Class 05: Data Visualization with GGPLOT

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background

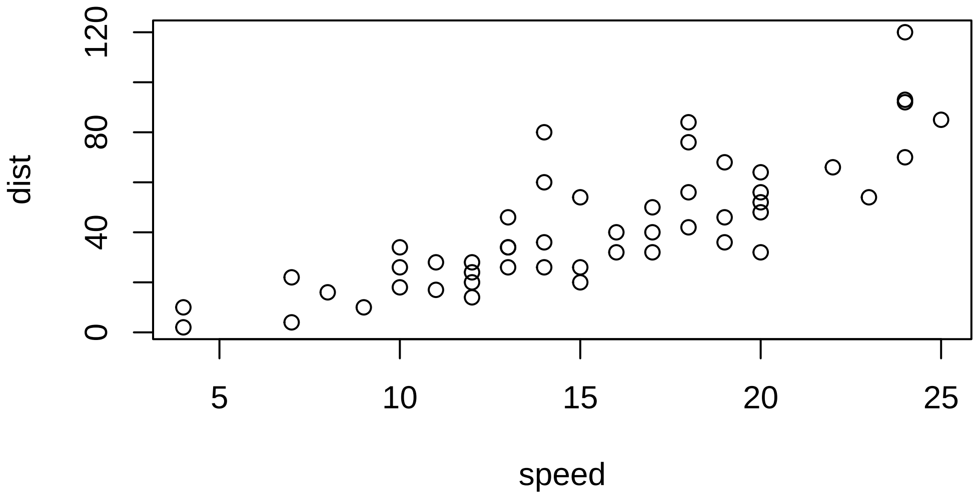
there are lots of ways to make plots in R these include so called base R like the `plot()` and add packages like **ggplot2**

same plot diff sysyems use `cars`

```
head(cars)
```

```
  speed dist
1     4    2
2     4   10
3     7    4
4     7   22
5     8   16
6     9   10
```

