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The Split-Apply-Combine Strategy for Data Analysis

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Abstract

Many data analysis problems involve the application of a split-apply-combine strategy, where you break up a big problem into manageable pieces, operate on each piece independently and then put all the pieces back together. This insight gives rise to a new R package that allows you to smoothly apply this strategy, without having to worry about the type of structure in which your data is stored.

The paper includes two case studies showing how these insights make it easier to work with batting records for veteran baseball players and a large 3d array of spatio-temporal ozone measurements.

Keywords: R, apply, split, data analysis.

1. Introduction

What do we do when we analyze data? What are common actions and what are common mistakes? Given the importance of this activity in statistics, there is remarkably little research on how data analysis happens. This paper attempts to remedy a very small part of that lack by describing one common data analysis pattern: Split-apply-combine. You see the split-apply-combine strategy whenever you break up a big problem into manageable pieces, operate on each piece independently and then put all the pieces back together. This crops up in all stages of an analysis:

- During data preparation, when performing group-wise ranking, standardization, or normalization, or in general when creating new variables that are most easily calculated on a per-group basis.

- When creating summaries for display or analysis, for example, when calculating marginal means, or conditioning a table of counts by dividing out group sums.

- During modeling, when fitting separate models to each panel of panel data. These models may be interesting in their own right, or used to inform the construction of a more sophisticated hierarchical model.

The split-apply-combine strategy is similar to the map-reduce strategy for processing large data, recently popularized by Google. In map-reduce, the map step corresponds to split and apply, and reduce corresponds to combine, although the types of reductions are much richer than those performed for data analysis. Map-reduce is designed for a highly parallel environment, where work is done by hundreds or thousands of independent computers, and for a wider range of data processing needs than just data analysis.

Just recognizing the split-apply-combine strategy when it occurs is useful, because it allows you to see the similarly between problems that previously might have appeared unconnected. This helps suggest appropriate tools and frees up mental effort for the aspects of the problem that are truly unique. This strategy can be used with many existing tools: APL's array operators (Friendly and Fox 1994), **Excel**'s pivot tables, the SQL `group by` operator, and the `by` argument to many SAS procedures. However, the strategy is even more useful when used with software specifically developed to support it; matching the conceptual and computational tools reduces cognitive impedance. This paper describes one implementation of the strategy in R (R Development Core Team 2010), the **plyr** package.

In general, **plyr** provides a replacement for loops for a large set of practical problems, and abstracts away from the details of the underlying data structure. An alternative to loops is not required because loops are slow (in most cases the loop overhead is small compared to the time required to perform the operation), but because they do not clearly express intent, as important details are mixed in with unimportant book-keeping code. The tools of **plyr** aim to eliminate this extra code and illuminate the key components of the computation.

Note that **plyr** makes the strong assumption that each piece of data will be processed only once and independently of all other pieces. This means that you can not use these tools when each iteration requires overlapping data (like a running mean), or it depends on the previous iteration (like in a dynamic simulation). Loops are still most appropriate for these tasks. If more speed is required, you can either recode the loops in a lower-level language (like C or Fortran) or solve the recurrence relation to find a closed form solution.

To motivate the development and use of **plyr**, Section 2 compares code that uses **plyr** functions with code that uses tools available in base R. Section 3 introduces the **plyr** family of tools, describes the three types of input and four types of output, and details the way in which input is split up and output is combined back together. The **plyr** package also provides a number of helper functions for error recovery, splatting, column-wise processing, and reporting progress, described in Section 4. Section 5 discusses the general strategy that these functions support, including two case studies that explore the performance of veteran baseball players, and the spatial-temporal variation of ozone. Finally, Section 6 maps existing R functions to their **plyr** counterparts and lists related packages. Section 7 describes future plans for the package.

This paper describes version 1.0 of **plyr**, which requires R 2.10.0 or later and has no run-time dependencies. The **plyr** package is available on the Comprehensive R Archive Network at `http://cran.r-project.org/web/packages/plyr`. Information about the latest version of the package can be found online at `http://had.co.nz/plyr`. To install it from within R, run `install.packages("plyr")`. The code used in this paper is available online in the supplemental materials.

Notation. *Array* includes the special cases of vectors (1d arrays) and matrices (2d arrays). Arrays can be made out of any *atomic* vector: Logical, character, integer, or numeric. A *list-array* is a non-atomic array (a list with dimensions), which can contain any type of data structure, such as a linear model or 2d kernel density estimate. *Dimension labels* refer to `dimnames()` for arrays; `rownames()` and `colnames()` for matrices and data frames; and `names()` for atomic vectors and lists.

2. Motivation

How does the explicit specification of this strategy help? What are the advantages of **plyr** over `for` loops or the built-in apply functions? This section compares **plyr** code to base R code with a teaser from Section 5.2, where we remove seasonal effects from 6 years of monthly satellite measurements, taken on a 24 × 24 grid. The 41 472 measurements are stored in a 24 × 24 × 72 array. A single location (`ozone[x, y, ]`) is a vector of 72 values (6 years × 12 months) .

We can crudely deseasonalize a location by looking at the residuals from a robust linear model:

```
R> one <- ozone[1, 1, ]
R>
R> month <- ordered(rep(1:12, length = 72))
R> model <- rlm(one ~ month - 1)
R> deseas <- resid(model)
R>
R> deseasf <- function(value) rlm(value ~ month - 1)
```

The challenge is to apply this function to each location, reassembling the output into the same form as the input, a 3d array. It would also be nice to keep the models in a 2d list-array, so we can reference a local model (`model[[1, 1]]`) in a similar way to referencing a local time series (`ozone[1, 1, ]`); keeping data-structures consistent reduces cognitive effort. In base R, we can tackle this problem with nested loops, or with the apply family of functions, as shown by Table 1.

The main disadvantage of the loops is that there is lot of book-keeping code: The size of the array is hard coded in multiple places and we need to create the output structures before filling them with data. The apply functions, `apply()` and `lapply()`, simplify the task, but there is not a straightforward way to go from the 2d array of models to the 3d array of residuals. In **plyr**, the code is much shorter because these details are taken care of:

```
R> models <- aaply(ozone, 1:2, deseasf)
R> deseas <- aaply(models, 1:2, resid)
```

You may be wondering what these function names mean. All **plyr** functions have a concise but informative naming scheme: The first and second characters describe the input and output data types. The input determines how the data should be split, and the output how it should be combined. Both of the functions used above input and output an *a*rray. Other data types are *l*ists and *d*ata frames. Because **plyr** caters for every combination of input and output

For loops

```
models <- as.list(rep(NA, 24 * 24))
dim(models) <- c(24, 24)

deseas <- array(NA, c(24, 24, 72))
dimnames(deseas) <- dimnames(ozone)

for (i in seq_len(24)) {
  for(j in seq_len(24)) {
    mod <- deseasf(ozone[i, j, ])

    models[[i, j]] <- mod
    deseas[i, j, ] <- resid(mod)
  }
}
```

Apply functions

```
models <- apply(ozone, 1:2, deseasf)
resids_list <- lapply(models, resid)

resids <- unlist(resids_list)
dim(resids) <- c(72, 24, 24)
deseas <- aperm(resids, c(2, 3, 1))
dimnames(deseas) <- dimnames(ozone)
```

Table 1: Compare of for loops and apply functions

data types in a consistent way, it is easy to use the data structure that feels most natural for a given problem.

For example, instead of storing the ozone data in a 3d array, we could also store it in a data frame. This type of format is more common if the data is ragged, irregular, or incomplete; if we did not have measurements at every possible location for every possible time point. Imagine the data frame is called `ozonedf` and has columns `lat`, `long`, `time`, `month`, and `value`. To repeat the deseasonalization task with this new data format, we first need to tweak our workhorse method to take a data frame as input:

```
R> deseasf_df <- function(df) {
+   rlm(value ~ month - 1, data = df)
+ }
```

Because the data could be ragged, it is difficult to use a `for` loop and we will use the base R functions `split()`, `lapply()` and `mapply()` to complete the task. Here the split-apply-combine strategy maps closely to built-in R functions: We split with `split()`, apply with `lapply()` and then combine the pieces into a single data frame with `rbind()`.

```
R> pieces <- split(ozonedf, list(ozonedf$lat, ozonedf$long))
R> models <- lapply(pieces, deseasf_df)
R>
R> results <- mapply(function(model, df) {
+   cbind(df[rep(1, 72), c("lat", "long")], resid(model))
+ }, models, pieces)
R> deseasdf <- do.call("rbind", results)
```

Most of the complication here is in attaching appropriate labels to the data. The type of labels needed depends on the output data structure, e.g., for arrays, dimnames are labels, while for data frames, values in additional columns are the labels. Here, we needed to use `mapply()` to match the models to their source data in order to extract informative labels. **plyr** takes care of adding the appropriate labels, so it only takes two lines:

```
R> models <- dlply(ozonedf, .(lat, long), deseasf_df)
R> deseas <- ldply(models, resid)
```

`dlply` takes a data frame and returns a list, and `ldply` does the opposite: It takes a list and returns a data frame. Compare this code to the code needed when the data was stored in an array.

The following section describes the **plyr** functions in more detail. If your interest has been whetted by this example, you might want to skip ahead to Section 5.2 to learn more about this example and see some plots of the data before and after removing the seasonal effects.

3. Usage

Table 2 lists the basic set of **plyr** functions. Each function is named according to the type of input it accepts and the type of output it produces: `a` = array, `d` = data frame, `l` = list, and `_` means the output is discarded. The input type determines how the big data structure is broken apart into small pieces, described in Section 3.1; and the output type determines how the pieces are joined back together again, described in Section 3.2.

