

# Package ‘neutralitytestr’

April 11, 2018

**Title** Test for a Neutral Evolutionary Model in Cancer Sequencing Data

**Version** 0.0.1

**Description** Package takes frequencies of mutations as reported by high throughput sequencing data from cancer and fits a theoretical neutral model of tumour evolution. Package outputs summary statistics and contains code for plotting the data and model fits. See Williams et al 2016 <doi:10.1038/ng.3489> and Williams et al 2017 <doi:10.1101/096305> for the details of the method.

**Depends** R (>= 3.4)

**License** MIT + file LICENSE

**Encoding** UTF-8

**LazyData** true

**Imports** dplyr, ggplot2, scales, pracma, ggpmisc, cowplot

**Suggests** knitr, rmarkdown, testthat

**VignetteBuilder** knitr

**URL** <https://github.com/marcjwilliams1/neutralitytestr>

**BugReports** <https://github.com/marcjwilliams1/neutralitytestr/issues>

**RoxygenNote** 6.0.1

**NeedsCompilation** no

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**Repository** CRAN

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lsq_plot	<i>Plot cumulative distribution lsq_plot Plots the cumulative distribution of the data as well as the best fit linear model line.</i>
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### Description

Plot cumulative distribution lsq\_plot Plots the cumulative distribution of the data as well as the best fit linear model line.

### Usage

```
lsq_plot(object)
```

### Arguments

object            neutrality test object

### Value

ggplot object.

### Examples

```
lsq_plot(neutralitytest(VAFselection, fmin = 0.1, fmax = 0.25))
```

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neutralitytest	<i>Testing for neutrality on cancer sequencing data</i>
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### Description

neutralitytest returns a neutralitytest object which contains the result of various test statistics to test for neutrality as described in Williams et al. Nature Genetics 2018.

### Usage

```
neutralitytest(VAF, fmin = 0.12, fmax = 0.24)
```

**Arguments**

VAF	Vector of variant allele frequencies (VAFs) from a deep sequencing experiment, numbers should be between 0 and 1
fmin	Minimum VAF of integration range, default is 0.12
fmax	Maximum VAF of integration range, default is 0.24

**Value**

neutralitytest object which contains test statistics which tests if the sequencing data is consistent a neutral evolutionary model. Test statistics are area between theoretical and empirical curves, kolmogorov distance, mean distance and R<sup>2</sup> statistics from linear model fit. Also returns an estimate of the mutation rate per tumour tumour doubling, the raw VAFs and cumulative distribution

**Examples**

```
neutralitytest(runif(100))
neutralitytest(VAFselection, fmin = 0.1, fmax = 0.25)
```

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neutralitytestr	neutralitytestr <i>package</i>
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**Description**

Package to test a neutral evolutionary model on deep sequencing data.

**Details**

See the README on [GitHub](#)

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normalized_plot	<i>Plot normalized cumulative distribution normalized_plot Plots the (normalized) cumulative distribution of the data as well as the theoretical expectation from a neutral evolutionary model.</i>
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**Description**

Plot normalized cumulative distribution normalized\_plot Plots the (normalized) cumulative distribution of the data as well as the theoretical expectation from a neutral evolutionary model.

**Usage**

```
normalized_plot(object)
```

**Arguments**

object	neutrality test object
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**Value**

ggplot object.

**Examples**

```
normalized_plot(neutralitytest(VAFselection, fmin = 0.1, fmax = 0.25))
```

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plot_all	<i>Plot all plots in the package and make composite figure. plot_all Plots histogram, linear model best fit plot and normalized plot and plot and makes composite figure.</i>
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**Description**

Plot all plots in the package and make composite figure. plot\_all Plots histogram, linear model best fit plot and normalized plot and plot and makes composite figure.

**Usage**

```
plot_all(object)
```

**Arguments**

object            neutrality test object

**Value**

ggplot object.

**Examples**

```
plot_all(neutralitytest(VAFselection, fmin = 0.1, fmax = 0.25))
```

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VAFneutral	<i>Synthetic sequencing data generated from a evolutionary based cancer simulation.</i>
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**Description**

This data is generated from a neutral evolutionary model where all subclonal mutations are neutral.

**Usage**

```
VAFneutral
```

**Format**

A vector with variant allele frequencies (VAFs) ranging from 0 to 1

**Source**

Generated using cancer sequencing simulation <https://github.com/marcjwilliams1/CancerSeqSim.jl>

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VAFselection	<i>Synthetic sequencing data generated from a evolutionary based cancer simulation.</i>
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**Description**

This data is generated from an evolutionary model where there is one subclonal population and all other mutations are neutral passengers.

**Usage**

```
VAFselection
```

**Format**

A vector with variant allele frequencies (VAFs) ranging from 0 to 1

**Source**

Generated using cancer sequencing simulation <https://github.com/marcjwilliams1/CancerSeqSim.jl>

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vaf_histogram	<i>Plot VAF histogram vaf_histogram Plots a histogram of the variant allele frequencies.</i>
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**Description**

Plot VAF histogram vaf\_histogram Plots a histogram of the variant allele frequencies.

**Usage**

```
vaf_histogram(object)
```

**Arguments**

object            neutrality test object

**Value**

ggplot object.

**Examples**

```
vaf_histogram(neutralitytest(VAFselection, fmin = 0.1, fmax = 0.25))
```

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