

# Package ‘samplesim’

October 31, 2017

**Type** Package

**Title** Sample size effects in stable isotope mixing solutions

**Version** 1.0

**Date** 2017-10-30

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**Description** This package allows the investigation of the effect of sample size on estimates and precision of stable isotope mixing solutions calculated with the package siar (written by Andrew Parnell et al.) or the package MixSIAR (written by Brian Stock et al.). Sample sizes are modified assuming a normal distribution with a user defined mean and standard deviation. Samples of different sizes are created from this distribution, and mixing proportions are estimated for several replicates of each sample size using the function siarmcmcdirchletv4 (package siar) or the function run\_model (package MixSIAR). Authors thank Rolf Ims for his contribution.

**License** GPL-2

**Depends** siar, MixSIAR, ggplot2

**Suggests** knitr, rmarkdown

**VignetteBuilder** knitr

**NeedsCompilation** no

**RemoteType** github

**RemoteHost** https://api.github.com

**RemoteRepo** samplesim

**RemoteUsername** ahasverus

**RemoteRef** master

**RemoteSha** 4bdf497a4edc7b6dce5a0df614d074b3b2f466b3

**GithubRepo** samplesim

**GithubUsername** ahasverus

**GithubRef** master

**GithubSHA1** 4bdf497a4edc7b6dce5a0df614d074b3b2f466b3

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samplesim-package	<i>Sample size effects in stable isotope mixing solutions</i>
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Description

This package allows the investigation of the effect of sample size on estimates and precision of stable isotope mixing solutions calculated with the package [siar](#) (written by Andrew Parnell et al.) or the package [MixSIAR](#) (written by Brian Stock et al.). Sample sizes are modified assuming a normal distribution with a user defined mean and standard deviation. Samples of different sizes are created from this distribution, and mixing proportions are estimated for several replicates of each sample size using the function `siarmcmcdirchletv4` (package `siar`) or the function `run_model` (package `MixSIAR`).

Details

Package: samplesim  
Type: Package  
Version: 1.0  
Date: 2017-10-30  
License: GPL-2

Author(s)

Nicolas Casajus, Nicolas Lecomte, Dorothee Ehrich  
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References

Lecomte N., Ehrich D., Casajus N., Berteaux D., Giroux M.-A., Yoccoz N.G. How many is enough? An R package for evaluating the effect of sample size on estimates and precision of stable isotope mixing solutions. Submitted in *Methods in Ecology and Evolution*.

See Also

[siar](#)

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credint	<i>samplesim internal function</i>
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**Description**

samplesim internal function.

**Details**

This function is a low level function. Not for a direct use.

**Author(s)**

Nicolas Casajus, Nicolas Lecomte, Dorothee Ehrich

**See Also**

[samplesim](#)

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credintt	<i>samplesim internal function</i>
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**Description**

samplesim internal function.

**Details**

This function is a low level function. Not for a direct use.

**Author(s)**

Nicolas Casajus, Nicolas Lecomte, Dorothee Ehrich

**See Also**

[samplesim](#)

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get_output	<i>Import samplesim simulation results</i>
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### Description

This function imports samplesim simulation results. More specifically it loads the median and width of credible intervals.

### Usage

```
get_output(name = "simulation_name", change = FALSE, reference = NULL)
```

### Arguments

name	Name of the simulation to extract results.
change	If TRUE, values are expressed as a percentage of change compared to a reference.
reference	The reference state to compute percentage of change. Default is the minimum value of sample size.

### Value

A data frame with five columns:

source	The source name.
size	The sample size.
replicate	The number of replicate.
value	The value of medians/widths of credible intervals.
type	The label of value (i.e. medians or widths)

If 'change' is TRUE, then the column replicate is omitted and results are aggregated over replicates.

### Author(s)

Nicolas Casajus, Nicolas Lecomte, Dorothee Ehrich

### References

Lecomte N., Ehrich D., Casajus N., Berteaux D., Giroux M.-A., Yoccoz N.G. How many is enough? An R package for evaluating the effect of sample size on estimates and precision of stable isotope mixing solutions. Submitted in Methods in Ecology and Evolution.

