

# Package ‘ALDEx2’

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**Type** Package

**Title** Analysis Of Differential Abundance Taking Sample Variation Into Account

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**Description** A differential abundance analysis for the comparison of two or more conditions. Useful for analyzing data from standard RNA-seq or meta-RNA-seq assays as well as selected and unselected values from in-vitro sequence selections. Uses a Dirichlet-multinomial model to infer abundance from counts, optimized for three or more experimental replicates. The method infers biological and sampling variation to calculate the expected false discovery rate, given the variation, based on a Wilcoxon Rank Sum test and Welch's t-test (via `aldex.ttest`), a Kruskal-Wallis test (via `aldex.kw`), a generalized linear model (via `aldex.glm`), or a correlation test (via `aldex.corr`). All tests report p-values and Benjamini-Hochberg corrected p-values.

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**URL** [https://github.com/ggloor/ALDEx\\_bioc](https://github.com/ggloor/ALDEx_bioc)

**BugReports** [https://github.com/ggloor/ALDEx\\_bioc/issues](https://github.com/ggloor/ALDEx_bioc/issues)

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ALDEx2m-package . . . . .	2
aldex . . . . .	3
aldex.clr . . . . .	5
aldex.clr-class . . . . .	6
aldex.corr . . . . .	8
aldex.effect . . . . .	9
aldex.expectedDistance . . . . .	11
aldex.glm . . . . .	12
aldex.glm.effect . . . . .	13
aldex.kw . . . . .	14
aldex.plot . . . . .	15
aldex.plotFeature . . . . .	17
aldex.set.mode . . . . .	18
aldex.ttest . . . . .	19
getDenom . . . . .	20
getFeatureNames . . . . .	21
getFeatures . . . . .	21
getMonteCarloInstances . . . . .	22
getMonteCarloReplicate . . . . .	23
getMonteCarloSample . . . . .	24
getReads . . . . .	25
getSampleIDs . . . . .	25
numConditions . . . . .	26
numFeatures . . . . .	27
numMCInstances . . . . .	28
selex . . . . .	28
synth2 . . . . .	29
<b>Index</b>	<b>30</b>

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ALDEx2m-package	<i>Analysis of differential abundance taking sample variation into account</i>
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**Description**

A differential abundance analysis for the comparison of two or more conditions. For example, single-organism and meta-RNA-seq high-throughput sequencing assays, or of selected and unselected values from in-vitro sequence selections. Uses a Dirichlet-multinomial model to infer abundance from counts, that has been optimized for three or more experimental replicates. Infers sampling variation and calculates the expected false discovery rate given the biological and sampling variation using the Wilcox rank test or Welches t-test (`aldex.ttest`) or the `glm` and Kruskal Wallis tests (`aldex.glm`). Reports both P and `fdr` values calculated by the Benjamini Hochberg correction.

**References**

Please use the citation given by `citation(package="ALDEx")`.

**See Also**

[aldex.clr](#), [aldex.ttest](#), [aldex.glm](#), [aldex.effect](#), [selex](#)

**Examples**

```
# see examples for the aldex.clr, aldex.ttest, aldex.effect, aldex.glm functions
```

---

```
aldex
```

*Compute an aldex Object*

---

**Description**

Welcome to the ALDEx2 package!

The `aldex` function is a wrapper that performs log-ratio transformation and statistical testing in a single line of code. Specifically, this function: (a) generates Monte Carlo samples of the Dirichlet distribution for each sample, (b) converts each instance using a log-ratio transform, then (c) returns test results for two sample (Welch's t, Wilcoxon) or multi-sample (glm, Kruskal-Wallis) tests. This function also estimates effect size for two sample analyses.

**Usage**

```
aldex(
  reads,
  conditions,
  mc.samples = 128,
  test = "t",
  effect = TRUE,
  include.sample.summary = FALSE,
  verbose = FALSE,
  denom = "all",
  iterate = FALSE,
  ...
)
```

**Arguments**

<code>reads</code>	A non-negative, integer-only data.frame or matrix with unique names for all rows and columns. Rows should contain genes and columns should contain sequencing read counts (i.e., sample vectors). Rows with 0 reads in each sample are deleted prior to analysis.
<code>conditions</code>	A character vector. A description of the data structure used for testing. Typically, a vector of group labels. For <code>aldex.glm</code> , use a <code>model.matrix</code> .
<code>mc.samples</code>	An integer. The number of Monte Carlo samples to use when estimating the underlying distributions. Since we are estimating central tendencies, 128 is usually sufficient.
<code>test</code>	A character string. Indicates which tests to perform. "t" runs Welch's t and Wilcoxon tests. "kw" runs Kruskal-Wallis and glm tests. "glm" runs a generalized linear model using a <code>model.matrix</code> . "corr" runs a correlation test using <code>cor.test</code> .
<code>effect</code>	A boolean. Toggles whether to calculate abundances and effect sizes. Applies to <code>test = "t"</code> and <code>test = "iterative"</code> .
<code>include.sample.summary</code>	A boolean. Toggles whether to include median clr values for each sample. Applies to <code>effect = TRUE</code> .

verbose	A boolean. Toggles whether to print diagnostic information while running. Useful for debugging errors on large datasets. Applies to <code>effect = TRUE</code> .
denom	A character string. Indicates which features to retain as the denominator for the Geometric Mean calculation. Using "iqlr" accounts for data with systematic variation and centers the features on the set features that have variance that is between the lower and upper quartile of variance. Using "zero" is a more extreme case where there are many non-zero features in one condition but many zeros in another. In this case the geometric mean of each group is calculated using the set of per-group non-zero features.
iterate	A boolean. Toggles whether to iteratively perform a test. For example, this will use the results from an initial "t" routine to seed the reference (i.e., denominator of Geometric Mean calculation) for a second "t" routine.
...	Arguments to embedded method (e.g., <code>glm</code> or <code>cor.test</code> ).

