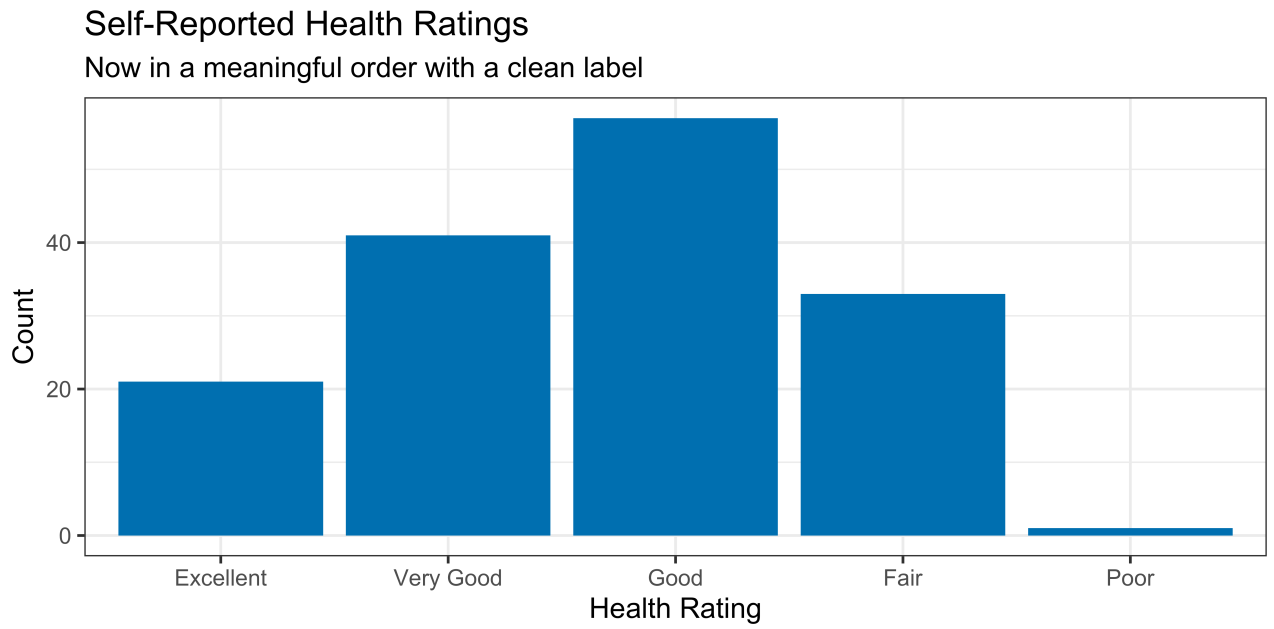
```r
# Cleaning Up Labels
nhanes.samp <- nhanes.samp %>%
  mutate(
    HealthGen = factor(HealthGen,
                       levels = c("Excellent", "Vgood", "Good", "Fair", "Poor"),
                       labels = c("Excellent", "Very Good", "Good", "Fair", "Poor"))
  )

levels(nhanes.samp$HealthGen)
```

```
[1] "Excellent" "Very Good" "Good"      "Fair"      "Poor"
```

The Fix: Ordered Factor in a Plot

```r
nhanes.samp %>%
  filter(!is.na(HealthGen)) %>%
  ggplot(aes(x = HealthGen)) +
  geom_bar(fill = "#0072B2") +
  labs(title = "Self-Reported Health Ratings",
       subtitle = "Now in a meaningful order with a clean label",
       x = "Health Rating",
       y = "Count") +
  theme_bw(base_size = 16)
```



Same code. The only thing that changed was making `HealthGen` a factor with meaningful levels.

`levels()` — Inspect and Verify

`levels()` is your diagnostic tool — use it to check that your factor is set up correctly:

```r
# What levels exist?
levels(nhanes.samp$HealthGen)
```

```
[1] "Excellent" "Very Good" "Good"      "Fair"      "Poor"
```

```r
# How many levels?
nlevels(nhanes.samp$HealthGen)
```

```
[1] 5
```

Important

Always check `levels()` after creating a factor. If the order isn't what you expect, fix it now — not after you've built plots and run models.

