



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 programming efficiency. It also implements a class-agnostic approach to R programming, supporting vector, matrix and data frame-like objects and their popular variants (e.g. `'factor'`, `'ts'`, `'xts'`, `'tibble'`, `'data.table'`, `'sf'`), 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, summary statistics, class-agnostic programming, R.

1. Introduction

collapse¹ is a large C/C++-based R package that provides an integrated suite of statistical and data manipulation functions. Most of these statistical functions are vectorized along multiple dimensions (notably along groups and columns) and perform high-cardinality operations² very efficiently. It also offers vectorizations for advanced operations such as weighted statistics (including mode and quantiles), functions and classes for fully indexed (time-aware) computations on time series and panel data, recursive (list-processing) tools to deal with nested data and advanced descriptive statistical tools. This functionality is supported by efficient algorithms for intensive operations like grouping, unique values, matching, ordering, etc., tailored to R's data structures and powerful data manipulation functions. The package also supplies many features for memory efficient R programming, such as data transforma-

¹Website: <https://sebkranz.github.io/collapse/>

²With many columns and/or groups relative to data size.

tion and math by reference and aversion of logical vectors. **collapse** is class-agnostic, i.e., it provides most statistical operations for atomic vectors, matrices, and data frames/lists, and seamlessly supports key variants of these objects used in the R ecosystem (e.g. *tibble*, *data.table*, *sf*, *xts*, *pdata.frame*). It is globally and interactively configurable, which includes setting different defaults for key function arguments (such as `na.rm` arguments to statistical functions, default `TRUE`), and modifying the package namespace itself.³

What is the purpose of combining all of this 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 performance and parsimony by avoiding R-level repetition⁴; (3) increase the memory efficiency and flexibility of R programs⁵; and (4) to create a new foundation package for statistics and data manipulation in R that implements successful ideas developed in the R ecosystem and other programming environments such as Python or STATA (StataCorp LLC. 2023), including some new ideas, in a stable, high performance, and broadly compatible manor.⁶

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 2023) provides an enhanced high-performance data frame with parsimonious data manipulation 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 2023) and **Rfast** (Papadakis *et al.* 2023) offer fast statistical calculations along the rows and columns of matrices and faster basic statistical procedures. **DescTools** (Signorell 2023) provides a wide variety of descriptive statistics, including weighted versions. **survey** (Lumley 2004) allows statistical computations on complex survey data. **labelled** (Larmarange 2023) provides tools to deal with labelled data. Packages like **tidyr** (Wickham *et al.* 2023b), **purrr** (Wickham and Henry 2023) and **rapply** (Chau 2022) provide some functions to deal with nested data and messy structures.

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

³**collapse**’s namespace is fully compatible with base R and the **tidyverse**, but can be interactively modified to overwrite key functions like `unique`, `match`, `%in%`, `table`, `subset`, `mutate`, `summarise` etc. with much faster **collapse** equivalents.

⁴Such as applying R functions across columns or split-apply-combine computing to apply functions across groups or other divisions of data.

⁵E.g. by avoiding object conversions and the need for certain classes to do certain things, such as converting to data frame or ‘*data.table*’ to do something “by groups” and then convert back to matrix to continue with linear algebra, and in general to reduce the need for metaprogramming.

⁶Examples of such ideas are **tidyverse** syntax, vectorized aggregations (**data.table**), data transformation by reference (Python, **pandas**), vectorized and verbose joins (**polars**, STATA), indexed time series and panel data (**xts**, **plm**), summary statistics for panel data (STATA), reshaping labelled data (myself) etc...

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 general (recursive) tools to deal with nested data, enhancing **tidyr**, **purrr** and **rrapply**. Finally, it provides a small but consistent and powerful set of descriptive statistical tools, yielding sufficient detail for most data exploration purposes and requiring users to invoke packages like **DescTools** or **survey** only for specific statistics. In summary, **collapse** is a foundation package for statistical computing and data manipulation in R that enhances and integrates seamlessly with the R ecosystem while being outstandingly computationally efficient. A significant benefit is that, rather than piecing together a somewhat fragmented ecosystem oriented at different classes and tasks, core computational tasks can be done with **collapse**, and easily extended by more specialized packages. This tends to result in R scripts that are shorter, more efficient, and more lightweight in dependencies.

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** (Wes 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,⁷ supports recursive operations, variable labels, verbosity for critical operations such as joins, and is extensively globally configurable. In short, it is very utile 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 columns⁸. Its vectorization capabilities are also limited to the statistical functions it provides and not, like **DataFrames.jl**, to any Julia function. However, as demonstrated below, the possibility of combining vectorized statistical functions also permits calculating 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
```

⁷Such as weighted statistics, including various quantile and mode estimators, support for fully time-aware computations on irregular series/panels, higher order centering, advanced (grouped, weighted, panel-decomposed) descriptive statistics etc., all supporting missing values.

⁸As 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 (except for joins where it remains competitive). There may be performance improvements for "long data" in the future, but, at present, the treatment of columns as fundamental units of computation is a tradeoff for the highly flexible class-agnostic architecture.

```

[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")
```

collapse is too large and complex to fully present it in a single article or even to present selected topics in depth. The following sections therefore briefly introduce its key components: (2) the *Fast Statistical Functions* and their (3) integration with data manipulation functions; (4) architecture for time series and panel data; (5) joins and reshaping; (6) list processing functions; (7) descriptive tools; and (8) global options (configurability). Section (9) provides a small benchmark, Section (10) concludes. For deeper engagement with **collapse**, the short vignette summarizing available [Documentation and Resources](#) is an excellent starting point.

2. Fast statistical functions

The **Fast Statistical Functions**, comprising `fsum()`, `fprod()`, `fmean()`, `fmedian()`, `fmode()`, `fvar()`, `fsd()`, `fmin()`, `fmax()`, `fnth()`, `ffirst()`, `flast()`, `fnoobs()` and `fndistinct()`, are a consistent set of S3-generic statistical functions providing fully vectorized statistical operations in R. Specifically, operations such as calculating the mean via the S3 generic `fmean()` function are vectorized across columns and groups. They may also involve weights or transformations of the original data. The basic syntax of these functions is

```

FUN(x, g = NULL, [w = NULL,] TRA = NULL, [na.rm = TRUE,]
    use.g.names = TRUE, drop = TRUE, [nthreads = 1L,] ...)

```

with arguments `x` - data (vector, matrix or data frame-like), `g` - groups (atomic vector, list of vectors, or ‘GRP’ object), `w` - weights, `TRA` - transformation, `na.rm` - missing values, `use.g.names` - attach group names upon aggregation (if `g` is used), `drop` - drop dimensions (i.e. simplify to atomic vector if `is.null(g)` and `x` is matrix or data frame-like), `nthreads` - multithreading⁹. The following examples, taken from the [collapse for tidyverse Users](#) vignette (and executed there, not here for parsimony) demonstrate their basic usage.

