

# Package ‘waldo’

July 13, 2020

**Title** Find Differences Between R Objects

**Version** 0.2.0

**Description** Compare complex R objects and reveal the key differences. Designed particularly for use in testing packages where being able to quickly isolate key differences makes understanding test failures much easier.

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**URL** <https://github.com/r-lib/waldo>

**BugReports** <https://github.com/r-lib/waldo/issues>

**Imports** cli, diffobj, fansi, glue, methods, rematch2, rlang, tibble

**Suggests** testthat, covr, R6

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.1.1

**NeedsCompilation** no

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**Repository** CRAN

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 compare

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*Compare two objects*


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### Description

This compares two R objects, identifying the key differences. It:

- Orders the differences from most important to least important.
- Displays the values of atomic vectors that are actually different.
- Carefully uses colour to emphasise changes (while still being readable when colour isn't available).
- Uses R code (not a text description) to show where differences arise.
- Where possible, it compares elements by name, rather than by position.
- Errs on the side of producing too much output, rather than too little.

`compare()` is an alternative to [`all.equal\(\)`](#).

### Usage

```
compare(
  x,
  y,
  ...,
  x_arg = "x",
  y_arg = "y",
  tolerance = NULL,
  ignore_srcref = TRUE,
  ignore_attr = FALSE,
  ignore_encoding = TRUE,
  ignore_function_env = FALSE,
  ignore_formula_env = FALSE
)
```

### Arguments

<code>x, y</code>	Objects to compare. <code>y</code> is treated as the reference object so messages describe how <code>x</code> is different to <code>y</code>
<code>...</code>	A handful of other arguments are supported with a warning for backward compatibility. These include: <ul style="list-style-type: none"> <li>• <code>all.equal()</code> arguments <code>checkNames</code> and <code>check.attributes</code></li> <li>• <code>testthat::compare()</code> argument <code>tol</code></li> </ul> All other arguments are ignored with a warning.
<code>x_arg, y_arg</code>	Name of <code>x</code> and <code>y</code> arguments, used when generated paths to internal components.

tolerance	If non-NULL, used as threshold for ignoring small floating point difference when comparing numeric vectors. Setting to any non-NULL value will cause integer and double vectors to be compared based on their values, rather than their types. It uses the same algorithm as <code>all.equal()</code> , i.e., first we generate <code>x_diff</code> and <code>y_diff</code> by subsetting <code>x</code> and <code>y</code> to look only locations with differences. Then we check that <code>mean(abs(x_diff - y_diff)) / mean(abs(y_diff))</code> (or just <code>mean(abs(x_diff - y_diff))</code> if <code>y_diff</code> is small) is less than <code>tolerance</code> .
ignore_srcref	Ignore differences in function <code>srcrefs</code> ? TRUE by default since the <code>srcref</code> does not change the behaviour of a function, only its printed representation.
ignore_attr	Ignore all differences in attributes? Only provided for backward compatibility with <code>all.equal()</code> . Using TRUE is not generally recommended because it will ignore many important functional differences.
ignore_encoding	Ignore string encoding? TRUE by default, because this is R's default behaviour. Use FALSE when specifically concerned with the encoding, not just the value of the string.
ignore_function_env, ignore_formula_env	Ignore the environments of functions and formulas, respectively? These are provided primarily for backward compatibility with <code>all.equal()</code> which always ignores these environments.

## Value

A character vector with class "waldo\_compare". If there are no differences it will have length 0; otherwise each element contains the description of a single difference.

## Examples

```
# Thanks to diffobj package comparison of atomic vectors shows differences
# with a little context
compare(letters, c("z", letters[-26]))
compare(c(1, 2, 3), c(1, 3))
compare(c(1, 2, 3), c(1, 3, 4, 5))
compare(c(1, 2, 3), c(1, 2, 5))

# More complex objects are traversed, stopping only when the types are
# different
compare(
  list(x = list(y = list(structure(1, z = 2))),
    list(x = list(y = list(structure(1, z = "a"))))
)

# Where possible, recursive structures are compared by name
compare(iris, rev(iris))

compare(list(x = "x", y = "y"), list(y = "y", x = "x"))
# Otherwise they're compared by position
compare(list("x", "y"), list("x", "z"))
compare(list(x = "x", x = "y"), list(x = "x", y = "z"))
```

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`compare_proxy`*Proxy for waldo comparison*

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**Description**

Use this generic to override waldo's default comparison if you need to override the defaults (typically because your object contains an external pointer).

waldo comes with methods for two common cases:

- `data.table`: the `.internal.selfref` attribute is set to `NULL`. This is an external pointer that is used for performance optimisation, and doesn't affect the data.
- `xml2::xml_node`: the underlying XML data is stored in memory in C, behind an external pointer, so the we best can do is to convert the object to a string.

**Usage**

```
compare_proxy(x)
```

**Arguments**

`x`                    An object.

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