Part 2: The `forcats` Package

Why `forcats`?

`factor()` works, but it requires you to type out every level by hand. The `forcats` package (part of the tidyverse) gives you shortcut functions for common tasks:

Function	What it does
`fct_relevel()`	Manually reorder specific levels
`fct_reorder()`	Reorder levels by a summary statistic
`fct_infreq()`	Order levels by frequency
`fct_rev()`	Reverse the current order
`fct_recode()`	Rename levels
`fct_collapse()`	Combine levels into groups

We'll focus on `fct_relevel()` and `fct_reorder()` — the two you'll use most.

Education Is Already a Factor

`Education` was already a factor in the dataset:

```r
class(nhanes.samp$Education)
```

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

```r
levels(nhanes.samp$Education)
```

```
[1] "8th Grade"       "9 - 11th Grade" "High School"    "Some College"  
[5] "College Grad"  
```

The levels are in a reasonable order — but what if we want to change the reference category for a model, or reorder by a statistic for a plot?

That's where `forcats` comes in.

`fct_relevel()` — Manual Reordering

Move specific levels to the front, or place them at a specific position:

```r
# Move "College Grad" to the first position
nhanes.samp %>%
  mutate(Education = fct_relevel(Education, "College Grad")) %>%
  pull(Education) %>%
  levels()
```

```
[1] "College Grad"   "8th Grade"      "9 - 11th Grade" "High School"
[5] "Some College"
```

```r
# Move "College Grad" to the last position
nhanes.samp %>%
  mutate(Education = fct_relevel(Education, "College Grad", after = Inf)) %>%
  pull(Education) %>%
  levels()
```

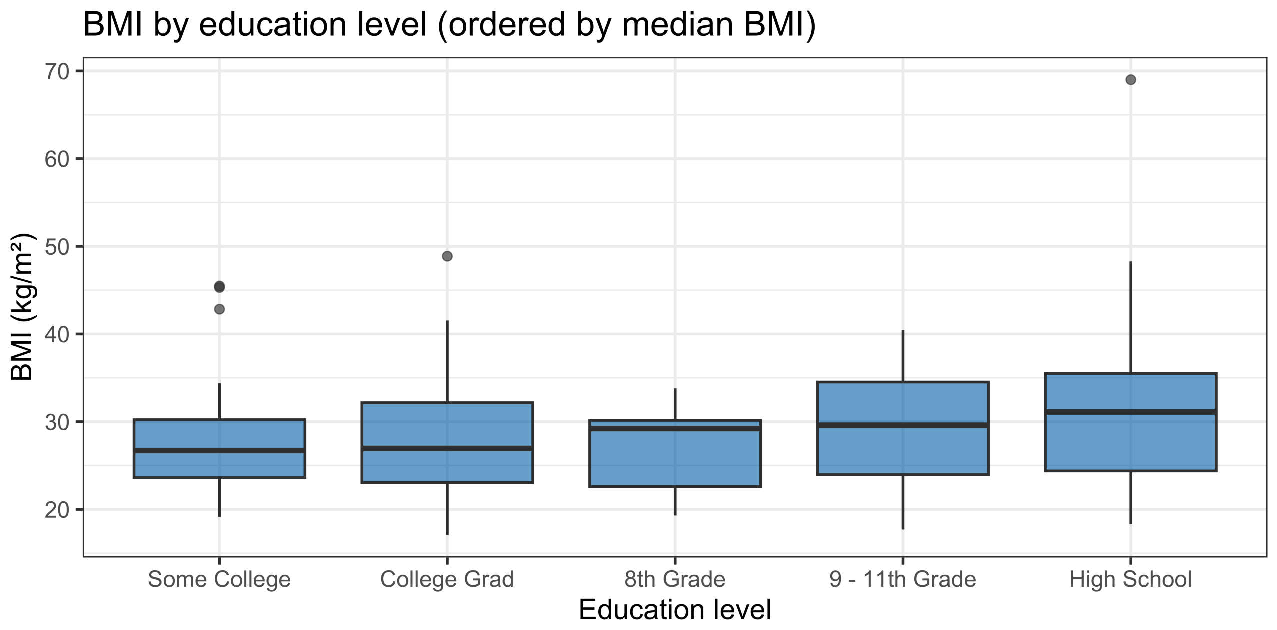
```
[1] "8th Grade"      "9 - 11th Grade" "High School"    "Some College"
[5] "College Grad"
```

`after = Inf` is the trick for "put it at the end."