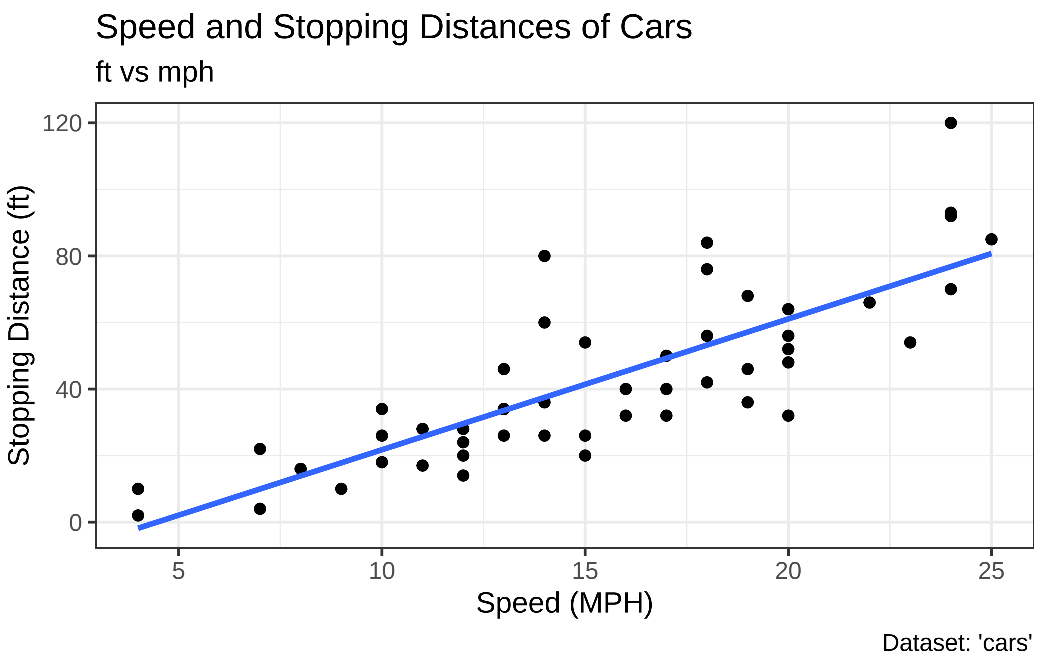
```
plot(cars)
```



first instiall `install.packages("ggplot2")` >**never run an install packages in code chunk bc will re install every render** when use add-on pkg need to load w `library()` every ggplot needs 3 things - data (eg data frame) - aes (map data to plot) - geom (plot type, lines etc)

```r
library(ggplot2)

#coment

ggplot(cars) +
  aes(x=speed, y=dist) +
  geom_point() +
  labs(title="Speed and Stopping Distances of Cars",
       x="Speed (MPH)",
       y="Stopping Distance (ft)",
       subtitle = "ft vs mph",
       caption="Dataset: 'cars'") +
  geom_smooth(method="lm", se=FALSE) +
  theme_bw()
```

```
`geom_smooth()` using formula = 'y ~ x'
```



aes

```
url <- "https://bioboot.github.io/bimm143_S20/class-material/up_down_expression.txt"
genes <- read.delim(url)
head(genes)
```

```
        Gene Condition1 Condition2      State
1      A4GNT -3.6808610 -3.4401355 unchanging
2       AAAS  4.5479580  4.3864126 unchanging
3      AASDH  3.7190695  3.4787276 unchanging
4       AATF  5.0784720  5.0151916 unchanging
5       AATK  0.4711421  0.5598642 unchanging
6 AB015752.4 -3.6808610 -3.5921390 unchanging
```

```
nrow(genes)
```

```
[1] 5196
```

```
colnames (genes)
```

```
[1] "Gene"       "Condition1" "Condition2" "State"
```

```r
ncol(genes)
```

```
[1] 4
```

```r
table(genes$State)
```

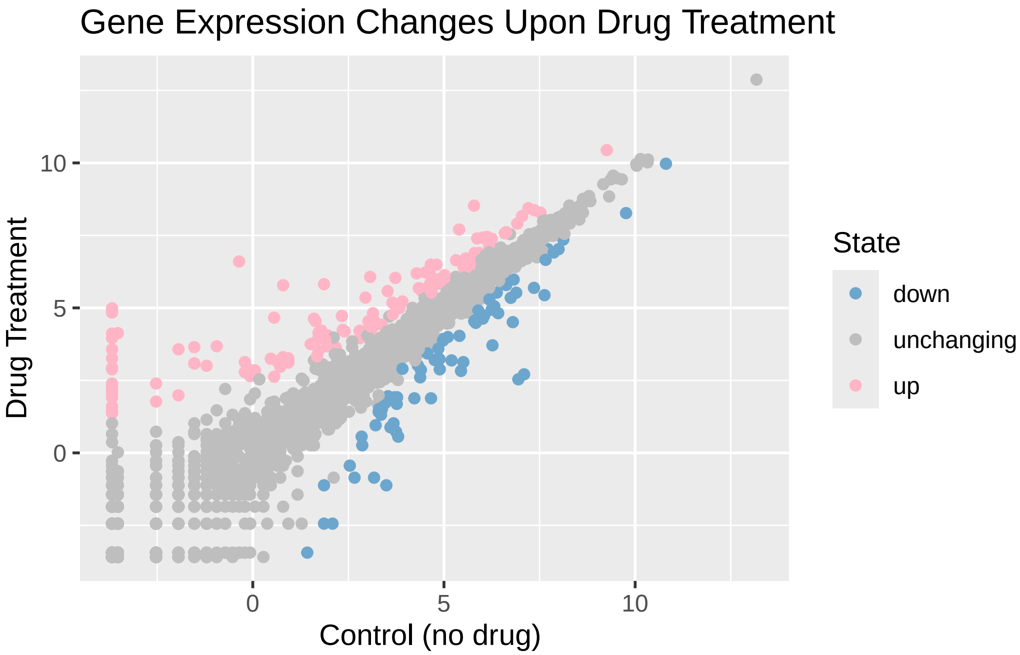
```

      down unchanging         up 
        72       4997        127 
```

```r
127/5196
```

```
[1] 0.02444188
```