```

fmean(mtcars$mpg)           # Vector
fmean(EuStockMarkets)      # Matrix
fmean(mtcars)              # Data Frame
fmean(mtcars$mpg, w = mtcars$wt) # Weighted mean
fmean(mtcars$mpg, g = mtcars$cyl) # Grouped mean
fmean(mtcars$mpg, g = mtcars$cyl, w = mtcars$wt) # Weighted group mean
fmean(mtcars[5:10], g = mtcars$cyl, w = mtcars$wt) # Of data frame
fmean(mtcars$mpg, g = mtcars$cyl, TRA = "fill") # Replace data by g. mean

```

⁹Not all functions are multithreaded, and parallelism is implemented differently for different functions (detailed in the documentation). The use of Single Instruction Multiple Data (SIMD) parallelism in single-threaded mode also implies limited gains from multithreading for simple operations such as `fsum()`.

2.1. Transformations

The `TRA` argument, more specifically, invokes the `TRA()` function for column-wise (grouped) replacing and sweeping operations (by reference). Its syntax is

```
TRA(x, STATS, FUN = "-", g = NULL, set = FALSE, ...)
```

where `STATS` is a vector/matrix/data.frame of statistics used to transform `x`. The `FUN` argument supports 11 different operations indicated using either an integer or string. `TRA()` is

<i>Int</i>	<i>String</i>	<i>Description</i>
0	"replace_na"/"na"	replace missing values in <code>x</code>
1	"replace_fill"/"fill"	replace data and missing values in <code>x</code>
2	"replace"	replace data but preserve missing values in <code>x</code>
3	"-"	subtract (i.e. center)
4	"-+"	center on overall average statistic
5	"/"	divide (i.e. scale)
6	"%"	compute percentages (i.e. divide and multiply by 100)
7	"+"	add
8	"*"	multiply
9	"%%"	modulus (i.e. remainder from division by <code>STATS</code>)
10	"-%%"	subtract modulus (i.e. make data divisible by <code>STATS</code>)

called internally in the *Fast Statistical Functions*, the `TRA` argument is passed to `FUN`. Thus `fmean(x, g, w, TRA = "-")` is equivalent to `TRA(x, fmean(x, g, w), "-", g)`. The `set` argument can also be passed to *Fast Statistical Functions* to toggle transformation by reference. The following examples demonstrate how this design allows flexible ad-hoc transformations using R's built-in `airquality` dataset with daily measurements for 5 months.

```
R> fnobs(airquality)
```

```

Ozone Solar.R   Wind   Temp   Month   Day
  116     146    153    153    153    153

```

This imputes `Ozone` and `Solar.R` by reference using the month median.

```
R> fmedian(airquality[1:2], airquality$Month, TRA = "replace_na", set = TRUE)
```

This performs different grouped and/or weighted transformations at once.

```

R> airquality |> fmutate(
+   rad_day = fsum(as.double(Solar.R), Day, TRA = "/"),
+   ozone_deg = Ozone / Temp,
+   ozone_amed = Ozone > fmedian(Ozone, Month, TRA = "fill"),
+   ozone_resid = fmean(Ozone, list(Month, ozone_amed), ozone_deg, "-")
+ ) |> head(3)

```

```

Ozone Solar.R Wind Temp Month Day rad_day ozone_deg ozone_amed ozone_resid
1    41     190  7.4  67    5    1  0.191   0.6119      TRUE    -10.279
2    36     118  8.0  72    5    2  0.135   0.5000      TRUE    -15.279
3    12     149 12.6  74    5    3  0.168   0.1622     FALSE     -3.035

```

2.2. Grouping objects and optimization

Whereas the `g` argument supports ad-hoc grouping with vectors and lists/data frames, the cost of grouping can be optimized by using factors or, even better, ‘GRP’ objects, which contain all information for **collapse**’s vectorized functions to operate across groups efficiently. These objects can be created with `GRP()`. The syntax is

```
GRP(X, by = NULL, sort = TRUE, decreasing = FALSE, na.last = TRUE,
    return.groups = TRUE, return.order = sort, method = "auto", ...)
```

The example below creates and displays a ‘GRP’ object from 3 columns in `mtcars`. The `by` argument also supports column names or indices, and `X` could also be an atomic vector.

```
R> str(g <- GRP(mtcars, ~ cyl + vs + am))
```

```
Class 'GRP'  hidden list of 9
 $ N.groups      : int 7
 $ group.id      : int [1:32] 4 4 3 5 6 5 6 2 2 5 ...
 $ group.sizes   : int [1:7] 1 3 7 3 4 12 2
 $ groups        : 'data.frame':      7 obs. of  3 variables:
  ..$ cyl: num [1:7] 4 4 4 6 6 8 8
  ..$ vs : num [1:7] 0 1 1 0 1 0 0
  ..$ am : num [1:7] 1 0 1 1 0 0 1
 $ group.vars    : chr [1:3] "cyl" "vs" "am"
 $ ordered       : Named logi [1:2] TRUE FALSE
  .. attr(*, "names")= chr [1:2] "ordered" "sorted"
 $ order         : int [1:32] 27 8 9 21 3 18 19 20 26 28 ...
  .. attr(*, "starts")= int [1:7] 1 2 5 12 15 19 31
  .. attr(*, "maxgrp")= int 12
  .. attr(*, "sorted")= logi FALSE
 $ group.starts: int [1:7] 27 8 3 1 4 5 29
 $ call          : language GRP.default(X = mtcars, by = ~cyl + vs + am)
```

‘GRP’ objects make grouped statistical computations in **collapse** fully programmable. Below, the object is used with the *Fast Statistical Functions* and some utility functions to aggregate the data (with optional weights) efficiently.

```
R> dat <- get_vars(mtcars, c("mpg", "disp")); w <- mtcars$wt
R> add_vars(g$groups,
+   fmean(dat, g, w, use.g.names = FALSE) |> add_stub("w_mean_"),
+   fsd(dat, g, w, use.g.names = FALSE) |> add_stub("w_sd_")) |> head(2)
```

```
   cyl vs am w_mean_mpg w_mean_disp w_sd_mpg w_sd_disp
1    4  0  1    26.00    120.3    0.000    0.0
2    4  1  0    23.02    137.1    1.236    11.6
```

Similar, data can be transformed, here also using the S3 generic `fscale()` function.

```
R> mtcars |> add_vars(fmean(dat, g, w, "-") |> add_stub("w_demean_"),
+                   fscale(dat, g, w) |> add_stub("w_scale_")) |> head(2)
```

	mpg	cyl	disp	hp	drat	wt	qsec	vs	am	gear	carb	w_demean_mpg
Mazda RX4	21	6	160	110	3.9	2.620	16.46	0	1	4	4	0.4357
Mazda RX4 Wag	21	6	160	110	3.9	2.875	17.02	0	1	4	4	0.4357

	w_demean_disp	w_scale_mpg	w_scale_disp
Mazda RX4	5.027	0.6657	0.6657
Mazda RX4 Wag	5.027	0.6657	0.6657

This programming access can become very useful. For example, the useR 2022 presentation [Slides 18-19](#) aggregates the [EORA Global Supply Chain Database](#) from the country to the world region level. After defining a single grouping object, a list of value-added shares matrices (VB) and outputs for years 1990-2021, is aggregated with no grouping cost using a single line of code like `lapply(VB_list, function(x) x$VB |> fsum(g) |> t() |> fmean(g, x$0) |> t())`. On an M1 Mac using 4 threads, this computation, involving 44.7 million summations and 2.6 million weighted means, takes only 0.33 seconds.¹⁰

3. Integration with data manipulation functions

collapse also provides a broad set of [fast data manipulation functions](#) familiar to R and **tidyverse** users, including `fselect()`, `fsubset()`, `fgroup_by()`, `fsummarise()`, `ftransform()`, `fmutate()`, `across()`, `frename()`, `fcount()`, etc. These are integrated with the *Fast Statistical Functions* to enable vectorized statistical operations in a familiar data frame oriented and **tidyverse**-like workflow. For example, the following code calculates