### See Also

[samplesim](#), [plot\\_samplesim](#)

### Examples

```
# See the vignette for a complete example.
```

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meansd.nd*samplesim internal function*

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**Description**

samplesim internal function.

**Details**

This function is a low level function. Not for a direct use.

**Author(s)**

Nicolas Casajus, Nicolas Lecomte, Dorothee Ehrich

**See Also**

[samplesim](#)

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plot\_isospace*Plot data in the isotope space*

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**Description**

This function represents the data in the isotope space to overlay consumer and sources isotope values.

**Usage**

```
plot_isospace(mix, source, discr, filename = "isospace", plot_save_pdf = FALSE, plot_save_png = FALSE)
```

**Arguments**

mix	The output returned by the <a href="#">load_mix_data</a> function and containing consumer isotope values. See the vignette for a complete example and the help page of the <a href="#">load_mix_data</a> function.
source	The output returned by the <a href="#">load_source_data</a> function and containing mean and standard deviation isotope values of sources (and in some case raw values). See the vignette for a complete example and the help page of the <a href="#">load_source_data</a> function.
discr	The output returned by the <a href="#">load_discr_data</a> function and containing discrimination values. See the vignette for a complete example and the help page of the <a href="#">load_discr_data</a> function.
filename	The name of the plot file(s) to save.
plot_save_pdf	Boolean. If TRUE, the plot(s) are saved as pdf.
plot_save_png	Boolean. If TRUE, the plot(s) are saved as png.

**Note**

User can also use the [plot\\_data](#) of the package MixSIAR.

**Author(s)**

Nicolas Casajus, Nicolas Lecomte, Dorothee Ehrich

**References**

Lecomte N., Ehrich D., Casajus N., Berteaux D., Giroux M.-A., Yoccoz N.G. How many is enough? An R package for evaluating the effect of sample size on estimates and precision of stable isotope mixing solutions. Submitted in Methods in Ecology and Evolution.

**See Also**

[samplesim](#), [get\\_output](#)

**Examples**

```
# See the vignette for a complete example.
```

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plot\_samplesim

*Plot samplesim simulation results*

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**Description**

This plot function is a graphical representation of the effects of sample size on estimates and precision of stable isotope mixing solutions. Two plots are currently available: a plot for the width of the credible interval and one for the median of the posterior distribution, both displayed for each sample size and each source.

**Usage**

```
plot_samplesim(name = "simulation_name", change = FALSE, reference = NULL)
```

**Arguments**

name	Name of the simulation to plot results.
change	If TRUE, values are expressed as a percentage of change compared to the reference.
reference	The reference state to compute percentage of change.

**Details**

This plot function automatically loads results data stored by the [samplesim](#) function from the simulation name. It produces two plots. The first plot presents the width of the credible interval displayed for each sample size and each source. The second represents the median of the posterior distribution for each sample size and each source.

**Author(s)**

Nicolas Casajus, Nicolas Lecomte, Dorothee Ehrich

## References

Lecomte N., Ehrich D., Casajus N., Berteaux D., Giroux M.-A., Yoccoz N.G. How many is enough? An R package for evaluating the effect of sample size on estimates and precision of stable isotope mixing solutions. Submitted in Methods in Ecology and Evolution.

## See Also

[samplesim](#), [get\\_output](#)

## Examples

```
# See the vignette for a complete example.
```

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samplesim	<i>Effect of sample size in stable isotope mixing models</i>
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## Description

This function allows investigating the effect of sample size on estimates and precision of stable isotope mixing solutions. User can modify the sample size for one chosen source, for all sources or for the consumer. See details section for further informations.