plot

```r
p <- ggplot(genes) +
    aes(x=Condition1, y=Condition2, col=State) +
    geom_point()
p + scale_colour_manual(values=c("skyblue3","gray","pink1")) +
    labs(title="Gene Expression Changes Upon Drug Treatment",
         x="Control (no drug) ",
         y="Drug Treatment")
```



gapminder install `install.packages("gapminder")`

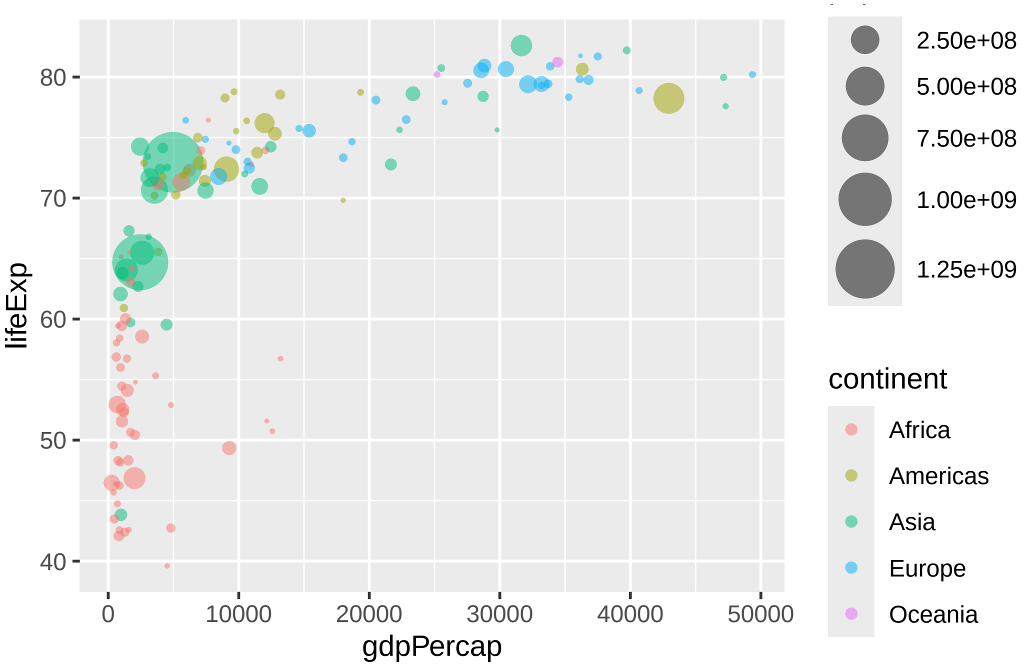
```
library(gapminder)
```

- dplyr *itals* **bold**

```
# install.packages("dplyr")  ## un-comment to install if needed
library(dplyr)
```