### Details

See "Examples" below for a description of the sample input.

### Value

Returns a number of values that depends on the set of options. See the return values of `aldex.ttest`, `aldex.kw`, `aldex.glm`, and `aldex.effect` for explanations and examples.

### Author(s)

Greg Gloor, Andrew Fernandes, and Matt Links contributed to the original package. Thom Quinn added the "glm" test method, the "corr" test method, and the "iterate" procedure.

### References

Please use the citation given by `citation(package="ALDEx2")`.

### See Also

[aldex](#), [aldex.clr](#), [aldex.ttest](#), [aldex.kw](#), [aldex.glm](#), [aldex.effect](#), [aldex.corr](#), [selex](#)

### Examples

```
# The 'reads' data.frame should have row
# and column names that are unique, and
# looks like the following:
#
#           T1a T1b T2  T3  N1  N2  Nx
# Gene_00001  0  0  2  0  0  1  0
# Gene_00002 20  8 12  5 19 26 14
# Gene_00003  3  0  2  0  0  0  1
# Gene_00004 75 84 241 149 271 257 188
# Gene_00005 10 16  4  0  4  10 10
# Gene_00006 129 126 451 223 243 149 209
#           ... many more rows ...

data(selex)
selex <- selex[1201:1600,] # subset for efficiency
conds <- c(rep("NS", 7), rep("S", 7))
```

```
x <- aldex(selex, conds, mc.samples=2, denom="all",
           test="t", effect=FALSE)
```

aldex.clr

*Compute an aldex.clr Object***Description**

Generate Monte Carlo samples of the Dirichlet distribution for each sample. Convert each instance using the centred log-ratio transform This is the input for all further analyses.

**Usage**

```
aldex.clr(reads, conds, mc.samples = 128, denom="all", verbose=FALSE, useMC=FALSE)
```

**Arguments**

reads	A data.frame or RangedSummarizedExperiment object containing non-negative integers only and with unique names for all rows and columns, where each row is a different gene and each column represents a sequencing read-count. Rows with 0 reads in each sample are deleted prior to analysis.
conds	A vector containing a descriptor for the samples, allowing them to be grouped and compared.
mc.samples	The number of Monte Carlo samples to use to estimate the underlying distributions; since we are estimating central tendencies, 128 is usually sufficient.
denom	An any variable (all, iqlr, zero, lvha, median,user) indicating features to use as the denominator for the Geometric Mean calculation The default "all" uses the geometric mean abundance of all features. Using "median" returns the median abundance of all features. Using "iqlr" uses the features that are between the first and third quartile of the variance of the clr values across all samples. Using "zero" uses the non-zero features in each group as the denominator. This approach is an extreme case where there are many nonzero features in one condition but many zeros in another. Using "lvha" uses features that have low variance (bottom quartile) and high relative abundance (top quartile in every sample). It is also possible to supply a vector of row indices to use as the denominator. Here, the experimentalist is determining a-priori which rows are thought to be invariant. In the case of RNA-seq, this could include ribosomal protein genes and other house-keeping genes.
verbose	Print diagnostic information while running. Useful only for debugging if fails on large datasets.
useMC	Use multicore by default (FALSE). Multi core processing will be attempted with the BiocParallel package. Serial processing will be used if this is not possible.

**Details**

An explicit description of the input format for the reads object is shown under 'Examples', below.

**Value**

The object produced by the `clr` function contains the `clr` transformed values for each Monte-Carlo Dirichlet instance, which can be accessed through `getMonteCarloInstances(x)`, where `x` is the `clr` function output. Each list element is named by the sample ID. `getFeatures(x)` returns the features, `getSampleIDs(x)` returns sample IDs, and `getFeatureNames(x)` returns the feature names.

**Author(s)**

Greg Gloor, Thom Quinn, Ruth Grace Wong, Andrew Fernandes, Matt Links and Jia Rong Wu contributed to this code.

**References**

Please use the citation given by `citation(package="ALDEX")`.

**See Also**

[aldex.ttest](#), [aldex.glm](#), [aldex.effect](#), [selex](#)

**Examples**

```
# The 'reads' data.frame or
# RangedSummarizedExperiment object should
# have row and column names that are unique,
# and looks like the following:
#
#           T1a T1b T2 T3 N1 N2 Nx
# Gene_00001  0  0  2  0  0  1  0
# Gene_00002 20  8 12  5 19 26 14
# Gene_00003  3  0  2  0  0  0  1
# Gene_00004 75 84 241 149 271 257 188
# Gene_00005 10 16  4  0  4  10 10
# Gene_00006 129 126 451 223 243 149 209
#           ... many more rows ...

data(selex)
#subset for efficiency
selex <- selex[1201:1600,]
conds <- c(rep("NS", 7), rep("S", 7))
x <- aldex.clr(selex, conds, mc.samples=2, denom="all", verbose=FALSE)
```

---

aldex.clr-class

*The aldex.clr class*


---

**Description**

The `aldex.clr` S4 class is a class which stores the data generated by the `aldex.clr` method.

## Details

An `aldex.clr` object contains the Monte Carlo Dirichlet instances derived from estimating the technical variance of the raw read count data. It is created by the `aldex.clr` function, which is invoked by the `aldex.clr` method. It consists of four attributes: the sample names, the feature names, the conditions vector (assigns each sample to a condition), and the Monte Carlo Dirichlet instances themselves. These can be accessed, along with information about the length of some attributes. A single Monte Carlo instance can also be retrieved.

