

# collapse: Advanced and Fast Statistical Computing and Data Transformation in R

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## Abstract

**collapse** is a large C/C++-based infrastructure package facilitating complex statistical computing, data transformation, and exploration tasks in R—at outstanding levels of performance and memory efficiency. It also implements a class-agnostic approach to R programming, supporting vector, matrix and data frame-like objects and their popular extensions (`'units'`, `'integer64'`, `'xts'`, `'tibble'`, `'data.table'`, `'sf'`, `'pdata.frame'`), enabling its seamless integration with large parts of the R ecosystem. This article introduces the package's key components and design principles in a structured way, supported by a rich set of examples. A small benchmark demonstrates its computational performance.

*Keywords:* statistical computing, vectorization, data manipulation and transformation, class-agnostic programming, summary statistics, C/C++, R.

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## 1. Introduction

**collapse** is a large C/C++-based R package that provides an integrated suite of statistical and data manipulation functions.<sup>1</sup> Its core functionality includes a rich set of S3 generic (grouped, weighted) statistical functions for vectors, matrices, and data frames, which provide efficient low-level vectorizations, OpenMP multithreading, and skip missing values by default (`na.rm = TRUE`). It also provides powerful data manipulation functions—such as vectorized and verbose hash-joins or fast (aggregation, recast) pivots—functions and classes for indexed (time-aware) computations on time series and panel data, recursive tools to deal with nested data, and advanced descriptive statistical tools. This functionality is supported by efficient algorithms for grouping, ordering, deduplication, and matching callable at both R and C levels. Lastly, it includes efficient object converters, functions for memory efficient R programming, such as (grouped) transformation and math by reference, and helper functions to handle variable labels, attributes, and missing data. **collapse** is **class-agnostic**, providing statistical operations for vectors, matrices, and data frames/lists, and seamlessly supporting extensions to these objects popular in the R ecosystem—notably, `'units'`, `'integer64'`, `'xts'`, `'tibble'`, `'data.table'`, `'sf'`, and `'pdata.frame'`. It is also globally and interactively configurable, allowing changing defaults of key function arguments, such as the `na.rm` arguments to statistical functions or `sort` arguments to grouping algorithms (default `TRUE`), and modifying the namespace to mask equivalent but less performant base R/**tidyverse** functions.<sup>2</sup>

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<sup>1</sup>Website: <https://sebkranz.github.io/collapse/>. Linecount (v2.1.2): R: 13,785, C: 19,013, C++: 9,844.

Exported namespace: 392 objects, of which 238 functions (excl. methods and shorthands), and 2 datasets.

<sup>2</sup>**collapse**'s namespace is fully compatible with base R and the **tidyverse** (Wickham *et al.* 2019), but can be interactively modified to mask/overwrite key functions with the much faster **collapse** equivalents. See Section 8.

Why combine all of these features in a package? The short answer is to make computations in R as flexible and powerful as possible. The more elaborate answer is to (1) facilitate complex data transformation, exploration, and computing tasks in R; (2) increase the performance and memory efficiency of R programs; and (3) create a new foundation package for statistics and data transformation that implements successful ideas in the R ecosystem and other programming environments in a stable, high performance, and broadly compatible manner.<sup>3</sup>

R already has a large and tested data manipulation and statistical computing ecosystem. Notably, the **tidyverse** (Wickham *et al.* 2019) provides a consistent toolkit for data manipulation in R, centered around the ‘**tibble**’ (Müller and Wickham 2023) object and tidy data principles (Wickham 2014). **data.table** (Dowle and Srinivasan 2025) provides an enhanced high-performance data frame with parsimonious syntax. **sf** (Pebesma 2018) provides a data frame for spatial data and supporting functionality. **tsibble** (Wang *et al.* 2020) and **xts** (Ryan and Ulrich 2023) provide classes and operations for time series data, the former via an enhanced ‘**tibble**’, the latter through an efficient matrix-based class. Econometric packages like **plm** (Croissant and Millo 2008) and **fixest** (Bergé 2018) also provide solutions to deal with panel data and irregularity in the time dimension. Packages like **matrixStats** (Bengtsson 2025) and **Rfast** (Papadakis *et al.* 2023) offer fast statistical calculations along the rows and columns of matrices as well as faster statistical procedures. **DescTools** (Signorell 2023) provides a wide variety of descriptive statistics, including weighted versions. **survey** (Lumley 2004) offers computations on complex surveys. **labelled** (Larmarange 2023) provides tools to deal with labelled data. Packages like **tidyr** (Wickham *et al.* 2024), **purrr** (Wickham and Henry 2023) and **rapply** (Chau 2022) provide functions to deal with nested or messy data.

**collapse** relates to and integrates key elements from these projects. It offers **tidyverse**-like data manipulation at the speed and stability of **data.table** for any data frame-like object. It can turn any vector/matrix/data frame into a time-aware indexed series or frame and perform operations such as lagging, differencing, scaling or centering, encompassing and enhancing core manipulation functionality of **plm**, **fixest**, and **xts**. It also performs fast (grouped, weighted) statistical computations along the columns of matrix-like objects, complementing and enhancing **matrixStats** and **Rfast**. Its low-level vectorizations and workhorse algorithms are accessible at the R and C-levels, unlike **data.table**, where most vectorizations and algorithms are internal. It also supports variable labels and intelligently preserves attributes of all objects, complementing **labelled**. It provides novel recursive tools to deal with nested data, enhancing **tidyr**, **purrr**, and **rapply**. Finally, it provides a small but consistent and powerful set of descriptive statistical tools, yielding sufficient detail for most data exploration purposes, requiring users to invoke packages like **DescTools** or **survey** only for specialized statistics.

In summary, **collapse** is a new foundation package for advanced statistical computing and data transformation in R that integrates seamlessly with the ecosystem and offers outstanding speed and memory efficiency. Thus, many core tasks can be done with **collapse**, and easily extended by specialized packages, yielding more lightweight, faster, and shorter R programs.

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<sup>3</sup>Such ideas include **tidyverse** syntax, vectorized aggregations (**data.table**), data transformation by reference (Python, **pandas**), vectorized and verbose joins (**polars**, STATA: StataCorp LLC. (2023)), indexed time series and panel data (**xts**, **plm**), summary statistics for panel data (STATA), variable labels (STATA), recast pivots (**reshape2**), etc...

Other programming environments such as Python and Julia now also offer computationally very powerful libraries for tabular data such as **DataFrames.jl** (Bouchet-Valat and Kamiński 2023), **Polars** (Vink *et al.* 2023), and **Pandas** (McKinney 2010; **pandas** Development Team 2023), and supporting numerical libraries such as **Numpy** (Harris *et al.* 2020), or **StatsBase.jl** (JuliaStats 2023). In comparison with these, **collapse** offers a class-agnostic approach bridging the divide between data frames and atomic structures, has more advanced statistical capabilities,<sup>4</sup> supports recast pivots and recursive operations on lists, variable labels, verbosity for critical operations such as joins, and is extensively globally configurable. In short, it is very useful for complex statistical workflows, rich datasets (e.g., surveys), and for integrating with different parts of the R ecosystem. On the other hand, **collapse**, for the most part, does not offer a sub-column-level parallel architecture and is thus not highly competitive with top frameworks, including **data.table**, on aggregating billion-row datasets with few columns.<sup>5</sup> Its vectorization capabilities are also limited to the statistical functions it provides and not, like **DataFrames.jl**, to any Julia function. However, as demonstrated in Section 3, vectorized statistical functions can be combined to calculate more complex statistics in a vectorized way.

The package has a built-in structured **documentation** facilitating its use. This documentation includes a central **overview page** linking to all other documentation pages and supplementary topic pages which briefly describe related functionality. The names of these extra pages are collected in a global macro `.COLLAPSE_TOPICS` and can be called directly with `help()`:

```
R> .COLLAPSE_TOPICS
```

```
[1] "collapse-documentation"      "fast-statistical-functions"
[3] "fast-grouping-ordering"      "fast-data-manipulation"
[5] "quick-conversion"           "advanced-aggregation"
[7] "data-transformations"        "time-series-panel-series"
[9] "list-processing"             "summary-statistics"
[11] "recode-replace"             "efficient-programming"
[13] "small-helpers"              "collapse-options"
```

```
R> help("collapse-documentation")
```

This article cannot fully present **collapse**, but the following sections introduce its key components, starting with (2) the *Fast Statistical Functions* and their (3) integration with data manipulation functions; (4) architecture for time series and panel data; (5) table joins and pivots; (6) list processing functions; (7) descriptive tools; and (8) global options. Section 9 provides a small benchmark, Section 10 concludes. For deeper engagement with **collapse**, consult the **documentation and resources**, including the **vignettes/cheatsheet/blog/talk + slides**.

<sup>4</sup>Such as weighted statistics, including several (weighted) quantile and mode estimators, support for fully time-aware computations on irregular series/panels, scaling and centering, advanced (grouped, weighted, panel-decomposed) descriptive statistics etc., all supporting missing values and vectors/matrices/data frames.

<sup>5</sup>As can be seen in the **DuckDB Benchmarks**: **collapse** is highly competitive on the 10-100 million observations datasets, but deteriorates in performance at larger data sizes. There may be performance improvements for very "long data" in the future, but, at present, the treatment of columns as fundamental units of computation (in most cases) is a tradeoff for the highly flexible class-agnostic architecture.

## 2. Fast statistical functions

The *Fast Statistical Functions*, comprising `fsum()`, `fprod()`, `fmean()`, `fmedian()`, `fmode()`, `fvar()`, `fsd()`, `fmin()`, `fmax()`, `fnth()`, `ffirst()`, `flast()`, `fnobs()`, and `fndistinct()`, are a consistent set of S3-generic statistical functions providing fully vectorized statistical operations in R.<sup>6</sup> Specifically, operations are vectorized across columns and groups, and may also involve weights or transformations of the input data. Their basic syntax is

```
FUN(x, g = NULL, w = NULL, TRA = NULL, na.rm = TRUE, use.g.names = TRUE, ...)
```

with arguments `x` - data (vector, matrix or data frame-like), `g` - groups (atomic vector, list of vectors, or ‘GRP’ object), `w` - sampling weights (only some functions), and `TRA` - transformation of `x`. The following examples with `fmean()` demonstrate their basic usage on the familiar `iris` dataset recording 50 measurements of 4 variables for 3 species of iris flowers.<sup>7</sup> All examples support weights (`w`), and `fmean()` can also be multithreaded across columns (`nthreads`).<sup>8</sup>

```
R> fmean(iris$Sepal.Length)
```

```
[1] 5.843
```

```
R> fmean(num_vars(iris))
```

```
Sepal.Length Sepal.Width Petal.Length Petal.Width
      5.843      3.057      3.758      1.199
```

```
R> identical(fmean(num_vars(iris)), fmean(as.matrix(num_vars(iris))))
```

```
[1] TRUE
```

```
R> fmean(iris$Sepal.Length, g = iris$Species)
```

```
setosa versicolor virginica
  5.006      5.936      6.588
```

```
R> fmean(num_vars(iris), g = iris$Species, nthreads = 4)
```

```
      Sepal.Length Sepal.Width Petal.Length Petal.Width
setosa      5.006      3.428      1.462      0.246
versicolor  5.936      2.770      4.260      1.326
virginica   6.588      2.974      5.552      2.026
```

<sup>6</sup>‘Vectorization’ in R/**collapse** means that these operations are implemented using compiled C/C++ code.