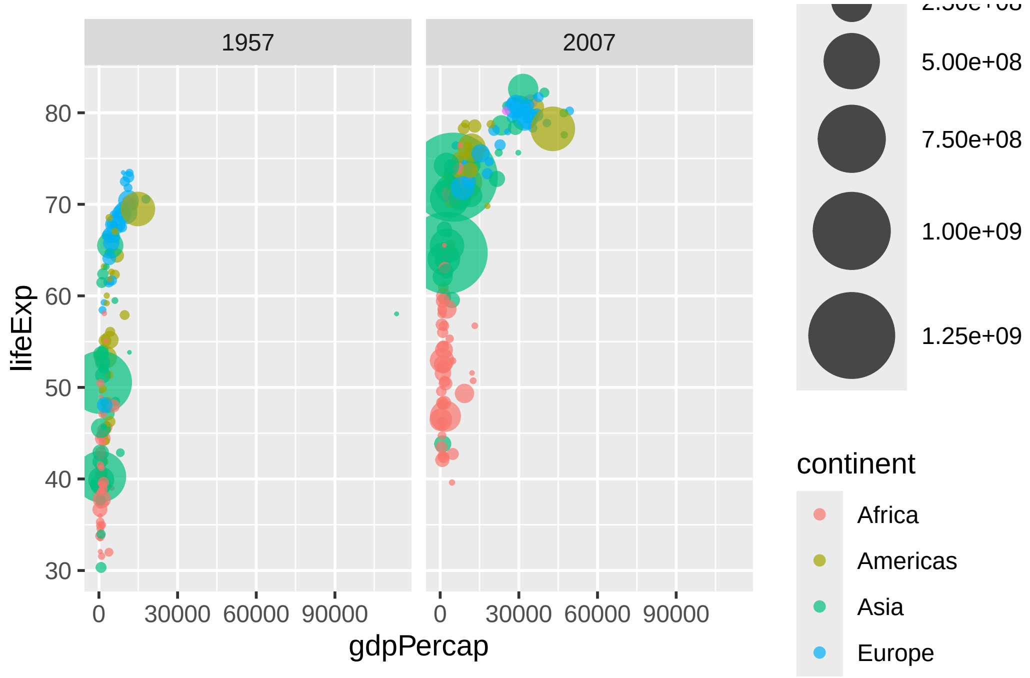
```

Attaching package: 'dplyr'

The following objects are masked from 'package:stats':

    filter, lag

The following objects are masked from 'package:base':

    intersect, setdiff, setequal, union
```

```
gapminder_2007 <- gapminder %>% filter(year==2007)

ggplot(gapminder_2007) +
  geom_point(aes(x=gdpPercap, y=lifeExp, color = continent, size = pop), alpha=.5) +
scale_size_area(max_size = 10)
```



1957

```
gapminder_1957 <- gapminder %>% filter(year==1957 | year==2007)

ggplot(gapminder_1957) +
  geom_point(aes(x=gdpPercap, y=lifeExp, color = continent, size = pop), alpha=.7) +
scale_size_area(max_size = 15)+
  facet_wrap(~year)
```