## Value

The `aldex.clr` object contains the `clr` transformed values for each Monte-Carlo Dirichlet instance, which can be accessed through `getMonteCarloInstances(x)`, where `x` is the `clr` function output. Each list element is named by the sample ID. `getFeatures(x)` returns the features, `getSampleIDs(x)` returns sample IDs, and `getFeatureNames(x)` returns the feature names.

## Methods

In the code below, `x` is an `aldex.clr` object, and `i` is a numeric whole number.

`getMonteCarloInstances(x)`: Returns `x`'s Monte Carlo Dirichlet instances.

`getSampleIDs(x)`: Returns the names of the samples. These can be used to access the original reads, as in `reads$sampleID` (if the reads are a data frame).

`getFeatures(x)`: Returns the names of the features as a vector.

`numFeatures(x)`: Returns the number of features associated with the data.

`numMCInstances(x)`: Returns the names of the keys that can be used to subset the data rows. The keys values are the `rsid`'s.

`getFeatureNames(x)`: Returns the names of the keys that can be used to subset the data rows. The keys values are the `rsid`'s.

`getReads(x)`: Returns the names of the keys that can be used to subset the data rows. The keys values are the `rsid`'s.

`numConditions(x)`: Returns the names of the keys that can be used to subset the data rows. The keys values are the `rsid`'s.

`getMonteCarloReplicate(x, i)`: Returns the names of the keys that can be used to subset the data rows. The keys values are the `rsid`'s.

## Author(s)

Greg Gloor, Ruth Grace Wong, Andrew Fernandes, Jia Rong Wu and Matt Links contributed to this code

## References

Please use the citation given by `citation(package="ALDEX")`.

## See Also

[aldex.clr.function](#)

**Examples**

```

# The 'reads' data.frame or
# SummarizedExperiment object should have
# row and column names that are unique,
# and looks like the following:
#
#           T1a T1b T2 T3 N1 N2 Nx
# Gene_00001  0  0  2  0  0  1  0
# Gene_00002 20  8 12  5 19 26 14
# Gene_00003  3  0  2  0  0  0  1
# Gene_00004 75 84 241 149 271 257 188
# Gene_00005 10 16  4  0  4  10 10
# Gene_00006 129 126 451 223 243 149 209
#           ... many more rows ...

data(selex)
#subset for efficiency
selex <- selex[1201:1600,]
conds <- c(rep("NS", 7), rep("S", 7))

# x is an object of type aldex.clr
x <- aldex.clr(selex, conds, mc.samples = 2, denom="all", verbose = FALSE)

# get all of the Monte Carlo Dirichlet instances
monteCarloInstances <- getMonteCarloInstances(x)

# get sample names
sampleIDs <- getSampleIDs(x)

# get features
features <- getFeatures(x)

# get number of features
numFeatures <- numFeatures(x)

# get number of Monte Carlo Dirichlet instances
numInstances <- numMCInstances(x)

# get names of features
featureNames <- getFeatureNames(x)

# get number of conditions
conditions <- numConditions(x)

# get number of conditions
reads <- getReads(x)

# retrieve the first Monte Carlo Dirichlet instance.
monteCarloInstance <- getMonteCarloReplicate(x,1)

```



**Description**

aldex.corr calculates the expected values for the correlation between each feature and a continuous variable, using data returned by aldex.clr and a vector of the continuous variable. Returns results of Pearson, Spearman and Kendall tests.

**Usage**

```
aldex.corr(clr, cont.var)
```

**Arguments**

clr                    An ALDEx2 object. The output of aldex.clr.  
cont.var              A continuous numeric vector

**Value**

Returns a data.frame of the average Pearson, Spearman and Kendall coefficients and their p-values for each feature, with FDR appended as a BH column.

**Author(s)**

Arianne Albert, Greg Gloor, Thom Quinn

**References**

Please use the citation given by `citation(package="ALDEx2")`.

**See Also**

[aldex](#), [aldex.clr](#), [aldex.ttest](#), [aldex.kw](#), [aldex.glm](#), [aldex.effect](#), [aldex.corr](#), [selex](#)

**Examples**

```
data(selex)
#subset for efficiency
selex <- selex[1:400,]
conds <- c(rep("N", 7), rep("S", 7))
cont.var <- c(rep(1, 7), rep(2, 7))
x <- aldex.clr(selex, conds)
corr.test <- aldex.corr(x, cont.var)
```

---

aldex.effect

*calculate effect sizes and differences between conditions*

---

**Description**

determines the median clr abundance of the feature in all samples and in groups determines the median difference between the two groups determines the median variation within each two group determines the effect size, which is the median of the ratio of the between group difference and the larger of the variance within groups

**Usage**

```
aldex.effect(clr, verbose = TRUE, include.sample.summary = FALSE, useMC=FALSE, CI=FALSE, glm.conds=
```

**Arguments**

<code>clr</code>	<code>clr</code> is the data output of <code>aldex.clr</code>
<code>verbose</code>	Print diagnostic information while running. Useful only for debugging if fails on large datasets
<code>include.sample.summary</code>	include median <code>clr</code> values for each sample, defaults to FALSE
<code>useMC</code>	use multicore by default (FALSE)
<code>CI</code>	give effect 95
<code>glm.conds</code>	give effect for <code>glm</code> contrasts, note: saved as list

**Details**

An explicit example for two conditions is shown in the ‘Examples’ below.

