



Base R Equivalents of dplyr Functions Part 1 – coalesce

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The dplyr `coalesce` function is incredibly useful and similar to the SQL `COALESCE` function. Given a set of vectors, it finds and keeps the first non-`NA` value at each position. For example, the following code returns the vector `c(1, 2, 3, 4)`.

```
library(dplyr)
coalesce(c(1, NA, 3, NA), c(2, 2, 4, 4))
```

```
[1] 1 2 3 4
```

- At position 1, the first non-`NA` value is 1 (from the first vector).
- At position 2, the first non-`NA` value is 2 (from the second vector, because the value at position 2 in the first vector is NA).
- At position 3, the first non-`NA` value is 3 (from the first vector).
- Finally, at position 4, the first non-`NA` value is 4 (from the second vector, because the value at position 4 in the first vector is NA).

The `coalesce` function is not limited to two vectors. You can use as many vectors as you'd like.

```
coalesce(c(1, 2, NA, NA), c(3, 3, 3, NA), c(4, 4, 4, 4))
```

```
[1] 1 2 3 4
```

The vectors must be of equal length or length 1. Vectors of length 1 will be recycled. The following:

```
coalesce(c(1, NA, NA, 5), 3)
```

```
[1] 1 3 3 5
```

Is equivalent to:

```
dplyr::coalesce(c(1, NA, NA, 5), c(3, 3, 3, 3))
```

```
[1] 1 3 3 5
```

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I most often use `coalesce` to replace all `NA` values in a vector with a single value. For example, the following code replaces all `NA` values with 0:

```
coalesce(c(1, NA, NA, 5, 6), 0)
[1] 1 0 0 5 6
```

Here are two alternative ways to do the same thing.

```
library(tidyr)
replace_na(c(1, NA, NA, 5, 6), 0) # this function is in the tidyr package
[1] 1 0 0 5 6

x <- c(1, NA, NA, 5, 6)
ifelse(is.na(x), 0, x)

[1] 1 0 0 5 6
```

Of the three options I have shown so far, I prefer `coalesce` and `replace_na`. (`coalesce` is a more general version of `replace_na`; `replace_na` takes a vector and a single value to replace the `NA` values in that vector with). If you want to go outside of base R and the tidyverse, `data.table::fcoalesce` is a much faster version of `dplyr::coalesce`.

Let's compare the speeds!

```
library(microbenchmark)
library(data.table)
set.seed(11)
x <- 1:10^7
x[sample(1:10^7, size = 10^6, replace = FALSE)] <- NA
microbenchmark(
  fcoalesce(x, 0L),
  coalesce(x, 0L),
  replace_na(x, 0L),
  ifelse(is.na(x), 0L, x),
  times = 5
)

Unit: milliseconds
expr      min       lq     mean   median      uq      max
fcoalesce(x, 0L) 14.4582 16.1549 18.47224 18.5650 19.1356 24.047
coalesce(x, 0L) 285.4586 289.1238 318.36890 292.7322 297.1620 427.367
replace_na(x, 0L) 37.2726 41.0626 51.48104 41.4943 52.0923 85.483
ifelse(is.na(x), 0L, x) 168.9397 178.8357 191.00360 180.9929 186.2458 240.003
neval
5
5
5
5
```

`data.table::fcoalesce` is the winner in terms of speed, followed by `replace_na`. Of the four methods above, `coalesce` and `fcoalesce` are the most general, since they are not limited to replacing all `NA` values with a single value.

Is there a base R equivalent to `dplyr::coalesce`? No. But we can easily create one using just base R code.

To think about how we would do that, let's start with two vectors:

```
x <- c(1, 2, NA, NA)
y <- c(2, 2, 3, NA)
coalesce(x, y)

[1] 1 2 3 NA
```



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How could we get the same results using the `ifelse` function? It's simple. We return the value in `y` when the value in `x` is `NA`.

```
ifelse(is.na(x), y, x)
```

```
[1] 1 2 3 NA
```

That's simple enough. But what if we want to use three vectors?

```
z <- c(4, 4, 4, 4)
coalesce(x, y, z)
```

```
[1] 1 2 3 4
```

We can start with our code from the case where we used two vectors.

```
output_step_1 <- ifelse(is.na(x), y, x)
```

When both `x` and `y` are `NA` (when `ifelse(is.na(x), y, x)` gives us `NA`), we want to use what is in `z`. Otherwise, we want to keep the results from step 1 above.

```
ifelse(is.na(output_step_1), z, output_step_1)
```

```
[1] 1 2 3 4
```

That worked! But what if we want to generalize this to any number of input vectors? We can use the base R function `Reduce`. For our case where we used `x`, `y`, and `z`, we could do:

```
Reduce(function(x, y) ifelse(is.na(x), y, x), list(x, y, z))
```

```
[1] 1 2 3 4
```

`Reduce(f, list(x, y, z))`, where `f` is a function of two variables, is the equivalent of `f(f(x, y), z)`. And `Reduce(f, list(x, y, z, a))` is equivalent to `f(f(f(x, y), z), a)`. The `Reduce` function is used to iteratively apply a function to elements of a list, reducing it to a single value. It takes a function with two parameters and applies it to the first two elements of the list, then applies the same function to the result and the next element, and so on, until all elements are combined into a single value.