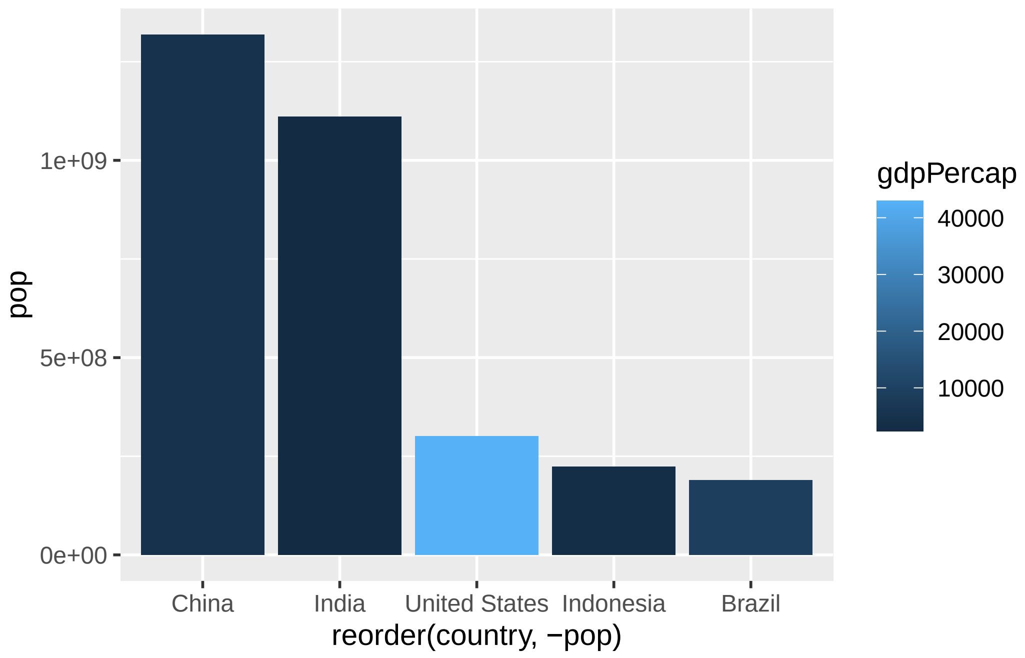


bars

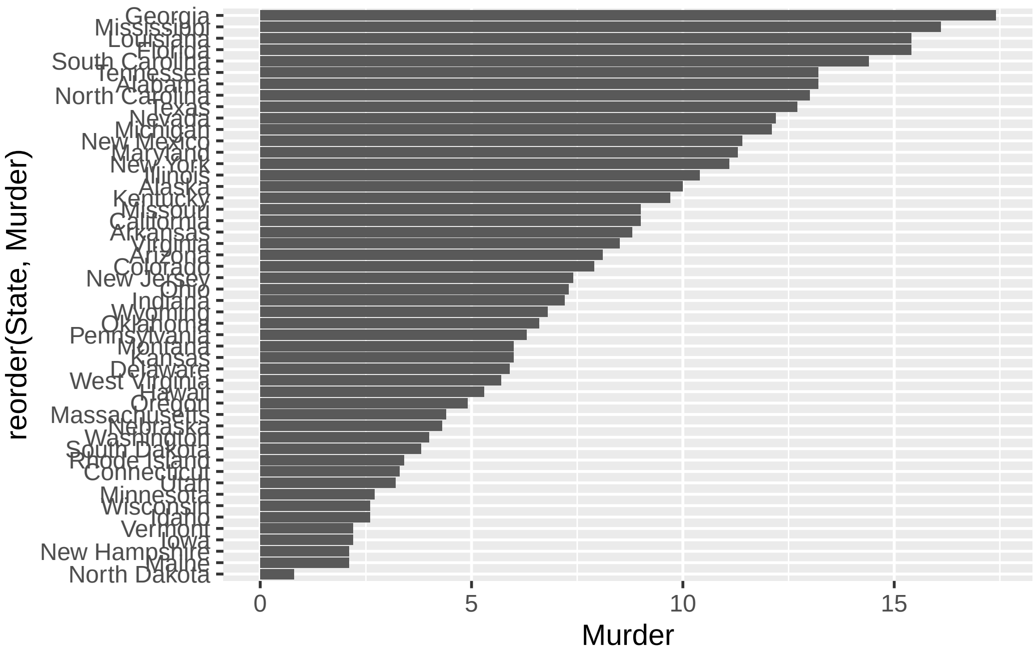
```
gapminder_top5 <- gapminder %>%
  filter(year==2007) %>%
  arrange(desc(pop)) %>%
  top_n(5, pop)

gapminder_top5
```

```
# A tibble: 5 x 6
  country       continent  year lifeExp        pop gdpPercap
  <fct>         <fct>     <int>   <dbl>      <int>     <dbl>
1 China         Asia       2007    73.0 1318683096     4959.
2 India         Asia       2007    64.7 1110396331     2452.
3 United States Americas   2007    78.2  301139947    42952.
4 Indonesia     Asia       2007    70.6  223547000     3541.
5 Brazil        Americas   2007    72.4  190010647     9066.
```