```
R> mtcars |>
+   fsubset(mpg > 11) |>
+   fgroup_by(cyl, vs, am) |>
+   fsummarise(across(c(mpg, carb, hp), fmean),
+               qsec_w_med = fmean(qsec, wt)) |> head(2)
```

	cyl	vs	am	mpg	carb	hp	qsec_w_med
1	4	0	1	26.0	2.000	91.00	16.70
2	4	1	0	22.9	1.667	84.67	21.04

the mean of columns `mpg`, `carb` and `hp`, and the weighted mean of `qsec`, after subsetting and grouping the data. This code is very fast (especially with many groups) because data does not need to be split by groups at all. There is also no need to call `lapply()` inside the `across()` statement: `fmean.data.frame()` is applied to a subset of the data containing

¹⁰Another example from my recent work involved numerically optimizing a parameter a in an equation of the form $y_j = \sum_i x_{ij}^a \forall j \in J$ where there are J groups (1 million in my case), and the optimal value of a is determined by the proximity of the aggregated vector \mathbf{y} to another vector \mathbf{z} . Thus each iteration of the numerical routine raises the vector \mathbf{x} to a different power (a), sums it in 1 million groups (j) to generate \mathbf{y} , and computes the Euclidean distance to \mathbf{z} (using `collapse::fdist`). Without grouping objects and vectorization, this would have been difficult to handle within reasonable computing times (a few seconds on the M1).

the three columns.¹¹ The *Fast Statistical Functions* also have a method for grouped data, so `fsummarise` is not always needed. The following code calculates weighted group means. By default (`keep.w = TRUE`) `fmean.grouped_df` also sums the weights in each group.

```
R> mtcars |>
+   fsubset(mpg > 11, cyl, vs, am, mpg, carb, hp, wt) |>
+   fgroup_by(cyl, vs, am) |>
+   fmean(wt) |> head(2)

  cyl vs am sum.wt   mpg carb   hp
1   4  0  1  2.140 26.00  2.00  91.0
2   4  1  0  8.805 23.02  1.72  83.6
```

3.1. Vectorizations for advanced tasks

`fsummarise()` and `fmutate()` can also evaluate other statistical functions in the classical way (split-apply-combine) and handle more complex expressions involving multiple columns and/or functions. However, using any *Fast Statistical Function* causes the whole expression to be vectorized, i.e., evaluated only once and not for every group. This eager vectorization approach is helpful for efficient grouped calculation of more complex statistics. The example below calculates grouped (`vs`) bivariate regression slopes (`mpg ~ carb`) in a vectorized way.

```
R> mtcars |>
+   fgroup_by(vs) |>
+   fmutate(dm_carb = fmean(carb, TRA = "-")) |>
+   fsummarise(slope = fsum(mpg, dm_carb) %/=% fsum(dm_carb^2))

  vs   slope
1  0 -0.5557
2  1 -2.0706
```

Apart from vectorization, this code avoids 3 intermediate copies: (1) `fmean(carb, TRA = "-")` avoids an expanded vector of group means, (2) `fsum(mpg, dm_carb)` uses the weights (`w`) argument to `fsum()` to avoid materializing a multiplication (as in `fsum(mpg * dm_carb)`), and (3) division by reference (`%/=%`) avoids allocating an additional vector for the final result. Under the hood, the expression boils down to an (expensive) grouping step, 5 allocations (of which 2 full length), and 6 loops in C to calculate the result. Any modern laptop can calculate 1 million regression slopes in less than 1 second like this.

collapse also supplies advanced statistics, such as weighted medians and modes. The following example calculates a weighted set of summary statistics by groups, with weighted quantiles type 8 following Hyndman and Fan (1996)¹², and a weighted maximum mode.¹³

¹¹Internally, the `g` argument of the statistical functions is set as a keyword argument by `fsummarise/across` and the function is evaluated on a suitable subset of columns. Thus `w` becomes the second positional argument...

¹²**collapse** calculates weighted quantiles by replacing the sample size with the sum of weights and 1 with the minimum non-zero weight in the respective quantile definition. See `fquantile` for more details.

¹³The weighted maximum mode is the largest element with the maximum sum of weights.


```
R> mtcars |>
+   fgroup_by(cyl, vs, am) |>
+   fmutate(o = radixorder(GRPid(), mpg)) |>
+   fsummarise(mpg_min = fmin(mpg),
+               mpg_Q1 = fnth(mpg, 0.25, wt, o = o, ties = "q8"),
+               mpg_mean = fmean(mpg, wt),
+               mpg_median = fmedian(mpg, wt, o = o, ties = "q8"),
+               mpg_mode = fmode(mpg, wt, ties = "max"),
+               mpg_Q3 = fnth(mpg, 0.75, wt, o = o, ties = "q8"),
+               mpg_max = fmax(mpg)) |> head(3)
```

	cyl	vs	am	mpg_min	mpg_Q1	mpg_mean	mpg_median	mpg_mode	mpg_Q3	mpg_max
1	4	0	1	26.0	26.00	26.00	26.00	26.0	26.00	26.0
2	4	1	0	21.5	21.90	23.02	23.16	24.4	24.38	24.4
3	4	1	1	21.4	22.37	27.74	28.28	30.4	31.51	33.9

Both weighted mode and quantiles have a sub-column parallel implementation,¹⁴ and, as in this case, can also harness an (optional) optimization by computing an overall ordering vector and passing it to the functions to avoid repeated sorting (using quickselect) of the same elements within each group. For advanced data aggregation, **collapse** also provides a convenience function, `collap()`, which (by default) uses `fmean` for numeric and `fmode` for non-numeric columns. Below, it aggregates GDP per Capita, Life Expectancy, and country name by World Bank Income Group, with population weights.¹⁵ This yields population-weighted statistics, the largest country, and each income group's total population (sum of weights) for each year, preserving (default `keep.col.order = TRUE`) the order of columns.

```
R> collap(wlddev, country + PCGDP + LIFEEX ~ year + income, w = ~ POP) |>
+   head(4)
```

	country	year	income	PCGDP	LIFEEX	POP
1	United States	1960	High income	12768.7	68.59	7.495e+08
2	Ethiopia	1960	Low income	658.5	38.33	1.474e+08
3	India	1960	Lower middle income	500.8	45.27	9.280e+08
4	China	1960	Upper middle income	1166.1	49.86	1.184e+09

4. Time series and panel data

collapse provides a flexible high-performance architecture to perform (*time aware*) computations on time series and panel series. In particular, the user enjoys great flexibility in deciding the desired degree of indexation and mode of computation. It is possible to apply time series and panel data transformations without any indexation 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. The following list summarizes **collapse**’s time series and panel data functions.

¹⁴Use `set_collapse(nthreads = #)` or the `nthreads` arguments to `fnth/fmedian/fmode` (default 1).

¹⁵`wlddev` is a dataset supplied by **collapse**, extracted from the World Bank World Development Indicators.

Classes, Constructors and Utilities

`findex_by()`, `findex()`, `unindex()`, `reindex()`, `timeid()`, `is_irregular()`,
`to_plm()` + rich set of S3 methods for 'indexed_frame', 'indexed_series' and 'index_df'.

Core Time-Based Functions

`flag()`, `fdiff()`, `fgrowth()`, `fcumsum()`, `psmat()` [panel data to array conversions]
`psacf()`, `pspacf()`, `psccf()` [autocorrelation functions for panel data]

Data Transformation Functions with Supporting Methods

`f[hd]between()`, `f[hd]within()`, `fscale()` [scaling and (higher-dimensional) centering]

Data Manipulation Functions with Supporting Methods

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

Summary Functions with Supporting Methods

`qsu()`, `varying()` [panel-variance decomposed statistics]

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 steps¹⁶. 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'.

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

```
Time Series:
```

```
Start = 1937
```

```
End = 1960
```

```
Frequency = 1
```

```
[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
```

The following code creates an irregular series by removing the 3rd and 15th observation and shows how indexation with the `t` argument accounts for this.

