You know it, I'm sure: You are developing a data transformation using lots of pipes. Then you need to remove one or more lines. You do this using comments.

So far so good. But if it's the last line you want to remove a simple comment will produce an error because of the trailing pipe symbol at the end of the second to last line.

Here's a solution:

Pipes

Magrittr

Let's say you are computing something like this:

```
 1  options(tidyverse.quiet = TRUE)
 2  library(tidyverse)
 3  options(dplyr.summarise.inform = FALSE)
 4
 5  starwars %>%
 6    mutate(
 7     mean_height = mean(height, na.rm = TRUE)
 8    ) %>%
 9    group_by(species, gender) %>%
10    summarize(
11      mean_height_species_gender = mean(height, na.rm = TRUE),
12      mean_height = first(mean_height)
13    ) %>%
14    mutate(
15      diff_mean_height = mean_height_species_gender - mean_height
16    ) %>%
17    select(gender, species, diff_mean_height) %>%
18    pivot_wider(names_from = 'gender', values_from = 'diff_mean_height',
    values_fill = NA)
```

```
 1  ## # A tibble: 38 x 4
 2  ## # Groups:    species [38]
 3  ##     species    masculine feminine  `NA`
 4  ##     <chr>          <dbl>    <dbl> <dbl>
 5  ##  1 Aleena         -95.4       NA    NA
 6  ##  2 Besalisk        23.6       NA    NA
 7  ##  3 Cerean          23.6       NA    NA
 8  ##  4 Chagrian        21.6       NA    NA
 9  ##  5 Clawdite         NA     -6.36    NA
10  ##  6 Droid          -34.4    -78.4    NA
11  ##  7 Dug            -62.4       NA    NA
12  ##  8 Ewok           -86.4       NA    NA
13  ##  9 Geonosian        8.64      NA    NA
14  ## 10 Gungan          34.3       NA    NA
15  ## # … with 28 more rows
```

Now you want to skip the last step pivoting the result. If you just comment out the last line, you'll get an error:

```
1  starwars %>%
2    mutate(
3     mean_height = mean(height, na.rm = TRUE)
4    ) %>%
5    group_by(species, gender) %>%
6    summarize(
7      mean_height_species_gender = mean(height, na.rm = TRUE),
8      mean_height = first(mean_height)
9    ) %>%
10   mutate(
11     diff_mean_height = mean_height_species_gender - mean_height
12   ) %>%
13   select(gender, species, diff_mean_height) %>%
14   # pivot_wider(names_from = 'gender', values_from = 'diff_mean_height',
   values_fill = NA)
```

```
1  ## Error: <text>:15:0: unexpected end of input
2  ## 13:   select(gender, species, diff_mean_height) %>%
3  ## 14:   # pivot_wider(names_from = 'gender', values_from =
   'diff_mean_height', values_fill = NA)
4  ##      ^
```

But if you use `identity()` as your last step everything is fine:

```
1  starwars %>%
2    mutate(
3     mean_height = mean(height, na.rm = TRUE)
4    ) %>%
5    group_by(species, gender) %>%
6    summarize(
7      mean_height_species_gender = mean(height, na.rm = TRUE),
8      mean_height = first(mean_height)
9    ) %>%
10   mutate(
11     diff_mean_height = mean_height_species_gender - mean_height
12   ) %>%
13   select(gender, species, diff_mean_height) %>%
14   # pivot_wider(names_from = 'gender', values_from = 'diff_mean_height',
   values_fill = NA) %>%
15   identity()
```

```
1  ## # A tibble: 42 x 3
2  ## # Groups:   species [38]
3  ##    gender    species   diff_mean_height
4  ##    <chr>     <chr>              <dbl>
5  ##  1 masculine Aleena             -95.4
```

```
 6 ##  2 masculine Besalisk          23.6
 7 ##  3 masculine Cerean            23.6
 8 ##  4 masculine Chagrian          21.6
 9 ##  5 feminine  Clawdite          -6.36
10 ##  6 feminine  Droid            -78.4
11 ##  7 masculine Droid            -34.4
12 ##  8 masculine Dug              -62.4
13 ##  9 masculine Ewok             -86.4
14 ## 10 masculine Geonosian          8.64
15 ## # … with 32 more rows
```