The effects of the input and outputs types are orthogonal, so instead of having to learn all 12 functions individually, it is sufficient to learn the three types of input and the four types of output. For this reason, we use the notation `d*ply` for functions with common input, a complete row of Table 2, and `*dply` for functions with common output, a column of Table 2.

The functions have either two or three main arguments, depending on the type of input:

- `a*ply(.data, .margins, .fun, ..., .progress = "none")`
- `d*ply(.data, .variables, .fun, ..., .progress = "none")`
- `l*ply(.data, .fun, ..., .progress = "none")`

The first argument is the `.data` which will be split up, processed and recombined. The second argument, `.variables` or `.margins`, describes how to split up the input into pieces. The third argument, `.fun`, is the processing function, and is applied to each piece in turn. All further arguments are passed on to the processing function. If you omit `.fun` the individual pieces

output *input*	array	data frame	list	discarded
array	`aaply`	`adply`	`alply`	`a_ply`
data frame	`daply`	`ddply`	`dlply`	`d_ply`
list	`laply`	`ldply`	`llply`	`l_ply`

Table 2: The 12 key functions of **plyr**. Arrays include matrices and vectors as special cases.

will not be modified, but the entire data structure will be converted from one type to another. The `.progress` argument controls display of a progress bar, and is described at the end of Section 4.

Note that all arguments start with "`.`". This prevents name clashes with the arguments of the processing function, and helps to visually delineate arguments that control the repetition from arguments that control the individual steps. Some functions in base R use all uppercase argument names for this purpose, but I think this method is easier to type and read.

3.1. Input

Each type of input has different rules for how to split it up, and these rules are described in detail in the following sections. In short:

- Arrays are sliced by dimension in to lower-d pieces: `a*ply()`.
- Data frames are subsetted by combinations of variables: `d*ply()`.
- Each element in a list is a piece: `l*ply()`.

Technical note. The way the input can be split up is determined not by the type of the data structure, but the methods that it responds to. An object split up by `a*ply()` must respond to `dim()` and accept multidimensional indexing; by `d*ply()`, must work with `split()` and be coercible to a list; by list, must work with `length()` and `[[`. This means that data frames can be passed to `a*ply()`, where they are treated like 2d matrices, and to `l*ply()` where they are treated as a list of vectors (the variables).

Input: Array (`a*ply`*)*

The `.margins` argument of `a*ply` describes which dimensions to slice along. If you are familiar with `apply`, `a*ply` works the same way. There are four possible ways to do this for the 2d case. Figure 1 illustrates three of them:

- `.margins = 1`: Slice up into rows.
- `.margins = 2`: Slice up into columns.
- `.margins = c(1,2)`: Slice up into individual cells.

The fourth way is to not split up the matrix at all, and corresponds to `.margins = c()`. However, there is not much point in using **plyr** to do this!

The 3d case is a little more complicated. We have three possible 2d slices, three 1d, and one 0d. These are shown in Figure 2. Note how the pieces of the 1d slices correspond to the intersection of the 2d slices. The margins argument works correspondingly for higher dimensions, with an combinatorial explosion in the number of possible ways to slice up the array.

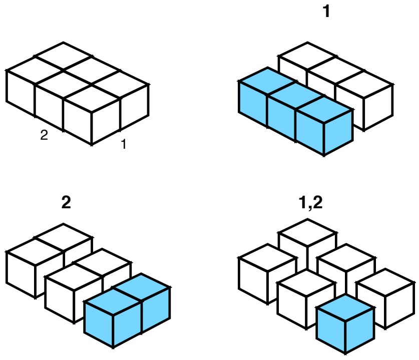


Figure 1: The three ways to split up a 2d matrix, labelled above by the dimensions that they slice. Original matrix shown at top left, with dimensions labelled. A single piece under each splitting scheme is colored blue.

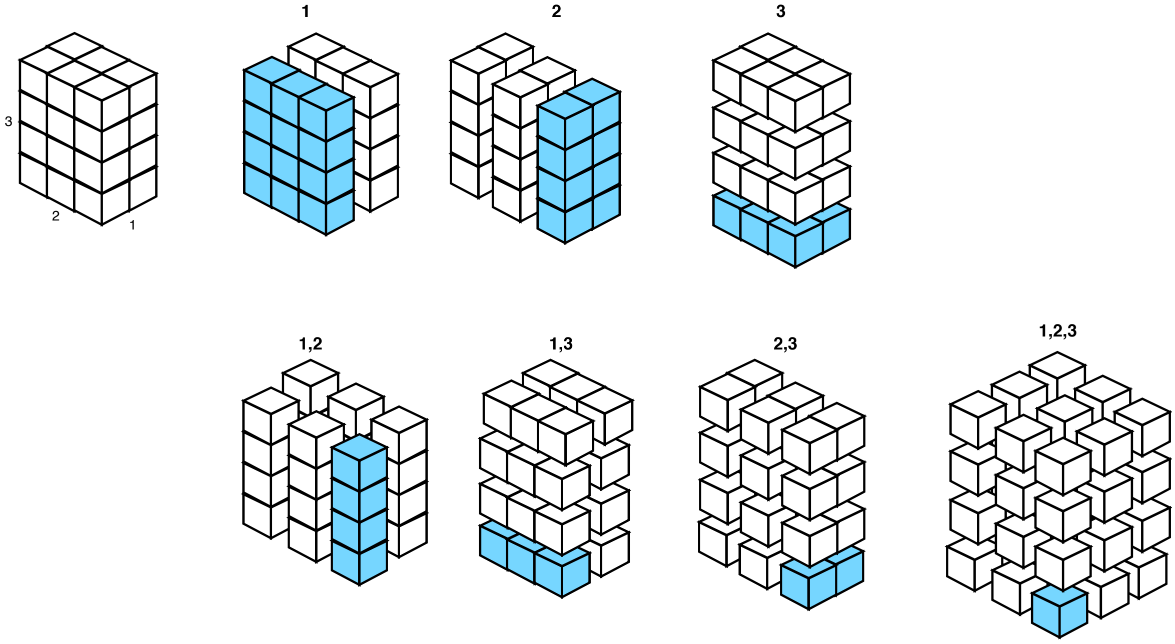
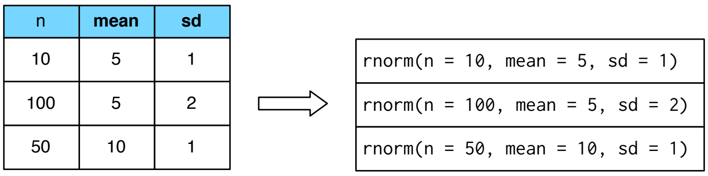


Figure 2: The seven ways to split up a 3d array, labelled above by the dimensions that they slice up. Original array shown at top left, with dimensions labelled. Blue indicates a single piece of the output.

Special case: `m*ply` A special case of operating on arrays corresponds to the `mapply` function of base R. `mapply` seems rather different at first glance: It accepts multiple inputs as separate arguments, compared to `a*ply` which takes a single array argument. However, the separate arguments to `mapply()` must have the same length, so conceptually it is the same underlying data structure. The **plyr** equivalents are named `maply`, `mdply`, `mlply` and `m_ply`.

`m*ply()` takes a matrix, list-array, or data frame, splits it up by rows and calls the processing function supplying each piece as its parameters. Figure 3 shows how you might use this to draw random numbers from normal distributions with varying parameters.



n	mean	sd
10	5	1
100	5	2
50	10	1

```
rnorm(n = 10, mean = 5, sd = 1)
rnorm(n = 100, mean = 5, sd = 2)
rnorm(n = 50, mean = 10, sd = 1)
```

Figure 3: Using `m*ply` with `rnorm()`, `m*ply(data, rnorm)`. The function is called once for each row, with arguments given by the columns. Arguments are matched by position, or name, if present.

Input: Data frame (`d*ply`)

When operating on a data frame, you usually want to split it up into groups based on combinations of variables in the data set. For `d*ply` you specify which variables (or functions of variables) to use. These variables are specified in a special way to highlight that they are computed first from the data frame, then the global environment (in which case it is your responsibility to ensure that their length is equal to the number of rows in the data frame).

- `.(var1)` will split the data frame into groups defined by the value of the `var1` variable. If you use multiple variables, `.(a, b, c)`, the groups will be formed by the interaction of the variables, and output will be labelled with all three variables. For array output, there will be three dimensions whose dimension names will be the values of a, b, and c in the input data frame; for data frame output there will be three extra columns with the values of a, b, and c; and for list output, the element names will be the values of a, b, and c appended together separated by periods, along with a `split_labels` attribute which contains the splits as a data frame.

- You can also use functions of variables: `.(round(a))`, `.(a * b)`. When outputting to a data frame, ugly names (produced by `make.names()`) may result, but you can override them by specifying names in the call: `.(product = a * b)`.

