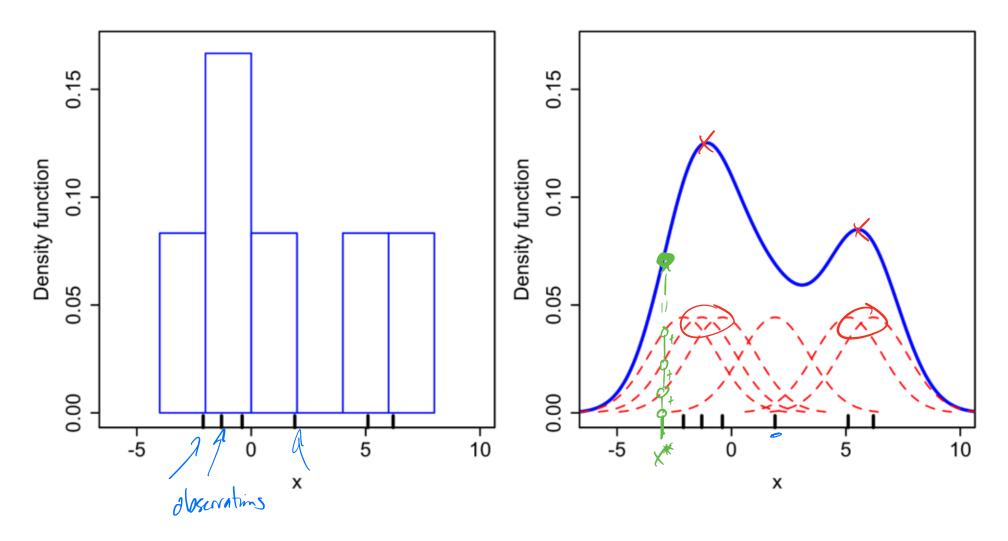
#### Kernel density estimation

**Goal**: estimate PDF f(x) for all possible values (assuming it is continuous & smooth)

Kernel density estimate: 
$$\hat{f}(x) = \frac{1}{n} \sum_{i=1}^n \frac{1}{h} K_h(x-x_i)$$

- n = sample size, x = new point to estimate f(x) (does NOT have to be in dataset!)
- $h = \mathsf{bandwidth}$ , analogous to histogram bin width, ensures  $\hat{f}(x)$  integrates to 1
- $x_i = i$ th observation in dataset
- $K_h(x-x_i)$  is the **Kernel** function, creates **weight** given distance of ith observation from new point
  - $lacksquare as |x-x_i| o \infty$  then  $K_h(x-x_i) o 0$ , i.e. further apart ith row is from x, smaller the weight
  - lacksquare as lacksquare and lacksquare are more evenly spread out (as  $h\downarrow$  more concentrated around x)
  - typically use Gaussian / Normal kernel:  $\propto e^{-(x-x_i)^2/2h^2}$
  - $K_h(x-x_i)$  is large when  $x_i$  is close to x

# Wikipedia example



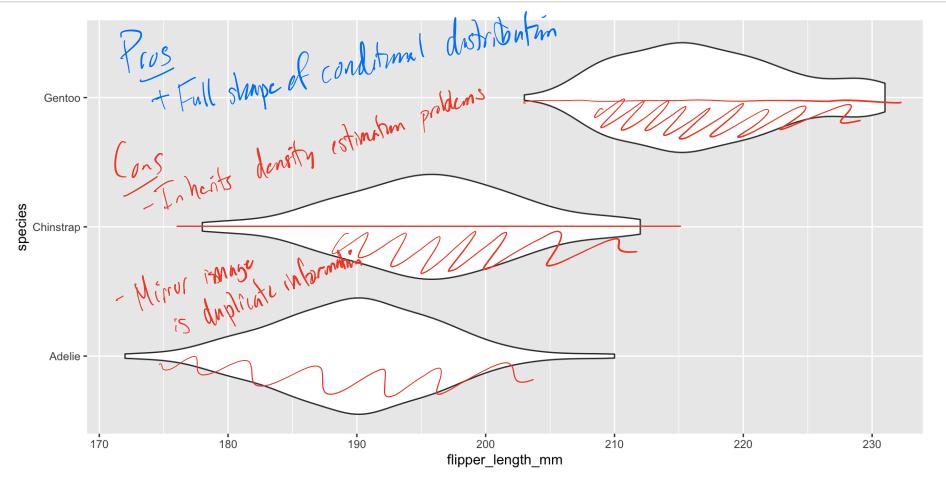
# We display kernel density estimates with

geom\_density() + Display full shape of distribution

+ Easily layer, add categorical
variables or color penguins |> ggplot(aes(x = flipper\_length\_mm)) + geom\_density() + 4 Theme bw() -Need to piele bandmidth & kerned 0.03 0.02 -0.01 0.00 170 180 190 200 210 220 230 flipper length mm

# Visualizing conditional distributions: violin plots

```
1 penguins |>
2    ggplot(aes(x = species, y = flipper_length_mm)) +
3    geom_violin() +
4    coord_flip()
```



#### Visualizing conditional distributions: ggbeeswarm

```
1 library(ggbeeswarm)
2 penguins |>
3    ggplot(aes(x = flipper_length_mm, y = species)) +
4    geom_beeswarm(cex = 1.5) +
5    theme_bw()
```