Base R (R >= 4.1.0)

This trick will also work with the new base R pipes:

```
 1  starwars |>
 2    mutate(
 3     mean_height = mean(height, na.rm = TRUE)
 4    ) |>
 5    group_by(species, gender) |>
 6    summarize(
 7      mean_height_species_gender = mean(height, na.rm = TRUE),
 8      mean_height = first(mean_height)
 9    ) |>
10    mutate(
11      diff_mean_height = mean_height_species_gender - mean_height
12    ) |>
13    select(gender, species, diff_mean_height) |>
14    # pivot_wider(names_from = 'gender', values_from = 'diff_mean_height',
15  values_fill = NA) |>
    identity()
```

```
 1 ## # A tibble: 42 x 3
 2 ## # Groups:   species [38]
 3 ##    gender    species   diff_mean_height
 4 ##    <chr>     <chr>                <dbl>
 5 ##  1 masculine Aleena             -95.4
 6 ##  2 masculine Besalisk            23.6
 7 ##  3 masculine Cerean              23.6
 8 ##  4 masculine Chagrian            21.6
 9 ##  5 feminine  Clawdite            -6.36
10 ##  6 feminine  Droid              -78.4
11 ##  7 masculine Droid              -34.4
12 ##  8 masculine Dug                -62.4
13 ##  9 masculine Ewok               -86.4
14 ## 10 masculine Geonosian            8.64
15 ## # … with 32 more rows
```
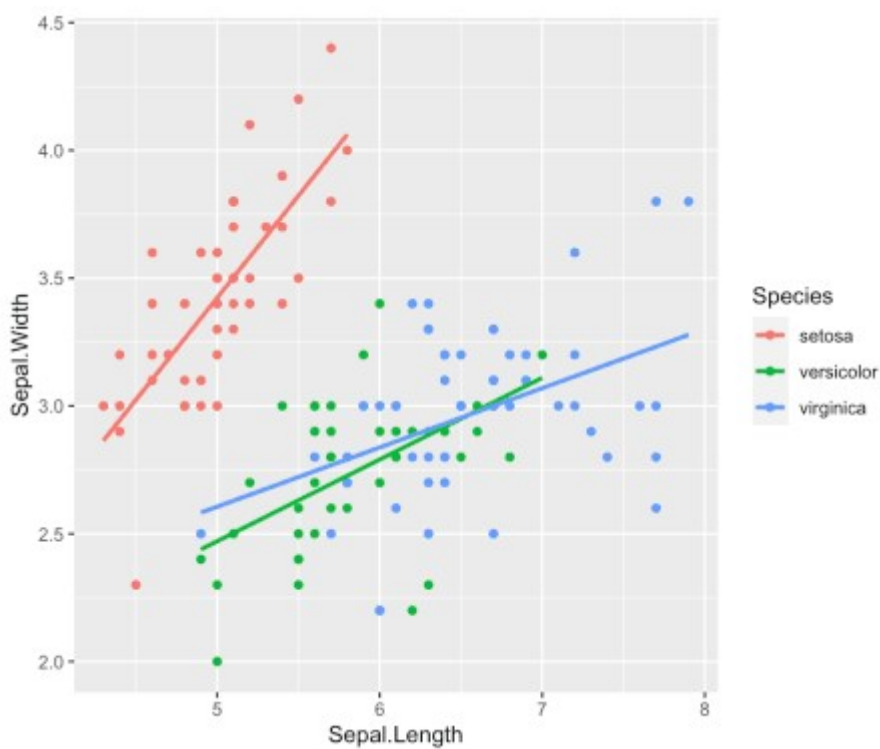
ggplot2

The same problem may occur building ggplots:

```
1  iris %>%
2    ggplot(aes(Sepal.Length, Sepal.Width, color = Species, group = Species)) +
3    geom_point() +
4    geom_smooth(method = "lm", se = FALSE, formula = "y ~ x") +
5    # facet_wrap(~Species) +
6    NULL
```


As you can see, I've added NUL1 at the end of the ggplot2-pipe. So I comment out the line
before without trouble.