Alternatively, you can use two more familiar ways of describing the splits:

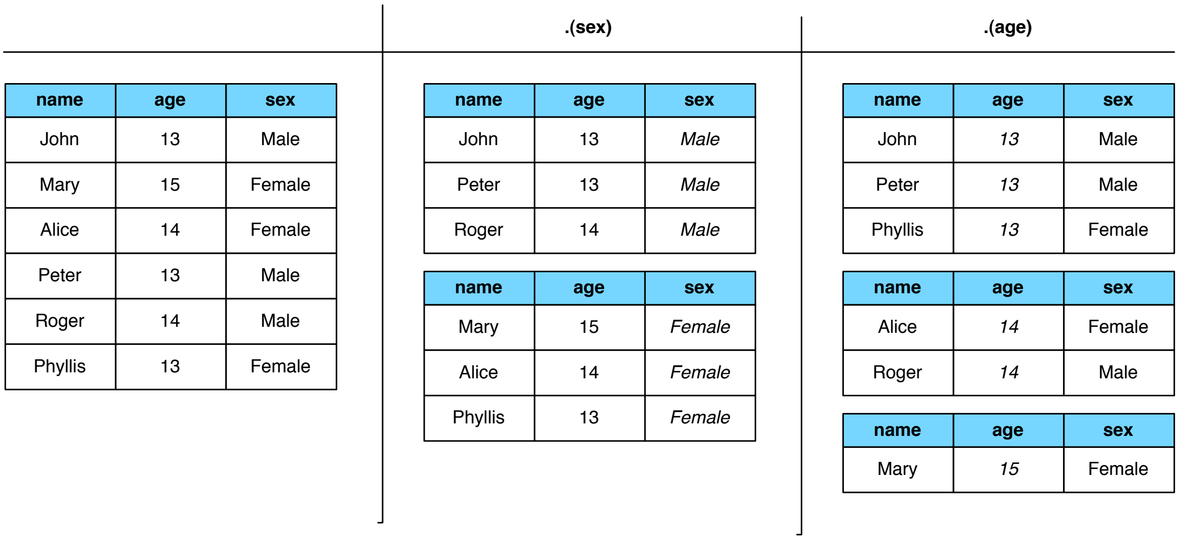
- As a character vector of column names: `c("var1", "var2")`.

- With a (one-sided) formula `~ var1 + var2`.

Figure 4 shows two examples of splitting up a simple data frame. Splitting up data frames is easier to understand (and to draw!) than splitting up arrays, because they are only 2 dimensional.

Input: List (`l*ply`)

Lists are the simplest type of input to deal with because they are already naturally divided into pieces: The elements of the list. For this reason, the `l*ply` functions do not need an argument that describes how to break up the data structure. Using `l*ply` is equivalent to using `a*ply` on a 1d array. `l*ply` can also be used with atomic vectors.



name	age	sex
John	13	Male
Mary	15	Female
Alice	14	Female
Peter	13	Male
Roger	14	Male
Phyllis	13	Female

.(sex)

name	age	sex
John	13	*Male*
Peter	13	*Male*
Roger	14	*Male*

name	age	sex
Mary	15	*Female*
Alice	14	*Female*
Phyllis	13	*Female*

.(age)

name	age	sex
John	*13*	Male
Peter	*13*	Male
Phyllis	*13*	Female

name	age	sex
Alice	*14*	Female
Roger	*14*	Male

name	age	sex
Mary	*15*	Female

Figure 4: Two examples of splitting up a data frame by variables. If the data frame was split up by both sex and age, there would only be one subset with more than one row: 13-year-old males.

Special case: `r*ply` A special case of operating on lists corresponds to `replicate()` in base R, and is useful for drawing distributions of random numbers. This is a little bit different to the other **plyr** methods. Instead of the `.data` argument, it has `.n`, the number of replications to run, and instead of a function it accepts a expression, which is evaluated afresh for each replication.

3.2. Output

The output type defines how the pieces will be joined back together and how they will be labelled. The labels are particularly important as they allow matching up of input and output.

The input and output types are the same, except there is an additional output data type, `_`, which discards the output. This is useful for functions like `plot()` and `write.table()` that are called only for their side effects, not their return value.

The output type also places some restrictions on what type of results the processing function should return. Generally, the processing function should return the same type of data as the eventual output, (i.e., vectors, matrices and arrays for `*aply` and data frames for `*dply`) but some other formats are accepted for convenience and are described in Table 3. These are explained in more detail in the individual output type sections.

Output: Array (`*aply`)

With array output the shape of the output array is determined by the input splits and the dimensionality of each individual result. Figures 5 and 6 illustrate this pictorially for simple 1d and 2d cases, and the following code shows another way to think about it.

```
R> x <- array(1:24, 2:4)
R> shape <- function(x) if (is.vector(x)) length(x) else dim(x)
```

Output	Processing function restrictions	Null output
`*aply`	atomic array, or list	`vector()`
`*dply` frame	data frame, or atomic vector	`data.frame()`
`*lply`	none	`list()`
`*_ply`	none	—

Table 3: Summary of processing function restrictions and null output values for all output types. Explained in more detail in each output section.

```
R> shape(x)

[1] 2 3 4

R>
R> shape(aaply(x, 2, function(y) 0))

[1] 3

R> shape(aaply(x, 2, function(y) rep(1,5)))

[1] 3 5

R> shape(aaply(x, 2, function(y) matrix(0,nrow=5,ncol=6)))

[1] 3 5 6

R> shape(aaply(x, 1, function(y) matrix(0,nrow=5,ncol=6)))

[1] 2 5 6
```

For array input, the pieces contribute to the output array in the expected way. The dimension labels of the output array will be the same as the dimension labels of the splits (i.e., the dimensions indexed by .margin in the input array.) List input is treated like a 1d array. For data frame input, the output array gets a dimension for each variable in the split, labelled by values of those variables.

The processing function should return an object of the same type and dimensionality each time it is called. This can be an atomic array (e.g., numeric, character, logical), or a list. If the object returned by the processing function is an array, its dimensions are included in the output array after the split dimensions. If it is a list, the output will be a list-array (i.e., a list with dimensions based on the split, and elements of the list are the objects returned by the processing function). If there are no results, `*aply` will return a logical vector of length 0.

All `*aply` functions have a `drop.` argument. When this is true, the default, any dimensions of length one will be dropped. This is useful because in R, a vector of length three is not equivalent to a 3×1 matrix or a $3 \times 1 \times 1$ array.

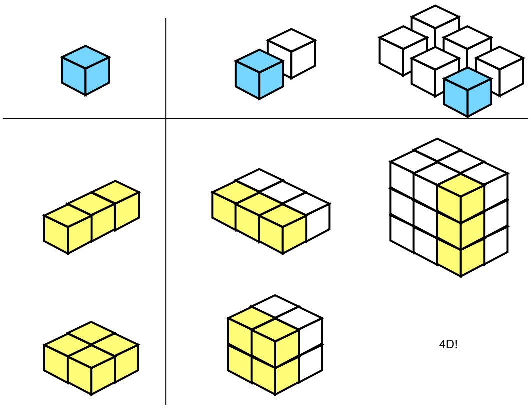


Figure 5: Results from outputs of various dimensionality from a *single* value, shown top left. Columns indicate input: (left) a vector of length two, and (right) a 3 × 2 matrix. Rows indicate the shape of a single processed piece: (top) a vector of length 3, (bottom) a 2 × 2 matrix. Extra dimensions are added perpendicular to existing ones. The array in the bottom-right cell is 4d and so is not shown.

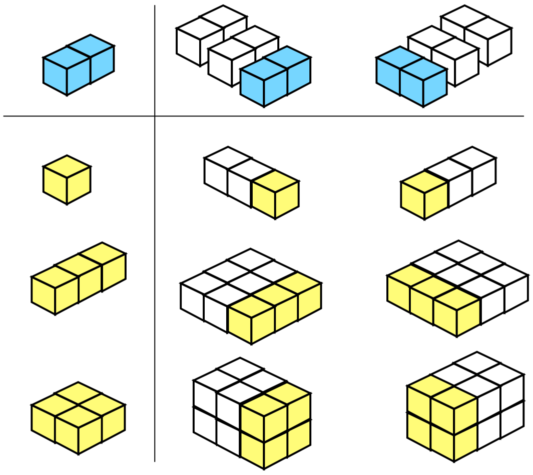
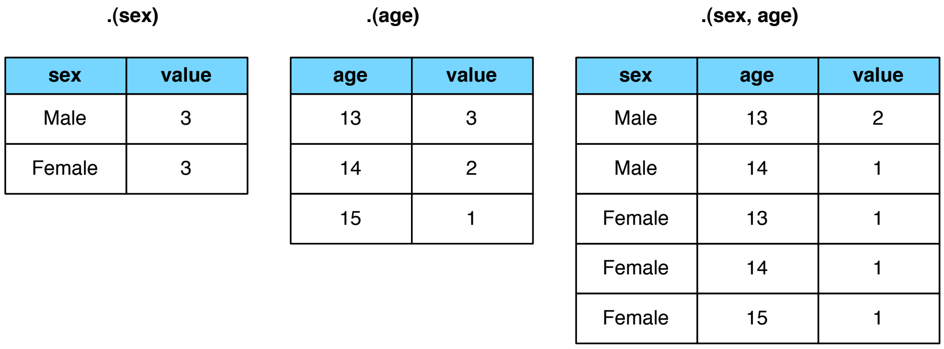


Figure 6: Results from outputs of various dimensionality from a *1d vector*, shown top left. Columns indicate input: (left) a 2 × 3 matrix split by rows and (right) and 3 × 2 matrix split by columns. Rows indicate the shape of a single processed piece: (top) a single value, (middle) a vector of length 3, and (bottom) a 2 × 2 matrix.

Output: Data frame (`*dply`)

When the output is a data frame, it will the results as well as additional label columns. These columns make it possible to merge the old and new data if required. If the input was a data frame, there will be a column for each splitting variable; if a list, a column for list names (if present); if an array, a column for each splitting dimension. Figure 7 illustrates this for data frame input.