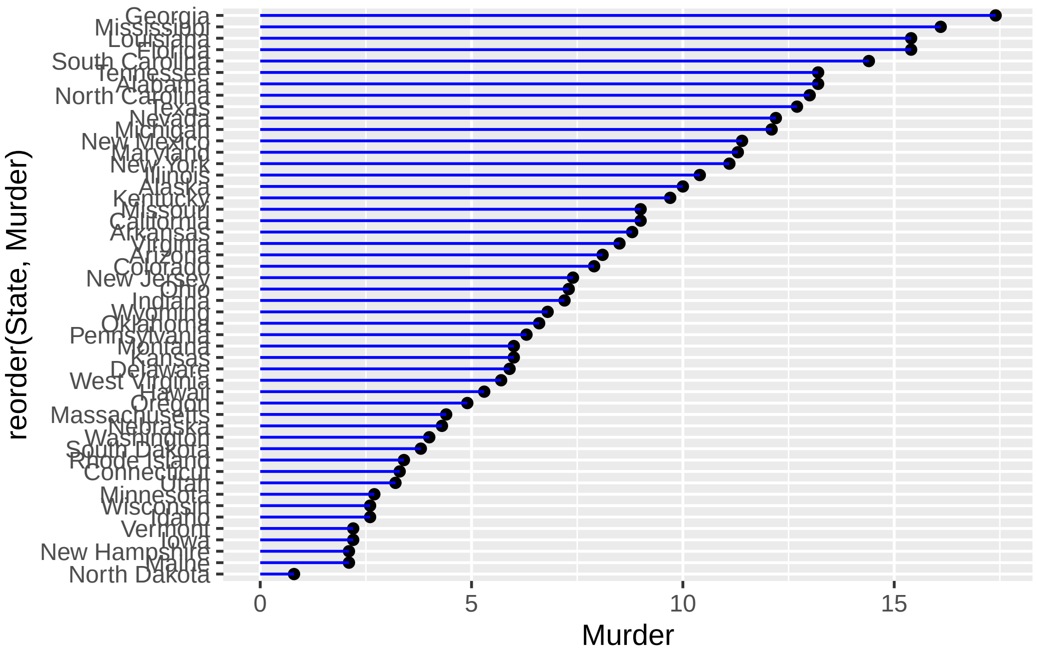
```
ggplot(gapminder_top5) +
  aes(x=reorder(country, -pop), y=pop, fill=gdpPercap) +
  geom_col()
```



```
USArrests$State <- rownames(USArrests)
ggplot(USArrests) +
  aes(x=reorder(State,Murder), y=Murder) +
  geom_col() +
  coord_flip()
```



```r
ggplot(USArrests) +
  aes(x=reorder(State,Murder), y=Murder) +
  geom_point() +
  geom_segment(aes(x=State,
                   xend=State,
                   y=0,
                   yend=Murder), color="blue") +
  coord_flip()
```



ani `install.packages("gifski")` `install.packages("gganimate")`

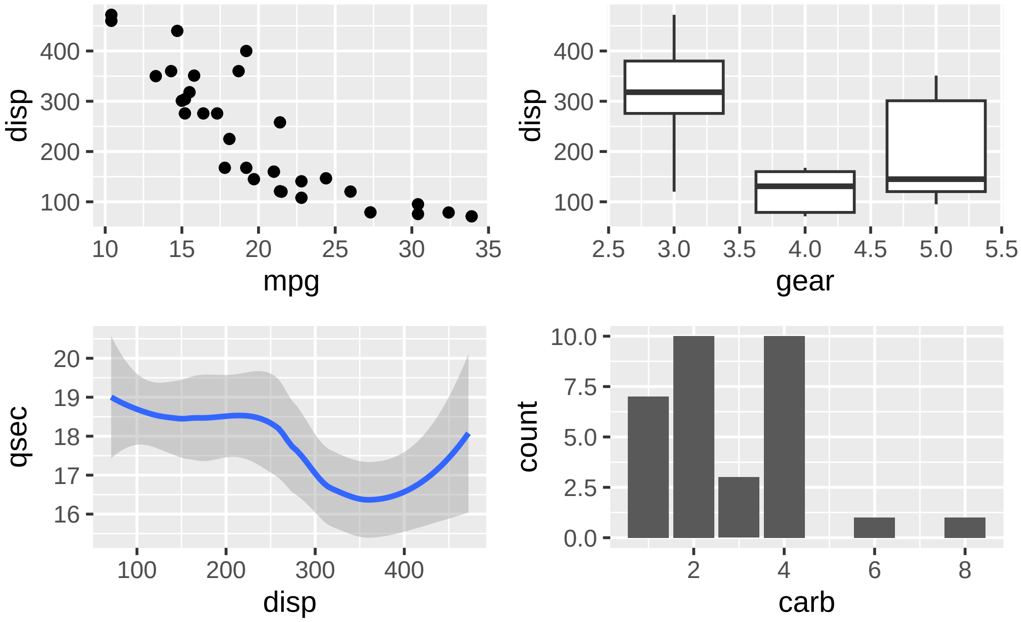
```
library(gapminder)
library(gganimate)
"
# Setup nice regular ggplot of the gapminder data
ggplot(gapminder, aes(gdpPercap, lifeExp, size = pop, colour = country)) +
  geom_point(alpha = 0.7, show.legend = FALSE) +
  scale_colour_manual(values = country_colors) +
  scale_size(range = c(2, 12)) +
  scale_x_log10() +
  # Facet by continent
  facet_wrap(~continent) +
  # Here comes the gganimate specific bits
  labs(title = 'Year: {frame_time}', x = 'GDP per capita', y = 'life expectancy') +
  transition_time(year) +
  shadow_wake(wake_length = 0.1, alpha = FALSE)
  "
```

```
[1] "\n# Setup nice regular ggplot of the gapminder data\nggplot(gapminder, aes(gdpPercap, li
```