`fct_reorder()` — Data-Driven Reordering

Order factor levels by a **summary statistic** of another variable. This is especially powerful for plots:

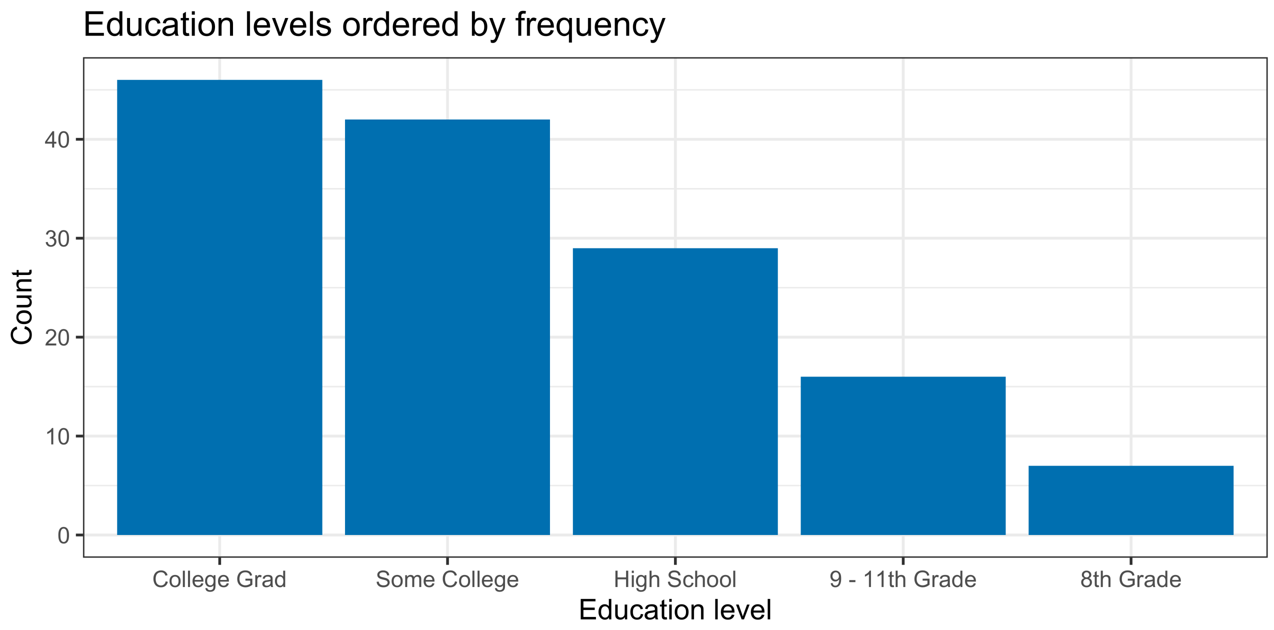
```r
nhanes.samp %>%
  filter(!is.na(Education), !is.na(BMI)) %>%
  mutate(Education = fct_reorder(Education, BMI, .fun = median)) %>%
  ggplot(aes(x = Education, y = BMI)) +
  geom_boxplot(fill = "#0072B2", alpha = 0.7) +
  labs(title = "BMI by education level (ordered by median BMI)",
       x = "Education level",
       y = "BMI (kg/m²)") +
  theme_bw(base_size = 16)
```