The processing functions should either return a data.frame, or an atomic vector of fixed length, which will be interpreted as a row of a data frame. In contrast to `*aply`, the shape of the results can vary: The piece-wise results are combined together with `rbind.fill()`, so



.(sex)

sex	value
Male	3
Female	3

.(age)

age	value
13	3
14	2
15	1

.(sex, age)

sex	age	value
Male	13	2
Male	14	1
Female	13	1
Female	14	1
Female	15	1

Figure 7: Illustrating the output from using `ddply()` on the example from Figure 4 with `nrow()`. Splitting variables shown above each example. Note how the extra labeling columns are added so that you can identify to which subset the results apply.

that any piece missing columns used in another piece will have those columns filled in with missing values. If there are no results, `*dply` will return an empty data frame. **plyr** provides an `as.data.frame` method for functions which can be handy: `as.data.frame(mean)` will create a new function which outputs a data frame.

Output: List (`*lply`)

This is the simplest output format, where each processed piece is joined together in a list. The list also stores the labels associated with each piece, so that if you use `ldply` or `laply` to further process the list the labels will appear as if you had used `aaply`, `adply`, `daply` or `ddply` directly. `llply` is convenient for calculating complex objects once (e.g., models), from which you later extract pieces of interest into arrays and data frames.

There are no restrictions on the output of the processing function. If there are no results, `*lply` will return a list of length 0.

Output: Discarded (`*_ply`)

Sometimes it is convenient to operate on a list purely for the side effects, e.g., plots, caching, and output to screen/file. In this case `*_ply` is a little more efficient than abandoning the output of `*lply` because it does not store the intermediate results.

The `*_ply` functions have one additional argument, `.print`, which controls whether or not each result should be printed. This is useful when working with **lattice** or **ggplot2** graphics.

4. Helpers

The **plyr** package also provides a number of helper function which take a function (or functions) as input and return a new function as output.

- `splat()` converts a function that takes multiple arguments to one that takes a list as its single argument. This is useful when you want a function to operate on a data frame, without manually pulling it apart. In this case, the column names of the data frame will match the argument names of the function. For example, compare the following two `ddply` calls, one with, and one without `spat`:

```
R> hp_per_cyl <- function(hp, cyl, ...) hp / cyl
R> splat(hp_per_cyl)(mtcars[1,])
R> splat(hp_per_cyl)(mtcars)
R>
R> ddply(mtcars, .(round(wt)), function(df) mean_hp_per_cyl(df$hp, df$cyl))
R> ddply(mtcars, .(round(wt)), splat(mean_hp_per_cyl))
```

Generally, splatted functions should have `...` as an argument, as this will consume unused variables without raising a error. For more information on how splat works, see `do.call`.

`m*ply` uses `splat()` to call the processing function given to it: `m*ply(a_matrix, FUN)` is equivalent to `a*ply(a_matrix, 1, splat(FUN)`.

- `each()` takes a list of functions and produces a function that runs each function on the inputs and returns a named vector of outputs. For example, `each(min, max)` is short hand for `function(x) c(min = min(x), max = max(x))`. Using `each()` with a single function is useful if you want a named vector as output.

- `colwise()` converts a function that works on vectors, to one that operates column-wise on a data frame, returning a data frame. For example, `colwise(median)` is a function that computes the median of each column of a data.frame.

  The optional `.if` argument specializes the function to only run on certain types of vector, e.g., `.if = is.factor` or `.if = is.numeric`. These two restrictions are provided in the pre-made `calcolwise` and `numcolwise`. Alternatively, you can provide a vector of column names, and `colwise()` only operate on those columns.

- `failwith()` sets a default value to return if the function throws an error. For example, `failwith(NA, f)` will return an `NA` whenever `f` throws an error.

  The optional `quiet` argument suppresses any notification of the error when `TRUE`.

- Given a function, `as.data.frame.function()` creates a new function which coerces the output of the input function to a data frame. This is useful when you are using `*dply()` and the default column-wise output is not what you want.

There is one additional helper function analogous to the base function ‘transform’, but instead of returning the original data frame with modified or new columns added to it, it returns just the modified or new columns in a new data frame. Because this is very useful for creating group-wise summaries, it is called `summarize()` (or `summarize()`).

Each **plyr** function also has a `.progress` argument which allows you to monitor the progress of long running operations. There are four different progress bars:

- `"none"`, the default. No progress bar is displayed.

- `"text"` provides a textual progress bar.

- "win" and "tk" provide graphical progress bars for Windows and systems with the **tcltk** package (Dalgaard 2001), including the base distribution of R for mac and linux.

This is useful because it allows you to gauge how long a task will take and so you know if you need to leave your computer on overnight, or try a different approach entirely. Psychologically, adding a progress bar also makes it feel like it takes much less time. The progress bars assume that processing each piece takes the same amount of time, so may not be 100% accurate.

5. Strategy

Having learned the basic structure and operation of the **plyr** family of functions, you will now see some examples of using them in practice. The following two case studies explore two data sets: A data frame of batting records from long-term baseball players, and a 3d array recording ozone measurements that vary over space and time. Neither of these data studies do more than scratch the surface of possible analyses, but do show of a number of different ways to use **plyr**.

Both cases follow a similar process:

1. Extract a subset of the data for which it is easy to solve the problem.
2. Solve the problem by hand, checking results as you go.
3. Write a function that encapsulates the solution.
4. Use the appropriate **plyr** function to split up the original data, apply the function to each piece and join the pieces back together.

The code shown in this paper is necessarily abbreviated. The data sets are large, and often only small subsets of the data are shown. The code focuses on data manipulation, and much of the graphics code is omitted. You are encouraged to experiment with the full code yourself, available as a supplement to this paper.

All plots are created using **ggplot2** (Wickham 2010), but the process is very similar regardless of the graphics package used.

5.1. Case study: Baseball

The baseball data set contains the batting records for all professional US players with 15 or more years of data. In this example we will focus on four of the variables in the data: id, which identifies the player, year the year of the record; rbi, runs batted in, the number of runs that the player made in the season; and ab, at bat or the number of times the player faced a pitcher. The other variables are described in ?baseball.

What we will explore is the performance of a batter over his career. To get started, we need to calculate the "career year", i.e. the number of years since the player started playing. This is easy to do if we have a single player:

```
R> baberuth <- subset(baseball, id == "ruthba01")
R> baberuth <- transform(baberuth, cyear = year - min(year) + 1)
```

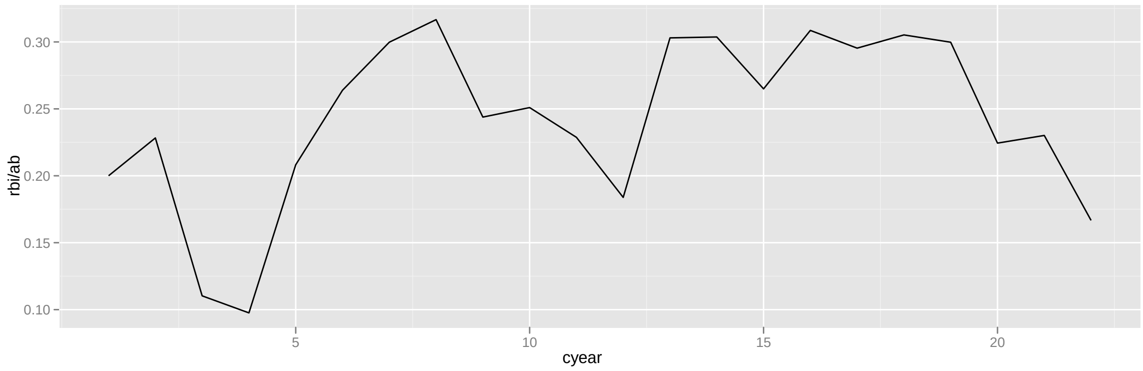


Figure 8: Runs per bat for Babe Ruth.

To do this for all players, we do not need to write our own function, because we can apply `transform()` to each piece:

```
R> baseball <- ddply(baseball, .(id), transform,
+   cyear = year - min(year) + 1)
```

To summarize the pattern across all players, we first need to figure out what the common patterns are. A time series plot of rbi/ab, runs per bat, is a good place to start. We do this for Babe Ruth, as shown in Figure 8, then write a function to do it for any player (taking care to ensure common scale limits) and then use `d_ply` to save a plot for every player to a pdf. We use two tricks here: `reorder` to sort the players in order of average rbi / ab, and `failwith` to ensure that even if a single plot does not work we will still get output for the others. We also restrict the data to focus only on records where `ab` is greater than 25: This prevents problems with a small number on the denominator.

```
R> baseball <- subset(baseball, ab >= 25)
R> xlim <- range(baseball$cyear, na.rm=TRUE)
R> ylim <- range(baseball$rbi / baseball$ab, na.rm=TRUE)
R> plotpattern <- function(df) {
+   qplot(cyear, rbi / ab, data = df, geom = "line",
+     xlim = xlim, ylim = ylim)
+ }
R>
R> pdf("paths.pdf", width = 8, height = 4)
R> d_ply(baseball, .(reorder(id, rbi / ab)), failwith(NA, plotpattern),
+   .print = TRUE)
R> dev.off()
```

Flicking through the 1145 plots reveals few common patterns, although many players do seem to have a roughly linear trend with quite a bit of noise. We will start by fitting a linear model to each player and then exploring the results. This time we will skip doing it by hand and go directly to the function. (Not recommended in practice!)

id	intercept	slope	rsquare
aaronha01	0.18	0.00	0.00
abernte02	0.00		0.00
adairje01	0.09	−0.00	0.01
adamsba01	0.06	0.00	0.03
adamsbo03	0.09	−0.00	0.11
adcocjo01	0.15	0.00	0.23