```
R> am_ir <- airmiles[-c(3, 15)]
```

```
R> t <- time(airmiles)[-c(3, 15)]
```

```
R> fgrowth(am_ir, t = t) |> round(2)
```

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

¹⁶This is premised on the observation that the most common form of temporal identifier is a numeric variable denoting calendar years.

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

	FG1	--	G1	L2G1	L3G1
[1,]	-14.167	412	NA	NA	NA
[2,]	NA	480	16.50	NA	NA
[3,]	-24.043	1052	NA	119.2	155.3
[4,]	-2.327	1385	31.65	NA	188.5

For these functions, there also exists shorthands in the form of statistical operators, e.g., `L()/D()/G()` are shorthands for `flag()/fdiff()/fgrowth()`, which facilitate their use inside formulas and also provide enhanced data frame interfaces for convenient ad-hoc computations. With panel data, `t` can be omitted, but this requires sorted data with consecutive groups.¹⁷

```
R> G(wlddev, c(1, 10), by = POP + LIFEEX ~ iso3c, t = ~ year) /> head(3)
```

	iso3c	year	G1.POP	L10G1.POP	G1.LIFEEX	L10G1.LIFEEX
1	AFG	1960	NA	NA	NA	NA
2	AFG	1961	1.917	NA	1.590	NA
3	AFG	1962	1.985	NA	1.544	NA

```
R> settransform(wlddev, POP_growth = G(POP, g = iso3c, t = year))
```

These functions and operators are also integrated with `fsummarise()` and `fmutate()` for vectorized grouped computations.

```
R> wlddev /> fgroup_by(iso3c) /> fselect(iso3c, year, POP, LIFEEX) />
+   fmutate(across(c(POP, LIFEEX), G, t = year)) /> head(2)
```

	iso3c	year	POP	LIFEEX	G1.POP	G1.LIFEEX
1	AFG	1960	8996973	32.45	NA	NA
2	AFG	1961	9169410	32.96	1.917	1.59

Similarly, functions to scale, center, and average data have groups (`g`) and also weights (`w`) arguments, and corresponding operators `STD()`, `[HD]W()`, `[HD]B()` to facilitate ad-hoc transformations. Below, two ways to perform grouped scaling are demonstrated. The operator version is slightly faster and renames the transformed columns by default (`stub = TRUE`).

```
R> iris /> fgroup_by(Species) /> fscale() /> head(2)
```

	Species	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width
1	setosa	0.2667	0.1899	-0.357	-0.4365
2	setosa	-0.3007	-1.1291	-0.357	-0.4365

```
R> STD(iris, ~ Species) /> head(2)
```

¹⁷This is because a group-lag is computed in a single pass, requiring all group elements to be consecutive.

	Species	STD.Sepal.Length	STD.Sepal.Width	STD.Petal.Length	STD.Petal.Width
1	setosa	0.2667	0.1899	-0.357	-0.4365
2	setosa	-0.3007	-1.1291	-0.357	-0.4365

The following example demonstrates a fixed-effects regression a la [Mundlak \(1978\)](#).

```
R> lm(mpg ~ carb + B(carb, cyl), data = mtcars) /> coef()
```

(Intercept)	carb	B(carb, cyl)
34.8297	-0.4655	-4.7750

collapse also offers higher-dimensional between and within transformations, powered by C++ code conditionally imported (and accessed directly) from **fixest**. The following detrends GDP per Capita and Life Expectancy at Birth using country-specific cubic polynomials.

```
R> HDW(wlddev, PCGDP + LIFEEX ~ iso3c * poly(year, 3), stub = F) /> head(2)
```

	PCGDP	LIFEEX
1	8.885	0.023614
2	13.685	0.006724

4.2. Indexed series and frames

For more complex use cases, indexation is very 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 be an 'indexed_frame' with any number of individual and/or time identifiers (e.g. an indexed 'data.table' is fully functional for other operations). The technical implementation of these classes is described in the [vignette on object handling](#) and, in more detail, in the [documentation](#). The basic syntax is:

```
data_ix = find_index_by(data, id1, ..., time)
data_ix$indexed_series
with(data, indexed_series)
index_df = find_index(data_ix)
```

Data can be indexed using one or more indexing variables. Unlike 'pdata.frame', an 'indexed_frame' is a deeply indexed structure, i.e., every series inside the frame is already an 'indexes_series' and contains, in its 'index_df' attribute, an external pointer to the 'index_df' attribute of the frame (to avoid duplication in memory). 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 manor in any caller environment (created by **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 also 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)
```

An example using the `wlddev` data follows:

```
R> wldi <- wlddev /> findex_by(iso3c, year)
R> wldi /> fsubset(-3, iso3c, year, PCGDP:POP) /> G() /> head(4)
```

	iso3c	year	G1.PCGDP	G1.LIFEEX	G1.GINI	G1.ODA	G1.POP
1	AFG	1960	NA	NA	NA	NA	NA
2	AFG	1961	NA	1.590	NA	98.75	1.917
3	AFG	1963	NA	NA	NA	NA	NA
4	AFG	1964	NA	1.448	NA	24.48	2.112

Indexed by: iso3c [1] | year [4 (61)]

The index statistics are: [N. ids] | [N. periods (total periods: (max-min)/GCD)]. This creates an ‘`indexes_series`’ of life expectancy and demonstrates its properties.

```
R> LIFEEXi = wldi$LIFEEX
R> str(LIFEEXi, width = 70, strict = "cut")
```

```
'indexed_series' num [1:13176] 32.4 33 33.5 34 34.5 ...
- attr(*, "label")= chr "Life expectancy at birth, total (years)"
- attr(*, "index_df")=Classes 'index_df', 'pindex' and 'data.frame'..
..$ iso3c: Factor w/ 216 levels "ABW","AFG","AGO",...: 2 2 2 2 2 2 ..
..$ year : Ord.factor w/ 61 levels "1960"<"1961"<...: 1 2 3 4 5 6 7..
..$ - attr(*, "label")= chr "Country Code"
..$ - attr(*, "label")= chr "Year"
```

```
R> c(is_irregular(LIFEEXi), is_irregular(LIFEEXi[-5]))
```

```
[1] FALSE TRUE
```

```
R> G(LIFEEXi[c(1:5, 7:10)])
```

```
[1] NA 1.590 1.544 1.494 1.448 NA 1.366 1.362 1.365
```

Indexed by: iso3c [1] | year [9 (61)]

The transformation and estimation below demonstrate the deep indexation of ‘`indexed_frame`’s, allowing correct computations in arbitrary data masking environments.

```
R> settransform(wldi, PCGDP_ld = Dlog(PCGDP))
R> lm(D(LIFEEX) ~ L(PCGDP_ld, 0:5) + B(PCGDP_ld), wldi) />
+ summary() /> coef() /> round(3)
```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	0.299	0.007	44.412	0.000
L(PCGDP_ld, 0:5)--	0.300	0.080	3.735	0.000
L(PCGDP_ld, 0:5)L1	0.269	0.081	3.332	0.001
L(PCGDP_ld, 0:5)L2	0.227	0.079	2.854	0.004
L(PCGDP_ld, 0:5)L3	0.200	0.078	2.563	0.010
L(PCGDP_ld, 0:5)L4	0.143	0.076	1.871	0.061
L(PCGDP_ld, 0:5)L5	0.095	0.073	1.301	0.193
B(PCGDP_ld)	-1.021	0.316	-3.234	0.001

The above example could also have been executed in one line as `lm(D(LIFEEX) ~ L(Dlog(PCGDP), 0:5) + B(Dlog(PCGDP)), wldi)`, log-differencing PCGDP twice.