**Value**

returns a dataframe with the following information:

<code>rab.all</code>	a vector containing the median <code>clr</code> value for each feature
<code>rab.win.conditionA</code>	a vector containing the median <code>clr</code> value for each feature in condition A
<code>rab.win.conditionB</code>	a vector containing the median <code>clr</code> value for each feature in condition B
<code>diff.btw</code>	a vector containing the per-feature median difference between condition A and B
<code>diff.win</code>	a vector containing the per-feature maximum median difference between Dirichlet instances within conditions
<code>effect</code>	a vector containing the per-feature effect size
<code>overlap</code>	a vector containing the per-feature proportion of effect size that is 0 or less

**Author(s)**

Greg Gloor, Andrew Fernandes, Matt Links

**References**

Please use the citation given by `citation(package="ALDEX")`.

**See Also**

[aldex.clr](#), [aldex.ttest](#), [aldex.glm](#), [selex](#)

**Examples**

```
# x is the output of the \code{x <- clr(data, mc.samples)} function
# conditions is a description of the data
# for the selex dataset, conditions <- c(rep("N", 7), rep("S", 7))
data(selex)
#subset for efficiency
selex <- selex[1201:1600,]
conds <- c(rep("NS", 7), rep("S", 7))
x <- aldex.clr(selex, conds, mc.samples=2, denom="all")
effect.test <- aldex.effect(x)
```

---

aldex.expectedDistance

*Calculate the expected values of distances between samples, given an aldex Object*

---

**Description**

Calculates the expected value of distances between samples, given an aldex Object, using the median value of distances derived from n Monte-Carlo replicates.

**Usage**

```
## S3 method for class 'expectedDistance'
aldex(clrData)
```

**Arguments**

clrData            an object of class aldex produced by the aldex function

**Details**

Generates a distance matrix for each Monte-Carlo instance in an aldex Object. Calculates the median distance value across all instances.

**Value**

Returns a dist Object.

**References**

Please use the citation given by `citation(package="ALDEX")`.

**See Also**

[aldex](#), [aldex.clr](#) `dist`

**Examples**

```

data(selex)
  #subset for efficiency
  selex <- selex[1201:1600,]
conds <- c(rep("NS", 7), rep("S", 7))
x <- aldex.clr(selex, conds, mc.samples = 128, denom = "all", verbose = FALSE)
x.dist <- aldex.expectedDistance(x)

```

aldex.glm

*Calculate glm test statistics using a model.matrix***Description**

aldex.glm calculates the expected values for each coefficient of a glm model on the data returned by aldex.clr. This function requires the user to define a model with model.matrix.

**Usage**

```
aldex.glm(clr, verbose = FALSE, ...)
```

**Arguments**

clr	An ALDEx2 object. The output of aldex.clr.
verbose	A boolean. Toggles whether to print diagnostic information while running. Useful for debugging errors on large datasets. Applies to effect = TRUE.
...	Arguments passed to glm.

**Value**

Returns a data.frame of the average coefficients and their p-values for each feature, with FDR appended as a BH column.

**Author(s)**

Thom Quinn

**References**

Please use the citation given by `citation(package="ALDEx2")`.

**See Also**

[aldex](#), [aldex.clr](#), [aldex.ttest](#), [aldex.kw](#), [aldex.glm](#), [aldex.effect](#), [aldex.corr](#), [selex](#)

**Examples**

```

data(selex)
#subset for efficiency
selex <- selex[1201:1600,]
covariates <- data.frame("A" = sample(0:1, 14, replace = TRUE),
                        "B" = c(rep(0, 7), rep(1, 7)))
mm <- model.matrix(~ A + B, covariates)
x <- aldex.clr(selex, mm, mc.samples=1, denom="all")
glm.test <- aldex.glm(x)

```

---

aldex.glm.effect	<i>calculate effect sizes and differences between all constrasts for the aldex.glm model matrix</i>
------------------	---

---

### Description

data for this function is saved in a list with entries named by contrast determines the median clr abundance of the feature in all samples and in groups determines the median difference between the two groups determines the median variation within each two group determines the effect size, which is the median of the ratio of the between group difference and the larger of the variance within groups

### Usage

```
aldex.glm.effect(clr, verbose = TRUE, include.sample.summary = FALSE, useMC=FALSE, CI=FALSE)
```

### Arguments

clr	clr is the data output of aldex.clr
verbose	Print diagnostic information while running. Useful only for debugging if fails on large datasets
include.sample.summary	include median clr values for each sample, defaults to FALSE
useMC	use multicore by default (FALSE)
CI	give effect 95

### Details

An explicit example for two conditions is shown in the ‘Examples’ below.

### Value

returns a dataframe with the following information:

rab.all	a vector containing the median clr value for each feature
rab.win.conditionA	a vector containing the median clr value for each feature in condition A
rab.win.conditionB	a vector containing the median clr value for each feature in condition B
diff.btw	a vector containing the per-feature median difference between condition A and B
diff.win	a vector containing the per-feature maximum median difference between Dirichlet instances within conditions
effect	a vector containing the per-feature effect size
overlap	a vector containing the per-feature proportion of effect size that is 0 or less

### Author(s)

Greg Gloor, Andrew Fernandes, Matt Links

## References

Please use the citation given by `citation(package="ALDEx")`.

## See Also

[aldex.clr](#), [aldex.effect](#), [aldex.ttest](#), [aldex.glm](#), [selex](#)

## Examples

```
# x is the output of the \code{x <- clr(data, mc.samples)} function
# conditions is a description of the data
# for the selex dataset, conditions <- c(rep("N", 7), rep("S", 7))
data(selex)
#subset for efficiency
selex <- selex[1201:1600,]
covariates <- data.frame("A" = sample(0:1, 14, replace = TRUE),
                        "B" = c(rep(0, 7), rep(1, 7)),
                        "Z" = sample(c(1,2,3), 14, replace=TRUE))
mm <- model.matrix(~ A + Z + B, covariates)
x <- aldex.clr(selex, mm, mc.samples=8, denom="all")
glm.effect <- aldex.glm.effect(x)
```

---

aldex.kw

*Calculate the Kruskal-Wallis test and glm ANOVA statistics*

---

## Description

`aldex.kw` calculates the expected values of the Kruskal-Wallis test and a glm ANOVA on the data returned by `aldex.clr`.

