

fct_inorder

Dataset

```
library(tidyverse)
tb <- tribble(
  ~cancer, ~cases, ~sex,
  "Colorectal", 66, "M",
  "Liver", 29, "M",
  "Skin", 21, "M",
  "Kidney", 17, "M",
  "Colorectal", 12, "F",
  "Skin", 17, "F",
)
tb$cancer <- tb$cancer |> factor()
tb$sex <- tb$sex |> factor()
tb
```

```
# A tibble: 6 x 3
  cancer    cases sex
  <fct>    <dbl> <fct>
1 Colorectal    66 M
2 Liver        29 M
3 Skin         21 M
4 Kidney       17 M
5 Colorectal    12 F
6 Skin         17 F
```

i Note

Default factor levels are placed alphabetically and are so plotted on ggplot2. To change the sequence use `fct_inorder`

```
levels(tb$cancer)
```

```
[1] "Colorectal" "Kidney"      "Liver"       "Skin"
```

```
tb$cancer <- fct_inorder(tb$cancer)  
levels(tb$cancer)
```

```
[1] "Colorectal" "Liver"       "Skin"        "Kidney"
```

i Note

There's also `fct_inseq` and `fct_infreq` (by number of observations with each level). They are found in the `forcats` package under `tidyverse`. Ref: https://forcats.tidyverse.org/reference/fct_inorder.html