`fct_infreq()` — Order by Frequency

Sometimes you just want categories ordered by how often they appear:

```r
nhanes.samp %>%
  filter(!is.na(Education)) %>%
  mutate(Education = fct_infreq(Education)) %>%
  ggplot(aes(x = Education)) +
  geom_bar(fill = "#0072B2") +
  labs(title = "Education levels ordered by frequency",
       x = "Education level",
       y = "Count") +
  theme_bw(base_size = 16)
```



`fct_recode()` — Rename Levels

Sometimes level names are too long, abbreviated, or inconsistent. `fct_recode()` lets you rename them:

```r
unique(nhanes.samp$HealthGen)
```

```
[1] Fair      Very Good <NA>      Good      Excellent Poor
Levels: Excellent Very Good Good Fair Poor
```

```r
nhanes.samp %>%
  mutate(
    Education = fct_recode(Education,
                           "Some HS" = "9 - 11th Grade",
                           "HS Grad" = "High School",
                           "College" = "College Grad")
  ) %>%
  pull(Education) %>%
  levels()
```

```
[1] "8th Grade"    "Some HS"      "HS Grad"      "Some College" "College"
```

Note

- The syntax is `"new name" = "old name"`. It feels backwards at first, but it follows the same `left = right` assignment pattern as `mutate()`. Only the levels you list are renamed — the rest stay as they are.
- Unlike the `labels` argument we used earlier, `fct_recode()` lets you pick and choose. If you only want to rename one category, the others will stay exactly as they were.

Why Factors Matter for Modeling (Preview)

When you fit a regression model, R automatically creates **dummy variables** from factors. The **first level** becomes the **reference category**.

```r
# Current reference level (first in the list)
levels(nhanes.samp$Education)[1]
```

```
[1] "8th Grade"
```

```r
# Change reference to "High School"
nhanes.samp %>%
  mutate(Education = fct_relevel(Education, "High School")) %>%
  pull(Education) %>%
  levels()
```

```
[1] "High School"    "8th Grade"      "9 - 11th Grade" "Some College"  
[5] "College Grad"  
```

Note

We'll come back to this in detail when we cover regression. For now, just know that the **first factor level = reference category** in any model.

Factor Tools Summary

Creating factors

- `factor(x, levels = c(...))` — full control
- `levels()` — inspect the result
- Always verify your levels are correct

Common tasks

- Reorder for plots → `fct_reorder()` or `fct_infreq()`
- Set reference level for modeling → `fct_relevel()`
- Rename levels → `fct_recode()`

Tip

The rule of thumb:

- **For plots:** use `fct_reorder()` to order by a statistic, or `fct_infreq()` to order by count
- **For models:** use `fct_relevel()` to set your reference category

Part 3: Wide vs. Long Data

The Conceptual Shift

Most data you receive is in **wide** format — one row per subject, multiple measurement columns.

But many R operations (especially `ggplot2`) need data in **long** format — one row per observation.

Note

This is not about right vs. wrong. It's about which shape your tool expects.

What Does “Wide” Data Look Like?

Each subject is **one row**, with measurements spread across columns:

```r
nhanes_wide <- nhanes.samp %>%
  select(ID, Age, BMI, BPSysAve, BPDiaAve) %>%
  head(5)

nhanes_wide
```

```
# A tibble: 5 × 5
     ID   Age   BMI BPSysAve BPDiaAve
  <int> <int> <dbl>    <int>    <int>
1 63147    41  30        112       76
2 67852    15  19.2      107       72
3 57165    48  27.4      123       69
4 68691     7  17.4       NA       NA
5 69465    50  26.9      152      103
```

Four measurement columns: `Age`, `BMI`, `BPSysAve`, `BPDiaAve`. This is the shape you’re used to seeing.

What Does "Long" Data Look Like?