## Usage

```
aldex.kw(clr, useMC = FALSE, verbose = FALSE)
```

## Arguments

<code>clr</code>	An ALDEx2 object. The output of <code>aldex.clr</code> .
<code>useMC</code>	Toggles whether to use multi-core.
<code>verbose</code>	A boolean. Toggles whether to print diagnostic information while running. Useful for debugging errors on large datasets. Applies to <code>effect = TRUE</code> .

## Value

Returns a `data.frame` with the following information:

<code>kw.ep</code>	a vector containing the expected p-value of the Kruskal-Wallis test for each feature
<code>kw.eBH</code>	a vector containing the corresponding expected value of the Benjamini-Hochberg corrected p-value for each feature
<code>glm.ep</code>	a vector containing the expected p-value of the glm ANOVA for each feature
<code>glm.eBH</code>	a vector containing the corresponding expected value of the Benjamini-Hochberg corrected p-value for each feature

**Author(s)**

Arianne Albert

**References**Please use the citation given by `citation(package="ALDEx2")`.**See Also**[aldex](#), [aldex.clr](#), [aldex.ttest](#), [aldex.kw](#), [aldex.glm](#), [aldex.effect](#), [aldex.corr](#), [selex](#)**Examples**

```
data(selex)
#subset for efficiency
selex <- selex[1201:1600,]
conds <- c(rep("A", 4), rep("B", 3), rep("C", 7))
x <- aldex.clr(selex, conds, mc.samples=1, denom="all")
kw.test <- aldex.kw(x)
```

aldex.plot

*Plot an aldex Object***Description**

Create 'MW'- or 'MA'-type plots from the given aldex object.

**Usage**

```
## S3 method for class 'plot'
aldex( x, ..., type=c("MW","MA"),
       xlab=NULL, ylab=NULL, xlim=NULL, ylim=NULL,
       all.col=rgb(0,0,0,0.2), all.pch=19, all.cex=0.4,
       called.col=red, called.pch=20, called.cex=0.6,
       thres.line.col=darkgrey, thres.lwd=1.5,
       test=welch, cutoff.pval=0.1, cutoff.effect=1, rare.col=black,
       rare=0, rare.pch=20, rare.cex=0.2 )
```

**Arguments**

<code>x</code>	an object of class aldex produced by the aldex function
<code>...</code>	optional, unused arguments included for compatibility with the S3 method signature
<code>type</code>	which type of plot is to be produced. MA is a Bland-Altman style plot; MW is a difference between to a variance within plot as described in: <a href="http://dx.doi.org/10.1080/10618600.2015">http://dx.doi.org/10.1080/10618600.2015</a>
<code>test</code>	the method of calculating significance, one of: welch = welch's t test; wilcox = wilcox rank test; glm = glm; kruskal = Kruskal-Wallace test
<code>cutoff.pval</code>	the Benjamini-Hochberg fdr cutoff, default 0.1
<code>cutoff.effect</code>	the effect size cutoff for plotting, default 1
<code>xlab</code>	the x-label for the plot, as per the parent plot function

ylab	the y-label for the plot, as per the parent plot function
xlim	the x-limits for the plot, as per the parent plot function
ylim	the y-limits for the plot, as per the parent plot function
all.col	the default colour of the plotted points
all.pch	the default plotting symbol
all.cex	the default symbol size
called.col	the colour of points with false discovery rate, $q \leq 0.1$
called.pch	the symbol of points with false discovery rate, $q \leq 0.1$
called.cex	the character expansion of points with false discovery rate, $q \leq 0.1$
thres.line.col	the colour of the threshold line where within and between group variation is equivalent
thres.lwd	the width of the threshold line where within and between group variation is equivalent
rare	relative abundance cutoff for rare features, default 0 or the mean abundance
rare.col	color for rare features, default black
rare.pch	the default symbol of rare features
rare.cex	the default symbol size of rare points

### Details

This particular specialization of the `plot` function is relatively simple and provided for convenience. For more advanced control of the plot is best to use the values returned by `summary(x)`.

### Value

None.

### References

Please use the citation given by `citation(package="ALDEx")`.

### See Also

[aldex](#), [aldex.effect](#), [aldex.ttest](#), [aldex.glm](#)

### Examples

```
# See the examples for 'aldex'.
```



---

aldex.plotFeature	<i>Show dispersion of the expected values returned by aldex.effect</i>
-------------------	--

---

### Description

aldex.plotFeature generates density plots showing the dispersion of the expected values given in the output from aldex.effect. The expected values are shown in the plots. This is a diagnostic visualization to help determine if the expected values are trustworthy

### Usage

```
aldex.plotFeature(  
  clrData,  
  featureName,  
  pooledOnly = FALSE,  
  densityOnly = FALSE  
)
```

### Arguments

clrData	the output object from aldex.clr
featureName	the name of the feature from the input data
pooledOnly	show only the pooled plots, default FALSE, shows all plots
densityOnly	show only the density plots, default FALSE includes expected values

### Author(s)

Brandon Lieng, Greg Gloor

### References

Please use the citation given by `citation(package="ALDEx2")`.