<sup>7</sup>`num_vars()` returns the numeric variables in a data frame-like object; `cat_vars()` the categorical ones.

<sup>8</sup>Not all functions are multithreaded, and parallelism is implemented differently for different functions, as detailed in the respective function documentation. The default use of single instruction multiple data (SIMD) parallelism also implies limited gains from multithreading for simple (non-grouped) operations.

## 2.1. Transformations

The TRA argument toggles (grouped) replacing and sweeping operations (by reference), generalizing `sweep(x, 2, STATS = fmean(x))`.<sup>9</sup> Table 1 lists the 11 possible TRA operations.

<i>String</i>	<i>Description</i>
"replace_na"/"na"	replace missing values in <code>x</code> by <code>STATS</code>
"replace_fill"/"fill"	replace data and missing values in <code>x</code> by <code>STATS</code>
"replace"	replace data by <code>STATS</code> but preserve missing values in <code>x</code>
"-"	subtract <code>STATS</code> (center)
"-+"	subtract <code>STATS</code> and add overall average statistic
"/"	divide by <code>STATS</code> (scale)
"%"	compute percentages (divide and multiply by 100)
"+"	add <code>STATS</code>
"*"	multiply by <code>STATS</code>
"%%"	modulus (remainder from division by <code>STATS</code> )
"-%%"	subtract modulus (make data divisible by <code>STATS</code> )

Table 1: Available TRA argument choices.

For example, option `TRA = "fill"` replaces elements with the corresponding statistics:

```
R> fmean(iris$Sepal.Length, g = iris$Species, TRA = "fill")[c(1:5, 51:55)]

[1] 5.006 5.006 5.006 5.006 5.006 5.936 5.936 5.936 5.936 5.936
```

Additionally, a `set` argument can be passed to *Fast Statistical Functions* to toggle transformation by reference. For example `fmean(iris$Sepal.Length, g = iris$Species, TRA = "fill", set = TRUE)` would modify `Sepal.Length` in-place and return the result invisibly.

Having grouping and data transformation functionality directly built into generic statistical functions facilitates and speeds up many common operations. It also avoids the need to convert atomic objects to data frames for grouped aggregations or transformations. The *Fast Statistical Functions* are complemented by a smaller set of *Data Transformation Functions*, including `TRA()`, infix functions such as `%r+%`, `%c+%`, `%+=%` and `setop()` for row/column-wise arithmetic operations (by reference), `dapply()` to apply functions across rows or columns of matrices/data frames, `BY()` for general split-apply-combine computing, and specialized functions such as `fscale()` or `f[hd]within()` for (grouped, weighted) scaling and centering:

```
R> BY(num_vars(iris), g = iris$Species, FUN = mad) |> head(1)
```

```
      Sepal.Length Sepal.Width Petal.Length Petal.Width
setosa      0.2965      0.3706      0.1483          0
```

```
R> fscale(iris$Sepal.Length, g = iris$Species) |> fsd(iris$Species)
```

```
      setosa versicolor virginica
      1          1          1
```

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<sup>9</sup>The TRA argument internally calls `TRA(x, STATS, FUN = "-", g = NULL, set = FALSE, ...)`.

### 3. Integration with data manipulation functions

**collapse** also provides a broad set of **Fast Data Manipulation Functions**, including `fselect()`, `fsubset()`, `fslice()`, `fgroup_by()`, `fsummarise()`, `fmutate()`, `frename()`, `fcount()`, etc. as optimized analogues to base R/**tidyverse** functions. These are integrated with the *Fast Statistical and Transformation Functions* to enable vectorized operations in a familiar data frame oriented and **tidyverse**-like workflow. I illustrate this using the included World Development Dataset (**wlddev**) recording five key indicators for 216 economies and years 1960-2020.

```
R> fndistinct(wlddev)
```

country	iso3c	date	year	decade	region	income	OECD	PCGDP
216	216	61	61	7	7	4	2	9470
LIFEEX	GINI	ODA	POP					
10548	368	7832	12877					

Below, I track changes in Life Expectancy at the country level, computing the range, average change per year, and correlation with GDP per Capita in log-differences<sup>10</sup> while also saving the latest measurements.<sup>11</sup> The `collap()` function called at the end to aggregate the country-level statistics across income groups is a convenience function for mixed-type aggregation.<sup>12</sup> By default, it uses `fmean()` for numeric data and `fmode()` for categorical data, here also applying population weights such that the most populous country in each group is kept.

```
R> wlddev |> fgroup_by(country, income) |>
+   fsummarise(n = fnobs(LIFEEX),
+             diff = fmax(LIFEEX) %-% fmin(LIFEEX),
+             mean_diff = fmean(fdiff(LIFEEX)),
+             cor_PCGDP = pwcor(Dlog(LIFEEX), Dlog(PCGDP)),
+             across(c(LIFEEX, PCGDP, POP), flast)) |>
+   collap(~ income, w = ~ POP, keep.w = FALSE) |> print(digits = 2)
```

	country	income	n	diff	mean_diff	cor_PCGDP	LIFEEX	PCGDP
1	United States	High income	60	13	0.23	-0.00828	81	44599
2	Ethiopia	Low income	60	26	0.43	0.27153	64	691
3	India	Lower middle income	60	24	0.41	-0.15366	69	2324
4	China	Upper middle income	60	27	0.45	0.00077	76	8749

With the exception of `pwcor(Dlog(LIFEEX), Dlog(PCGDP))`, which is evaluated for every country, all other expressions in `fsummarise()` and also the final `collap()` call are fully vectorized, i.e., evaluated only once with grouping information passed directly to the `g` arguments of *Fast Statistical and Transformation Functions*. Using subtraction by reference in the range is thus memory efficient as the executed expression is equivalent to `fmax(LIFEEX, country)`

<sup>10</sup>`Dlog()` is a shorthand for `fdiff(log(x))` in **collapse**, `pwcor()` wraps `cor(..., use = "pairwise.complete.obs")`.

<sup>11</sup>Note that `fsummarise()` never re-groups data, making a call to `fungroup()` redundant.

<sup>12</sup>See also [this blog post on aggregating survey data using collapse](#) which showcases more aspects of the `collap()` function using real census data.



`%-=% fmin(LIFFEX, country). across()` also directly invokes `flast.data.frame()` on the subset of columns. *Fast Statistical Functions* also have a method for grouped data, hence `fsummarise()` is not always needed. Below, I average the data with population weights.<sup>13</sup>

```
R> wlddev |> fsubset(year >= 2015, income, PCGDP:POP) |>
+   fgroup_by(income) |> fmean(POP)
```

	income	sum.POP	PCGDP	LIFEEX	GINI	ODA
1	High income	5.901e+09	43340	80.70	36.14	81398948
2	Low income	3.296e+09	663	63.05	39.13	2466732035
3	Lower middle income	1.490e+10	2177	68.31	36.48	2234540565
4	Upper middle income	1.318e+10	8168	75.51	41.68	-86630117

Using the *Fast Statistical Functions* directly often results in more efficient code. For example, computing population shares for each year as `fmutate(wlddev, POP_share = fsum(POP, year, TRA = "/"))` is considerably more efficient than `wlddev |> fgroup_by(year) |> fmutate(POP_share = fsum(POP, TRA = "/")) |> fungroup()`, which in turn is more efficient than `POP / fsum(POP)` (extra allocation) or `proportions(POP)` (split-apply-combine).

**collapse** thus offers several ways to reach the same outcome. This may be confusing, but all options can be distinguished in efficiency terms. It is thus useful to be mindful of computer resources and attempt to craft minimalistic solutions. For example, I recently combined multiple spatial datasets on points of interest (POIs) and needed to deduplicate them. I decided to keep the richest source for each location and POI type. After creating POI confidence, location, and type indicators comparable across sources (datasets), my deduplication expression ended up being a single line of the form `fsubset(data, source == fmode(source, list(location, type), confidence, "fill"))`—which retains POIs from the confidence-weighted most frequent (i.e., richest) source by location and type. This is very efficient because it avoids materializing intermediate datasets and relegates all computations to `fmode()`.

### 3.1. Vectorizations for advanced tasks

`fsummarise()` and `fmutate()` follow an eager vectorization approach, implying that using any *Fast Statistical Function* in an expression causes the whole expression to be vectorized. This only applies to visible expressions, **collapse** cannot read the contents of custom functions, thus such functions are always evaluated split-apply-combine. The eager vectorization approach enables efficient grouped calculation of more complex statistics. Below, I forecast the population of each region via linear regression (`POP ~ year`) in a fully vectorized way.

```
R> wlddev |> collap(POP ~ region + year, FUN = fsum) |>
+   fmutate(POP = POP / 1e6) |> fgroup_by(region) |>
+   fmutate(dmy = fmean(year, TRA = "-")) |>
+   fsummarise(beta = fsum(POP, dmy) %/=% fsum(dmy, dmy),
+             POP20 = flast(POP)) |>
+   fmutate(POP21 = POP20 + beta, POP22 = POP21 + beta,
+           POP23 = POP22 + beta, POP24 = POP23 + beta)
```

<sup>13</sup>Functions like `fmean()`, when called on a grouped data frame with weights, by default (`keep.w = TRUE`) sum the weights column and retain it after the grouping columns to permit further weighted operations.

	region	beta	POP20	POP21	POP22	POP23	POP24
1	East Asia & Pacific	18.731	2291.4	2310.2	2328.9	2347.6	2366.4
2	Europe & Central Asia	2.463	921.2	923.7	926.1	928.6	931.0
3	Latin America & Caribbean	6.460	646.4	652.9	659.4	665.8	672.3
4	Middle East & North Africa	5.409	456.7	462.1	467.5	472.9	478.3
5	North America	2.301	365.9	368.2	370.5	372.8	375.1
6	South Asia	19.640	1835.8	1855.4	1875.1	1894.7	1914.3
7	Sub-Saharan Africa	12.852	1103.5	1116.3	1129.2	1142.0	1154.9

When `fsummarise()` evaluates an expression involving *Fast Statistical Functions*, it sets their `g` argument with a grouping ('GRP') object that is directly handed to C/C++, and also sets `use.g.names = FALSE`. Hence, `weights (w)` becomes the second positional argument. Similarly, `fmutate()` sets `g` and `TRA = "fill"`, which can be overwritten by the user (here with `TRA = "-"`). The expression `fsum(x, dmy) %/=% fsum(dmy, dmy)`, amounting to `cov(x, y)/var(y)`, is thus vectorized across groups and memory efficient—leveraging the `weights (w)` argument to `fsum()` to compute products (`v * dmy` and `dmy * dmy`) on the fly and division by reference (`%/=%`) to avoid an additional allocation. In a 2023 [blog post](#), I forecasted high-resolution population estimates for South Africa like this. Using 1 *km*<sup>2</sup> [WorldPop](#) data available for years 2014-2020, running 1.6 million cell-regressions and obtaining 2 forecasts for 2021 and 2022 took only 0.3 seconds on my M1 Mac. Another neat example from the community, shared by Andrew Ghazi in a [blog post](#), vectorizes an expression to compute the *p* value, `2 * pt(abs(fmean(x) * sqrt(6) / fsd(x)), 5, lower.tail = FALSE)`, across 300,000 groups for a simulation study, yielding a 70x performance increase over `dplyr`.