## Usage

```
samplesim(package = "siar", mix, source, discr, type = NULL,
  nsamples = NULL, modify = NULL, nrep = 100, interval = 90,
  name = NULL, resid_err = TRUE, process_err = FALSE,
  run = "test", alpha.prior = 1)
```

## Arguments

package	The package name to be used to estimate mixing proportions. Must be one of 'siar' or 'mixsiar'.
mix	The output returned by the <a href="#">load_mix_data</a> function and containing consumer isotope values. See the vignette for a complete example and the help page of the <a href="#">load_mix_data</a> function.
source	The output returned by the <a href="#">load_source_data</a> function and containing mean and standard deviation isotope values of sources (and in some case raw values). See the vignette for a complete example and the help page of the <a href="#">load_source_data</a> function.
discr	The output returned by the <a href="#">load_discr_data</a> function and containing discrimination values. See the vignette for a complete example and the help page of the <a href="#">load_discr_data</a> function.
type	Character indicating the type of analysis to run. Must be one of 'one source', 'all sources' or 'consumer'.
nsamples	A vector with the sample sizes to simulate.
modify	The source name to modify (case sensitive). This argument has to be specified when type is 'one source'. Otherwise it will be ignored.

nrep	An integer specifying the number of replicates for each sample sizes. Default is 100.
interval	An integer indicating the width of credible interval to use for precision estimation. Default is 90.
name	A character string giving the name of the simulation. If NULL the simulation will be named by the time of the simulation. This name will serve to create a directory in which results will be stored.
resid_err	Boolean indicating if residual error is included in the model. See <a href="#">run_model</a> for further informations. Only necessary if package = mixsiar.
process_err	Boolean indicating if process error is included in the model. See <a href="#">run_model</a> for further informations. Only necessary if package = mixsiar.
run	String or list specifying MCMC parameters. See <a href="#">run_model</a> for further informations. Only necessary if package = mixsiar.
alpha.prior	Numeric. Dirichlet prior on p.global. See <a href="#">run_model</a> for further informations. Only necessary if package = mixsiar.

### Details

This function assesses the sensitivity of isotopes mixing models to variation in numbers of samples from source tissues. This tool can be used prior to full-blown studies in a similar manner than power analyses. It used the function [siarmcmcdirichletv4](#) developed by Andrew Parnell et al. and available in the package [siar](#). Alternatively, it can be used with the function [run\\_model](#) developed by Brian Stock et al. and available in the package [MixSIAR](#). User can choose to sample one particular source (argument type sets to 'one source') or all the sources in the same type (argument type sets to 'all sources'). User can also choose to modify consumer data (argument type sets to 'consumer'). Sample sizes are modified assuming a normal distribution with a user defined mean and standard deviation. Samples of different sizes are created from this distribution, and mixing proportions are estimated for several replicates of each sample size with the function [siarmcmcdirichletv4](#) or [run\\_model](#).

### Value

This function does not return any object in the R console. Results are stored in a directory (argument 'name') and contain four R objects.

intervals	A four dimensions array with the upper and lower bounds of the credible interval for each sample size, replicate and source. First dimension represents lower and upper bounds; second dimension corresponds to the number of sources; third dimension is the number of replicates; and fourth dimension is the number of sample size.
widths	A three dimensions array with the width (precision) of credible intervals for each source, each replicate and each sample size. First dimension corresponds to the number of replicates; second dimension is the number of sources; and third dimension represents the number of sample size.
medians	A three dimensions array with the median (estimate) of credible intervals for each source, each replicate and each sample size. Dimensions are the same as for widths object.
datasets	A four dimensions array with all resampled datasets.

A logfile is also written and contains all parameters of the simulation.



**Note**

The use of *samplesim* with the package *MixSIAR* requires the installation of the software JAGS. See the [MixSIAR](#) documentation for further details.

**Author(s)**

Nicolas Casajush, Nicolas Lecomte, Dorothee Ehrlich

**References**

Lecomte N., Ehrlich D., Casajush N., Berteaux D., Giroux M.-A., Yoccoz N.G. How many is enough? An R package for evaluating the effect of sample size on estimates and precision of stable isotope mixing solutions. Submitted in *Methods in Ecology and Evolution*.

**See Also**

[plot\\_samplesim](#), [siarmcmcdirichletv4](#), [run\\_model](#)

**Examples**

```
# See the vignette for a complete example.
```

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