### See Also

[aldex.clr](#), [aldex.effect](#), [selex](#)

### Examples

```
data(selex)  
#subset for efficiency  
selex <- selex[1201:1600,]  
conds <- c(rep("NS", 7), rep("S", 7))  
x <- aldex.clr(selex, conds, mc.samples=4, denom="all")  
aldex.plotFeature(x, "S:D:A:D")
```

---

aldex.set.mode                    *identify set of denominator features for log-ratio calculation*

---

### Description

calculate the features that are to be used as the denominator for the Geometric Mean calculation in `clr_function.R`

### Usage

```
aldex.set.mode(reads, conds, denom="all")
```

### Arguments

reads	A data frame containing the samples and features per sample.
conds	A vector describing which samples belong to what condition.
denom	Character argument specifying which indices to return. 'all' returns all features in both conditions. 'zero' returns the nonzero count features per condition. 'iqlr' returns the features whose variance falls within the inter-quantile range of the CLR-transformed data. In cases of malformed or null queries, input defaults to 'all'. Additionally, the input can be a numeric vector, which contains a set of row indices to center the data against. Only for advanced users who can pre-determine the invariant set of features within their data.

### Details

An explicit example for two conditions is shown in the 'Examples' below.

### Value

Outputs a vector containing indices per condition.

### Author(s)

Jia Rong Wu

### References

Please use the citation given by `citation(package="ALDEx")`.

### See Also

[aldex.clr](#), [aldex.ttest](#), [aldex.effect](#), [selex](#)

### Examples

```
# x is the output of the \code{x <- clr(data, mc.samples)} function
# conditions is a description of the data
# for the selex dataset, conditions <- c(rep("N", 7), rep("S", 7))
# input can be "all", "iqlr", "zero" or numeric for advanced users
data(selex)
#subset for efficiency
```

```

selex <- selex[1201:1600,]
conds <- c(rep("NS", 7), rep("S", 7))
x <- aldex.clr(selex, conds, mc.samples=2, denom="all")

```

aldex.ttest

*Calculate Wilcoxon Rank Sum test and Welch's t-test statistics***Description**

aldex.ttest calculates the expected values of the Wilcoxon Rank Sum test and Welch's t-test on the data returned by aldex.clr.

**Usage**

```
aldex.ttest(clr, paired.test = FALSE, hist.plot = FALSE, verbose = FALSE)
```

**Arguments**

clr	An ALDEx2 object. The output of aldex.clr.
paired.test	Toggles whether to calculate paired tests.
hist.plot	Toggles whether to plot a histogram of p-values for the first Dirichlet Monte Carlo instance.
verbose	A boolean. Toggles whether to print diagnostic information while running. Useful for debugging errors on large datasets. Applies to effect = TRUE.

**Value**

Returns a data.frame with the following information:

we.ep	a vector containing the expected p-value of Welch's t-test for each feature
we.eBH	a vector containing the corresponding expected value of the Benjamini-Hochberg corrected p-value for each feature
wi.ep	a vector containing the expected p-value of the Wilcoxon Rank Sum test for each feature
wi.eBH	a vector containing the corresponding expected value of the Benjamini-Hochberg corrected p-value for each feature

**Author(s)**

Greg Gloor

**References**

Please use the citation given by citation(package="ALDEx2").

**See Also**

[aldex](#), [aldex.clr](#), [aldex.ttest](#), [aldex.kw](#), [aldex.glm](#), [aldex.effect](#), [aldex.corr](#), [selex](#)

**Examples**

```

data(selex)
#subset for efficiency
selex <- selex[1201:1600,]
conds <- c(rep("NS", 7), rep("S", 7))
x <- aldex.clr(selex, conds, mc.samples=2, denom="all")
ttest.test <- aldex.ttest(x)

```

---

getDenom

*getDenom*


---

**Description**

Returns the denominator used as the basis for the log-ratio, for an `aldex.clr` object.

**Usage**

```
getDenom(.object)
```

**Arguments**

<code>.object</code>	A <code>aldex.clr</code> object containing the Monte Carlo Dirichlet instances derived from estimating the technical variance of the raw read count data, along with sample and feature information.
----------------------	--

**Details**

Returns the denominator used to calculate the log-ratios. "all" is the centred log-ratio. "iqlr" is the interquartile log-ratio. A vector of numbers is the offset of the variables used in the denominator

**Value**

A vector of values.

**See Also**

`aldex.clr`

**Examples**

```

data(selex)
#subset for efficiency
selex <- selex[1201:1600,]
conds <- c(rep("NS", 7), rep("S", 7))
x <- aldex.clr(selex, conds, mc.samples = 2, denom = "iqlr", verbose = FALSE)
Denom <- getDenom(x)

# to find the names of housekeeping genes used
getFeatureNames(x)[getDenom(x)]

```

---

getFeatureNames	<i>getFeatureNames</i>
-----------------	------------------------

---

**Description**

Returns the names of the features as a vector, for an `aldex.clr` object.

**Usage**

```
getFeatureNames(.object)
```

**Arguments**

<code>.object</code>	A <code>aldex.clr</code> object containing the Monte Carlo Dirichlet instances derived from estimating the technical variance of the raw read count data, along with sample and feature information.
----------------------	--

**Details**

Returns the names of the keys that can be used to subset the data rows. The keys values are the `rsid`'s.

**Value**

A vector of feature names.

**See Also**

`aldex.clr`

**Examples**

```
data(selex)
#subset for efficiency
selex <- selex[1201:1600,]
conds <- c(rep("NS", 7), rep("S", 7))
x <- aldex.clr(selex, conds, mc.samples = 2, denom="all", verbose = FALSE)
featureNames <- getFeatureNames(x)
```

---

getFeatures	<i>getFeatures</i>
-------------	--------------------

---

**Description**

Returns the features as a vector, for an `aldex.clr` object.

**Usage**

```
getFeatures(.object)
```

**Arguments**

`.object` A `aldex.clr` object containing the Monte Carlo Dirichlet instances derived from estimating the technical variance of the raw read count data, along with sample and feature information.