In comparison with existing solutions, the flexibility of this architecture is new to the R ecosystem: A `'pdata.frame'` or `'fixest_panel'` only works inside **plm**/**fixest** estimation functions¹⁸. Time series classes like `'xts'` and `'tsibble'` also do not provide deeply indexed structures for time series operations 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 (such as `'sf'` to create a spatiotemporal panel), as long as **collapse**'s functions (`flag()/L()` etc.) are used to perform the time-based computations. The `'index_df'` attached to these objects can be used with other general tools such as `collapse::BY()` to perform grouped computations on these objects with 3rd-party functions. An example of calculating a 5-year rolling average is given below. Last but not least, the performance of these classes is second to none, as demonstrated in the useR 2022 presentation [on slide 40](#).

```
R> BY(LIFEEXi, findex(LIFEEXi)$iso3c, data.table::frollmean, 5) |> head(10)
```

```
[1]    NA    NA    NA    NA 33.46 33.96 34.46 34.95 35.43 35.92
```

```
Indexed by: iso3c [1] | year [10 (61)]
```

5. Table joins and pivots

While **collapse** has a broad set of [Data Manipulation Functions](#), its implementations of table joins and pivots is particularly noteworthy since they offer several new features such as various verbose options for table joins, pivots supporting variable labels, and `'recast'` pivots.

5.1. Joins

Compared to commercial environments such as STATA, the implementation of joins in most open-source software, including R, is non-verbose, i.e., provides no information on how many and which records were joined from both tables. This is somewhat unsatisfying and often provokes manual efforts to validate the join operation. `collapse::join` provides a rich set of options to make table join operations intelligible. Its syntax is:

¹⁸And, in the case of **fixest**, inside **data.table** due to dedicated methods.

```
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, ...)
```

By default (`verbose = 1`), it prints information about the join operation and number of records joined. Users can request the generation of a 'join' column, akin to STATA's '`__merge`' column, indicating the origin of records in the joined table, as shown below.

```
R> df1 <- data.frame(id1 = c(1, 1, 2, 3),
+                   id2 = c("a", "b", "b", "c"),
+                   name = c("John", "Jane", "Bob", "Carl"),
+                   age = c(35, 28, 42, 50))
R> df2 <- data.frame(id1 = c(1, 2, 3, 3),
+                   id2 = c("a", "b", "c", "e"),
+                   salary = c(60000, 55000, 70000, 80000),
+                   dept = c("IT", "Marketing", "Sales", "IT"))
R> join(df1, df2, on = c("id1", "id2"), how = "full", column = TRUE)
```

```
full join: df1[id1, id2] 3/4 (75%) <m:m> df2[id1, id2] 3/4 (75%)
  id1 id2 name age salary      dept  .join
1   1   a John  35  60000      IT matched
2   1   b Jane  28    NA    <NA>    df1
3   2   b Bob   42  55000 Marketing matched
4   3   c Carl  50  70000    Sales matched
5   3   e <NA>  NA  80000      IT    df2
```

An alternative to the join column is to request an attribute that also summarizes the join operation, including the output of `fmatch()` (the workhorse of `join()` if `sort = FALSE`). Users can also invoke the `validate` argument to check the uniqueness of the join keys in either table: passing a '1' for a non-unique key produces an error.

```
R> join(df1, df2, on = c("id1", "id2"), validate = "1:1", attr = "join") />
+   attr("join") /> str(width = 70, strict = "cut")
```

```
left join: df1[id1, id2] 3/4 (75%) <1:1> df2[id1, id2] 3/4 (75%)
List of 3
 $ call      : language join(x = df1, y = df2, on = c("id1", "id2"), v"..
 $ on.cols:List of 2
  ..$ x: chr [1:2] "id1" "id2"
  ..$ y: chr [1:2] "id1" "id2"
 $ match     : 'qG' int [1:4] 1 NA 2 3
  ..- attr(*, "N.nomatch")= int 1
  ..- attr(*, "N.groups")= int 4
  ..- attr(*, "N.distinct")= int 3
```

A few further particularities are worth highlighting. First, `collapse::join` is also class-agnostic and preserves the attributes of `x`. It supports 6 different join operations ("`left`",

"right", "inner", "full", "semi" or "anti") and default to "left", so the default behavior simply adds columns to `x`. By default (`sort = FALSE`), the order of rows in `x` is also preserved. Setting `sort = TRUE` sorts all records in the joined table by the keys.¹⁹ Additionally, by default (`multiple = FALSE`), only the first matches from both tables are joined to avoid silent cartesian duplication of records. In multi-match settings, this will be reflected by few records from `y` being used. `fmatch()` also has a built-in overidentification check, which issues a warning if more key columns than necessary to identify the records are provided.

```
R> df2$name = df1$name
R> join(df1, df2) /> capture.output(type="m") /> strwrap(77) /> cat(sep="\n")
```

```
left join: df1[id1, id2, name] 1/4 (25%) <m:m> df2[id1, id2, name] 1/4 (25%)
  id1 id2 name age salary dept
1   1   1  a John  35  60000  IT
2   1   2  b Jane  28     NA <NA>
3   2   2  b Bob   42     NA <NA>
4   3   3  c Carl  50     NA <NA>
Warning in fmatch(x[ixon], y[iyon], nomatch = NA_integer_, count = count, :
Overidentified match/join: the first 2 of 3 columns uniquely match the
records. With overrides > 0, fmatch() continues to match columns. Consider
removing columns or setting overrides = 0 to terminate the algorithm after 2
columns (the results may differ, see ?fmatch). Alternatively set overrides = 2
to silence this warning.
```

A final noteworthy feature is the handling of duplicate non-id columns in both tables.

```
R> join(df1, df2, on = c("id1", "id2"))

left join: df1[id1, id2] 3/4 (75%) <m:m> df2[id1, id2] 3/4 (75%)
duplicate columns: name => renamed using suffix '_df2' for y
  id1 id2 name age salary      dept name_df2
1   1   1  a John  35  60000        IT      John
2   1   2  b Jane  28     NA        <NA>    <NA>
3   2   2  b Bob   42  55000 Marketing    Jane
4   3   3  c Carl  50  70000      Sales      Bob
```

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. Another option, `drop.dup.cols = "x"/"y"` can be used to simply drop duplicate columns from `x` or `y` before the join operation.

5.2. Pivots

The reshaping/pivoting functionality of commercial and open source software is also unsatisfying for complex datasets such as surveys or disaggregated production, trade, or financial

¹⁹This 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.

sector data, where variable names resemble codes and variable labels are essential to making sense of the data. Such datasets can only be reshaped by losing these labels or additional manual efforts to retain them. Modern R packages also offer different functions for different reshaping operations, 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. Finally, since the depreciation of `reshape(2)` (Wickham 2007), there is no modern replacement for `reshape2::recast()`. This requires R users to consecutively call two reshaping functions, incurring a high cost in terms of syntax and memory for such frequently required data transpositions.