Table 4: The first few rows of the `bcoefs` data frame. Note that the player ids from the original data have been preserved.

```
R> model <- function(df) {
+   lm(rbi / ab ~ cyear, data=df)
+ }
R> model(baberuth)


Call:
lm(formula = rbi/ab ~ cyear, data = df)

Coefficients:
(Intercept)        cyear
    0.20320      0.00341


R> bmodels <- dlply(baseball, .(id), model)
```

Now we have a list of 1145 models, one for each player. To do something interesting with these, we need to extract some summary statistics. We will extract the coefficients of the model (the slope and intercept), and a measure of model fit (R^2) so we can ensure we are not drawing conclusions based on models that fit the data very poorly. The first few rows of `coef` are shown in Table 4.

```
R> rsq <- function(x) summary(x)$r.squared
R> bcoefs <- ldply(bmodels, function(x) c(coef(x), rsquare = rsq(x)))
R> names(bcoefs)[2:3] <- c("intercept", "slope")
```

Figure 9 displays the distribution of R^2 across the models. The models generally do a very bad job of fitting the data, although there are few with an R^2 very close to 1. We can see the data that generated these perfect fits by merging the coefficients with the original data, and then selecting records with an R^2 of 1:

```
R> baseballcoef <- merge(baseball, bcoefs, by = "id")
R> subset(baseballcoef, rsquare > 0.999)$id

 [1] "bannifl01" "bannifl01" "bedrost01" "bedrost01" "burbada01" "burbada01"
 [7] "carrocl02" "carrocl02" "cookde01"  "cookde01"  "davisma01" "davisma01"
```

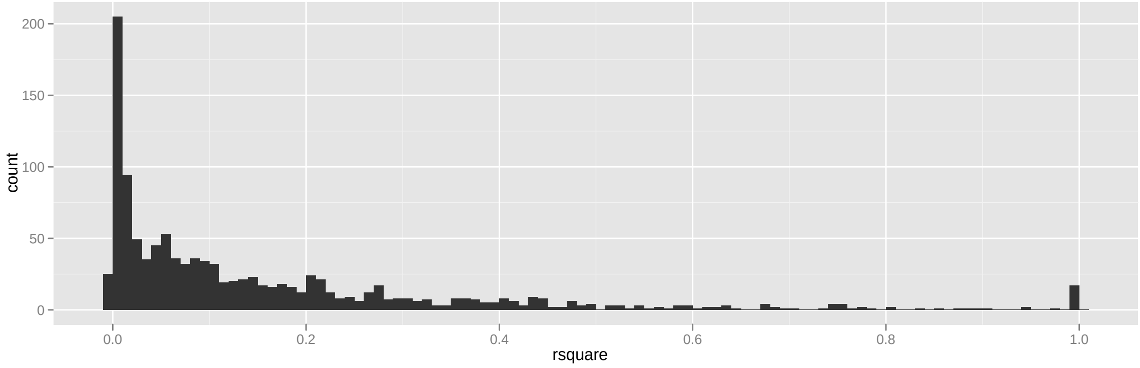


Figure 9: Histogram of model R^2 with bin width of 0.05. Most models fit very poorly!

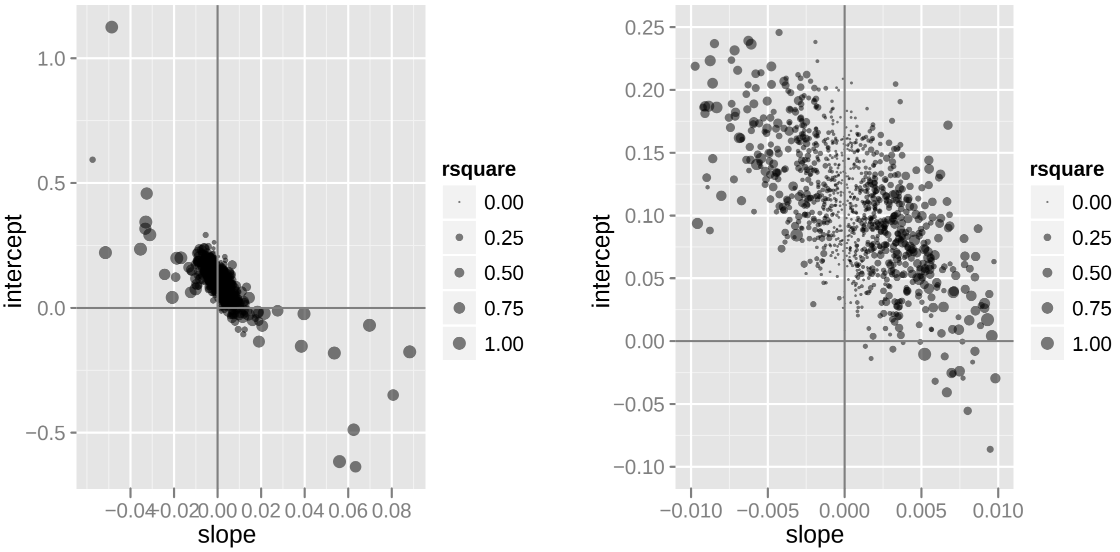


Figure 10: A scatterplot of model intercept and slope, with one point for each model (player). The size of the points is proportional to the R^2 of the model. Vertical and horizontal lines emphasize the x and y origins.

```
[13] "jacksgr01" "jacksgr01" "lindbpa01" "lindbpa01" "oliveda02" "oliveda02"
[19] "penaal01"  "penaal01"  "powerte01" "powerte01" "splitpa01" "splitpa01"
[25] "violafr01" "violafr01" "wakefti01" "wakefti01" "weathda01" "weathda01"
[31] "woodwi01"  "woodwi01"
```

All the models with a perfect fit only have two data points. Figure 10 is another attempt to summarize the models. These plots show a negative correlation between slope and intercept, and the particularly bad models have estimates for both values close to 0.

This concludes the baseball player case study, which used used `ddply`, `d_ply`, `dlply` and `ldply`. Our statistical analysis was not very sophisticated, but the tools of **plyr** made it very easy to work at the player level. This is an sensible first step when creating a hierarchical model.

5.2. Case study: Ozone

In this case study we will analyze a 3d array that records ozone levels over a 24 × 24 spatial grid at 72 time points (Hobbs, Wickham, Hofmann, and Cook 2010). This produces a 24 × 24 × 72 3d array, containing a total of 41 472 data points. Figure 11 shows one way of displaying this data. Conditional on spatial location, each star glyph shows the evolution of ozone levels for each of the 72 months (6 years, 1995–2000). The construction of the glyph is described in Figure 12; it is basically a time series in polar coordinates. The striking seasonal patterns make it difficult to see if there are any long-term changes. In this case study, we will explore how to separate out and visualize the seasonal effects.

Again we will start with the simplest case: A single time point, from location (1, 1). Figure 13 displays this in two ways: As a single line over time, or a line for each year over the months. This plot illustrates the striking seasonal variation at this time point. The following code sets up some useful variables.

```
R> value <- ozone[1, 1, ]
R> time <- 1:72 / 12
R> month.abbr <- c("Jan", "Feb", "Mar", "Apr", "May",
+   "Jun", "Jul", "Aug", "Sep", "Oct", "Nov", "Dec")
R> month <- factor(rep(month.abbr, length = 72), levels = month.abbr)
R> year <- rep(1:6, each = 12)
```

We are going to use a quick and dirty method to remove the seasonal variation: Residuals from a robust linear model (Venables and Ripley 2002) that predicts the amount of ozone for each month. We could use a regular linear model, but then our seasonal estimates might be thrown off by an unusual month. Figure 14 shows the deseasonalized trend from location (1, 1).

```
R> library("MASS")
R>
R> deseas1 <- rlm(value ~ month - 1)
R> summary(deseas1)


Call: rlm(formula = value ~ month - 1)
Residuals:
   Min     1Q Median     3Q    Max
 -18.7   -3.3    1.0    3.0   11.3

Coefficients:
         Value  Std. Error t value
monthJan 264.40   2.75      96.19
monthFeb 259.20   2.75      94.30
monthMar 255.00   2.75      92.77
monthApr 252.00   2.75      91.68
```

