

# Package ‘multifwf’

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**Type** Package

**Title** Read Fixed Width Format Files Containing Lines of Different Type

**Version** 0.2.2

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**Description** Read a table of fixed width formatted data of different types into a data.frame for each type.

**Depends** R (>= 3.1.1)

**License** GPL (>= 2)

**URL** <https://github.com/prontog/multifwf>

**BugReports** <https://github.com/prontog/multifwf/issues>

**RoxygenNote** 5.0.1

**Imports** utils

**Suggests** testthat

**NeedsCompilation** no

**Repository** CRAN

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## R topics documented:

multifwf . . . . .	2
read.multi.fwf . . . . .	2

<b>Index</b>	<b>5</b>
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 multifwf

*Read Fixed Width Format Files containing lines of different Type*


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### Description

Read a table of fixed width formatted data of different types into a `data.frame` for each type.

### Details

The only function you're likely to need from **multifwf** is `read.multi.fwf`.

### Author(s)

Panos Rontogiannis <p.g.ronto@gmail.com>

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 read.multi.fwf

*Read Fixed Width Format Files containing lines of different Type*


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### Description

Read a table of fixed width formatted data of different types into a `data.frame` for each type.

### Usage

```
read.multi.fwf(file, multi.specs, select, header = FALSE, sep = "\t",
  skip = 0, n = -1, bufferize = 2000, ...)
```

### Arguments

<code>file</code>	the name of the file which the data are to be read from. Alternatively, <code>file</code> can be a <a href="#">connection</a> , which will be opened if necessary, and if so closed at the end of the function call.						
<code>multi.specs</code>	A named list of <code>data.frames</code> containing the following columns: <table> <tr> <td><code>widths</code></td> <td>see <a href="#">read.fwf</a></td> </tr> <tr> <td><code>col.names</code></td> <td>see <a href="#">read.table</a></td> </tr> <tr> <td><code>row.names</code></td> <td>see <a href="#">read.table</a></td> </tr> </table>	<code>widths</code>	see <a href="#">read.fwf</a>	<code>col.names</code>	see <a href="#">read.table</a>	<code>row.names</code>	see <a href="#">read.table</a>
<code>widths</code>	see <a href="#">read.fwf</a>						
<code>col.names</code>	see <a href="#">read.table</a>						
<code>row.names</code>	see <a href="#">read.table</a>						

For more info on these fields see [read.fwf](#).

Note that each list item should have a name. This is important for the `select` function.

<code>select</code>	A function to select the type of a line. This selector should have parameters:
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<code>line</code>	the line
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specs the multi.specs list that was passed to read.multi.fwf

The select function should return the name of the spec that matches the line. read.multi.fwf will then use this name to select the a spec from the passed multi.spec. This is why multi.spec should be a named list. If there is no match then NULL can be returned.

header	a logical value indicating whether the file contains the names of the variables as its first line. If present, the names must be delimited by sep.
sep	character; the separator used internally; should be a character that does not occur in the file (except in the header).
skip	number of initial lines to skip; see <a href="#">read.fwf</a> .
n	the maximum number of records (lines) to be read, defaulting to no limit.
buffersize	Maximum number of lines to read at one time
...	further arguments to be passed to <a href="#">read.fwf</a> .

### Details

Known bugs: Warnings on connections that are left open. Haven't figured this out yet. Somehow some files are left opened.

### Value

Return value is a named list with an item for each spec in multi.spec. If there was at least one line in file, matching a spec, then the named item will be a [data.frame](#). Otherwise it will be NULL.

### Author(s)

Panos Rontogiannis <[p.g.ronto@gmail.com](mailto:p.g.ronto@gmail.com)>

### See Also

[read.fwf](#)

### Examples

```
ff <- tempfile()
cat(file = ff, '123456', '287654', '198765', sep = '\n')
specs <- list()
specs[['sp1']] = data.frame(widths = c(1, 2, 3),
                             col.names = c('Co11', 'Co12', 'Co13'))
specs[['sp2']] = data.frame(widths = c(3, 2, 1),
                             col.names = c('C1', 'C2', 'C3'))

myselector <- function(line, specs) {
  s <- substr(line, 1, 1)
  spec_name = ''
  if (s == '1')
    spec_name = 'sp1'
```

```
    else if (s == '2')
      spec_name = 'sp2'

    spec_name
  }

read.multi.fwf(ff, multi.specs = specs, select = myselector)
#> sp1: 1 23 456 \ 1 98 765, sp2: 287 65 4

unlink(ff)
```

# Index

`connection`, [2](#)

`data.frame`, [2](#), [3](#)

`multifwf`, [2](#)

`multifwf-package (multifwf)`, [2](#)

`read.fwf`, [2](#), [3](#)

`read.multi.fwf`, [2](#), [2](#)

`read.table`, [2](#)