`collapse::pivot` provides a modern class-agnostic implementation of reshaping for R that addresses these shortcomings: it has a single intuitive syntax to perform 'longer', 'wider', and 'recast' pivots, can handle complex labelled data without loss of information, and offers best-in-R computational performance and memory efficiency. Its syntax is:

```

pivot(data, ids = NULL, values = NULL, names = NULL, labels = NULL,
      how = "longer", na.rm = FALSE, factor = c("names", "labels"),
      check.dups = FALSE, nthreads = 1, fill = NULL, drop = TRUE,
      sort = FALSE, transpose = FALSE)

```

Below, its use is demonstrated with a generated dataset about fruits. We could also think about a survey with households and individuals, or sectors and firms. Variable labels are stored in `attr(column, "label")`. The [documentation](#) provides more elaborate examples with real data.

```

R> data <- data.frame(type = rep(c("A", "B"), each = 2),
+                    type_name = rep(c("Apples", "Bananas"), each = 2),
+                    id = rep(1:2, 2), r = abs(rnorm(4)), h = abs(rnorm(4)*2))
R> setrelabel(data, id = "Fruit Id", r = "Fruit Radius", h = "Fruit Height")
R> print(data)

```

	type	type_name	id	r	h
1	A	Apples	1	0.9322	0.4315
2	A	Apples	2	0.2230	0.7225
3	B	Bananas	1	0.8147	0.4918
4	B	Bananas	2	0.5642	2.4131

```

R> vlabels(data)

```

type	type_name	id	r	h
NA	NA	"Fruit Id"	"Fruit Radius"	"Fruit Height"

To reshape this dataset into a longer format, it suffices to call `pivot(data, ids = c(...))`. If `labels = "lab_name"` is specified, variable labels are saved to an additional column named 'lab_name'. In addition, `names = list(variable = "var_name", value = "val_name")` can be passed to assign alternative names to the 'variable' and 'value' columns, respectively.

```
R> (dl <- pivot(data, ids = c("type", "type_name", "id"), labels = "label"))
```

	type	type_name	id	variable	label	value
1	A	Apples	1	r Fruit Radius	0.9322	
2	A	Apples	2	r Fruit Radius	0.2230	
3	B	Bananas	1	r Fruit Radius	0.8147	
4	B	Bananas	2	r Fruit Radius	0.5642	
5	A	Apples	1	h Fruit Height	0.4315	
6	A	Apples	2	h Fruit Height	0.7225	
7	B	Bananas	1	h Fruit Height	0.4918	
8	B	Bananas	2	h Fruit Height	2.4131	

```
R> vlabels(dl)
```

type	type_name	id	variable	label	value
NA	NA	"Fruit Id"	NA	NA	NA

In general, `pivot()` only requires essential information and intelligently guesses the rest. For example, the same result could have been obtained by `pivot(data, values = c("r", "h"), labels = "label")`. An exact reverse operation can also be performed by specifying as little as `pivot(dl, labels = "label", how = "w")`.

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.²⁰ *Note* how the labels are combined with existing labels such that also this operation is without loss of information. It is, however, a destructive operation, i.e., with 2 or more columns selected through `values`, `pivot()` is not able to reverse it. Further arguments like `na.rm`, `fill`, `sort`, and `transpose` can be used to control the casting process.

```
R> (dw <- pivot(data, "id", names = "type", labels = "type_name", how = "w"))
```

	id	r_A	r_B	h_A	h_B
1	1	0.9322	0.8147	0.4315	0.4918
2	2	0.2230	0.5642	0.7225	2.4131

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

	Variable	Label
1	id	Fruit Id
2	r_A Fruit Radius - Apples	
3	r_B Fruit Radius - Bananas	
4	h_A Fruit Height - Apples	
5	h_B Fruit Height - Bananas	

²⁰multiple columns with names and labels could be selected, which would be combined using "_" for names and " - " for labels.

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

```
R> (dr <- pivot(data, ids = "id", names = list(from = "type"),
+             labels = list(from = "type_name", to = "label"), how = "r"))
```

	id	variable	label	A	B
1	1	r	Fruit Radius	0.9322	0.8147
2	2	r	Fruit Radius	0.2230	0.5642
3	1	h	Fruit Height	0.4315	0.4918
4	2	h	Fruit Height	0.7225	2.4131

```
R> vlabels(dr)
```

	id	variable	label	A	B
"Fruit Id"		NA	NA	"Apples"	"Bananas"

As with the other pivots, this operation does not incur any loss of information. A suitable reverse operation also exists: `pivot(dr, "id", names = list(to = "type"), labels = list(from = "label", to = "type_name"), how = "r")`. More features of `pivot()` are demonstrated in the [documentation examples](#). Notably, it is also possible to perform longer and recast pivots without id variables. The recast pivot without IDs resembles a generalization of `data.table::transpose`, albeit slightly less efficient.

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 object, performance statistics, and predictions) 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, e.g., in response to nested user inputs in shiny apps. Except for certain recursive functions found in packages such as **purrr**, **tidyr**, **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 a (nested) list.

```
R> (dl <- mtcars |> rsplit(mpg + hp + carb ~ vs + am)) |> str(max.level = 2)
```

```
List of 2
```

```
$ 0:List of 2
```

```
..$ 0:'data.frame':      12 obs. of  3 variables:
..$ 1:'data.frame':       6 obs. of  3 variables:
```

```
$ 1:List of 2
..$ 0:'data.frame':      7 obs. of  3 variables:
..$ 1:'data.frame':      7 obs. of  3 variables:
```

If a nested structure is not wanted, argument `flatten = TRUE` lets `rsplit()` operate like a faster version of `split()`. With a single column on the LHS of the formula, the default (`simplify = TRUE`) returns a nested list of atomic vectors. Having created a nested list, `rapply2d()` is used to fit a linear model on each frame,²¹ followed by `get_elem()` to obtain the coefficient matrices. `get_elem()` offers several options for filtering lists but, by default, simplifies the list tree as much as possible while maintaining existing hierarchies. In this case, it returns the same nested list with coefficient matrices in all final nodes.

```
R> nest_lm_coef <- dl |>
+   rapply2d(lm, formula = mpg ~ .) |>
+   rapply2d(summary, classes = "lm") |>
+   get_elem("coefficients")
R> nest_lm_coef |> str(give.attr = FALSE, strict = "cut")
```

```
List of 2
 $ 0:List of 2
  ..$ 0: num [1:3, 1:4] 15.8791 0.0683 -4.5715 3.655 0.0345 ...
  ..$ 1: num [1:3, 1:4] 26.9556 -0.0319 -0.308 2.293 0.0149 ...
 $ 1:List of 2
  ..$ 0: num [1:3, 1:4] 30.896903 -0.099403 -0.000332 3.346033 0.03587 ...
  ..$ 1: num [1:3, 1:4] 37.0012 -0.1155 0.4762 7.3316 0.0894 ...
```

At last, `unlist2d()` is applied to unlist the nested list to a data frame. This function can create a data frame (or ‘`data.table`’) representation of any nested list containing data 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.

```
R> nest_lm_coef |> unlist2d(c("vs", "am"), row.names = "variable") |> head(2)

  vs am    variable Estimate Std. Error t value Pr(>|t|)
1  0  0 (Intercept) 15.87915     3.65495   4.345 0.001865
2  0  0          hp   0.06832     0.03449   1.981 0.078938
```

This example does not represent an optimal workflow for this specific task²² but exemplifies the power of these tools to create, query, and combine nested data in very general ways. **collapse**’s list processing toolkit provides further useful functions such as `t_list()` to turn lists of lists inside out, `has_elem()` to check for the existence of elements, `ldepth()` to return the maximum level of recursion, and `is_unlistable()` to check whether a list has atomic

²¹`rapply2d()` is just a recursive wrapper around `lapply()`, with different defaults than `rapply()`. Notably, by default, it excludes data frames from being considered as sub-lists and does not simplify the result.