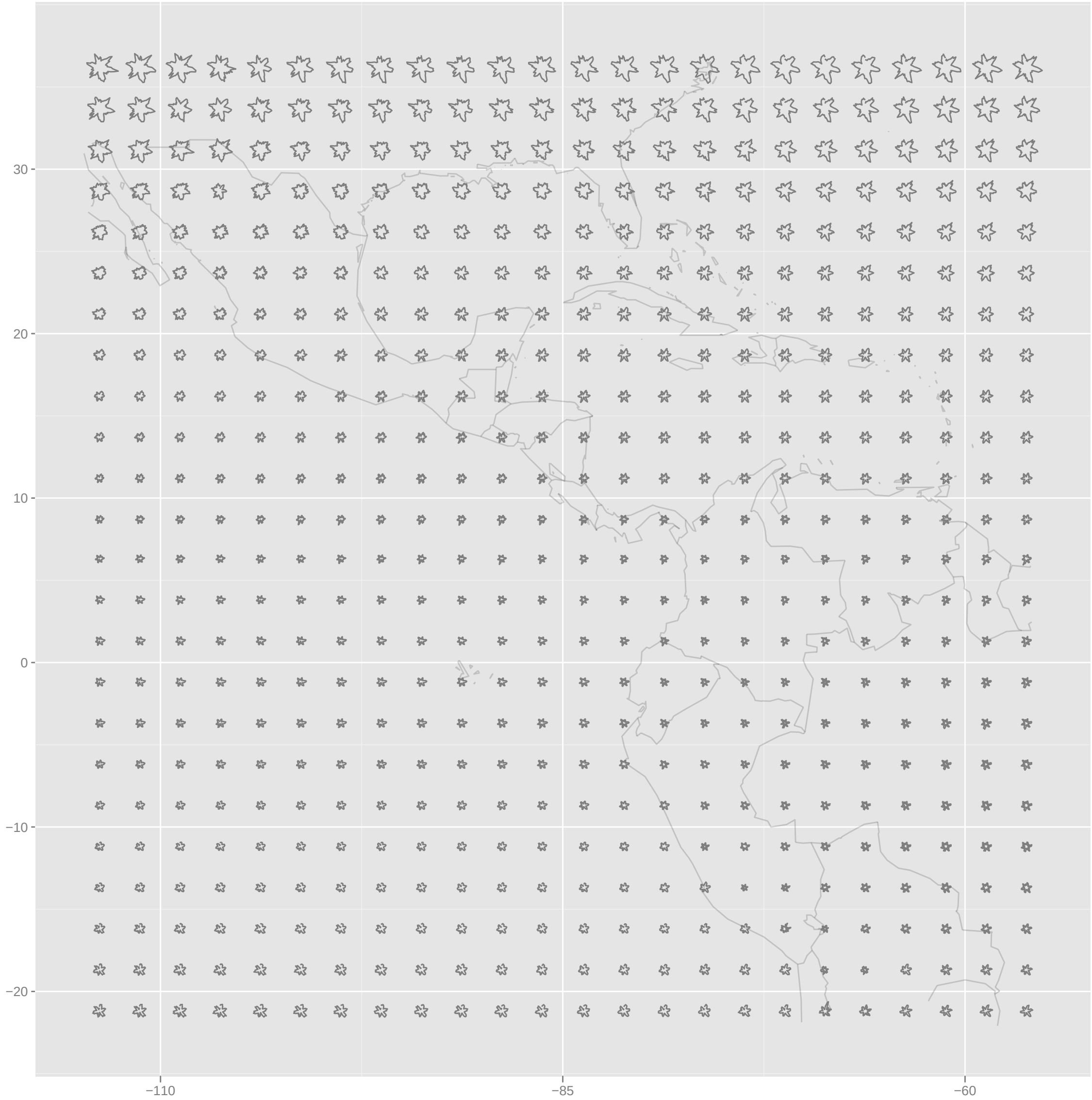


Figure 11: Star glyphs showing variation in ozone over time at each spatial location.

```
monthMay 258.51   2.75      94.05
monthJun 265.34   2.75      96.53
monthJul 274.00   2.75      99.68
monthAug 276.67   2.75     100.66
monthSep 277.00   2.75     100.78
monthOct 285.00   2.75     103.69
monthNov 283.60   2.75     103.18
monthDec 273.20   2.75      99.39

Residual standard error: 4.45 on 60 degrees of freedom
```

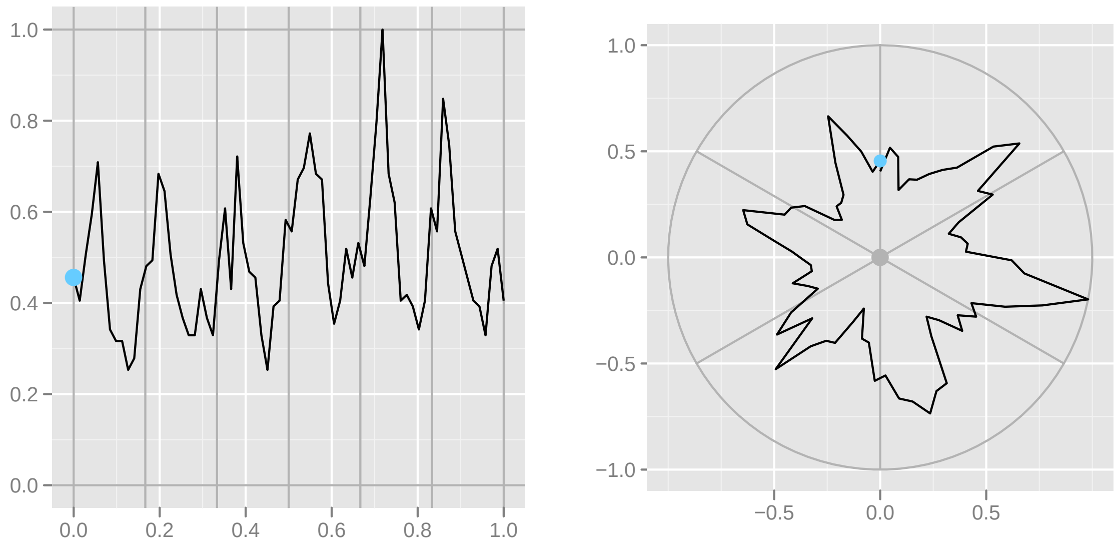


Figure 12: Star glyphs are time-series (left) plotted in polar coordinates (right). Both time and ozone value have been scaled to lie between 0 and 1: The smallest value in the entire dataset will be 0 and the largest will be 1. Grey lines indicate these boundaries, as well as the boundaries between the six years. A red point shows the position of the first value: it is close to the last value in the glyph. This glyph is the glyph on the top-left of Figure 11.

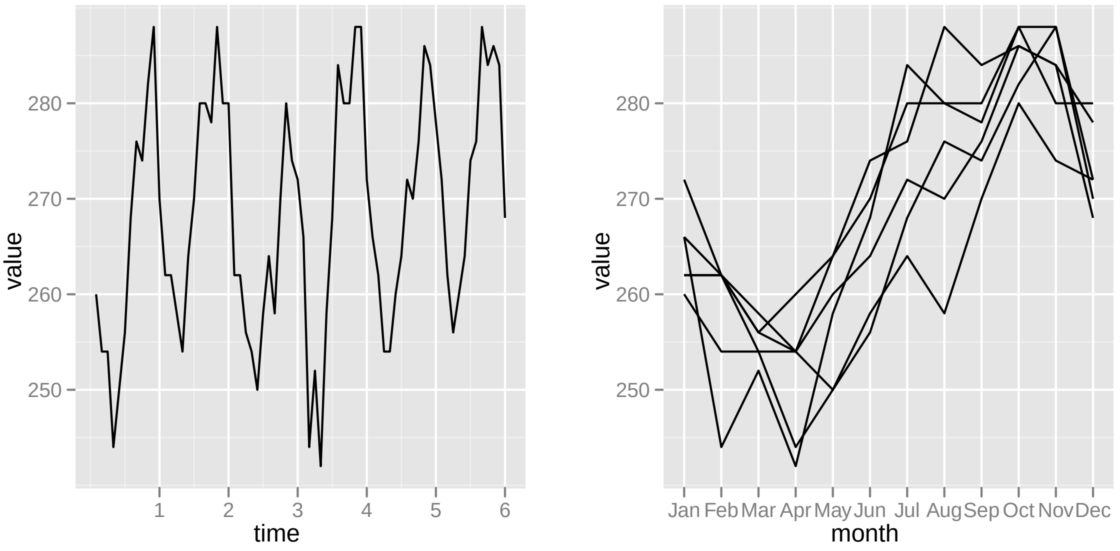


Figure 13: Two ways of displaying the seasonal changes. (Left) A single time series over all six years and (right) a line for each year.

```
R> coef(deseas1)
```

```
monthJan monthFeb monthMar monthApr monthMay monthJun monthJul monthAug
```

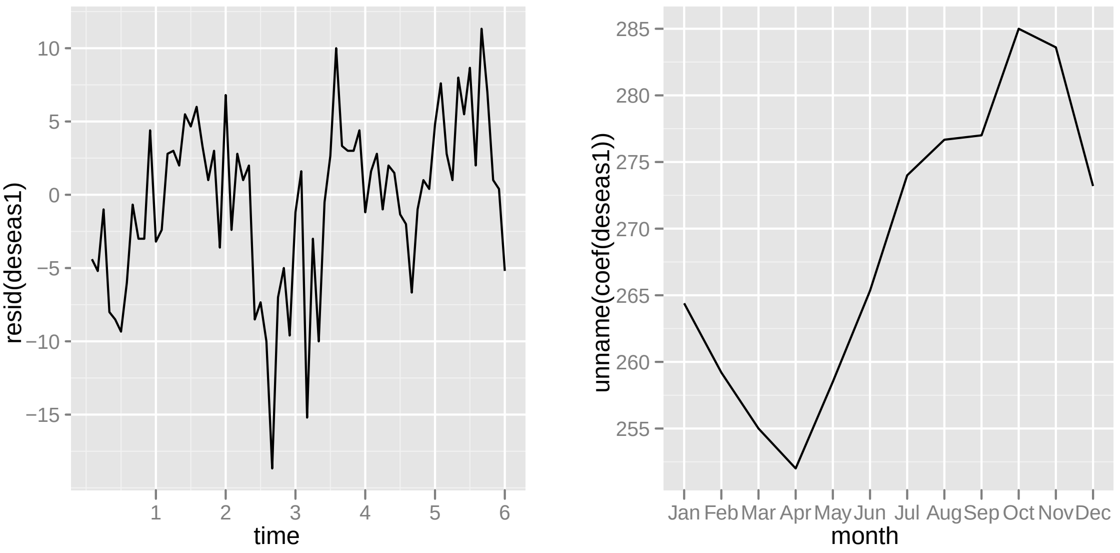


Figure 14: Deseasonalized ozone trends. (Left) Deseasonalized trend over six years. (Right) Estimates of seasonal effects. Compare to Figure 13.

```
     264       259       255       252       259       265       274       277
monthSep monthOct monthNov monthDec
     277       285       284       273
```