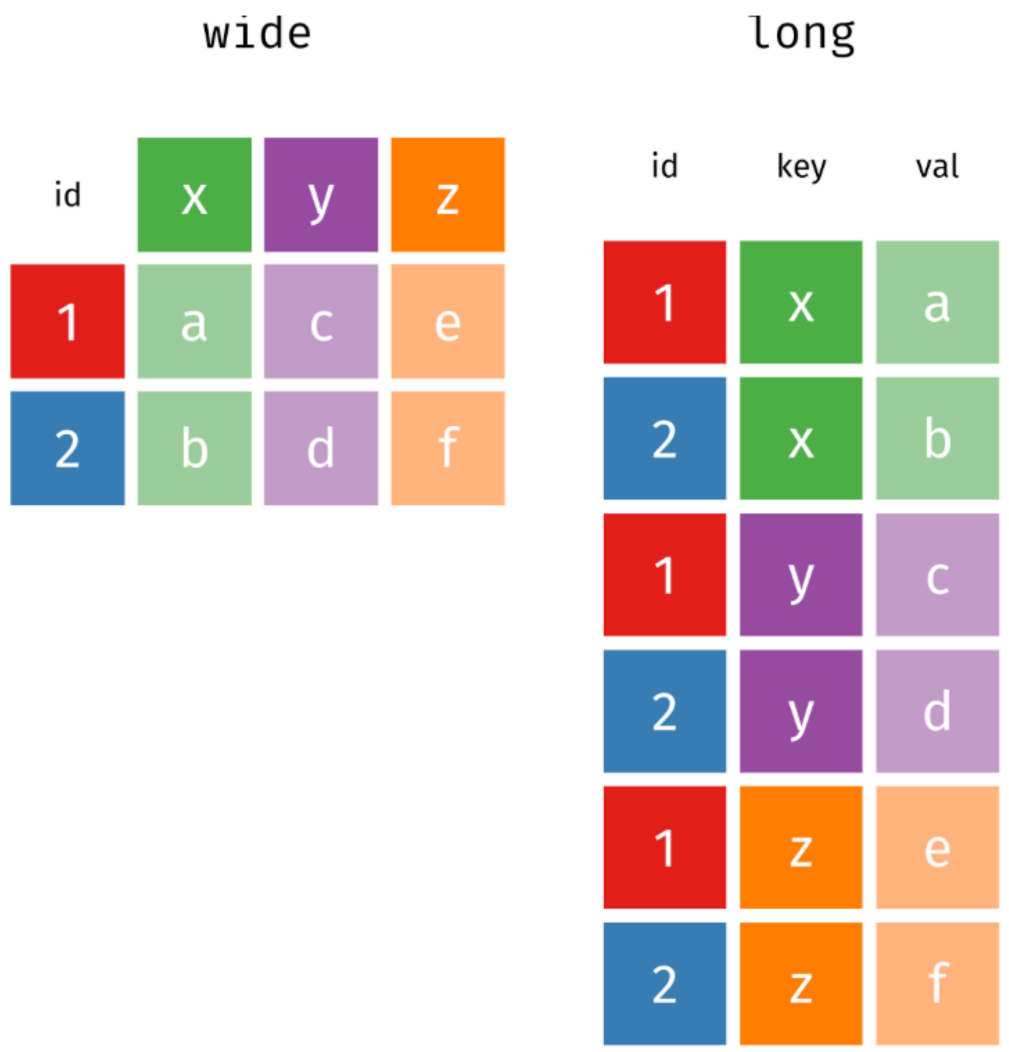
Each measurement is **its own row**:

```r
nhanes_long <- nhanes_wide %>%
  pivot_longer(
    cols = c(Age, BMI, BPSysAve, BPDiaAve),
    names_to = "measure",
    values_to = "value"
  )

nhanes_long
```

```
# A tibble: 20 × 3
      ID measure  value
   <int> <chr>    <dbl>
 1 63147 Age       41
 2 63147 BMI       30
 3 63147 BPSysAve 112
 4 63147 BPDiaAve  76
 5 67852 Age       15
 6 67852 BMI       19.2
 7 67852 BPSysAve 107
 8 67852 BPDiaAve  72
 9 57165 Age       48
10 57165 BMI       27.4
11 57165 BPSysAve 123
12 57165 BPDiaAve  69
13 68691 Age        7
14 68691 BMI       17.4
15 68691 BPSysAve  NA
```