**collapse** also vectorizes advanced statistics. The following calculates a weighted set of summary statistics by groups, with weighted quantiles type 8 following [Hyndman and Fan \(1996\)](#).<sup>14</sup>

```
R> wlddev |> fsubset(is.finite(POP)) |> fgroup_by(region) |>
+   fmutate(o = radixorder(GRPid(), LIFEEX)) |>
+   fsummarise(min = fmin(LIFEEX),
+             Q1 = fnth(LIFEEX, 0.25, POP, o = o, ties = "q8"),
+             mean = fmean(LIFEEX, POP),
+             median = fmedian(LIFEEX, POP, o = o),
+             Q3 = fnth(LIFEEX, 0.75, POP, o = o, ties = "q8"),
+             max = fmax(LIFEEX))
```

	region	min	Q1	mean	median	Q3	max
1	East Asia & Pacific	18.91	65.28	68.45	69.67	73.86	85.08
2	Europe & Central Asia	45.37	68.68	72.30	71.58	76.67	85.42
3	Latin America & Caribbean	41.76	65.17	69.16	70.87	74.48	82.19
4	Middle East & North Africa	29.92	61.96	66.65	69.12	72.64	82.80
5	North America	68.90	73.57	75.54	75.62	78.38	82.05
6	South Asia	32.45	55.08	60.19	62.00	66.67	78.92
7	Sub-Saharan Africa	26.17	46.51	52.53	52.23	58.32	74.51

Weighted quantiles have a sub-column parallel implementation,<sup>15</sup> and, as shown above, can

<sup>14</sup>**collapse** computes weighted quantiles in a theoretically consistent way, see [fquantile](#) for details.

<sup>15</sup>Use `set_collapse(nthreads = #)` or the `nthreads` arguments to `fnth()/fmedian()/fmode()` (default 1).



also harness an (optional) optimization utilizing an overall ordering vector (combining groups and the data column) to avoid repeated partial sorting of the same elements within groups.

### 3.2. Grouping objects and lower-level API

Whereas the `g` argument supports ad-hoc grouping with vectors and lists/data frames, for repeated operations the cost of grouping can be minimized by using factors (see `?qF` for efficient factor generation) or ‘GRP’ objects as inputs. The latter contain all information **collapse**’s statistical functions may require to operate across groups and are thus passed to internal C/C++ code without checks. They can be created with `GRP()`. Its basic syntax is:

```
GRP(X, by = NULL, sort = TRUE, return.groups = TRUE, method = "auto", ...)
```

Below, I create a ‘GRP’ object from two columns in the World Development Dataset (`wlddev`). The `by` argument also supports column names/indices, and `X` could also be an atomic vector.

```
R> str(g <- GRP(wlddev, ~ income + OECD))

Class 'GRP'  hidden list of 9
 $ N.groups      : int 6
 $ group.id      : int [1:13176] 3 3 3 3 3 3 3 3 3 3 ...
 $ group.sizes   : int [1:6] 2745 2074 1830 2867 3538 122
 $ groups        : 'data.frame':      6 obs. of  2 variables:
  ..$ income: Factor w/ 4 levels "High income",...: 1 1 2 3 4 4
  ..- attr(*, "label")= chr "Income Level"
  ..$ OECD   : logi [1:6] FALSE TRUE FALSE FALSE FALSE TRUE
  ..- attr(*, "label")= chr "Is OECD Member Country?"
 $ group.vars    : chr [1:2] "income" "OECD"
 $ ordered       : Named logi [1:2] TRUE FALSE
  ..- attr(*, "names")= chr [1:2] "ordered" "sorted"
 $ order         : int [1:13176] 245 246 247 248 249 250 251 252 253 254 ...
  ..- attr(*, "starts")= int [1:6] 1 2746 4820 6650 9517 13055
  ..- attr(*, "maxgrp")= int 3538
  ..- attr(*, "sorted")= logi FALSE
 $ group.starts  : int [1:6] 245 611 1 306 62 7687
 $ call          : language GRP.default(X = wlddev, by = ~income + OECD)
```

‘GRP’ objects make grouped statistical computations in **collapse** fully programmable. I can employ the object with the *Fast Statistical Functions* and some utilities<sup>16</sup> to efficiently aggregate GDP per capita, life expectancy, and country name, with population weights.

```
R> add_vars(g$groups,
+   get_vars(wlddev, "country") |> fmode(g, wlddev$POP, use = FALSE),
+   get_vars(wlddev, c("PCGDP", "LIFEEX")) |> fmean(g, wlddev$POP, use = F),
+   get_vars(wlddev, "POP") |> fsum(g, use = FALSE))
```

<sup>16</sup>`add_vars()` is a fast `cbind.data.frame()` which also has an assignment method, and `get_vars()` enables fast and secure extraction of data frame columns.

	income	OECD	country	PCGDP	LIFEEX	POP
1	High income	FALSE	Saudi Arabia	22426.7	73.00	3.114e+09
2	High income	TRUE	United States	31749.6	75.84	5.573e+10
3	Low income	FALSE	Ethiopia	557.1	53.51	2.095e+10
4	Lower middle income	FALSE	India	1238.8	60.59	1.138e+11
5	Upper middle income	FALSE	China	3820.6	68.21	1.114e+11
6	Upper middle income	TRUE	Mexico	8311.2	69.06	8.162e+09

The above is equivalent to `collap(wlddev, country + PCGDP + LIFEEX ~ income + OECD, w = ~ POP)`, which internally toggles many of the same function calls.

Similarly, data can be transformed, here using `fwithin()` to level average differences in economic status, adding back the overall mean after subtracting out group means:<sup>17</sup>

```
R> add_vars(wlddev) <- get_vars(wlddev, c("PCGDP", "LIFEEX")) |>
+   fwithin(g, mean = "overall.mean") |> add_stub("center_")
```

The low-level API is useful for package development and standard-evaluation programming, as further elucidated in the [vignette on developing with collapse](#). Users should note that **collapse** does not provide metaprogramming capabilities in its non-standard evaluation functions—such as [quosures](#) or [indirection](#) familiar to **tidyverse** users. Instead, there exist standard-evaluation equivalents to some of these functions which typically end with a `v` (for 'variables'), such as `collapv()`, `fslicev()`, `ftransformv()`, etc. In other cases, such as those typically handled by `fsummarise()` or `fmutate()`, users may need to use the low-level API for programming, or resort to `substitute()` and friends. The main reason for not providing higher-level metaprogramming capabilities is to keep all functions as simple as possible. It also compels users to think deeper about their programs and devise more efficient solutions.

These metaprogramming restrictions are also vindicated by internally complex data manipulation functions producing greater overheads that can noticeably add up in larger scripts:<sup>18</sup>

```
R> bmark(collapse = collapse::fsummarise(mtcars, sum = sum(mpg)),
+       dplyr = dplyr::summarise(mtcars, sum = sum(mpg)))
```

	expression	min	median	mem_alloc	n_itr	n_gc	total_time
1	collapse	3.61µs	4.26µs	14.33KB	9999	1	43.81ms
2	dplyr	211.27µs	240.26µs	3.92MB	7651	52	1.86s

Grouped programming using 'GRP' objects and *Fast Statistical Functions* is also particularly powerful with vectors and matrices. In the [useR 2022 presentation](#), I aggregate global input-output tables stored as matrices (`x`) from the country to the region level using a single grouping object and expressions of the form `x |> fsum(g) |> t() |> fsum(g) |> t()`.<sup>19</sup>

<sup>17</sup>`add_stub()` adds a prefix (or suffix if `pre = FALSE`) to columns  $\rightarrow$  `center_PCGDP` and `center_LIFEEX`.

<sup>18</sup>`bmark()` is a slim wrapper around `bench::mark()`. See the Computational details section.

<sup>19</sup>Another recent application with vectors involved numerically optimizing a parameter  $a$  in an equation of the form  $\sum_i x_{ij}^a \forall j \in J$  so as to minimize the deviation from a target  $y_j$  where there are  $J$  groups (1 million in my case) - see the first example in [this blog post](#) for an illustration.

## 4. Time series and panel series

**collapse** also provides a flexible high-performance architecture to perform time aware computations on time series and panel series. In particular, users can either apply time series and panel data transformations by passing individual and/or time identifiers to the respective functions in an ad-hoc fashion, or by using ‘`indexed_frame`’ and ‘`indexes_series`’ classes, which implement full and deep indexation for worry-free application in many contexts. Table 2 compactly summarizes **collapse**’s architecture for time series and panel data.

### *Classes, constructors and utilities*

`findex_by()`, `findex()`, `unindex()`, `reindex()`, `timeid()`, `is_irregular()`,  
`to_plm()` + S3 methods for ‘`indexed_frame`’, ‘`indexed_series`’ and ‘`index_df`’

### *Core time-based functions*

`flag()`, `fdiff()`, `fgrowth()`, `fcumsum()`, `psmat()`  
`psacf()`, `pspacf()`, `psccf()`

### *Data transformation functions with supporting methods*

`fscale()`, `f[hd]between()`, `f[hd]within()`

### *Data manipulation functions with supporting methods*

`fsubset()`, `funique()`, `roworder[v]()` (internal), `na_omit()` (internal)

### *Summary functions with supporting methods*

`varying()`, `qsu()`

Table 2: Time series and panel data architecture.

### 4.1. Ad-hoc computations

Time series functions such as `fgrowth()` to compute growth rates are S3 generic and can be applied to most time series classes. In addition to a `g` argument for grouped computation, these functions also have a `t` argument for indexation. If `t` is a plain numeric vector or a factor, it is coerced to integer and interpreted as time steps.<sup>20</sup> But first, a basic example:

```
R> fgrowth(airmiles) |> round(2)
```

Time Series:

Start = 1937

End = 1960

Frequency = 1

---

<sup>20</sup>This is premised on the observation that the most common form of temporal identifier is a plain numeric vector representing calendar years. Users need to manually call `timeid()` on plain numeric vectors with decimals to yield an appropriate integer representation. If `t` is a numeric time object (e.g., ‘`Date`’, ‘`POSIXct`’, etc.), then it is internally passed through `timeid()` which computes the greatest common divisor (GCD) and generates an integer time-id. For the GCD approach to work, `t` must have an appropriate class, e.g., for monthly/quarterly data, `zoo::yearmon()/zoo::yearqtr()` should be used instead of ‘`Date`’ or ‘`POSIXct`’.

```
[1]    NA 16.50 42.29 54.03 31.65  2.38 15.23 33.29 54.36 76.92  2.71 -2.10
[13] 12.91 18.51 32.03 18.57 17.82 13.61 18.19 12.83 13.32  0.01 15.49  4.25
```

To illustrate the full capabilities of these time series functions, I generate a sector-level trade dataset of export values (*v*) by country (*c*), sector (*s*), and year (*y*). Like many detailed trade datasets, it is unbalanced—not all sectors/products are exported by country *c* in all years.

```
R> set.seed(101)
R> exports <- expand.grid(y = 2001:2010, c = paste0("c", 1:10),
+   s = paste0("s", 1:10)) /> fmutate(v = abs(rnorm(1e3))) />
+   colorder(c, s) /> fsubset(-sample.int(1e3, 500))
```

The following extracts one country-sector series from the `exports` dataset. It is irregular, missing years 2003 and 2006.<sup>21</sup> Indexation using the `t` argument then allows for correct (time-aware) computations in this context without the need to ‘expand’ the data/fill gaps.

```
R> .c(y, v) %=% fsubset(exports, c == "c1" & s == "s7", -c, -s)
R> print(y)
```

```
[1] 2001 2002 2004 2005 2007 2008 2009 2010
```

```
R> fgrowth(v, t = y) /> round(2)
```

```
[1]    NA 175.52    NA -22.37    NA 624.27 -79.01 534.56
```

```
R> fgrowth(v, -1:3, t = y) /> head(4)
```

	FG1	--	G1	L2G1	L3G1
[1,]	-63.71	0.3893	NA	NA	NA
[2,]	NA	1.0726	175.52	NA	NA
[3,]	28.82	0.8450	NA	-21.22	117.05
[4,]	NA	0.6559	-22.37	NA	-38.85

Functions `flag()/fdiff()/fgrowth()` also have associated ‘operators’ `L()/D()/G()` to facilitate their use inside formulas and provide an enhanced data frame interface for convenient ad-hoc computations. With panel data, `t` can be omitted, but this requires sorted data with consecutive groups. Below, I demonstrate two ways to compute a sequence of lagged growth rates using either `G()` or `fgrowth()` and `tfm()`—a shorthand for `ftransform()`.<sup>22</sup>

```
R> G(exports, -1:2, by = v ~ c + s, t = ~ y) /> head(3)
```

	c	s	y	FG1.v	v	G1.v	L2G1.v
1	c1	s1	2002	-18.15	0.5525	NA	NA
2	c1	s1	2003	214.87	0.6749	22.17	NA
3	c1	s1	2004	-31.02	0.2144	-68.24	-61.2

<sup>21</sup>`%=%` is an infix operator for the `massign()` function in **collapse** which is a multivariate version of `assign()`.