patchwork `install.packages("patchwork")`

```r
library(patchwork)

# Setup some example plots
p1 <- ggplot(mtcars) + geom_point(aes(mpg, disp))
p2 <- ggplot(mtcars) + geom_boxplot(aes(gear, disp, group = gear))
p3 <- ggplot(mtcars) + geom_smooth(aes(disp, qsec))
p4 <- ggplot(mtcars) + geom_bar(aes(carb))

# Use patchwork to combine them here:
(p1 | p2 ) /
     (p3|p4)
```

```
`geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```



```r
sessionInfo()
```

```
R version 4.5.2 (2025-10-31)
Platform: aarch64-apple-darwin20
Running under: macOS Sequoia 15.6.1

Matrix products: default
```

```
BLAS:   /System/Library/Frameworks/Accelerate.framework/Versions/A/Frameworks/vecLib.framewo
LAPACK: /Library/Frameworks/R.framework/Versions/4.5-arm64/Resources/lib/libRlapack.dylib;

locale:
[1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8

time zone: America/Los_Angeles
tzcode source: internal

attached base packages:
[1] stats     graphics  grDevices utils     datasets  methods   base

other attached packages:
[1] patchwork_1.3.2  gganimate_1.0.11 dplyr_1.1.4      gapminder_1.0.1
[5] ggplot2_4.0.1

loaded via a namespace (and not attached):
 [1] Matrix_1.7-4       gtable_0.3.6       jsonlite_2.0.0     crayon_1.5.3
 [5] compiler_4.5.2     tidyselect_1.2.1   progress_1.2.3     splines_4.5.2
 [9] scales_1.4.0       yaml_2.3.12        fastmap_1.2.0      lattice_0.22-7
[13] R6_2.6.1           labeling_0.4.3     generics_0.1.4     knitr_1.51
[17] tibble_3.3.1       pillar_1.11.1      RColorBrewer_1.1-3 rlang_1.1.7
[21] utf8_1.2.6         stringi_1.8.7      xfun_0.55          S7_0.2.1
[25] cli_3.6.5          tweenr_2.0.3       withr_3.0.2        magrittr_2.0.4
[29] mgcv_1.9-3         digest_0.6.39      grid_4.5.2         rstudioapi_0.18.0
[33] hms_1.1.4          lifecycle_1.0.5    nlme_3.1-168       prettyunits_1.2.0
[37] vctrs_0.7.0        evaluate_1.0.5     glue_1.8.0         farver_2.1.2
[41] gifski_1.32.0-2    rmarkdown_2.30     tools_4.5.2        pkgconfig_2.0.3
[45] htmltools_0.5.9
```