Package 'waldo'

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Title Find Differences Between R Objects

Version 0.4.0

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://waldo.r-lib.org>, <https://github.com/r-lib/waldo>

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

Imports cli, diffobj (>= 0.3.4), fansi, glue, methods, rematch2, rlang
(>= 1.0.0), tibble

Suggests covr, R6, testthat (>= 3.0.0), withr, xml2

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R topics documented:

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compare   *Compare two objects*

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().](all.equal())

Usage

```
compare(
  x,
  y,
  ...,
  x_arg = "old",
  y_arg = "new",
  tolerance = NULL,
  max_diffs = if (in_ci()) Inf else 10,
  ignore_srcref = TRUE,
  ignore_attr = "waldo_opts",
  ignore_encoding = TRUE,
  ignore_function_env = FALSE,
  ignore_formula_env = FALSE,
  list_as_map = FALSE
)
```

Arguments

x, y   Objects to compare. x is treated as the reference object so messages describe
              how y is different to x.

...   A handful of other arguments are supported with a warning for backward com-
              parability. These include:

              - all.equal() arguments checkNames and check.attributes
              - testthat::compare() argument tol

              All other arguments are ignored with a warning.

x_arg, y_arg	Name of x and y arguments, used when generated paths to internal components. These default to "old" and "new" since it's most natural to supply the previous value then the new value.
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 [all.equal()](), i.e., first we generate x_diff and y_diff by subsetting x and y to look only locations with differences. Then we check that mean(abs(x_diff -y_diff)) / mean(abs(y_diff)) (or just mean(abs(x_diff -y_diff)) if y_diff is small) is less than tolerance.
max_diffs	Control the maximum number of differences shown. The default shows 10 differences when run interactively and all differences when run in CI. Set max_diffs = Inf to see all differences.
ignore_srcref	Ignore differences in function srcrefs? TRUE by default since the srcref does not change the behaviour of a function, only its printed representation.
ignore_attr	Ignore differences in specified attributes? Supply a character vector to ignore differences in named attributes. By default the "waldo_opts" attribute is listed in ignore_attr so that changes to it are not reported; if you customize ignore_attr, you will probably want to do this yourself.
	For backward compatibility with all.equal(), you can also use TRUE, to all ignore differences in all attributes. This is not generally recommended as it is a blunt tool that 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 all.equal() which always ignores these environments.
list_as_map	Compare lists as if they are mappings between names and values. Concretely, this drops NULLs in both objects and sorts named components.

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.

Controlling comparisons

There are two ways for an object (rather than the person calling compare() or expect_equal() to control how it is compared to other objects. First, if the object has an S3 class, you can provide a [compare_proxy()]() method that provides an alternative representation of the object; this is particularly useful if important data is stored outside of R, e.g. in an external pointer.

Alternatively, you can attach an attribute called "waldo_opts" to your object. This should be a list of compare options, using the same names and possible values as the arguments to this function. This option is ignored by default (ignore_attr) so that you can set the options in the object

that you control. (If you don't want to see the attributes interactively, you could attach them in a compare_proxy() method.)

Options supplied in this way also affect all the children. This means options are applied in the following order, from lowest to highest precedence:

1. Defaults from `compare()`.

2. The `waldo_opts` for the parents of x.

3. The `waldo_opts` for the parents of y.

4. The `waldo_opts` for x.

5. The `waldo_opts` for y.

6. User-specified arguments to `compare()`.

Use these techniques with care. If you accidentally cover up an important difference you can create a confusing situation where x and y behave differently but `compare()` reports no differences in the underlying objects.

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*

Description

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

waldo comes with methods for a few common cases:

- data.table: the `.internal.selfref` and `index` attributes are set to `NULL`. Both attributes are used for performance optimisation, and don'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.
- Classes from the `RProtoBuf` package: like XML objects, these store data in memory in C++ and only expose string names to R. Fortunately, these have well-understood string representations that we can use for comparisons. See https://developers.google.com/protocol-buffers/docs/reference/cpp/google.protobuf.text_format

Usage

```
compare_proxy(x, path = "x")
```

Arguments

x	An object.
path	Path

Value

A list with two components:

- `object`: the modified object
- `path`: an updated path showing what modification was applied

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