<sup>22</sup>Several key functions in **collapse** have syntactic shorthands. The `list(v = v)` is needed here to prevent `fgrowth()` from creating a matrix with the growth rates, ensuring that the ‘list’ method applies.

```
R> tfm(exports, fgrowth(list(v = v), -1:2, g = list(c, s), t = y)) |> head(3)
```

```
   c  s    y      v  FG1.v  G1.v L2G1.v
1 c1 s1 2002 0.5525 -18.15    NA     NA
2 c1 s1 2003 0.6749 214.87  22.17    NA
3 c1 s1 2004 0.2144 -31.02 -68.24 -61.2
```

These functions and operators are also integrated with `fgroup_by()` and `fmutate()` for vectorized computations. But, as mentioned earlier, ad-hoc grouping is always more efficient.

```
R> A <- exports |> fgroup_by(c, s) |> fmutate(gv = G(v, t = y)) |> fungroup()
R> head(B <- exports |> fmutate(gv = G(v, g = list(c, s), t = y)), 4)
```

```
   c  s    y      v    gv
1 c1 s1 2002 0.5525    NA
2 c1 s1 2003 0.6749  22.17
3 c1 s1 2004 0.2144 -68.24
4 c1 s1 2005 0.3108  44.98
```

```
R> identical(A, B)
```

```
[1] TRUE
```

## 4.2. Indexed series and frames

For more complex use cases, indexation is convenient. **collapse** supports **plm**'s `'pseries'` and `'pdata.frame'` classes through dedicated methods. Flexibility and performance considerations lead to the creation of new classes `'indexes_series'` and `'indexed_frame'` which inherit from the former. Any data frame-like object can become an `'indexed_frame'` and behave as usual for other operations. The technical implementation of these classes is described in the [vignette on object handling](#) and, in more detail, in the [documentation](#). Their basic syntax is:

```
data_ix <- findex_by(data, id1, ..., time)
data_ix$indexed_series; with(data, indexed_series)
index_df <- findex(data_ix)
```

Data can be indexed using one or more indexing variables. Unlike `'pdata.frame'`, an `'indexed_frame'` is a deeply indexed structure—every series inside the frame is already an `'indexes_series'`. A comprehensive set of [methods for subsetting and manipulation](#), and applicable `'pseries'` and `'pdata.frame'` methods for time series and transformation functions like `flag()/L()` ensure that these objects behave in a time-/panel-aware manner in any caller environment (`with()`, `lm()`, etc.). Indexation can be undone using `unindex()` and redone with `reindex()` and a suitable `'index_df'`. `'indexes_series'` can be atomic vectors or matrices (including objects such as `'ts'` or `'xts'`) and can be created directly using `reindex()`.

```
data <- unindex(data_ix)
data_ix <- reindex(data, index = index_df)
indexed_series <- reindex(vec/mat, index = vec/index_df)
```

It is worth highlighting that the flexibility of this architecture is new to the R ecosystem: A ‘pdata.frame’ or ‘fixest\_panel’ only works inside **plm/fixest** estimation functions.<sup>23</sup> Time series classes like ‘xts’ and ‘tsibble’ also do not provide deeply indexed structures or native handling of irregularity in basic operations. ‘indexed\_series’ and ‘indexed\_frame’, on the other hand, work ‘anywhere’, and can be superimposed on any suitable object, as long as **collapse**’s functions (`flag()/L()`, etc.) are used to perform the time-based computations.

An example using the `exports` data follows. Note that data need not be sorted for indexing.

```
R> exportsi <- exports /> findex_by(c, s, y)
R> exportsi /> G() /> head(5)
```

```
      c  s    y  G1.v
1 c1 s1 2002    NA
2 c1 s1 2003  22.17
3 c1 s1 2004 -68.24
4 c1 s1 2005  44.98
5 c1 s1 2006 277.76
```

```
Indexed by:  c.s [1] | y [5 (10)]
```

```
R> exportsi /> findex() /> print(2)
```

```
      c.s    y
1 c1.s1 2002
2 c1.s1 2003
---
499 c10.s10 2007
500 c10.s10 2009
```

```
c.s [100] | y [10]
```

The index statistics are: [N. ids] | [N. periods (total periods: (max-min)/GCD)].

```
R> vi <- exportsi$v; str(vi, width = 70, strict = "cut")
```

```
'indexed_series' num [1:500] 0.552 0.675 0.214 0.311 1.174 ...
- attr(*, "index_df")=Classes 'index_df', 'pindex' and 'data.frame'..
..$ c.s: Factor w/ 100 levels "c1.s1","c2.s1",...: 1 1 1 1 1 1 1 1 ..
..$ y : Ord.factor w/ 10 levels "2001"<"2002"<...: 2 3 4 5 6 7 8 9..
..- attr(*, "nam")= chr [1:3] "c" "s" "y"
```

```
R> is_irregular(vi)
```

```
[1] TRUE
```

---

<sup>23</sup>And, in the case of **fixest**, inside **data.table** due to dedicated methods.



```
R> vi |> psmat() |> head(3)
```

```
      2001  2002  2003  2004  2005  2006  2007  2008  2009  2010
c1.s1   NA 0.552 0.675 0.214 0.311 1.17 0.619 0.1127 0.917 0.223
c2.s1   NA 0.795    NA    NA 0.237    NA    NA 0.0585 0.818    NA
c3.s1   NA 0.709 0.268 1.464    NA    NA 0.467 0.1193 0.467    NA
```

```
R> fdiff(vi) |> psmat() |> head(3)
```

```
      2001 2002  2003  2004  2005  2006  2007  2008  2009  2010
c1.s1   NA   NA 0.122 -0.461 0.0964 0.863 -0.555 -0.506 0.804 -0.694
c2.s1   NA   NA    NA    NA    NA    NA    NA    NA 0.759    NA
c3.s1   NA   NA -0.441 1.196    NA    NA    NA -0.348 0.348    NA
```

`psmat()`, for panel-series to matrix, generates a matrix/array from panel data. Thanks to deep indexing, indexed computations work in arbitrary data masking environments:

```
R> settransform(exportsi, v_ld = Dlog(v))
R> lm(v_ld ~ L(v_ld, 1:2), exportsi) |> summary() |> coef() |> round(3)
```

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	-0.008	0.141	-0.058	0.954
L(v_ld, 1:2)L1	-0.349	0.115	-3.042	0.004
L(v_ld, 1:2)L2	-0.033	0.154	-0.215	0.831

Indexed series/frames also support transformation such as grouped scaling with `fscale()` or demeaning with `fwthin()`. Functions `psacf()`/`pspacf()`/`psccf()` provide panel-data autocorrelation functions, which are computed using group-scaled and suitably lagged panel-series. The ‘`index_df`’ attached to these objects can also be used with other general tools such as `collapse::BY()` to perform grouped computations using 3rd-party functions. An example of calculating a 5-year rolling average is given below (`ix()` abbreviates `findex()`).

```
R> BY(vi, ix(vi)$c.s, data.table::frollmean, 5) |> head(10)
```

```
[1]    NA    NA    NA    NA 0.5853 0.5986 0.4861 0.6267 0.6092    NA
```

```
Indexed by:  c.s [2] | y [9 (10)]
```

## 5. Table joins and pivots

Among all [data manipulation functions](#) `collapse` provides, its implementations of table [joins](#) and [pivots](#) are particularly noteworthy since they offer several new features, including rich verbosity for table joins, pivots supporting variable labels, and recast pivots. Both implementations provide outstanding computational performance, syntax, and memory efficiency.

## 5.1. Joins

Compared to commercial software such as STATA (StataCorp LLC. 2023), the implementation of joins in most open-source software provides no information on how many records were joined from both tables. This often provokes manual efforts to validate the join operation. `collapse::join()` provides many options to understand table join operations. Its syntax is:

```
join(x, y, on = NULL, how = "left", suffix = NULL, validate = "m:m",
     multiple = FALSE, sort = FALSE, keep.col.order = TRUE,
     drop.dup.cols = FALSE, verbose = 1, column = NULL, attr = NULL, ...)
```

It defaults to left join and only takes first matches from `y` (`multiple = FALSE`), thus, it simply adds columns to `x`, which is efficient and sufficient/desired in many cases. By default (`verbose = 1`), it prints information about the join operation and number of records joined.

To demonstrate `join()`, I generate a small database for a bachelor in economics curriculum. It has a `teacher` table of 4 teachers (`id`: PK) and a linked (`id`: FK) `course` table of 5 courses.

```
R> teacher <- data.frame(id = 1:4, names = c("John", "Jane", "Bob", "Carl"),
+   age = c(35, 32, 42, 67), subject = c("Math", "Econ", "Stats", "Trade"))
R> course <- data.frame(id = c(1, 2, 2, 3, 5), semester = c(1, 1, 2, 1, 2),
+   course = c("Math I", "Microecon", "Macroecon", "Stats I", "History"))
R> join(teacher, course, on = "id")
```

```
left join: teacher[id] 3/4 (75%) <1:1st> course[id] 3/5 (60%)
  id names age subject semester   course
1  1  John  35    Math         1   Math I
2  2  Jane  32    Econ         1 Microecon
3  3   Bob  42   Stats         1   Stats I
4  4  Carl  67   Trade        NA      <NA>
```

Users can request the generation of a `.join` column (`column = "name"/TRUE`), akin to STATA's `_merge` column, to indicate the origin of records in the joined table—useful with a full join:

```
R> join(teacher, course, how = "full", multiple = TRUE, column = TRUE)
```

```
full join: teacher[id] 3/4 (75%) <1:1.33> course[id] 4/5 (80%)
  id names age subject semester   course   .join
1  1  John  35    Math         1   Math I matched
2  2  Jane  32    Econ         1 Microecon matched
3  2  Jane  32    Econ         2 Macroecon matched
4  3   Bob  42   Stats         1   Stats I matched
5  4  Carl  67   Trade        NA      <NA> teacher
6  5 <NA>  NA    <NA>         2   History  course
```

