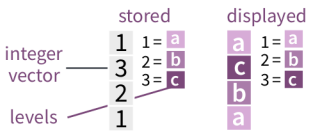
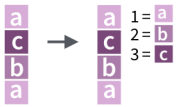
Factors with forcats : : CHEAT SHEET

The **forcats** package provides tools for working with factors, which are R's data structure for categorical data.

Factors

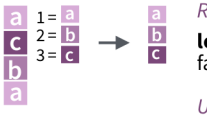
R represents categorical data with factors. A **factor** is an integer vector with a **levels** attribute that stores a set of mappings between integers and categorical values. When you view a factor, R displays not the integers, but the values associated with them.





Create a factor with factor()

factor(x = character(), levels, labels = levels, exclude = NA, ordered = is.ordered(x), nmax = NA) Convert a vector to a factor. Also **as_factor**.
f <- factor(c("a", "c", "b", "a"), levels = c("a", "b", "c"))

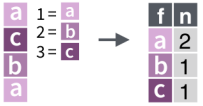


Return its levels with levels()

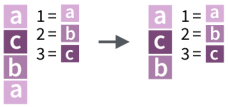
levels(x) Return/set the levels of a factor. *levels(f); levels(f) <- c("x","y","z")*

Use unclass() to see its structure

Inspect Factors

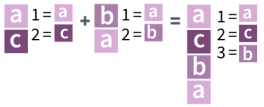


fct_count(f, sort = FALSE) Count the number of values with each level. *fct_count(f)*

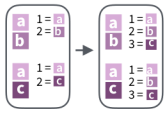


fct_unique(f) Return the unique values, removing duplicates. *fct_unique(f)*

Combine Factors

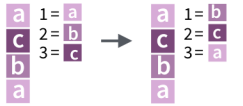


fct_c(…) Combine factors with different levels.
f1 <- factor(c("a", "c"))
f2 <- factor(c("b", "a"))
fct_c(f1, f2)



fct_unify(fs, levels = lvls_union(fs)) Standardize levels across a list of factors.
fct_unify(list(f2, f1))

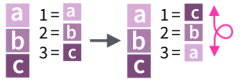
Change the order of levels



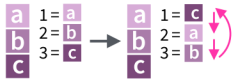
fct_relevel(.f, ..., after = 0L) Manually reorder factor levels.
fct_relevel(f, c("b", "c", "a"))

fct_infreq(f, ordered = NA) Reorder levels by the frequency in which they appear in the data (highest frequency first).
f3 <- factor(c("c", "c", "a"))
fct_infreq(f3)

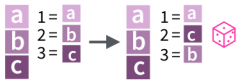
fct_inorder(f, ordered = NA) Reorder levels by order in which they appear in the data.
fct_inorder(f2)



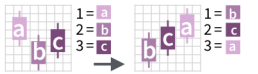
fct_rev(f) Reverse level order.
f4 <- factor(c("a","b","c"))
fct_rev(f4)



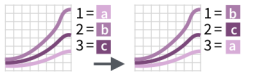
fct_shift(f) Shift levels to left or right, wrapping around end.
fct_shift(f4)



fct_shuffle(f, n = 1L) Randomly permute order of factor levels.
fct_shuffle(f4)

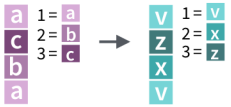


fct_reorder(.f, .x, .fun=median, ..., .desc = FALSE) Reorder levels by their relationship with another variable.
boxplot(data = iris, Sepal.Width ~ fct_reorder(Species, Sepal.Width))

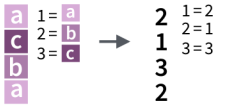


fct_reorder2(.f, .x, .y, .fun = last2, ..., .desc = TRUE) Reorder levels by their final values when plotted with two other variables.
ggplot(data = iris, aes(Sepal.Width, Sepal.Length, color = fct_reorder2(Species, Sepal.Width, Sepal.Length))) + geom_smooth()

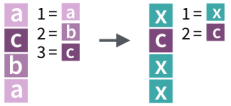
Change the value of levels



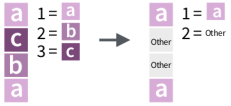
fct_recode(.f, ...) Manually change levels. Also **fct_relabel** which obeys purrr::map syntax to apply a function or expression to each level.
fct_recode(f, v = "a", x = "b", z = "c")
fct_relabel(f, ~ paste0("x", .x))



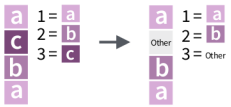
fct_anon(f, prefix = "")) Anonymize levels with random integers. *fct_anon(f)*



fct_collapse(.f, ...) Collapse levels into manually defined groups.
fct_collapse(f, x = c("a", "b"))

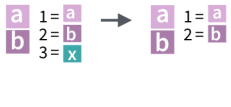


fct_lump(f, n, prop, w = NULL, other_level = "Other", ties.method = c("min", "average", "first", "last", "random", "max")) Lump together least/most common levels into a single level. Also **fct_lump_min**.
fct_lump(f, n = 1)



fct_other(f, keep, drop, other_level = "Other") Replace levels with "other."
fct_other(f, keep = c("a", "b"))

Add or drop levels



fct_drop(f, only) Drop unused levels.
f5 <- factor(c("a","b"),c("a","b","x"))
f6 <- fct_drop(f5)

fct_expand(f, …) Add levels to a factor. *fct_expand(f6, "x")*

fct_explicit_na(f, na_level="(Missing)") Assigns a level to NAs to ensure they appear in plots, etc.
fct_explicit_na(factor(c("a", "b", NA)))

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