We next turn this into a function and fit the model to each spatial location. This does take a little while, but we are fitting 576 models! As is common when fitting large numbers of models, some of the models does not fit very well, and `rlm()` does not converge. We figure out where these lie by looking at the `converged` attribute for each model. In a real analysis it would be important to figure why these locations are troublesome and deal with them appropriately, but here we will just ignore them.

```
R> deseasf <- function(value) rlm(value ~ month - 1, maxit = 50)
R> models <- alply(ozone, 1:2, deseasf)

Warning message: rlm failed to converge in 50 steps
Warning message: rlm failed to converge in 50 steps
Warning message: rlm failed to converge in 50 steps
Warning message: rlm failed to converge in 50 steps
Warning message: rlm failed to converge in 50 steps
Warning message: rlm failed to converge in 50 steps
Warning message: rlm failed to converge in 50 steps

R> failed <- laply(models, function(x) !x$converged)
```

From those models we extract the deseasonalized values (the residuals) and the seasonal coefficients. Looking at the dimensionality we see that they are in the same format as the original data. We also carefully label the new dimensions. This is important: Just as data frames should have descriptive variable names, arrays should always have descriptive dimension labels.

```
R> coefs <- laply(models, coef)
R> dimnames(coefs)[[3]] <- month.abbr
R> names(dimnames(coefs))[3] <- "month"
R>
R> deseas <- laply(models, resid)
R> dimnames(deseas)[[3]] <- 1:72
R> names(dimnames(deseas))[3] <- "time"
R>
R> dim(coefs)

[1] 24 24 12

R> dim(deseas)

[1] 24 24 72
```

We now have a lot of data to try and understand: For each of the 576 locations we have 12 estimates of monthly effects, and 72 residuals. There are many different ways we could visualize this data. Figures 15 and 16 visualize these results with star glyph plots. For plotting, it is more convenient to have the data in data frames. There are a few different ways to do this: We can convert from the 3d array to a data frame with `melt()` from the **reshape** package, or use `ldply()` instead of `laply()`. For this example, we will use a combination of these techniques. We will convert the original array to a data frame, add on some useful columns, and then perform the same steps as above with this new format. Notice how our effort labeling the array dimensions pays off with informative column names in `coefs_df`: `lat`, `long` and `month`.

```
R> coefs_df <- melt(coefs)
R> head(coefs_df)

    lat long month value
1 -21.2 -114   Jan   264
2 -18.7 -114   Jan   261
3 -16.2 -114   Jan   261
4 -13.7 -114   Jan   259
5 -11.2 -114   Jan   256
6  -8.7 -114   Jan   255

R> coefs_df <- ddply(coefs_df, .(lat, long), transform,
+   avg = mean(value),
+   std = value / max(value)
+ )
R> head(coefs_df)
```

```
    lat long month value avg   std
1 -21.2 -114   Jan   264 269 0.928
2 -21.2 -114   Feb   259 269 0.909
3 -21.2 -114   Mar   255 269 0.895
4 -21.2 -114   Apr   252 269 0.884
5 -21.2 -114   May   259 269 0.907
6 -21.2 -114   Jun   265 269 0.931
```

```
R>
R> deseas_df <- melt(deseas)
R> head(deseas_df)
```

```
    lat long time value
1 -21.2 -114    1 -4.40
2 -18.7 -114    1 -3.33
3 -16.2 -114    1 -2.96
4 -13.7 -114    1 -5.00
5 -11.2 -114    1 -4.00
6  -8.7 -114    1 -3.00
```

The star glyphs show temporal patterns conditioned on location. We can also look at spatial pattern conditional on time. One way to do this is to draw tile plots where each cell of the 24×24 grid is colored according to its value. The following code sets up a function with constant scales to do that. Figure 17 shows the spatial variation of seasonal coefficients for January and July.

```
R> coef_limits <- range(coefs_df$value)
R> coef_mid <- mean(coefs_df$value)
R> monthsurface <- function(mon) {
+   df <- subset(coefs_df, month == mon)
+   qplot(long, lat, data = df, fill = value, geom="tile") +
+   scale_fill_gradient(limits = coef_limits,
+     low = brightblue, high = "yellow") +
+     map + opts(aspect.ratio = 1)
+ }
```

We could do the same thing for the values themselves, but we would probably want to make an animation rather than looking at all 72 plots individually. The `*_ply` functions are useful for making animations because we are only calling the plotting function for its side effects, not because we are interested in its value.

```
> pdf("ozone-animation.pdf", width = 8, height = 8)
> l_ply(month.abbr, monthsurface, .print = TRUE)
> dev.off()
```

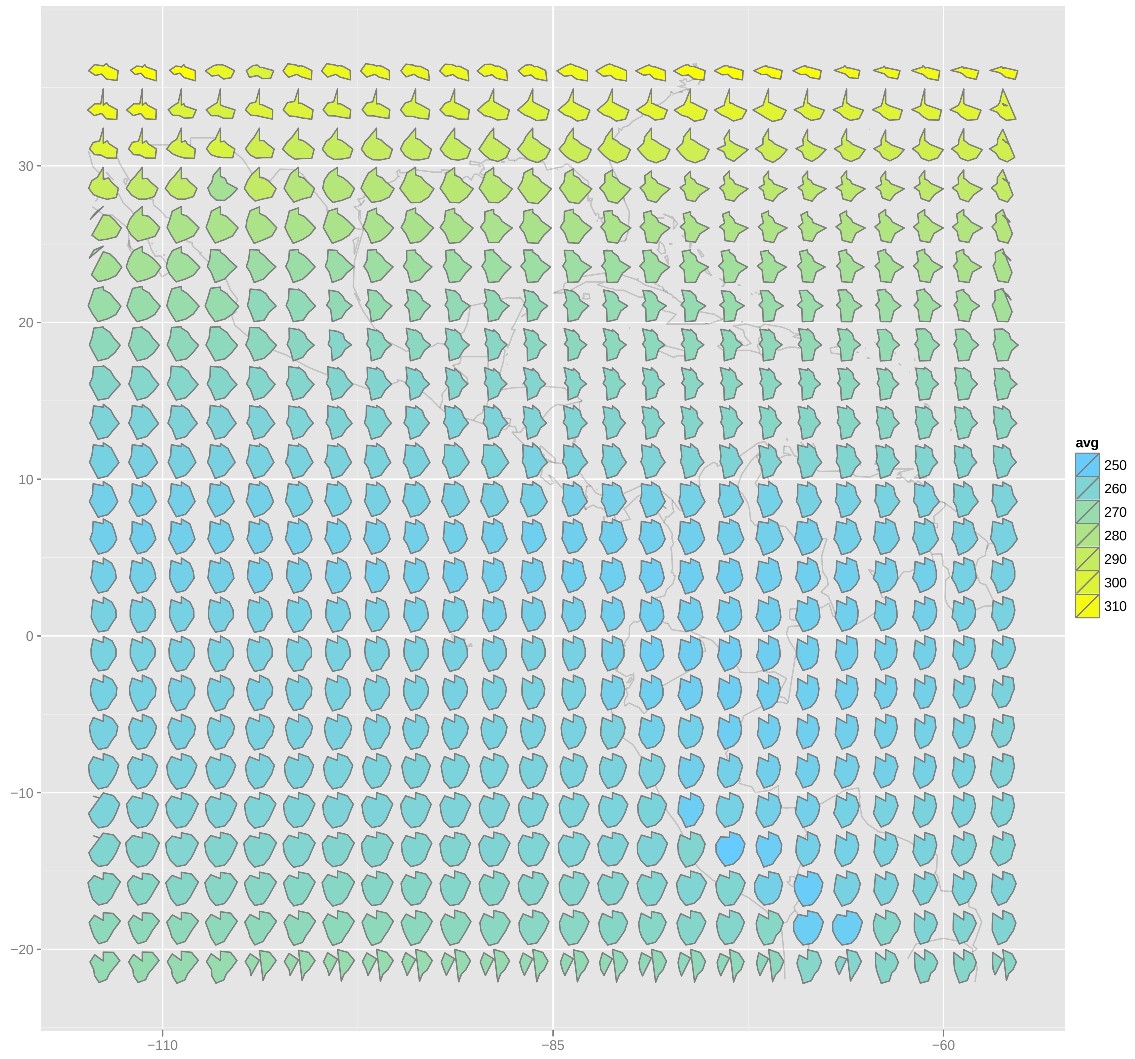


Figure 15: Star glyphs showing seasonal variation. Each star shows the twelve estimates of monthly seasonal effects, standardized to have maximum one. This focuses on the overall pattern of changes, rather than the absolute values, given by the glyph colour. Note the strong spatial correlation: Nearby glyphs have similar shapes.

