fct_inorder

Dataset

```r
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