## Regular expressions and reshaping using data tables and the nc package

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**Abstract** Regular expressions are powerful tools for extracting tables from non-tabular text data. Capturing regular expressions that describe information to extract from column names can be especially useful when reshaping a data table from wide (one row with many columns) to tall (one column with many rows). We present the R package **nc**, which provides functions for data reshaping, regular expressions, and a uniform interface to three C libraries (PCRE, RE2, ICU). We describe the main features of **nc**, then provide detailed comparisons with related R packages (**stats**, **utils**, **data.table**, **tidyr**, **reshape2**, **cdata**).

## Introduction

Regular expressions are powerful tools for text processing that are available in many programming languages, including R. A regular expression *pattern* defines a set of *matches* in a *subject* string. For example, the pattern .\*[.].\* matches zero or more non-newline characters, followed by a period, followed by zero or more non-newline characters. It would match the subjects Sepal.Length and Petal.Width, but it would not match in the subject Species.

The focus of this article is patterns with capture groups, which are typically defined using parentheses. For example, the pattern (.\*)[.](.\*) results in the same matches as the pattern in the previous paragraph, and it additionally allows the user to capture and extract the substrings by group index (e.g. group 1 matches Sepal, group 2 matches Length).

Named capture groups allow extracting the a substring by name rather than by index. Using names rather than indices is useful in order to create more readable regular expressions (names document the purpose of each sub-pattern), and to create more readable R code (it is easier to understand the intent of named references than numbered references). For example, the pattern (?<part>.\*)[.](?<dimension>.\*) documents that the flower part appears before the measurement dimension; the part group matches Sepal and the dimension group matches Length.

Recently, Hocking (2019a) proposed a new syntax for defining named capture groups in R code. Using this new syntax, named capture groups are specified using R arguments, which results in code that is easier to read and modify than capture groups defined in string literals. For example, the pattern in the previous paragraph can be written as part=".\*", "[.]", dimension=".\*". Sub-patterns can be grouped for clarity and/or re-used using lists, and numeric data may be extracted by specifying group-specific type conversion functions.

In this article our original contribution is the R package nc which provides a new implementation of the previously proposed syntax for named capture regular expressions, in addition to several new features for data reshaping. The main new ideas are (1) using un-named capture groups in the regex string literal to provide a uniform interface to three regex C libraries, (2) integration of capture groups and data.table functionality (Dowle and Srinivasan, 2019), and (3) specifying wide-to-tall reshape operations with a concise syntax which results in less repetitive user code than other packages. A secondary contribution of this article is a detailed comparison of current R functions for reshaping data with regular expressions.

The organization of this article is as follows. The rest of this introduction provides an overview of current R packages for regular expressions and data reshaping. The second section describes the proposed functions of the nc package. The third section provides detailed comparisons with other R packages, in terms of syntax and computation times. The article concludes with a summary and discussion.

## Related work

There are many R functions which can extract tables from non-tabular text using regular expressions. Base R includes base::regexpr and base::gregexpr as well as utils::strcapture. CRAN packages include namedCapture (Hocking, 2019b), rematch2 (Csárdi, 2017), rex (Ushey et al., 2017), stringr (Wickham, 2018), stringi (Gagolewski, 2018), tidyr (Wickham and Henry, 2018), and re2r (Wenfeng, 2017). Hocking (2019a) provides a detailed comparison of these packages in terms of features, syntax, and computation time.

For reshaping data from wide (one row with many columns) to tall (one column with many rows),

there are several different R functions that provide similar functionality. Each function supports a different set of features (Table 1):

single refers to support for converting input columns of the same type to a single output column.

multiple refers to support for converting input columns of possibly different types to multiple output columns; "sorted" means that conversion works correctly only if the columns are sorted in a regular order, e.g. Sepal.Length, Sepal.Width, Petal.Length, Petal.Width; "unsorted" means that conversion works correctly even if the columns are not sorted, e.g. Sepal.Length, Sepal.Width, Petal.Width, Petal.Length.

regex refers to support for regular expressions; "match" means a pattern is used to match the input column names; "capture" means that the capture groups in the specified pattern are used to create new output columns, which is especially useful when the names consist of several distinct variables, e.g. Sepal.Length; "no" means that regular expressions are not directly supported (although base::grep can always be used).

na.rm refers to support for removing missing values.