Visualizing the Transformation (1/2)

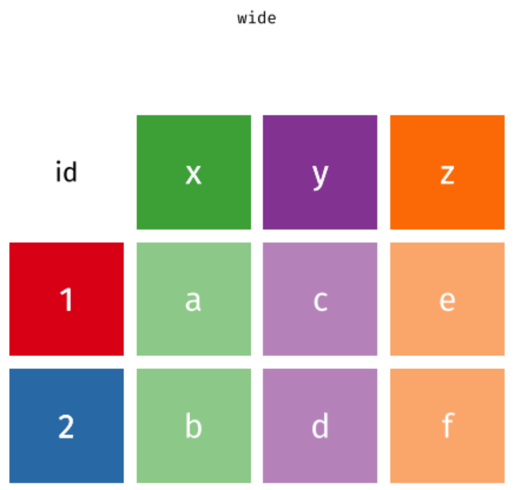


id	x	y	z
1	a	c	e
2	b	d	f

id	key	val
1	x	a
2	x	b
1	y	c
2	y	d
1	z	e
2	z	f

Visual by Garrick Aden-Buie/tidyexplain

Visualizing the Transformation (2/2)


wide

id	x	y	z
1	a	c	e
2	b	d	f

Why Does the Shape Matter?

Wide format is good for:

- Human readability
- Summary tables
- Spreadsheet-style work
- Most statistical tests in R

Long format is good for:

- `ggplot2` — faceting, color mapping
- Grouped operations with `group_by()`
- Repeated measures analysis
- Any time you want to treat variable names as data

Important

ggplot2's golden rule: if you want different variables to be distinguished by color, facet, or grouping, they usually need to be in the **same column** — which means long format.

Part 4: Pivoting

`pivot_longer()` — Wide to Long

`pivot_longer()` takes multiple columns and stacks them into two new columns: one for the **variable names** and one for the **values**.

```r
nhanes.samp %>%
  select(ID, BMI, BPSysAve, BPDiaAve) %>%
  head(4) %>%
  pivot_longer(
    cols = c(BMI, BPSysAve, BPDiaAve),        # columns to stack
    names_to = "measurement",        # new column for variable names
    values_to = "value"              # new column for the values
  )
```

```
# A tibble: 12 × 3
      ID measurement value
   <int> <chr>       <dbl>
 1 63147 BMI          30  
 2 63147 BPSysAve    112  
 3 63147 BPDiaAve     76  
 4 67852 BMI          19.2
 5 67852 BPSysAve    107  
 6 67852 BPDiaAve     72  
 7 57165 BMI          27.4
 8 57165 BPSysAve    123  
 9 57165 BPDiaAve     69  
10 68691 BMI          17.4
11 68691 BPSysAve     NA  
12 68691 BPDiaAve     NA  
```

`pivot_longer()` — The Three Arguments

```r
pivot_longer(
  cols = c(BMI, BPSysAve, BPDiaAve),     # 1. Which columns to pivot
  names_to = "measurement",              # 2. Name for the new "names" column
  values_to = "value"                    # 3. Name for the new "values" column
)
```

Argument	Question it answers
`cols`	Which columns are being stacked?
`names_to`	What should we call the column that holds the old column names?
`values_to`	What should we call the column that holds the values?

Tip

Think of it as: “I want to make this data **longer** by stacking these columns.”

`pivot_longer()` — Why the Dimensions Change

```r
nhanes_subset <- nhanes.samp %>%
  select(ID, BMI, BPSysAve, BPDiaAve)

# Wide: one row per subject
dim(nhanes_subset)
```

```
[1] 200   4
```

```r
# Long: one row per subject × measurement
nhanes_subset %>%
  pivot_longer(cols = c(BMI, BPSysAve, BPDiaAve),
               names_to = "measurement",
               values_to = "value") %>%
  dim()
```

```
[1] 600   3
```

We pivoted **3 columns**, so we get **3× the rows** and go from 4 columns down to 3 (ID + the two new columns).