An alternative is to request an attribute (`attr = "name"/TRUE`) that also summarizes the join operation, including the output of `fmatch()`—the workhorse of `join()` if `sort = FALSE`.

```
R> join(teacher, course, multiple = TRUE, attr = "jn") |> attr("jn") |> str()

left join: teacher[id] 3/4 (75%) <1:1.33> course[id] 4/5 (80%)
List of 3
 $ call      : language join(x = teacher, y = course, multiple = TRUE,"..
 $ on.cols:List of 2
  ..$ x: chr "id"
  ..$ y: chr "id"
 $ match    : 'qG' int [1:5] 1 2 3 4 NA
  ..- attr(*, "N.nomatch")= int 1
  ..- attr(*, "N.groups")= int 5
  ..- attr(*, "N.distinct")= int 4
```

Users can also invoke the `validate` argument to examine the uniqueness of the join keys in either table: passing a '1' produces an error if the key is not unique.

```
R> join(teacher, course, on = "id", validate = "1:1") |>
+   tryCatch(error = function(e) strwrap(e) |> cat(sep = "\n"))
```

```
Error in join(teacher, course, on = "id", validate = "1:1"): Join is
not 1:1: teacher (x) is unique on the join columns; course (y) is
not unique on the join columns
```

Similarly, the `require` argument allows users to demand a minimum matching success rate.

```
R> join(teacher, course, on = "id", require = list(x = 0.8)) |>
+   tryCatch(error = function(e) substr(e, 102, 200) |> cat())
```

```
Matched 75.0% of records in table teacher (x), but 80.0% is required
```

A few further particularities are worth highlighting. First, `join()` is class-agnostic and preserves the attributes of `x` (any list-based object). It supports 6 different join operations ("left", "right", "inner", "full", "semi", or "anti" join). This demonstrates the latter:

```
R> for (h in c("semi", "anti")) join(teacher, course, how = h) |> print()
```

```
semi join: teacher[id] 3/4 (75%) <1:1st> course[id] 3/5 (60%)
  id names age subject
1  1  John  35    Math
2  2  Jane  32    Econ
3  3   Bob  42    Stats
anti join: teacher[id] 3/4 (75%) <1:1st> course[id] 3/5 (60%)
  id names age subject
1  4  Carl  67    Trade
```

By default (`sort = FALSE`), the order of rows in `x` is preserved. Setting `sort = TRUE` sorts all records in the joined table by the keys.<sup>24</sup> The join relationship is indicated inside the `<>` as the number of records joined from each table divided by the number of unique matches.

---

<sup>24</sup>This is done using a separate sort-merge-join algorithm, so it is faster than performing a hash join (using `fmatch()`) followed by sorting, particularly if the data is already sorted on the keys.

```
R> course$names <- teacher$names[course$id]
R> join(teacher, course, on = "id", how = "inner", multiple = TRUE)
```

```
inner join: teacher[id] 3/4 (75%) <1:1.33> course[id] 4/5 (80%)
duplicate columns: names => renamed using suffix '_course' for y
```

	id	names	age	subject	semester	course	names_course
1	1	John	35	Math	1	Math I	John
2	2	Jane	32	Econ	1	Microecon	Jane
3	2	Jane	32	Econ	2	Macroecon	Jane
4	3	Bob	42	Stats	1	Stats I	Bob

As shown above, `join()`'s handling of duplicate columns in both tables is rather special. By default (`suffix = NULL`), `join()` extracts the name of the y table and appends y-columns with it. x-columns are not renamed. This is congruent to the principle of adding columns to x and altering this table as little as possible. Alternatively, option `drop.dup.cols = "x"/"y"` can be used to remove duplicate columns from either x or y before the join operation.

```
R> join(teacher, course, on = "id", multiple = TRUE, drop.dup.cols = "y")
```

```
left join: teacher[id] 3/4 (75%) <1:1.33> course[id] 4/5 (80%)
duplicate columns: names => dropped from y
```

	id	names	age	subject	semester	course
1	1	John	35	Math	1	Math I
2	2	Jane	32	Econ	1	Microecon
3	2	Jane	32	Econ	2	Macroecon
4	3	Bob	42	Stats	1	Stats I
5	4	Carl	67	Trade	NA	<NA>

A final noteworthy feature is that `fmatch()` has a built-in overidentification check, which warns if more key columns than necessary to identify the records are provided. This check only triggers with 3+ id columns as for efficiency reasons the first two ids are hashed jointly. `join()` is thus a highly efficient, versatile, and verbose implementation of table joins for R.

## 5.2. Pivots

The reshaping/pivoting functionality of both commercial and open-source software is also presently unsatisfactory for complex datasets such as surveys or disaggregated production, trade, or financial sector data, where variable names resemble codes and variable labels are essential to making sense of the data. Such datasets can presently only be reshaped by losing these labels or additional manual efforts to retain them. Modern R packages also offer different reshaping functions, such as `data.table::melt()/tidyr::pivot_longer()` to combine columns and `data.table::dcast()/tidyr::pivot_wider()` to expand them, requiring users to learn both. Since the depreciation of `reshape(2)` (Wickham 2007), there is also no modern replacement for `reshape2::recast()`, requiring R users to consecutively call two functions.

`collapse::pivot` provides a class-agnostic implementation of reshaping for R that addresses these shortcomings. It has a single intuitive syntax to perform 'longer', 'wider', and 'recast' pivots and supports complex labelled data without loss of information. Its basic syntax is:

```
pivot(data, ids = NULL, values = NULL, names = NULL, labels = NULL,
      how = "longer", na.rm = FALSE, check.dups = FALSE, ...)
```

The demonstration below employs the included Groningen Growth and Development Centre 10-Sector Database (**GGDC10S**) providing long-run internationally comparable data on sectoral productivity performance in Africa, Asia, and Latin America. While the database covers 10 sectors, for the demonstration I only retain Agriculture, Mining, and Manufacturing.<sup>25</sup>

```
R> data <- GGDC10S />
+   fmutate(Label = ifelse(Variable == "VA", "Value Added", "Employment")) />
+   fsubset(is.finite(AGR), Country, Variable, Label, Year, AGR:MAN)
R> namlab(data, N = TRUE, Ndistinct = TRUE, class = TRUE)
```

	Variable	Class	N	Ndist	Label
1	Country	character	4364	43	Country
2	Variable	character	4364	2	Variable
3	Label	character	4364	2	<NA>
4	Year	numeric	4364	67	Year
5	AGR	numeric	4364	4353	Agriculture
6	MIN	numeric	4355	4224	Mining
7	MAN	numeric	4355	4353	Manufacturing

To reshape this dataset into a longer format, it suffices to call `pivot(data, ids = 1:4)`. If `labels = "name"` is specified, variable labels stored in `attr(column, "label")` are saved to an additional column. In addition, `names = list(variable = "var_name", value = "val_name")` can be passed to set alternative names for the variable and value columns.

```
R> head(dl <- pivot(data, ids = 1:4, names = list("Sectorcode", "Value"),
+         labels = "Sector", how = "longer"))
```

	Country	Variable	Label	Year	Sectorcode	Sector	Value
1	BWA	VA	Value Added	1964	AGR	Agriculture	16.30
2	BWA	VA	Value Added	1965	AGR	Agriculture	15.73
3	BWA	VA	Value Added	1966	AGR	Agriculture	17.68
4	BWA	VA	Value Added	1967	AGR	Agriculture	19.15
5	BWA	VA	Value Added	1968	AGR	Agriculture	21.10
6	BWA	VA	Value Added	1969	AGR	Agriculture	21.86

`pivot()` only requires essential information and intelligently guesses the rest. For example, the same result could have been obtained by specifying `values = c("AGR", "MIN", "MAN")` instead of `ids = 1:4`. An exact reverse operation can also be specified as `pivot(dl, 1:4, "Value", "Sectorcode", "Sector", "wider")`, with `dl` the long data.

The second option is a wider pivot with `how = "wider"`. Here, `names` and `labels` can be used to select columns containing the names of new columns and their labels.<sup>26</sup> Note below

<sup>25</sup>The "Label" column is added for demonstration purposes. `namlab()` provides a compact overview of variable names and labels stored in `attr(column, "label")`, with (optional) additional information/statistics.

<sup>26</sup>If multiple columns are selected, they are combined using "\_" for names and " - " for labels.

how the labels are combined with existing labels such that also this operation is without loss of information. It is, however, a destructive operation—with 2 or more columns selected through `values`, `pivot()` is not able to reverse it. Further arguments like `na.rm`, `fill`, `drop`, `sort`, and `transpose` can be used to control the casting process/output.

```
R> head(dw <- pivot(data, c("Country", "Year"), names = "Variable",
+                      labels = "Label", how = "w"))
```

	Country	Year	AGR_VA	AGR_EMP	MIN_VA	MIN_EMP	MAN_VA	MAN_EMP
1	BWA	1964	16.30	152.1	3.494	1.9400	0.7366	2.420
2	BWA	1965	15.73	153.3	2.496	1.3263	1.0182	2.330
3	BWA	1966	17.68	153.9	1.970	1.0022	0.8038	1.282
4	BWA	1967	19.15	155.1	2.299	1.1192	0.9378	1.042
5	BWA	1968	21.10	156.2	1.839	0.7855	0.7503	1.069
6	BWA	1969	21.86	157.4	5.245	2.0314	2.1396	2.124

```
R> namlab(dw)
```

	Variable	Label
1	Country	Country
2	Year	Year
3	AGR_VA	Agriculture - Value Added
4	AGR_EMP	Agriculture - Employment
5	MIN_VA	Mining - Value Added
6	MIN_EMP	Mining - Employment
7	MAN_VA	Manufacturing - Value Added
8	MAN_EMP	Manufacturing - Employment

For the recast pivot (`how = "recast"`), unless a column named `variable` exists in the data, the source and (optionally) destination of variable names needs to be specified using a list passed to `names`, and similarly for `labels`. Again, taking along labels is entirely optional—omitting either the labels-list's `from` or `to` element will omit the respective operation.

```
R> head(dr <- pivot(data, c("Country", "Year"),
+                      names = list(from = "Variable", to = "Sectorcode"),
+                      labels = list(from = "Label", to = "Sector"), how = "r"))
```

	Country	Year	Sectorcode	Sector	VA	EMP
1	BWA	1964	AGR	Agriculture	16.30	152.1
2	BWA	1965	AGR	Agriculture	15.73	153.3
3	BWA	1966	AGR	Agriculture	17.68	153.9
4	BWA	1967	AGR	Agriculture	19.15	155.1
5	BWA	1968	AGR	Agriculture	21.10	156.2
6	BWA	1969	AGR	Agriculture	21.86	157.4

```
R> vlabels(dr)[3:6]
```



Sectorcode	Sector	VA	EMP
NA	NA	"Value Added"	"Employment"

This (`dr`) is the tidy format (Wickham 2014) where each variable is a separate column. It is analytically more useful, e.g., to compute labor productivity as `settransform(dr, LP = VA / EMP)` or to estimate a panel-regression with sector fixed-effects. The recast pivot is thus a natural operation to change data representation. As with the other pivots, it preserves all information and can be reversed by simply swapping the contents of the `from` and `to` keywords.