**Details**

Returns the features as a vector, for an `aldex.clr` object.

**Value**

A vector of features.

**See Also**

`aldex.clr`

**Examples**

```
data(selex)
  #subset for efficiency
  selex <- selex[1201:1600,]
conds <- c(rep("NS", 7), rep("S", 7))
x <- aldex.clr(selex, conds, mc.samples = 2, denom="all", verbose = FALSE)
features <- getFeatures(x)
```

---

`getMonteCarloInstances`

*getMonteCarloInstances*

---

**Description**

Returns the Monte Carlo Dirichlet instances used to create an `aldex.clr` object.

**Usage**

```
getMonteCarloInstances(.object)
```

**Arguments**

`.object` A `aldex.clr` object containing the Monte Carlo Dirichlet instances derived from estimating the technical variance of the raw read count data, along with sample and feature information.

**Details**

Returns the Monte Carlo Dirichlet instances used to create an `aldex.clr` object.

**Value**

A list of data frames of Monte Carlo Dirichlet instances derived from estimating the technical variance of the raw read count data.

**See Also**

aldex.clr

**Examples**

```

data(selex)
  #subset for efficiency
  selex <- selex[1201:1600,]
conds <- c(rep("NS", 7), rep("S", 7))
x <- aldex.clr(selex, conds, mc.samples = 2, denom = "all", verbose = FALSE)
monteCarloInstances <- getMonteCarloInstances(x)

```

---

getMonteCarloReplicate

*getMonteCarloReplicate*


---

**Description**

Returns a single Monte Carlo Dirichlet replicate generated from analysis, for an `aldex.clr` object.

**Usage**

```
getMonteCarloReplicate(.object, i)
```

**Arguments**

<code>.object</code>	A <code>aldex.clr</code> object containing the Monte Carlo Dirichlet replicates derived from estimating the technical variance of the raw read count data, along with sample and feature information.
<code>i</code>	The numeric index of the desired replicate.

**Details**

Returns the designated Monte Carlo Dirichlet replicate generated from analysis.

**Value**

A data frame representing the designated Monte Carlo Dirichlet replicate generated from analysis.

**See Also**

aldex.clr

**Examples**

```

data(selex)
  #subset for efficiency
  selex <- selex[1201:1600,]
conds <- c(rep("NS", 7), rep("S", 7))
x <- aldex.clr(selex, conds, mc.samples = 2, denom = "all", verbose = FALSE)
monteCarloReplicate <- getMonteCarloReplicate(x,1)

```

---

`getMonteCarloSample`    *getMonteCarloSample*

---

### **Description**

Returns a set of Monte Carlo Dirochlet replicates for one sample generated from analysis, for an `aldex.clr` object.

### **Usage**

```
getMonteCarloSample(.object, i)
```

### **Arguments**

<code>.object</code>	A <code>aldex.clr</code> object containing the Monte Carlo Dirochlet instances derived from estimating the technical variance of the raw read count data, along with sample and feature information.
<code>i</code>	The numeric index of the desired sample.

### **Details**

Returns the designated Monte Carlo Dirochlet replicates for one sample generated from analysis.

### **Value**

A data frame representing the designated Monte Carlo Dirochlet replicates for one sample generated from analysis.

### **See Also**

`aldex.clr`

### **Examples**

```
data(selex)
#subset for efficiency
selex <- selex[1201:1600,]
conds <- c(rep("NS", 7), rep("S", 7))
x <- aldex.clr(selex, conds, mc.samples = 2, denom = "all", verbose = FALSE)
monteCarloSample <- getMonteCarloSample(x,1)
```



---

`getReads`*getReads*

---

**Description**

Returns the count table used as input for analysis, for an `aldex.clr` object.

**Usage**

```
getReads(.object)
```

**Arguments**

`.object` A `aldex.clr` object containing the Monte Carlo Dirichlet instances derived from estimating the technical variance of the raw read count data, along with sample and feature information.

**Details**

Returns the count table.

**Value**

A data frame representing the count table used as input for analysis.

**See Also**

`aldex.clr`

**Examples**

```
data(selex)
#subset for efficiency
selex <- selex[1201:1600,]
conds <- c(rep("NS", 7), rep("S", 7))
x <- aldex.clr(selex, conds, mc.samples = 2, denom = "all", verbose = FALSE)
reads <- getReads(x)
```

---

`getSampleIDs`*getSampleIDs*

---

**Description**

Returns the names of the samples for an `aldex.clr` object. These can be used to access the original reads, as in `reads$sampleID` (if the reads are a data frame).

**Usage**

```
getSampleIDs(.object)
```

**Arguments**

`.object` A `aldex.clr` object containing the Monte Carlo Dirichlet instances derived from estimating the technical variance of the raw read count data, along with sample and feature information.

**Details**

Returns the names of the samples. These can be used to access the original reads, as in `reads$sampleID` (if the reads are a data frame).

**Value**

A vector of sample names.

**See Also**

`aldex.clr`

**Examples**

```
data(selex)
#subset for efficiency
selex <- selex[1201:1600,]
conds <- c(rep("NS", 7), rep("S", 7))
x <- aldex.clr(selex, conds, mc.samples = 2, denom = "all", verbose = FALSE)
sampleIDs <- getSampleIDs(x)
```

---

`numConditions`

*numConditions*

---

**Description**

Returns the number of conditions compared for analysis, for an `aldex.clr` object.

**Usage**

```
numConditions(.object)
```

**Arguments**

`.object` A `aldex.clr` object containing the Monte Carlo Dirichlet instances derived from estimating the technical variance of the raw read count data, along with sample and feature information.

**Details**

Returns the number of conditions compared.