To use `Reduce` to mimic `coalesce(x, y, z, ...)`, we need to apply the logic `f <- function(x, y) { ifelse(is.na(x), y, x)}` over and over starting from left to right. In other words, for three vectors `x`, `y`, and `z`, we need to do:

```
f <- function(x, y) {
  ifelse(is.na(x), y, x)
}
f(f(x, y), z)
```

```
[1] 1 2 3 4
```

Which is equivalent to

```
Reduce(f, list(x, y, z))
```

```
[1] 1 2 3 4
```

So a very simple base R function equivalent to the `coalesce` function is:

```
coalesce_base_r <- function(...) {
  args <- list(...)
  Reduce(function(x, y) ifelse(is.na(x), y, x), args)
}
```

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Let's see if it produces identical results to `dplyr::coalesce` :

```
set.seed(11)
x <- 1:10^7
y <- 1:10^7
x[sample(1:10^7, size = 10^6, replace = FALSE)] <- NA
y[sample(1:10^7, size = 10^6, replace = FALSE)] <- NA
z <- 1L

dplyr_result <- coalesce(x, y, z)
base_r_result <- coalesce_base_r(x, y, z)
identical(dplyr_result, base_r_result)
```

[1] TRUE

We get identical results!

Let's compare the speed:

```
microbenchmark(coalesce(x, y, z), coalesce_base_r(x, y, z), times = 5)
```

	expr	min	lq	mean	median	uq	max
coalesce(x, y, z)	299.6434	321.6311	355.9083	357.0767	385.4815	415.709	
coalesce_base_r(x, y, z)	349.0094	406.5152	400.0490	412.2628	413.9706	418.487	
neval	5	5	5	5	5	5	

Our base R version of `coalesce` is almost identical in speed dplyr's!

But our function contains some flaws. dplyr's `coalesce` function forces the vectors passed to it to either be of the same length or be of length 1. If we try:

```
coalesce(c(1, 2, 3, NA, 6), c(4, 5))
```

```
Error in `coalesce()`:
! Can't recycle `..1` (size 5) to match `..2` (size 2).
```

We get an error, since the first vector has length 5 and the second has length 2.

Here's a better base R version of `coalesce` :

```
coalesce_base <- function(...) {
  args <- list(...)

  # Check for NULL, zero-length vectors, and collect lengths
  lengths <- sapply(args, function(x) {
    if (is.null(x) || length(x) == 0) {
      stop("Arguments must not be NULL or zero-length vectors")
    }
    length(x)
  })

  # Determine the maximum length
  max_length <- max(lengths)

  # Check if lengths are consistent.
  # Only allow vectors of length equal to max length or length of 1
  if (any(lengths != max_length & lengths != 1)) {
    stop("All arguments must have the same length,
         except for vectors of length 1 which can be recycled")
  }

  # Use Reduce with ifelse to coalesce
  Reduce(function(x, y) ifelse(is.na(x), y, x), args)
}

# Example usage:
v1 <- c(NA, 2, NA, 4, NA)
v2 <- c(1, NA, 3, NA, NA)
```

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```
v3 <- 0
coalesce_base(v1, v2, v3)
```

```
[1] 1 2 3 4 0
```

Again, let's compare the speed of our function to `dplyr::coalesce` and

```
data.table::fcoalesce .
```

```
microbenchmark(fcoalesce(x, y, z),
               coalesce(x, y, z),
               coalesce_base_r(x, y, z),
               times = 5)
```

	expr	min	lq	mean	median	uq
fcoalesce(x, y, z)	16.9233	17.5952	19.12082	17.6570	19.5384	
coalesce(x, y, z)	304.2171	321.0251	343.79622	355.3758	358.6747	
coalesce_base_r(x, y, z)	344.0853	357.0263	383.64736	386.5437	388.1294	
max	23.8902	5				
379.6884	5					
442.4521	5					

`data.table::fcoalesce` is the clear winner when it comes to speed! Our function is almost identical in speed to `dplyr::coalesce`!

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