`pivot()` also supports fast aggregation pivots, the default being `FUN = "last"`, which simply overwrites values in appearance order if the combination of `ids` and `names` does not fully identify the data. The latter can be checked with `check.dups = TRUE`. There are a small number of internal functions: `"first"`, `"last"`, `"sum"`, `"mean"`, `"min"`, `"max"`, and `"count"`. These carry out computations 'on the fly' and are thus extremely fast. `pivot()` also supports *Fast Statistical Functions*, which will yield vectorized aggregations, but require a deep copy of the columns aggregated which is avoided using the internal functions. The following example performs aggregation across years with the internal mean function during a recast pivot.

```
R> head(dr_agg <- pivot(data, "Country", c("AGR", "MIN", "MAN"), how = "r",
+   names = list(from = "Variable", to = "Sectorcode"),
+   labels = list(from = "Label", to = "Sector"), FUN = "mean"))
```

	Country	Sectorcode	Sector	VA	EMP
1	BWA	AGR	Agriculture	462.2	188.06
2	ETH	AGR	Agriculture	34389.9	17624.34
3	GHA	AGR	Agriculture	1549.4	3016.04
4	KEN	AGR	Agriculture	139705.9	5348.91
5	MWI	AGR	Agriculture	28512.6	2762.62
6	MUS	AGR	Agriculture	3819.6	59.34

The [documentation examples](#) demonstrate more features of `pivot()`. Notably, it can also perform longer and recast pivots without id variables, like `data.table::transpose()`.

## 6. List processing

Often in programming, nested structures are needed. A typical use case involves running statistical procedures for multiple configurations of variables and parameters and saving multiple objects (such as a model predictions and performance statistics) in a list. Nested data is also often the result of web scraping or web APIs. A typical use case in development involves serving different data according to user choices. Except for certain recursive functions found in packages such as **purrr**, **tidyr**, or **rrapply**, R lacks a general recursive toolkit to create, query, and tidy nested data. **collapse**'s [list processing functions](#) attempt to provide a basic toolkit.

To create nested data, `rsplit()` generalizes `split()` and (recursively) splits up data frame-like objects into (nested) lists. For example, we can split the `GGDC10S` data by country and variable, such that, for example, agricultural employment in Argentina can be accessed as:<sup>27</sup>

<sup>27</sup>If a nested structure is not needed, `flatten = TRUE` lets `rsplit()` operate like a faster version of `split()`.

```
R> dl <- GGDC10S |> rsplit( ~ Country + Variable)
R> dl$ARG$EMP$AGR[1:12]
```

```
[1] 1800 1835 1731 2030 1889 1843 1789 1724 1678 1725 1650 1553
```

This is a convenient data representation for *Shiny Apps* where we can let the user choose data (e.g., `dl[[input$country]][[input$variable]][[input$sector]]`) without expensive subsetting operations. As mentioned, such data representation can also be the result of an API call parsing JSON or a nested loop or `lapply()` call. Below, I write a nested loop running a regression of agriculture on mining and manufacturing output and employment.

```
R> result <- list()
R> for (country in c("ARG", "BRA", "CHL")) {
+   for (variable in c("EMP", "VA")) {
+     m <- lm(log(AGR+1) ~ log(MIN+1) + log(MAN+1) + Year,
+             data = dl[[country]][[variable]])
+     result[[country]][[variable]] <- list(model = m, BIC = BIC(m),
+                                           summary = summary(m))
+   }
+ }
```

This programming may not be ideal for this particular use case as I could have used data frame-based tools and saved the result in a column.<sup>28</sup> However, there are limits to such workflows. For example, I recently trained a complex ML model for different variables and parameters, which involved loading a different dataset at each iteration. Loops are useful in such cases, and lists a natural vehicle to structure complex outputs. The main issue with nested lists is that they are complex to query. What if we want to know just the  $R^2$  of these 6 models? We would need to use, e.g., `result$ARG$EMP$summary$r.squared` for each model.

This nested list-access problem was the main reason for creating `get_elem()`: an efficient recursive list-filtering function which, by default, simplifies the list tree as much as possible.

```
R> str(r_sq_l <- result |> get_elem("r.squared"))
```

```
List of 3
 $ ARG:List of 2
  ..$ EMP: num 0.907
  ..$ VA : num 1
 $ BRA:List of 2
  ..$ EMP: num 0.789
  ..$ VA : num 0.999
 $ CHL:List of 2
  ..$ EMP: num 0.106
  ..$ VA : num 0.999
```

---

<sup>28</sup>E.g., `GGDC10S |> fgroup_by(Country, Variable) |> fsummarise(result = my_fun(lm(log(AGR+1) log(MIN+1) + log(MAN+1) + Year)))` with `my_fun <- function(m) list(list(m, BIC(m), summary(m)))`.

```
R> rowbind(r_sq_l, idcol = "Country", return = "data.frame")
```

	Country	EMP	VA
1	ARG	0.9068	0.9996
2	BRA	0.7888	0.9988
3	CHL	0.1058	0.9991

Note how the "summary" branch was eliminated since it is common to all final nodes; `result |> get_elem("r.squared", keep.tree = TRUE)` could have been used to keep it. `rowbind()` then efficiently combines lists of lists. We can also apply `t_list()` to turn the list inside-out:

```
R> r_sq_l |> t_list() |> rowbind(idcol = "Variable", return = "data.frame")
```

	Variable	ARG	BRA	CHL
1	EMP	0.9068	0.7888	0.1058
2	VA	0.9996	0.9988	0.9991

`rowbind()` is limited if `get_elem()` returns a more nested or asymmetric list, potentially with vectors/arrays in the final nodes. Suppose we want to extract the coefficient matrices:

```
R> result$ARG$EMP$summary$coefficients
```

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	26.583617	1.2832583	20.7157	1.747e-28
log(MIN + 1)	0.083168	0.0352493	2.3594	2.169e-02
log(MAN + 1)	-0.064413	0.0767614	-0.8391	4.048e-01
Year	-0.009683	0.0005556	-17.4278	1.003e-24

For such cases, `unlist2d()` provides a complete recursive generalization of `unlist()`. It creates a 'data.frame' or 'data.table' representation of any nested list using recursive row-binding and coercion operations, while generating (optional) id variables representing the list tree and (optionally) saving row names of matrices or data frames. In the present example

```
R> result |> get_elem("coefficients") |> get_elem(is.matrix) |>
+   unlist2d(idcols = c("Country", "Variable"),
+   row.names = "Covariate") |> head(3)
```

	Country	Variable	Covariate	Estimate	Std. Error	t value	Pr(> t )
1	ARG	EMP	(Intercept)	26.58362	1.28326	20.7157	1.747e-28
2	ARG	EMP	log(MIN + 1)	0.08317	0.03525	2.3594	2.169e-02
3	ARG	EMP	log(MAN + 1)	-0.06441	0.07676	-0.8391	4.048e-01

where `get_elem(is.matrix)` is needed because the models also contain "coefficients".

This exemplifies the power of these tools to create, query, and combine nested data in very general ways. Further useful functions include `has_elem()` to check for the existence of

elements, `ldepth()` to return the maximum level of recursion, `is_unlistable()` to check whether a list has atomic elements in all final nodes, `[ir]reg_elem()` to recursively extract the (non-)atomic elements, and `rapply2d()` to apply functions to nested lists of data objects.

## 7. Summary statistics

**collapse**'s **summary statistics functions** offer a parsimonious yet powerful toolkit to examine complex datasets. A particular focus has been on providing tools for examining longitudinal (panel) data. Recall the indexed World Development panel dataset (**wlddev**). The function `varying()` can be used to examine which of these variables are time-varying.

```
R> varying(wlddev, ~ iso3c)
```

country	date	year	decade	region
FALSE	TRUE	TRUE	TRUE	FALSE
income	OECD	PCGDP	LIFEEX	GINI
FALSE	FALSE	TRUE	TRUE	TRUE
ODA	POP	center_PCGDP	center_LIFEEX	
TRUE	TRUE	TRUE	TRUE	

A related exercise is to decompose the variance of a panel series into variation between countries and variation within countries over time. Using the (de-)meaning functions `fbetween()`/`fwithin()` supporting 'indexed\_series' (see Table 2), this is easily demonstrated.

```
R> LIFEEXi <- reindex(wlddev$LIFEEX, wlddev$iso3c)
R> all.equal(fvar(LIFEEXi), fvar(fbetween(LIFEEXi)) + fvar(fwithin(LIFEEXi)))
```

```
[1] TRUE
```

The `qsu()` (quick-summary) function provides an efficient method to compute this decomposition, considering the group-means instead of the between transformation<sup>29</sup> and adding the overall mean back to the within transformation to preserve the scale of the data.

```
R> qsu(LIFEEXi)
```

	N/T	Mean	SD	Min	Max
Overall	11670	64.2963	11.4764	18.907	85.4171
Between	207	64.9537	9.8936	40.9663	85.4171
Within	56.3768	64.2963	6.0842	32.9068	84.4198

The decomposition above implies more variation in life expectancy between countries than within countries over time. It can also be computed for different subgroups and with sampling weights. `qsu()` also has a data frame method, and by default computes simple statistics:<sup>30</sup>

<sup>29</sup>This is more efficient and equal to using the between transformation if the panel is balanced.

<sup>30</sup>The `pid` argument to `qsu()` can also be used to pass identifiers for panel-decomposition, e.g., `pid = iso3c`. With indexed data, it is automatically set to the first column in the index (`effect = 1`).

```
R> qsu(wlddev, by = LIFEEX ~ income, w = ~ POP)
```

	N	WeightSum	Mean	SD	Min	Max
High income	3828	5.87959699e+10	75.6926	4.5346	42.672	85.4171
Low income	1792	2.09491614e+10	53.5061	8.8691	26.172	74.43
Lower middle income	2790	1.13837685e+11	60.5865	8.3607	18.907	76.699
Upper middle income	3249	1.19295269e+11	68.2698	7.1889	36.535	80.279

For greater detail, `descr()` provides a rich (grouped, weighted) statistical description. It does not support panel-variance decompositions like `qsu()`, but also computes detailed (grouped, weighted) frequency tables for categorical data and is thus very useful with mixed-type data.

```
R> wlda15 <- wlddev |> fsubset(year >= 2015) |> fgroup_by(iso3c) |> flast()
R> wlda15 |> descr(by = income + LIFEEX ~ OECD)
```

Dataset: wlda15, 2 Variables, N = 216

Grouped by: OECD [2]

	N	Perc
FALSE	180	83.33
TRUE	36	16.67

income (factor): Income Level

Statistics (N = 216)

	N	Perc	Ndist
FALSE	180	83.33	4
TRUE	36	16.67	2

Table (Freq Perc)

	FALSE		TRUE		Total	
High income	45	25.0	34	94.4	79	36.6
Upper middle income	58	32.2	2	5.6	60	27.8
Lower middle income	47	26.1	0	0.0	47	21.8
Low income	30	16.7	0	0.0	30	13.9

LIFEEX (numeric): Life expectancy at birth, total (years)

Statistics (N = 200, 7.41% NAs)

	N	Perc	Ndist	Mean	SD	Min	Max	Skew	Kurt
FALSE	164	82	164	71.25	7.06	53.28	85.08	-0.5	2.61
TRUE	36	18	36	80.83	2.55	75.05	84.36	-0.92	2.72

Quantiles

	1%	5%	10%	25%	50%	75%	90%	95%	99%
FALSE	54.3	58.38	61.25	66.43	72.56	76.68	78.93	80.88	83.77
TRUE	75.12	75.83	76.8	79.04	81.77	82.63	83.21	83.54	84.13

It also has a `stepwise` argument to describe one variable at a time, allowing users to naturally 'click-through' the variables in a large dataset while spreading the computational burden. The

[documentation](#) provides more details and examples. Both `qsu()` and `descr()` come with an `as.data.frame()` method for efficient tidying and easy further analysis.