**Value**

A numeric representing the number of conditions compared.

**See Also**`aldex.clr`**Examples**

```
data(selex)
  #subset for efficiency
  selex <- selex[1201:1600,]
conds <- c(rep("NS", 7), rep("S", 7))
x <- aldex.clr(selex, conds, mc.samples = 2, denom = "all", verbose = FALSE)
conditions <- numConditions(x)
```

---

`numFeatures`*numFeatures*

---

**Description**

Returns the number of features associated with the data, for an `aldex.clr` object.

**Usage**

```
numFeatures(.object)
```

**Arguments**

`.object` A `aldex.clr` object containing the Monte Carlo Dirichlet instances derived from estimating the technical variance of the raw read count data, along with sample and feature information.

**Details**

Returns the number of features associated with the data.

**Value**

A numeric representing the number of features associated with the data.

**See Also**`aldex.clr`**Examples**

```
data(selex)
  #subset for efficiency
  selex <- selex[1201:1600,]
conds <- c(rep("NS", 7), rep("S", 7))
x <- aldex.clr(selex, conds, mc.samples = 2, denom = "all", verbose = FALSE)
numFeatures <- numFeatures(x)
```

---

numMCInstances	<i>numMCInstances</i>
----------------	-----------------------

---

**Description**

Returns the number of Monte Carlo Dirichlet instances generated for analysis, for an `aldex.clr` object.

**Usage**

```
numMCInstances(.object)
```

**Arguments**

<code>.object</code>	A <code>aldex.clr</code> object containing the Monte Carlo Dirichlet instances derived from estimating the technical variance of the raw read count data, along with sample and feature information.
----------------------	--

**Details**

Returns the number of Monte Carlo Dirichlet instances generated for analysis.

**Value**

A numeric representing the number of Monte Carlo Dirichlet instances generated for analysis.

**See Also**

`aldex.clr`

**Examples**

```
data(selex)
#subset for efficiency
selex <- selex[1201:1600,]
conds <- c(rep("NS", 7), rep("S", 7))
x <- aldex.clr(selex, conds, mc.samples = 2, denom = "all", verbose = FALSE)
numInstances <- numMCInstances(x)
```

---

selex	<i>Selection-based differential sequence variant abundance dataset</i>
-------	--

---

**Description**

This data set gives the differential abundance of 1600 enzyme variants grown under selective (NS) and selective (S) conditions

**Usage**

```
selex
```

**Format**

A dataframe of 1600 features and 14 samples. The first 7 samples are non-selected, the last 7 are selected.

**Source**

McMurrough et al (2014) PNAS doi:10.1073/pnas.1322352111

**References**

McMurrough et al (2014) PNAS doi:10.1073/pnas.1322352111

---

synth2

*Synthetic asymmetric dataset*

---

**Description**

This synthetic dataset contains 2 percent sparsity as 0 values asymmetrically distributed. It is used as a test dataset.

**Usage**

selex

**Format**

A dataframe of 1000 features and 16 samples. The first 8 samples contain 20 features set to 0, the last 8 samples contain counts.

**Source**

Gloor et al (2017) notes

# Index

- \* **classes**
  - aldex.clr-class, 6
- \* **datasets**
  - selex, 28
  - synth2, 29
- \* **methods**
  - aldex.clr-class, 6
- \* **package**
  - ALDEx2m-package, 2
  
- aldex, 3, 4, 9, 11, 12, 15, 16, 19
- aldex.clr, 2, 4, 5, 9–12, 14, 15, 17–19
- aldex.clr, data.frame-method (aldex.clr), 5
- aldex.clr, matrix-method (aldex.clr), 5
- aldex.clr, RangedSummarizedExperiment-method (aldex.clr), 5
- aldex.clr-class, 6
- aldex.clr.function, 7
- aldex.clr.function (aldex.clr), 5
- aldex.corr, 4, 8, 9, 12, 15, 19
- aldex.effect, 2, 4, 6, 9, 9, 12, 14–19
- aldex.expectedDistance, 11
- aldex.glm, 2, 4, 6, 9, 10, 12, 12, 14–16, 19
- aldex.glm.effect, 13
- aldex.kw, 4, 9, 12, 14, 15, 19
- aldex.plot, 15
- aldex.plotFeature, 17
- aldex.set.mode, 18
- aldex.ttest, 2, 4, 6, 9, 10, 12, 14–16, 18, 19, 19
- ALDEx2m (ALDEx2m-package), 2
- ALDEx2m-package, 2
  
- getDenom, 20
- getDenom, aldex.clr-method (getDenom), 20
- getFeatureNames, 21
- getFeatureNames, aldex.clr-method (getFeatureNames), 21
- getFeatures, 21
- getFeatures, aldex.clr-method (getFeatures), 21
- getMonteCarloInstances, 22
- getMonteCarloInstances, aldex.clr-method (getMonteCarloInstances), 22
- getMonteCarloReplicate, 23
- getMonteCarloReplicate, aldex.clr, numeric-method (getMonteCarloReplicate), 23
- getMonteCarloSample, 24
- getMonteCarloSample, aldex.clr, numeric-method (getMonteCarloSample), 24
- getReads, 25
- getReads, aldex.clr-method (getReads), 25
- getSampleIDs, 25
- getSampleIDs, aldex.clr-method (getSampleIDs), 25
  
- numConditions, 26
- numConditions, aldex.clr-method (numConditions), 26
- numFeatures, 27
- numFeatures, aldex.clr-method (numFeatures), 27
- numMCInstances, 28
- numMCInstances, aldex.clr-method (numMCInstances), 28
  
- selex, 2, 4, 6, 9, 10, 12, 14, 15, 17–19, 28
- synth2, 29