pivot_wider() — Long to Wide

pivot_wider() does the reverse — it spreads rows back into columns:

```r
nhanes_long_example <- nhanes.samp %>%
  select(ID, BMI, BPSysAve, BPDiaAve) %>%
  head(4) %>%
  pivot_longer(cols = c(BMI, BPSysAve, BPDiaAve),
               names_to = "measurement",
               values_to = "value")

# Now spread it back to wide
nhanes_long_example %>%
  pivot_wider(
    names_from = "measurement",     # column whose values become new column names
    values_from = "value"           # column whose values fill the new columns
  )
```

```
# A tibble: 4 × 4
     ID   BMI BPSysAve BPDiaAve
  <int> <dbl>    <dbl>    <dbl>
1 63147  30        112       76
2 67852  19.2      107       72
3 57165  27.4      123       69
4 68691  17.4       NA       NA
```

`pivot_wider()` — The Two Arguments

```r
pivot_wider(
  names_from = "measurement",     # 1. Which column has the new column names?
  values_from = "value"           # 2. Which column has the values to fill in?
)
```

Argument	Question it answers
`names_from`	Which column's values should become new column names?
`values_from`	Which column's values should fill those new columns?

Tip

Think of it as: "I want to make this data **wider** by spreading this column into multiple columns."

Putting It Together: Pivot → Plot

A Three-Step Workflow

Suppose we want to compare the distributions of `BMI`, `BPSysAve`, and `BPDiaAve` side by side. In wide format, this is awkward. In long format, it's one `ggplot()` call:

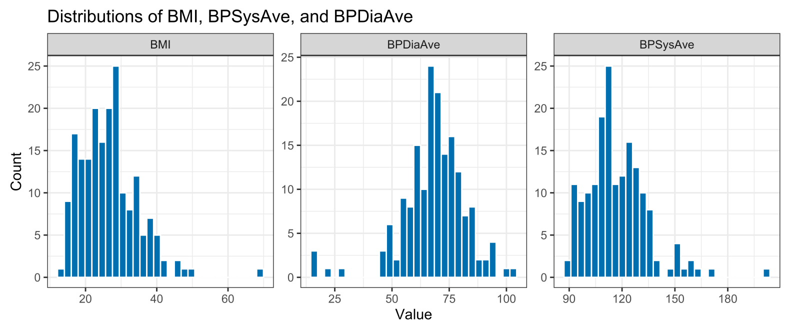
Step 1: Select the relevant columns

Step 2: Pivot to long format

Step 3: Plot with faceting

Pivot → Plot in Action

```r
nhanes.samp %>%
  select(ID, BMI, BPSysAve, BPDiaAve) %>%
  pivot_longer(
    cols = c(BMI, BPSysAve, BPDiaAve),
    names_to = "measurement",
    values_to = "value"
  ) %>%
  ggplot(aes(x = value)) +
  geom_histogram(bins = 30, fill = "#0072B2", color = "white") +
  facet_wrap(~ measurement, scales = "free") +
  labs(title = "Distributions of BMI, BPSysAve, and BPDiaAve",
       x = "Value",
       y = "Count") +
  theme_bw(base_size = 16)
```



One pipeline. Three plots. This is why reshaping matters.

Key Takeaways

Factors

- Characters have no order — factors do
- `factor(x, levels = ...)` for full control
- `fct_reorder()` for data-driven plot ordering
- `fct_relevel()` to set reference categories

Reshaping

- Wide = one row per subject, many measurement columns
- Long = one row per observation
- `pivot_longer()` — wide to long (for plotting, grouping)
- `pivot_wider()` — long to wide (for tables, summaries)

Tip

The rules:

Factors: If your plot categories are in the wrong order, it's a factor problem.

Reshaping: If `ggplot` wants your data in a different shape, pivot it.

References

Factors

- R for Data Science: Factors
- forcats documentation
- Be the boss of your factors — STAT 545

Reshaping data

- R for Data Science: Pivoting
- tidyr documentation
- Garrick Aden-Buie’s site — excellent visual explanations