A final noteworthy function from **collapse**'s descriptive statistics toolkit is `qtab()`, an enhanced drop-in replacement for `table()`. It is enhanced both in a statistical and a computational sense, providing a remarkable performance boost, an option `sort = FALSE` to preserve the first-appearance-order of vectors being cross-tabulated, support for frequency weights (`w`), and the ability to compute different statistics representing table entries using these weights—vectorized when using *Fast Statistical Functions*, as demonstrated below.

```
R> wlda15 /> with(qtab(OECD, income))
```

	income			
OECD	High income	Low income	Lower middle income	Upper middle income
FALSE	45	30	47	58
TRUE	34	0	0	2

This shows the total population (latest post-2015 estimates) in millions.

```
R> wlda15 /> with(qtab(OECD, income, w = POP) / 1e6)
```

	income			
OECD	High income	Low income	Lower middle income	Upper middle income
FALSE	93.01	694.89	3063.54	2459.71
TRUE	1098.75	0.00	0.00	211.01

This shows the average life expectancy in years. The use of `fmean()` toggles an efficient vectorized computation of the table entries (i.e., `fmean()` is only called once).

```
R> wlda15 /> with(qtab(OECD, income, w = LIFEEX, wFUN = fmean))
```

	income			
OECD	High income	Low income	Lower middle income	Upper middle income
FALSE	78.75	62.81	68.30	73.81
TRUE	81.09			76.37

Finally, this calculates a population-weighted average of life expectancy in each group.

```
R> wlda15 /> with(qtab(OECD, income, w = LIFEEX, wFUN = fmean,
+                      wFUN.args = list(w = POP)))
```

	income			
OECD	High income	Low income	Lower middle income	Upper middle income
FALSE	77.91	63.81	68.76	75.93
TRUE	81.13			76.10



‘qtab’ objects inherit the ‘table’ class, thus all ‘table’ methods apply. Apart from the above functions, **collapse** also provides functions `pwcor()`, `pwcov()`, and `pwnobs()` for convenient (pairwise, weighted) correlations, covariances, and observations counts, respectively.

## 8. Global options

**collapse** is **globally configurable** to an extent few packages are: the default values of key function arguments governing the behavior of its algorithms, and the exported namespace, can be adjusted interactively through the `set_collapse()` function. These options are saved in an internal environment called `.op`. Its contents can be accessed using `get_collapse()`.

The current set of options comprises the default behavior for missing values (`na.rm` arguments in all statistical functions and algorithms), sorted grouping (`sort`), multithreading and algorithmic optimizations (`nthreads`, `stable.algo`), presentational settings (`stub`, `digits`, `verbose`), and, surpassing all else, the package namespace itself (`mask`, `remove`).

As evident from previous sections, **collapse** provides performance-improved or otherwise enhanced versions of functionality already present in base R (like the *Fast Statistical Functions*, `funique()`, `fmatch()`, `fsubset()`, `ftransform()`, etc.) and other packages (esp. **dplyr** (Wickham *et al.* 2023): `fselect()`, `fsummarise()`, `fmutate()`, `frename()`, etc.). The objective of being namespace compatible warrants such a naming convention, but this has a syntactical cost, particularly when **collapse** is the primary data manipulation package.

To reduce this cost, **collapse**’s `mask` option allows masking existing R functions with the faster **collapse** versions by creating additional functions in the namespace and instantly exporting them. All **collapse** functions starting with ‘f’ can be passed to the option (with or without the ‘f’), e.g., `set_collapse(mask = c("subset", "transform"))` creates `subset <- fsubset` and `transform <- ftransform` and exports them. Special functions are “n”, “table”/“qtab”, and “%in%”, which create `n <- GRPN` (for use in (f)summarise/(f)mutate), `table <- qtab`, and replace `%in%` with a fast version using `fmatch()`, respectively. There are also several **convenience keywords to mask related groups of functions**. The most powerful of these is “all”, which masks all f-functions and special functions, as shown below.

```
set_collapse(mask = "all")
wlddev |> subset(year >= 1990 & is.finite(GINI)) |>
  group_by(year) |>
  summarise(n = n(), across(PCGDP:GINI, mean, w = POP))
with(mtcars, table(cyl, vs, am))
sum(mtcars)
diff(EuStockMarkets)
mean(num_vars(iris), g = iris$Species)
unique(wlddev, cols = c("iso3c", "year"))
range(wlddev$date)
wlddev |> index_by(iso3c, year) |>
  mutate(PCGDP_lag = lag(PCGDP),
         PCGDP_growth = growth(PCGDP)) |> unindex()
```

The above is now 100% **collapse** code. Similarly, using this option, all code in this article could have been written without `f`-prefixes. Thus, **collapse** is able to offer a fast and syntactically clean experience of R—without the need to even restart the session. Masking is completely and interactively reversible: calling `set_collapse(mask = NULL)` instantly removes the additional functions. Option `remove` can further be used to remove (un-export) any **collapse** function, allowing manual conflict management. Function `fastverse::fastverse_conflicts()` from the related **fastverse** project (Krantz 2024) can be used to display namespace conflicts with **collapse**. Invoking either `mask` or `remove` detaches **collapse** and re-attaches it at the top of the search path, letting its namespace to take precedence over other packages.

Such global powers confer responsibilities upon package developers, as further elucidated in the [vignette on developing with collapse](#). As a general rule, options `mask` and `remove` should be off-limits inside packages, and other options need to be reset immediately using `on.exit()`.

## 9. Benchmark

This section provides several simple benchmarks to show that **collapse** provides best-in-R performance for statistics and data manipulation on moderately sized datasets. They are executed on a 2024 Apple MacBook Pro with 48GB M4 Pro chip. It also discusses results from [3rd party benchmarks](#) involving **collapse**. The first set of benchmarks show that **collapse** provides faster computationally intensive operations like unique values and matching on large integer and character vectors. It creates integer/character vectors of 10 million obs, with 1000 unique integers and 5776 unique strings, respectively, which are deduplicated/matched in the benchmark. These fast basic operations impact many critical components of the package.

```
R> set.seed(101)
R> int <- 1:1000; g_int <- sample.int(1000, 1e7, replace = TRUE)
R> char <- c(letters, LETTERS, month.abb, month.name)
R> g_char <- sample(char <- outer(char, char, paste0), 1e7, TRUE)
R> bmark(base_int = unique(g_int), collapse_int = funique(g_int))
```

	expression	min	median	mem_alloc	n_itr	n_gc	total_time
1	base_int	41.49ms	43.2ms	166.2MB	47	47	2.04s
2	collapse_int	5.47ms	9.28ms	38.2MB	220	44	2.01s

```
R> bmark(base_char = unique(g_char), collapse_char = funique(g_char))
```

	expression	min	median	mem_alloc	n_itr	n_gc	total_time
1	base_char	68.7ms	70ms	166.2MB	28	28	2.01s
2	collapse_char	13.8ms	15.7ms	38.2MB	123	21	2.01s

```
R> bmark(base_int = match(g_int, int), collapse_int = fmatch(g_int, int))
```

	expression	min	median	mem_alloc	n_itr	n_gc	total_time
1	base_int	15.13ms	15.58ms	76.3MB	38	67	608.03ms
2	collapse_int	5.47ms	7.74ms	38.2MB	196	49	1.43s

```
R> bmark(base_char = match(g_char, char), data.table_char =
+       chmatch(g_char, char), collapse_char = fmatch(g_char, char))
```

	expression	min	median	mem_alloc	n_itr	n_gc	total_time
1	base_char	60.8ms	62.4ms	114.5MB	32	32	2.07s
2	data.table_char	31.9ms	34ms	38.1MB	58	18	2.02s
3	collapse_char	19.6ms	21.8ms	38.1MB	90	18	2.01s

The second set below shows that **collapse**'s statistical functions are very efficient on aggregating a numeric matrix with 10,000 rows and 1000 columns. They are faster than base R even without multithreading, but using 4 threads in this case induces a sizeable difference.

```
R> set_collapse(na.rm = FALSE, sort = FALSE, nthreads = 4)
R> m <- matrix(rnorm(1e7), ncol = 1000)
R> bmark(R = colSums(m), collapse = fsum(m))
```

	expression	min	median	mem_alloc	n_itr	n_gc	total_time
1	R	5.67ms	6.21ms	7.86KB	324	0	2s
2	collapse	280.93µs	321.64µs	7.86KB	6143	1	2s

```
R> bmark(R = colMeans(m), collapse = fmean(m))
```

	expression	min	median	mem_alloc	n_itr	n_gc	total_time
1	R	6.01ms	6.21ms	32.09KB	324	0	2s
2	collapse	278.92µs	322.14µs	7.86KB	6164	0	2s

```
R> bmark(MS = matrixStats::colMedians(m), collapse = fmedian(m))
```

	expression	min	median	mem_alloc	n_itr	n_gc	total_time
1	MS	78.7ms	79.7ms	238.9KB	26	0	2.07s
2	collapse	19.4ms	19.6ms	27.2KB	101	0	2.02s

Below, I also show a grouped version summing the columns within 1000 random groups.

```
R> g <- sample.int(1e3, 1e4, TRUE)
R> bmark(R = rowsum(m, g), collapse = fsum(m, g))
```

	expression	min	median	mem_alloc	n_itr	n_gc	total_time
1	R	5.36ms	5.59ms	7.87MB	319	20	1.79s
2	collapse	923.24µs	1.14ms	7.71MB	1279	60	1.58s

I now turn to basic operations on a medium sized real-world database recording all flights from New York City (EWR, JFK, and LGA) in 2023—provided by the **nycflights23** package. The **flights** table has 435k flights, and grouping it by day and route yields 76k unique trips.

```
R> fastverse_extend(nycflights23, dplyr, data.table); setDTthreads(4)
R> list(flights, airports, airlines, planes, weather) |> supply(nrow)
```

```
[1] 435352 1255 14 4840 26207
```

```
R> flights |> fselect(month, day, origin, dest) |> fnunique()
```

```
[1] 75899
```

In the following, I select 6 numeric variables and sum them across the 76k trips using **dplyr**, **data.table**, and **collapse**. Ostensibly, despite `sum()` being 'primitive' (implemented in C), there is a factor 100 between **dplyr**'s split-apply-combine and **collapse**'s fully vectorized execution.

```
R> vars <- .c(dep_delay, arr_delay, air_time, distance, hour, minute)
R> bmark(dplyr = flights |> group_by(month, day, origin, dest) |>
+       summarise(across(all_of(vars), sum), .groups = "drop"),
+       data.table = qDT(flights)[, lapply(.SD, sum), .SDcols = vars,
+       by = .(month, day, origin, dest)],
+       collapse = flights |> fgroup_by(month, day, origin, dest) |>
+       get_vars(vars) |> fsum())
```

	expression	min	median	mem_alloc	n_itr	n_gc	total_time
1	dplyr	437.44ms	471.82ms	50.5MB	5	50	2.35s
2	data.table	7.56ms	8.59ms	20.8MB	208	18	2s
3	collapse	3ms	3.75ms	9.2MB	467	21	2s

Below, I also benchmark the mean and median functions in the same way. It is evident that with non-primitive R functions the split-apply-combine logic becomes even more costly.

	expression	min	median	mem_alloc	n_itr	n_gc	total_time
1	dplyr_mean	1.17s	1.18s	48.57MB	2	42	2.36s
2	data.table_mean	7.64ms	8.79ms	18.93MB	190	18	2s
3	collapse_mean	3.28ms	3.77ms	9.11MB	470	17	2.01s

	expression	min	median	mem_alloc	n_itr	n_gc	total_time
1	dplyr_median	4.05s	4.05s	52.8MB	1	86	4.05s
2	data.table_median	21.45ms	22.51ms	18.9MB	86	8	2.01s
3	collapse_median	9.7ms	10.34ms	11.1MB	171	11	2s

