```
> # Load wine dataset
> wine <- read_csv("wine_dataset.csv")
Rows: 178 Columns: 14
── Column specification ────────────────────────────────────────────────────────
Delimiter: ","
dbl (14): alcohol, malic_acid, ash, alcalinity_of_ash, magnesium, total_ph...

ℹ Use `spec()` to retrieve the full column specification for this data.
ℹ Specify the column types or set `show_col_types = FALSE` to quiet this message.
> # Inspect structure
> head(wine)
# A tibble: 6 × 14
  alcohol malic_acid   ash alcalinity_of_ash magnesium total_phenols
    <dbl>      <dbl> <dbl>             <dbl>     <dbl>         <dbl>
1    14.2       1.71  2.43              15.6       127          2.8
2    13.2       1.78  2.14              11.2       100          2.65
3    13.2       2.36  2.67              18.6       101          2.8
4    14.4       1.95  2.5               16.8       113          3.85
5    13.2       2.59  2.87              21         118          2.8
6    14.2       1.76  2.45              15.2       112          3.27
# ℹ 8 more variables: flavanoids <dbl>, nonflavanoid_phenols <dbl>,
#   proanthocyanins <dbl>, color_intensity <dbl>, hue <dbl>,
#   `od280/od315_of_diluted_wines` <dbl>, proline <dbl>, target <dbl>
> glimpse(wine)
Rows: 178
Columns: 14
$ alcohol                         <dbl> 14.23, 13.20, 13.16, 14.37, 13.24, 14…
$ malic_acid                      <dbl> 1.71, 1.78, 2.36, 1.95, 2.59, 1.76, 1…
$ ash                             <dbl> 2.43, 2.14, 2.67, 2.50, 2.87, 2.45, 2…
$ alcalinity_of_ash               <dbl> 15.6, 11.2, 18.6, 16.8, 21.0, 15.2, 1…
```

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SUBJECT - Data Analysis with SAS / SPSS / R

```
> glimpse(wine)
Rows: 178
Columns: 14
$ alcohol                         <dbl> 14.23, 13.20, 13.16, 14.37, 13.24, 14…
$ malic_acid                      <dbl> 1.71, 1.78, 2.36, 1.95, 2.59, 1.76, 1…
$ ash                             <dbl> 2.43, 2.14, 2.67, 2.50, 2.87, 2.45, 2…
$ alcalinity_of_ash               <dbl> 15.6, 11.2, 18.6, 16.8, 21.0, 15.2, 1…
$ magnesium                       <dbl> 127, 100, 101, 113, 118, 112, 96, 121…
$ total_phenols                   <dbl> 2.80, 2.65, 2.80, 3.85, 2.80, 3.27, 2…
$ flavanoids                      <dbl> 3.06, 2.76, 3.24, 3.49, 2.69, 3.39, 2…
$ nonflavanoid_phenols            <dbl> 0.28, 0.26, 0.30, 0.24, 0.39, 0.34, 0…
$ proanthocyanins                 <dbl> 2.29, 1.28, 2.81, 2.18, 1.82, 1.97, 1…
$ color_intensity                 <dbl> 5.64, 4.38, 5.68, 7.80, 4.32, 6.75, 5…
$ hue                             <dbl> 1.04, 1.05, 1.03, 0.86, 1.04, 1.05, 1…
$ `od280/od315_of_diluted_wines`  <dbl> 3.92, 3.40, 3.17, 3.45, 2.93, 2.85, 3…
$ proline                         <dbl> 1065, 1050, 1185, 1480, 735, 1450, 12…
$ target                          <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0…
> # Sort by alcohol content (lowest first)
> wine_sorted_alcohol <- wine |>
+   arrange(alcohol)
> head(wine_sorted_alcohol, 5)
# A tibble: 5 × 14
  alcohol malic_acid   ash alcalinity_of_ash magnesium total_phenols
    <dbl>      <dbl> <dbl>             <dbl>     <dbl>          <dbl>
1    11.0       1.51  2.2               21.5        85           2.46
2    11.4       0.74  2.5               21          88           2.48
3    11.4       2.4   2.42              20          96           2.9
4    11.5       3.74  1.82              19.5       107           3.18
5    11.6       2.05  3.23              28.5       119           3.18
# i 8 more variables: flavanoids <dbl>, nonflavanoid_phenols <dbl>,
```

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```
# ℹ 8 more variables: flavanoids <dbl>, nonflavanoid_phenols <dbl>,
#   proanthocyanins <dbl>, color_intensity <dbl>, hue <dbl>,
#   `od280/od315_of_diluted_wines` <dbl>, proline <dbl>, target <dbl>
> # Sort by quality (highest quality wines first)
> wine_sorted_quality_desc <- wine |>
+   arrange(desc(quality))
```

```
Error in `arrange()`:
ℹ In argument: `..1 = quality`.
Caused by error:
! object 'quality' not found
Run `rlang::last_trace()` to see where the error occurred.
```

```
> head(wine_sorted_quality_desc, 5)
```

```
Error: object 'wine_sorted_quality_desc' not found
```

Show Traceback
Rerun with Debug

```
> # Sort by type of acid: first fixed acidity ascending,
> # then within each group sort by volatile acidity descending
> wine_multi_sort <- wine |>
+   arrange(fixed.acidity, desc(volatile.acidity))
```

```
Error in `arrange()`:
ℹ In argument: `..1 = fixed.acidity`.
Caused by error:
! object 'fixed.acidity' not found
Run `rlang::last_trace()` to see where the error occurred.
```

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```
Error in `arrange()`:
i In argument: `..1 = fixed.acidity`.
Caused by error:
! object 'fixed.acidity' not found
Run `rlang::last_trace()` to see where the error occurred.
```

```
> head(wine_multi_sort, 10)
```

```
Error: object 'wine_multi_sort' not found
```

Show Traceback
Rerun with Debug

```
> # Filter wines with high alcohol content (> 12%)
> # Then sort by sulphates (ascending)
> high_alcohol_sorted <- wine |>
+   filter(alcohol > 12) |>
+   arrange(sulphates)
```

```
Error in `arrange()`:
i In argument: `..1 = sulphates`.
Caused by error:
! object 'sulphates' not found
Run `rlang::last_trace()` to see where the error occurred.
```

```
> cat("Top 5 high-alcohol wines with lowest sulphates:\n")
Top 5 high-alcohol wines with lowest sulphates:
> high_alcohol_sorted |>
```

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