**types** refers to support for converting captured text to numeric output columns.

**list** refers to support for output of list columns.

Base R provides stats::reshape and utils::stack for reshaping data from wide to tall. TODO

The tidyr package provides two functions for reshaping data from wide to tall format: gather and pivot\_longer. The older gather function only supports converting input columns to a single output column (not multiple). The input columns to convert may not be directly specified using regular expressions; instead R expressions such as x:y can be used to indicate all columns starting from x and ending with y. It does support limited type conversion; if the convert=TRUE argument is specified, the utils::type.convert function is used to convert the input column names to numeric, integer, or logical. In contrast the newer pivot\_longer also supports multiple output columns (even if input columns are unsorted), and regular expressions for capturing new output columns from the input column names (but grep must be used to specify the input columns to convert). Limited type conversion is also supported in pivot\_longer, via the names\_ptypes argument, which should be a list with names corresponding to output columns and values corresponding to prototypes (zero-length atomic vectors, e.g. numeric()). Both functions support list columns and removing missing values, although different arguments are used (na.rm for gather, values\_drop\_na for pivot\_longer).

The reshape2 and data.table packages each provide a melt function for converting data from wide to tall (Wickham, 2007; Dowle and Srinivasan, 2019). The older reshape2 version only supports converting input columns to a single output column, whereas the newer data.table version also supports multiple output columns. Regular expressions are not supported in reshape2, but can be used with data.table::patterns to match input column names to convert (although the output can be incorrect if columns are not sorted in a regular order). Neither function supports type conversion, and both functions support removing missing values from the output using the na.rm argument. List column output is supported in data.table but not reshape2.

The cdata package provides several functions for data reshaping, including rowrecs\_to\_blocks and unpivot\_to\_blocks which can convert data from tall to wide (Mount and Zumel, 2019). TODO

```
> nc::capture_melt_single
function (subject.df, ..., id.vars = NULL, variable.name = "variable",
    value.name = "value", na.rm = FALSE, verbose = getOption("datatable.verbose"))
{
    if (!is.data.frame(subject.df)) {
        stop("subject must be a data.frame")
    }
    variable <- names(subject.df)
    match.dt <- capture_first_vec(variable, ..., nomatch.error = FALSE)
    no.match <- apply(is.na(match.dt), 1, all)
    if (all(no.match)) {
        stop("no column names match regex below\n", var_args_list(...)$pattern)
    }
    names.dt <- data.table(variable, match.dt)[!no.match]
    if (is.null(id.vars)) {
        id.vars <- which(no.match)
    }
    tall.dt <- melt(data.table(subject.df), id.vars = id.vars,
        measure.vars = which(!no.match), variable.name = variable.name,</pre>
```

pkg::function	single	multiple	regex	na.rm	types	list
nc::capture_melt_multiple	no	unsorted	capture	yes	any	yes
nc::capture_melt_single	yes	no	capture	yes	any	yes
tidyr::pivot_longer	yes	unsorted	capture	yes	some	yes
stats::reshape	yes	sorted	match	no	no	no
data.table::melt,patterns	yes	sorted	match	yes	no	yes
tidyr::gather	yes	no	no	yes	some	yes
reshape2::melt	yes	no	no	yes	no	no
cdata::rowrecs_to_blocks	yes	unsorted	no	no	no	yes
cdata::unpivot_to_blocks	yes	no	no	no	no	yes
utils::stack	yes	no	no	no	no	no

**Table 1:** Reshaping functions in R support various features: "single" for converting input columns into a single output column; "multiple" for converting input columns (either "sorted" in a regular order, or "unsorted" for any order) into multiple output columns of different types; "regex" for regular expressions to only "match" input column names or to "capture" and create new output column names; "na.rm" for removal of missing values; "types" for converting input column names to non-character output columns; "list" for output of list columns.

```
value.name = value.name, na.rm = na.rm, variable.factor = FALSE,
        value.factor = FALSE, verbose = verbose)
    on.vec <- structure("variable", names = variable.name)</pre>
    tall.dt[names.dt, on = on.vec]
<br/>
<br/>
bytecode: 0x2f814e8>
<environment: namespace:nc>
attr(,"ex")
function ()
    library(data.table)
    iris.dt <- data.table(observation = 1:nrow(iris), iris)</pre>
    (iris.tall <- nc::capture_melt_single(iris.dt, part = ".*",</pre>
        "[.]", dim = ".*"))
    (iris.part.cols <- dcast(iris.tall, observation + Species +</pre>
        dim ~ part))
    iris.part.cols[Sepal < Petal]</pre>
    (iris.dim.cols <- dcast(iris.tall, observation + Species +</pre>
        part ~ dim))
    iris.dim.cols[Length < Width]</pre>
<environment: namespace:nc>
```

**Reproducible research statement.** The source code for this article can be freely downloaded from https://github.com/tdhock/nc-article

## **Bibliography**

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