5.3. Other uses

The `transform()`, `summarise()` and `subset()` functions work well in combination with **plyr**. Transform makes it very easy to perform randomization within groups. For example the following expression returns a data frame like `coefs_df`, but with the values in the `time` column randomized within each latitude/longitude grouping:

```
ddply(coefs_df, .(lat, long), transform, time = sample(time))
```

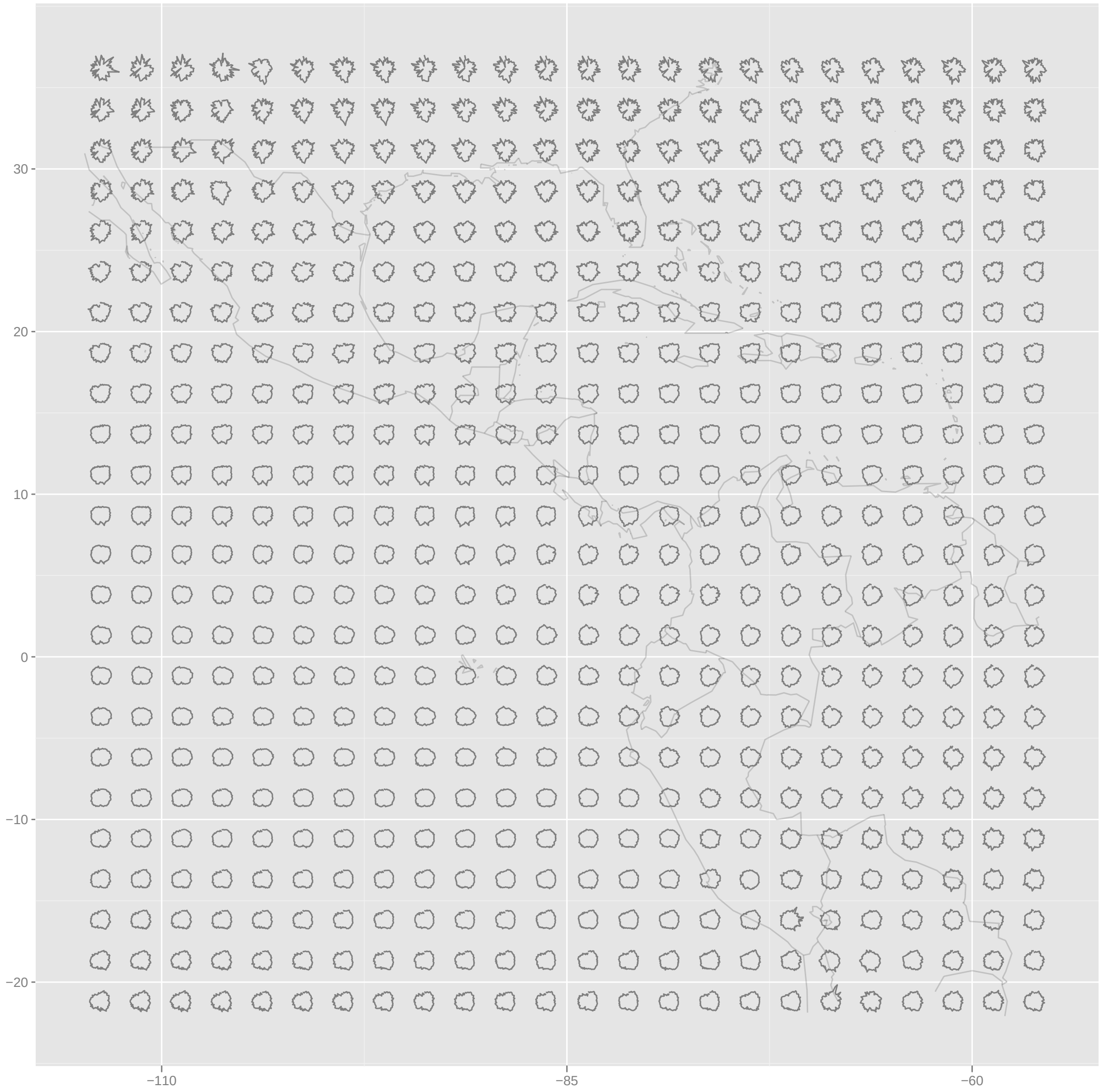


Figure 16: Star glyphs showing deseasonalized trends. Each star shows six years of data, with seasonal trend removed. This plot contains a lot of data—over 40,000 observations—and rewards detailed study. Looking at a printed version also helps as the resolution of a printer (600 dpi) is much higher than that of the screen (∼100 dpi). Interesting features include the higher variability in the North, locations in the mountains of South America with a large difference between starting and ending temperatures, and an unusual month common to many of the locations in the Pacific.

This technique is useful for performing block bootstrapping and other related permutation tests, and is related to the `ave` function in base R. Scaling variables within a group is also trivial:

```
ddply(coefs_df, .(lat, long), transform, value = scale(value))
```

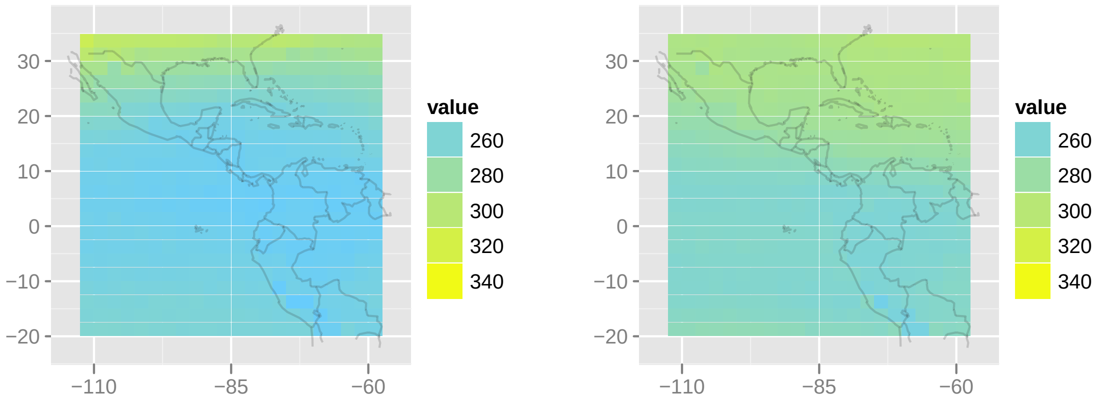


Figure 17: Tile plots of coefficients for January (left) and July (right).

We can create group-wise summaries with `summarise()` (or `summarize()`). For example, it is easy to summarize the range of ozone at each location:

```
ddply(coefs_df, .(lat, long), summarise,
  ozone_min = min(value), ozone_max = max(ozone))
```

Group-wise subsetting is easy with `subset()`. For example, if we wanted to extract the observation in each group with the lowest value ozone of ozone, it is just as easy:

```
ddply(coefs_df, .(lat, long), subset, value == min(value))
```

For simulations, `mdply()` can be very useful, because it is easy to generate a grid of parameter values and then evaluate them. This can also be useful when testing many possible combinations to input to a function.

```
mdply(expand.grid(mean = 1:5, sd = 1:5), as.data.frame(rnorm), n = 10)
```

6. Related work

There are a number of other approaches to solving the problems that **plyr** solves. You can always use loops, but loops create a lot of book-keeping code that obscures the intent of your algorithm. This section describes other high-level approaches similar to **plyr**.

Table 5 describes the functions in base R that work similarly to functions in **plyr**. The built-in R functions focus mainly on arrays and lists, not data frames, and most attempt to return an atomic data structure if possible, and if not, a list. This ambiguity of the output type is

Base function	Input	Output	**plyr** function
`aggregate`	d	d	`ddply` + `colwise`
`apply`	a	a/l	`aaply` / `alply`
`by`	d	l	`dlply`
`lapply`	l	l	`llply`
`mapply`	a	a/l	`maply` / `mlply`
`replicate`	r	a/l	`raply` / `rlply`
`sapply`	l	a	`laply`

Table 5: Mapping between apply functions and **plyr** functions.

fine for interactive use, but does make programming with these functions tricky. Compared to `aaply`, `apply` returns the new dimensions first, rather than last, which means it is not idempotent when used with the `identity` function. In contrast, `aaply(x, a, identity) == aperm(x, unique(c(a, seq_along(dim(x)))))` for all `a`.

Related functions `tapply` and `sweep` have no corresponding function in **plyr**, and remain useful. `merge` is useful for combining summaries with the original data.

Contributed packages also tackle this problem:

- The **doBy** (Højsgaard 2006, 2011) package provides versions of `order`, `sample`, `split`, `subset`, `summary` and `transform` that make it easy to perform each of these operations on subsets of data frames, joining the results back into a data frame. These functions are rather like a specialized version of `ddply` with a formula based interface, which, particularly for `summary`, makes it easy to only operate on selected columns.

- The **abind** (Plate and Heiberger 2011) package provides the `abind()` function which can be used to construct multidimensional arrays in a similar way to the `*aply` functions.

- The **gdata** (Warnes 2010) package contains a bundle of helpful data manipulation functions, including `frameApply` which works like `ddply` or `dlply` depending on its arguments.

- The **scope** (Bergsma 2007) package provides `scope`, `scoop`, `skim`, `score` and `probe` which provide a composable set of functions for operating symbolically on subsets of data frames.

- The **reshape** (Wickham 2007) package is similar to **Excel** pivot tables and provides tools for rearranging matrices and data frames. The `cast` function in the **reshape** package is closely related to `aaply`.

- The **sqldf** (Grothendieck 2010) package allows you to use SQL commands with R data frames. This gives the user access to a powerful set-based data access language.

7. Conclusion

Speed-wise **plyr** is competitive with R for small to moderate sized datasets, and generally a little faster for large datasets split by many different values. It is more memory-efficient than the naïve split-apply-combine approach because **plyr** is careful not to make an extra copy of the data in the split step. Further efficiency gains are possible, particularly by implementing key parts C for maximum speed and memory efficiency. The basic algorithm of **plyr** is trivially parallelizable, and future versions will integrate with the **foreach** package (REvolution Computing 2009) to make use of multiple cores and multiple machines.

More generally, what are other common strategies used in data analysis? How can we identify these strategies and then develop software to support them? It is difficult to step back and identify these patterns as trivial details may obscure the common components; it took four years of thinking about related problems before I recognized this split-apply-combine strategy. However, the task is important because the patterns are so useful. Personally, identifying the split-apply-combine strategy has made it much easier for me to solve common data analysis problems, and I have also found useful when teaching others how to do data analysis.

8. Acknowledgements

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