²²A better way of achieving the same result would be `mtcars |> fgroup_by(vs, am) |> fsummarise(qDF(lmtest::coeftest(lm(mpg ~ hp + carb)), "variable"))`.

elements in all final nodes. A non-recursive and class-agnostic `rowbind()` function also exists to efficiently bind lists of data frame-like objects (like `data.table::rbindlist`).

7. Summary statistics

`collapse`'s **Summary Statistics Functions** provide a parsimonious and powerful toolset to examine complex datasets. A particular focus has been on providing tools for examining longitudinal (panel) data. Recall the indexed world development panel (`wldi`) from Section (4). The function `varying()` indicates which of these variables are time-varying:

```
R> varying(wldi)
```

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

```
R> varying(wldi, any_group = FALSE) |> head(3)
```

	country	date	year	decade	region	income	OECD	PCGDP	LIFEEX	GINI	ODA	POP
ABW	FALSE	TRUE	TRUE	TRUE	FALSE	FALSE	FALSE	TRUE	TRUE	NA	TRUE	TRUE
AFG	FALSE	TRUE	TRUE	TRUE	FALSE	FALSE	FALSE	TRUE	TRUE	NA	TRUE	TRUE
AGO	FALSE	TRUE	TRUE	TRUE	FALSE	FALSE	FALSE	TRUE	TRUE	TRUE	TRUE	TRUE

Country-variance can be examined using `varying(wldi, effect = "year")`. For non-indexed data, `varying()` also has a `g` argument. A related exercise is to decompose the variance of a panel series into a component due to variation between countries and one capturing variance within countries over time. Using the `W()`/`B()` operators and the `LIFEEXi` 'indexed_series' from Section (4), this is easily demonstrated

```
R> all.equal(fvar(W(LIFEEXi)) + fvar(B(LIFEEXi)), fvar(LIFEEXi))
```

```
[1] TRUE
```

The function `qsu()` (quick-summary) provides an efficient method to approximately compute this decomposition, considering the group-means instead of the between transformation²³ and adding the 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

²³This is more efficient and equal to using the between transformation if the panel is balanced.

This decomposition shows more variation in life expectancy between countries than within countries over time. It can also be computed for different subgroups, such as OECD members and non-members, and with sampling weights, such as population. `qsu()` can also return Pearson's measures of higher-order statistics.

```
R> qsu(LIFEEXi, g = wlddev$OECD, w = wlddev$POP, higher = TRUE) |> aperm()
```

```
, , FALSE
```

	N/T	Mean	SD	Min	Max	Skew	Kurt
Overall	9503	63.5476	9.2368	18.907	85.4171	-0.7394	2.7961
Between	171	63.5476	6.0788	43.0905	85.4171	-0.8041	3.082
Within	55.5731	65.8807	6.9545	30.3388	82.8832	-1.0323	4.0998

```
, , TRUE
```

	N/T	Mean	SD	Min	Max	Skew	Kurt
Overall	2156	74.9749	5.3627	45.369	84.3563	-1.2966	6.5505
Between	36	74.9749	2.9256	66.2983	78.6733	-1.3534	4.5999
Within	59.8889	65.8807	4.4944	44.9513	77.2733	-0.627	3.9839

The output shows that the variation in life expectancy is significantly larger for non-OECD countries and that for these countries, the between- and within-country variation is approximately equal in magnitude.²⁴ For more detailed (grouped, weighted) statistics, `descr()` provides a rich statistical description of variables in a dataset.

```
R> descr(wlddev, LIFEEX ~ OECD, w = ~ replace_na(POP))
```

```
Dataset: wlddev, 1 Variables, N = 13176, WeightSum = 313233706778
```

```
Grouped by: OECD [2]
```

	N	Perc	WeightSum	Perc
FALSE	10980	83.33	2.49344474e+11	79.6
TRUE	2196	16.67	6.38892329e+10	20.4

```
-----
```

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

Statistics (N = 11659, 11.51% NAs)

	N	Perc	Ndist	Mean	SD	Min	Max	Skew	Kurt
FALSE	9503	81.51	8665	63.55	9.24	18.91	85.42	-0.74	2.8
TRUE	2156	18.49	2016	74.97	5.36	45.37	84.36	-1.3	6.55

Quantiles

	1%	5%	10%	25%	50%	75%	90%	95%	99%
FALSE	41.39	45.78	49.08	57.51	65.98	70.14	74.12	75.63	76.91
TRUE	56.65	65.98	69.7	71.85	75.38	78.64	81.26	82.43	83.6

²⁴`qsu()` also has a convenient formula interface to perform these transformations in an ad-hoc fashion, e.g., the above can be obtained using `qsu(wlddev, LIFEEX ~ OECD, iso3c, POP, higher = TRUE)`, without prior indexation.

While `descr()` does not support panel-variance decompositions like `qsu()`, it also provides detailed (grouped, weighted) frequency tables for categorical data and is thus very useful for complex survey data. A `stepwise` argument toggles describing one variable at a time, allowing users to naturally ‘click-through’ a large dataset rather than printing a massive output to the console. More details and examples are in the [documentation](#). Both `qsu()` and `descr()` provide an `as.data.frame()` method for efficient tidying and further analysis.

A final noteworthy function from **collapse**’s descriptive statistics toolkit is `qtab()`, an enhanced drop-in replacement for `base::table`. It is enhanced both in a statistical and 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> library(magrittr) # World after 2015 (latest country data)
R> wlda15 <- wlddev |> fsubset(year >= 2015) |> fgroup_by(iso3c) |> flast()
R> wlda15 %%% 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 %%% qtab(OECD, income, w = POP) %>% divide_by(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 invoked once).

```
R> wlda15 %%% qtab(OECD, income, w = LIFEEX, wFUN = fmean) %>% replace_na(0)
```

	income			
OECD	High income	Low income	Lower middle income	Upper middle income
FALSE	78.75	62.81	68.30	73.81
TRUE	81.09	0.00	0.00	76.37

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

```
R> wlda15 %%% qtab(OECD, income, w = LIFEEX, wFUN = fmean,
+                  wFUN.args = list(w = POP)) %>% replace_na(0)
```

	income			
OECD	High income	Low income	Lower middle income	Upper middle income
FALSE	77.91	63.81	68.76	75.93
TRUE	81.13	0.00	0.00	76.10

‘qtab’ objects inherit the ‘table’ class, thus all ‘table’ methods apply. Apart from the above functions, **collapse** also provides functions **pwcor**, **pwcov**, **pwnobs** for convenient (pairwise, weighted) correlations, covariances, and observations counts, and also functions **psacf**, **pspacf** and **psccf** for auto- and cross-covariance and correlation function estimation on panel series.

8. Global options

collapse is **globally configurable** to an extent few packages are: the default value 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` (for safety and performance reasons) visible in the **documentation of some functions**. 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.* 2023a): `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 used as the primary data manipulation framework.