So far, **data.table**, by virtue of its internal vectorizations (also via dedicated grouped C implementations of simple functions), is competitive.<sup>31</sup> Below, I compute the range of one column (`x`) using `max(x) - min(x)`. As elucidated in Section 3, this expression is also vectorized in **collapse**, where it amounts to `fmax(x, g) - fmin(x, g)`, but not in **data.table**.

```
R> bmark(dplyr = flights |> group_by(month, day, origin, dest) |>
+       summarise(rng = max(arr_delay) - min(arr_delay), .groups = "drop"),
+       data.table = qDT(flights)[, .(rng = max(arr_delay) - min(arr_delay)),
+       by = .(month, day, origin, dest)],
+       collapse = flights |> fgroup_by(month, day, origin, dest) |>
+       fsummarise(rng = fmax(arr_delay) - fmin(arr_delay)))
```

<sup>31</sup>Much longer data will likely also favor **data.table** over **collapse** due to its sub-column-level parallel grouping and implementation of simple functions like `sum()` and `mean()`, see, e.g., the [DuckDB Benchmarks](#).

	expression	min	median	mem_alloc	n_itr	n_gc	total_time
1	dplyr	90.25ms	99.01ms	20.18MB	20	44	2.09s
2	data.table	59.54ms	63.14ms	5.77MB	32	27	2.04s
3	collapse	5.32ms	5.88ms	6.8MB	303	11	2s

I also benchmark table joins and pivots. The following demonstrates how all tables can be joined together using **collapse** and its default first-match left-join, which preserves **flights**.

```
R> flights |> join(weather, on = c("origin", "time_hour")) |>
+   join(planes, on = "tailnum") |> join(airports, on = c(dest = "faa")) |>
+   join(airlines, on = "carrier") |> dim()
```

```
left join: flights[origin, time_hour] 434526/435352 (99.8%) <21.94:1st> weat
duplicate columns: year, month, day, hour => renamed using suffix '_weather'
left join: x[tailnum] 424068/435352 (97.4%) <87.62:1st> planes[tailnum] 4840
duplicate columns: year => renamed using suffix '_planes' for y
left join: x[dest] 435352/435352 (100%) <3689.42:1st> airports[faa] 118/1255
left join: x[carrier] 435352/435352 (100%) <31096.57:1st> airlines[carrier]
duplicate columns: name => renamed using suffix '_airlines' for y
[1] 435352      48
```

The verbosity of `join()` is essential to understanding what has happened here—how many records from each table were matched and which duplicate non-id columns were suffixed with the (default) *y*-table name. Normally, I would set `drop.dup.cols = "y"` as it seems not useful to preserve them here, but the other packages don't have this option. For the benchmark, I set `verbose = 0` in **collapse** and employ the fastest syntax for **dplyr** and **data.table**:<sup>32</sup>

	expression	min	median	mem_alloc	n_itr	n_gc	total_time
1	dplyr_joins	140.85ms	173.7ms	559.4MB	12	28	2.12s
2	data.table_joins	99.45ms	132.9ms	491MB	15	36	2.11s
3	collapse_joins	9.15ms	11.2ms	89.7MB	142	40	2.01s

Evidently, the vectorized hash join provided by **collapse** is 10x faster than **data.table** on this database, at a substantially lower memory footprint. It remains competitive on **big data**.<sup>33</sup>

Last but not least, I benchmark pivots, starting with a long pivot that simply melts the 6 columns aggregated beforehand into one column, duplicating all other columns 6 times:

```
R> bmark(tidyr = tidyr::pivot_longer(flights, cols = vars),
+       data.table = qDT(flights) |> melt(measure = vars),
+       collapse = pivot(flights, values = vars))
```

	expression	min	median	mem_alloc	n_itr	n_gc	total_time
1	tidyr	58.2ms	58.2ms	255MB	1	27	58.2ms
2	data.table	41.9ms	43.9ms	209MB	14	22	613.6ms
3	collapse	13ms	15.3ms	209MB	34	57	512.9ms

<sup>32</sup>`left_join(..., multiple = "first")` for **dplyr** and `y[x, on = ids, mult = "first"]` for **data.table**.

<sup>33</sup>**data.table** joins utilize multithreaded radix-ordering—a very different logic more useful for big data.

Memory-wise, **collapse** and **data.table** are equally efficient, but **collapse** is faster, presumably due to more extensive use of `memset()` to copy values in C or smaller R-level overheads.

To complete the picture, I also perform a wide pivot where the 6 columns are summed (for efficiency) across the 3 origin airports and expanded to create 18 airport-value columns.

```
R> bmark(tidyr = tidyr::pivot_wider(flights, id_cols = .c(month, day, dest),
+   names_from = "origin", values_from = vars, values_fn = sum),
+   data.table = dcast(qDT(flights), month + day + dest ~ origin,
+   value.var = vars, fun = sum),
+   collapse_fsum = pivot(flights, .c(month, day, dest), vars,
+   "origin", how = "wider", FUN = fsum),
+   collapse_itnl = pivot(flights, .c(month, day, dest), vars,
+   "origin", how = "wider", FUN = "sum"))
```

	expression	min	median	mem_alloc	n_itr	n_gc	total_time
1	tidyr	353.82ms	383.22ms	143MB	5	37	2s
2	data.table	222.83ms	230.79ms	21.7MB	9	40	2.08s
3	collapse_fsum	5.04ms	7.01ms	39.1MB	233	23	2.07s
4	collapse_itnl	4.12ms	4.51ms	12.4MB	392	8	2.01s

Again, **collapse** is fastest, as it offers full vectorization, either via `fsum()`, which translates to `fsum(x, g, TRA = "fill")` before pivoting and thus entails a full deep copy of the **vars** columns, or via an optimized internal sum function which sums values 'on the fly' during the reshaping process. **data.table** is not vectorized here but at least memory efficient.

In summary, these benchmarks show that **collapse** provides outstanding performance and memory efficiency on a typical medium-sized real-world database popular in the R community.

## 9.1. Other benchmarks

The [DuckDB Benchmarks](#) compare many software packages for database-like operations using large datasets (big data) on a linux server. The January 2025 run distinguishes 6 packages that consistently achieve outstanding performances: **DuckDB**, **Polars**, **ClickHouse**, **Apache Datafusion**, **data.table**, and **collapse**. Of these, **DuckDB**, **ClickHouse**, and **Datafusion** are vectorized database (SQL) engines, and **Polars** is a Python/Rust DataFrame library and SQL engine. These four are supported by (semi-)commercial entities, leaving **data.table** as the only fully community-led project, and **collapse** as the only project that is single-authored and without financial support. The benchmarks show that **collapse** achieves the highest relative performance on 'smaller' datasets (10-100 million rows) and performing advanced operations.

Since June 2024, there is also an independent [database-like operations benchmark](#) by [Adrian Antico](#) using a windows server and executing scripts inside IDEs (VScode, Rstudio), on which **collapse** achieved the overall fastest runtimes. I also very recently started a [user-contributed benchmark Wiki](#) as part of the [fastverse project](#) promoting high-performance software for R, where users can freely contribute benchmarks involving, but not limited to, **fastverse** packages. These benchmarks align in showing that **collapse** offers a computationally outstanding experience, particularly for medium-sized datasets, complex tasks, and personal computers.



## 9.2. Limitations and outlook

**collapse** maximizes three principal objectives: being class-agnostic/fully compatible with the R ecosystem (supporting statistical operations on vector, matrix and data.frame-like objects), being statistically advanced, and being fast. This warranted some design choices away from maximum performance for large data manipulation.<sup>34</sup> Its limited use of multithreading and SIMD instructions, partly by design constraints and by R’s C API, and the use of standard types for internal indexing, imposes hard-limits—the maximum integer in R is 2,147,483,647 → the maximum vector length **collapse** supports. It is and will remain an in-memory tool.

Despite these constraints, **collapse** provides very respectable performance even on very large datasets by virtue of its algorithmic and memory efficiency. It is, together with the popular **data.table** package offering more sub-column-level parallel architecture for basic operations, well-positioned to remain a premier tool for in-memory statistics and data manipulation.

## 10. Conclusion

**collapse** was first released to CRAN in March 2020, and has grown and matured considerably over the course of 5 years. It has become a new foundation package for statistical computing and data transformation in R—one that is statistically advanced, class-agnostic, flexible, fast, lightweight, stable, and able to manipulate complex scientific data with ease. As such, it opens up new possibilities for statistics, data manipulation, and package development in R.

This article provided a quick guide to the package, articulating its key ideas and design principles and demonstrating all core features. At this point the API is stable—it has changed very little over the 5 years and no further changes are planned. Compatibility with R version 3.5.0 will be maintained for as long as possible. Minor new features are currently planned.

For deeper engagement with **collapse**, visit its [website](#) or start with the vignette summarizing all available [documentation and resources](#). Users can also follow **collapse** on [Twitter/X](#) and [Bluesky](#) to be notified about major updates and participate in community discussions.

Last but not least, **collapse** users are encouraged to also familiarize themselves with the **fastverse**,<sup>35</sup> a suite of complementary high-performance packages for statistical computing and data manipulation in R which offer more advanced tools in several statistical computing domains. The **fastverse** metapackage also provides a lightweight framework to jointly load and manage these packages, as well as to build customized and fully separate package verses.

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<sup>34</sup>Which nowadays would demand creating a multithreaded, vectorized query engine with optimized memory buffers/vector types to take full advantage of SIMD processing as in **DuckDB** or **Polars**. Such an architecture is very difficult to square with R vectors and R’s 30-year old C API.

<sup>35</sup>Website: <https://fastverse.github.io/fastverse/>

## Computational details

The results in this paper were obtained using R (R Core Team 2025) 4.4.3 with **collapse** 2.1.2, **data.table** 1.17.0, **dplyr** 1.1.4, **tidyr** 1.3.1, **matrixStats** 1.5.0, **fastverse** 0.3.4, and **bench** 1.1.4 (Hester and Vaughan 2025). All packages used are available from the Comprehensive R Archive Network (CRAN) at <https://CRAN.R-project.org/>. The benchmark was run on an Apple MacBook Pro (2024) with 48GB M4 Pro chip. Packages were compiled from source using Apple Clang version 17.0.0 with OpenMP enabled and the -O2 flag.

The `bmark()` function used for benchmarking is defined as follows:

```
bmark <- function(...) {  
  bench::mark(..., min_time = 2, check = FALSE) |>  
    janitor::clean_names() |>  
    fselect(expression, min, median, mem_alloc, n_itr, n_gc, total_time) |>  
    fmutate(expression = names(expression)) |>  
    dapply(as.character) |> qDF()  
}
```

## Acknowledgments

The source code of **collapse** has been heavily inspired by (and partly copied from) **data.table** (Matt Dowle and Arun Srinivasan), R's source code (R Core Team and contributors worldwide), the **kit** package (Morgan Jacob), and **Rcpp** (Dirk Eddelbuettel). Packages **plm** (Yves Croissant, Giovanni Millo, and Kevin Tappe) and **fixest** (Laurent Berge) have also provided a lot of inspiration (and a port to its demeaning algorithm in the case of **fixest**). I also thank many people from diverse fields for helpful answers on Stackoverflow and many other people for encouragement, feature requests, and helpful issues and suggestions.

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