

Package ‘amregtest’

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Title Runs Allelematch Regression Tests

Version 1.0.5

Description Automates regression testing of package 'allelematch'. Over 2500 tests covers all functions in 'allelematch', reproduces the examples from the documentation and includes negative tests. The implementation is based on 'testthat'.

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amExample1	<i>Example 1 High quality data set</i>
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Description

This is sample data copied from [amExampleData](#) in version 5.2.1 of package [allelematch](#). We use this data to test 'allelematch' backwards compatibility.

Format

Data frame with samples in rows, and alleles in columns. Missing data is represented as "-99".

Details

The data in this example is simulated to represent a high quality data set that might result from a laboratory protocol where samples were run multiple times to confirm their identity. It has no genotyping error, a near-zero missing data load, and approximately 60% of the individuals have been artificially resampled more than once.

References

<https://github.com/cran/allelematch>

amExample2	<i>Example 2 Good quality data set</i>
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Description

This is sample data copied from [amExampleData](#) in version 5.2.1 of package [allelematch](#).

Format

Data frame with samples in rows, and alleles in columns. Missing data is represented as "-99".

Details

The data in this example have also been simulated, this time to reflect the qualities of good quality data set, where genotyping error and missing data exist, but these can be confidently handled by `allelematch` without manual intervention. At each locus a random 4% of heterozygotes lost their second allele to simulate an allele dropout, and a random 4% of samples at each locus had alleles set to missing.

References

<https://github.com/cran/allelematch>

amExample3

Example 3 Marginal quality data set

Description

This is sample data copied from `amExampleData` in version 5.2.1 of package `allelematch`.

Format

Data frame with samples in rows, and alleles in columns. Missing data is represented as "-99".

Details

The data in this example have been simulated to represent a data set of marginal quality where the use of `allelematch` combined with careful manual review of the results is required to achieve a confident assessment of the unique genotypes. At each locus a random 4% of heterozygotes lost their second allele to simulate an allele dropout, and a random 10% of samples at each locus had alleles set to missing.

References

<https://github.com/cran/allelematch>

amExample4

Example 4 Low quality data set

Description

This is sample data copied from `amExampleData` in version 5.2.1 of package `allelematch`.

Format

Data frame with samples in rows, and alleles in columns. Missing data is represented as "-99".

Details

For this example we have simulated a low quality data set where uncertainty created by genotyping error and missing data, combined with a lack of information in the form of allelic diversity across loci will result in a low confidence assessment of the unique genotypes. At each locus a random 6% of heterozygotes lost their second allele to simulate an allele dropout, and a random 20% of samples at each locus had alleles set to missing.

References

<https://github.com/cran/allelematch>

amExample5

Example 5 Wildlife data set

Description

This is sample data copied from `amExampleData` in version 5.2.1 of package `allelematch`.

Format

Data frame with samples in rows, and alleles in columns. Missing data is represented as "-99".

Details

In this final example we use real data from the non-invasive sampling of a wildlife population. The data have been anonymized by changing sampling details. A single column giving the gender is also available and we show how this can be used as an extra locus. Missing data is also more common at some loci than at others, with a total load of about 10%.

References

<https://github.com/cran/allelematch>

amregtest

Package Overview

Description

Package 'amregtest' automates regression testing of package `allelematch`.

The API is simple. There are only three functions:

<code>artRun</code>	Executes the test, or a subset of the tests
<code>artList</code>	Lists the available tests without running them
<code>artVersion</code>	Shows the installed versions of 'allelematch' and 'amregtest'

The prefix "art" is short for "Allelematch Regression Test".
See [artData](#) for a description of data sets used as input.

References

[amregtest-package](#)
<https://github.com/cran/allelematch>
[allelematchSuppDoc.pdf](#)

artData	<i>Example data used by amregtest</i>
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Description

This example data is used when testing allelematch backwards compatibility using [artRun](#). The tests load this data and passes it to [amDataset](#).

It includes data that was imported from version 5.2.1 of [allelematch](#). It was still unchanged in 5.2.5.

amExample1	Example 1 High quality data set
amExample2	Example 2 Good quality data set
amExample3	Example 3 Marginal quality data set
amExample4	Example 4 Low quality data set
amExample5	Example 5 Wildlife data set

See [allelematchSuppDoc.pdf](#) for a more detailed description.

It also includes a large data set gathered from field work:

ggSample	Very large wildlife data set
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Format

Data frames with varying numbers of samples in rows, and alleles in columns. Missing data is represented as "-99".

References

<https://github.com/cran/allelematch>
[allelematchSuppDoc.pdf](#)

artList	<i>Lists available tests in amregtest without running them</i>
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Description

Use the output to select a value for parameter filter to [artRun](#). Useful when debugging.

Usage

```
artList(verbose = TRUE)
```

Arguments

verbose logical. If TRUE (the default), prints additional info to stdout

Value

A character vector containing the names of all the tests

See Also

[artVersion](#) and [artRun](#)

Examples

```
# See what version of packages 'allelematch' and 'amregtest'
# are currently loaded:
artVersion()

# List the available tests:
artList()

# Run all the tests:
# artRun() # Takes several minutes

# Run the first of the available tests:
artRun(filter="allelematch_1-amDataset$")
```

artRun	<i>Runs the regression test</i>
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Description

Runs regression tests on package [allelematch](#) to make sure it is backwards compatible.

The full set of tests will take a couple of minutes.

Call [artList](#) to see the available tests with without running them.

Usage

```
artRun(filter = "", verbose = TRUE)
```

Arguments

filter	If specified, only tests with names matching this perl regular expression will be executed. Character vector of length 1. See also artList
verbose	logical. If TRUE (the default), prints version of tested allelematch to stdout

Details

If any of the test executed with [artRun](#) should fail, then we want to be able to run that specific test under the debugger.

Set a breakpoint in `allelematch.R` and call `artRun(filter="<the test that reproduces the problem>")`

Note that it is the last loaded version of `allelematch` that will be executed, not the last edited. In RStudio, CTRL+SHIFT+B will build, install and load.

Value

A list (invisibly) containing data about the test results as returned by [testthat::test_package](#)

See Also

[artVersion](#) and [artList](#)

Examples

```
# See what version of packages 'allelematch' and 'amregtest'
# are currently loaded:
artVersion()

# List the available tests:
artList()
```

```
# Run all the tests:
# artRun() # Takes several minutes

# Run the first of the available tests:
artRun(filter="allelematch_1-amDataset$")
```

artVersion	Returns package version
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Description

Displays version of this package ([amregtest](#)) and of [allelematch](#), together with build timestamps.

The version is specified in the file DESCRIPTION, tag "Version: ".

Usage

```
artVersion(verbose = TRUE)
```

Arguments

verbose	logical. If TRUE (the default), prints additional info to stdout, including versions and build timestamps of 'allelematch' and 'amregtest'.
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Value

The loaded version of this package ([amregtest-package](#)) in a character vector of length one

See Also

[artList](#), [artRun](#) and [amregtest](#)

Examples

```
# See what version of packages 'allelematch' and 'amregtest'
# are currently loaded:
artVersion()

# List the available tests:
artList()

# Run all the tests:
# artRun() # Takes several minutes

# Run the first of the available tests:
artRun(filter="allelematch_1-amDataset$")
```


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