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” and “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 a couple of **convenience keywords to mask groups of functions**. The most powerful of these is “all”, which masks all f-functions + specials, as shown below.

```
set_collapse(mask = "all", na.rm = FALSE, sort = FALSE, nthreads = 4)
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_diff = PCGDP - PCGDP_lag,
         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**, together with namespace masking, provides a fast experience of R - within GNU R - without the need to even restart the session. Masking is completely interactive and reversible within the active session: calling `set_collapse(mask = NULL)` instantly removes the additional functions. Option `remove` can further be used to remove any **collapse** function from the list of exported functions, allowing manual conflict management. Function `fastverse::fastverse_conflicts()` from the related [fastverse project](https://github.com/ropensci/fastverse)²⁵ can be used to display namespace conflicts with **collapse**. Invoking either `mask` or `remove` detaches **collapse** and reattaches it at the top of the search path, letting its namespace to take precedence over other packages.

9. Benchmark

This section offers a small benchmark to demonstrate that **collapse** provides best-in-R performance for many basic statistical and data manipulation tasks. They are executed on an Apple M1 MacBook Pro with 16 GB unified memory. The [DuckDB Benchmarks](https://github.com/ropensci/duckdb-benchmarks) compare more software packages on larger datasets, using a large server with many (slow) cores.

```

R> setDTthreads(4)
R> set_collapse(na.rm = FALSE, sort = FALSE, nthreads = 4)
R> set.seed(101)
R> m <- matrix(rnorm(1e7), ncol = 1000)
R> data <- qDT(replicate(100, rnorm(1e5), simplify = FALSE))
R> g <- sample.int(1e4, 1e5, TRUE)
R> microbenchmark(R = colMeans(m),
+                 Rfast = Rfast::colmeans(m, parallel = TRUE, cores = 4),
+                 collapse = fmean(m))

```

Unit: milliseconds

	expr	min	lq	mean	median	uq	max	neval
	R	9.632	9.837	9.959	9.852	9.940	12.70	100
	Rfast	1.315	1.805	2.257	1.840	1.917	11.92	100
	collapse	1.321	1.432	1.847	1.506	1.603	16.33	100

²⁵Website: <https://fastverse.github.io/fastverse/>

```
R> microbenchmark(R = rowsum(data, g, reorder = FALSE),
+                 data.table = data[, lapply(.SD, sum), by = g],
+                 collapse = fsum(data, g))
```

Unit: milliseconds

	expr	min	lq	mean	median	uq	max	neval
	R	10.715	11.19	11.550	11.295	11.61	16.89	100
	data.table	9.154	18.70	19.743	19.229	20.19	30.22	100
	collapse	2.330	2.89	3.619	3.078	3.71	15.94	100

```
R> add_vars(data) <- g
R> microbenchmark(data.table = data[, lapply(.SD, median), by = g],
+                 collapse = data |> fgroup_by(g) |> fmedian())
```

Unit: milliseconds

	expr	min	lq	mean	median	uq	max	neval
	data.table	136.36	137.50	140.23	138.54	140.62	173.7	100
	collapse	68.42	76.85	82.25	80.28	83.36	163.3	100

```
R> d <- data.table(g = unique(g), x = 1, y = 2, z = 3)
R> microbenchmark(data.table = d[data, on = "g"],
+                 collapse = join(data, d, on = "g", verbose = 0))
```

Unit: milliseconds

	expr	min	lq	mean	median	uq	max	neval
	data.table	8.915	10.881	16.398	13.166	16.903	73.045	100
	collapse	1.228	1.379	1.452	1.413	1.459	2.337	100

```
R> microbenchmark(data.table = melt(data, "g"),
+                 collapse = pivot(data, "g"))
```

Unit: milliseconds

	expr	min	lq	mean	median	uq	max	neval
	data.table	11.79	12.84	17.99	15.87	17.68	73.75	100
	collapse	11.73	13.77	20.37	15.69	18.17	76.75	100

```
R> settransform(data, id = rowid(g))
R> cols = grep("^V", names(data), value = TRUE)
R> microbenchmark(data.table = dcast(data, g ~ id, value.var = cols),
+                 collapse = pivot(data, ids = "g", names = "id", how = "w"))
```

Unit: milliseconds

	expr	min	lq	mean	median	uq	max	neval
	data.table	60.01	69.99	90.12	74.28	111.73	157.7	100
	collapse	32.59	41.80	63.15	48.87	63.98	177.0	100

The benchmark below further shows that **collapse** provides faster algorithms for basic computationally intensive operations such as unique values and matching. These algorithms power much of its functionality, such as efficient factor generation with `qF()`, cross-tabulation with `qtab()`, `join()`'s, `pivot()`'s, etc.

```
R> set.seed(101)
R> g_int <- sample.int(1e3, 1e7, replace = TRUE)
R> char <- c(letters, LETTERS, month.abb, month.name)
R> char <- outer(char, char, paste0)
R> g_char <- sample(char, 1e7, replace = TRUE)
R> microbenchmark(base_int = unique(g_int), collapse_int = funique(g_int),
+                 base_char = unique(g_char), collapse_char = funique(g_char))
```

Unit: milliseconds

	expr	min	lq	mean	median	uq	max	neval
	base_int	60.07	61.852	67.56	65.613	68.55	133.05	100
	collapse_int	6.69	9.222	10.34	9.581	10.18	17.56	100
	base_char	91.79	94.570	102.38	99.497	103.65	170.41	100
	collapse_char	22.29	23.879	26.83	24.577	27.58	80.46	100

```
R> microbenchmark(base_int = match(g_int, 1:1000),
+                 collapse_int = fmatch(g_int, 1:1000),
+                 base_char = match(g_char, char),
+                 data.table_char = chmatch(g_char, char),
+                 collapse_char = fmatch(g_char, char), times = 10)
```

Unit: milliseconds

	expr	min	lq	mean	median	uq	max	neval
	base_int	26.873	26.993	28.261	27.094	27.306	33.25	10
	collapse_int	8.603	8.633	9.352	8.662	8.723	15.53	10
	base_char	84.091	84.726	86.127	85.100	86.008	91.23	10
	data.table_char	40.970	41.169	42.597	41.307	41.407	48.49	10
	collapse_char	30.482	30.541	30.774	30.622	30.803	31.47	10

Apart from the raw algorithmic efficiency demonstrated here, **collapse** is often more efficient than other solutions by simply doing less. For example, if grouping columns are factor variables, **collapse**'s algorithms in `funique()`, `group()` or `fmatch()`, etc., use the values as hashes without checking for collisions. Similarly, if data is already sorted/unique, it is directly returned by functions like `roworder()/funique()`.

10. Conclusion

It is coming close to 4 years since the first CRAN release of **collapse** in March 2020, and since then, the package has grown and matured considerably. At the time of writing this article, it has been downloaded >1.5 million times off CRAN and is known and used by thousands of R users. In this article, I have articulated key ideas and design principles and demonstrated some core features of the package. In summary, my work with R as an applied economist has led me to believe that there should be a new foundation package for statistical computing and data manipulation in R that is statistically advanced, class-agnostic, flexible, fast, lightweight, stable, and able to manipulate complex scientific data with ease. **collapse** is my attempt at providing such a package, and the feedback I have received over the years, particularly from users in academia, government, and international organizations, is a strong indication that I have responded to a need felt in larger parts of the R community. As mentioned, a single article cannot summarize **collapse**, but there is an excellent [website](#) with comprehensive [Documentation Resources](#).

Computational details

The results in this paper were obtained using R ([R Core Team 2023](#)) 4.3.0 with **collapse** 2.0.10, **data.table** 1.15.0, **Rfast** 2.1.0, **fixest** 0.11.3, **magrittr** ([Bache and Wickham 2022](#)) 2.0.3 and **microbenchmark** ([Mersmann 2023](#)) 1.4.10. 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 M1 MacBook Pro (2020) with 16GB unified memory. Packages were compiled from source using Homebrew Clang version 16.0.4 with OpenMP enabled and the -O3 optimization flag.

Acknowledgments

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