

# Package: simphony (via r-universe)

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**Type** Package

**Title** Simulating Large-Scale, Rhythmic Data

**Version** 1.0.3

**Description** A tool for simulating rhythmic data: transcriptome data using Gaussian or negative binomial distributions, and behavioral activity data using Bernoulli or Poisson distributions. See Singer et al. (2019) <[doi:10.7717/peerj.6985](https://doi.org/10.7717/peerj.6985)>.

**URL** <https://simphony.hugheylab.org>,  
<https://github.com/hugheylab/simphony>

**License** GPL-2

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.2.1

**Roxygen** list(markdown = TRUE)

**Depends** R (>= 3.4)

**Imports** data.table (>= 1.11.4), foreach (>= 1.4.4)

**Suggests** ggplot2 (>= 3.0.0), kableExtra (>= 0.9.0), knitr (>= 1.20),  
limma (>= 3.34.9), precrec (>= 0.9.1), rmarkdown (>= 1.9),  
testthat (>= 2.0.0)

**VignetteBuilder** knitr

**Repository** <https://hugheylab.r-universe.dev>

**RemoteUrl** <https://github.com/hugheylab/simphony>

**RemoteRef** HEAD

**RemoteSha** f5a705e50e644d1e787bf860a658bf2d6b0757e4

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defaultDispFunc	<i>Default function for mapping expected counts to dispersion.</i>
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### Description

The function was estimated from circadian RNA-seq data from mouse liver (PRJNA297287), using local regression in DESeq2. In a negative binomial distribution,  $variance = mean + mean^2 * dispersion$ .

### Usage

```
defaultDispFunc(x)
```

### Arguments

x                    Numeric vector of mean counts.

### Format

An object of class function of length 1.

### Value

Numeric vector of dispersions.

### See Also

[simphony\(\)](#)

### Examples

```
means = 2^(6:10)
dispersions = defaultDispFunc(means)
```

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getExpectedAbund	<i>Calculate expected abundance</i>
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### Description

Calculate expected abundance for multiple features at multiple timepoints in multiple conditions.

### Usage

```
getExpectedAbund(  
  featureMetadata,  
  times = NULL,  
  sampleMetadata = NULL,  
  byCondGroup = is.null(times)  
)
```

### Arguments

featureMetadata	data.table with columns feature, base, rhyFunc, amp, period, and phase, where every row corresponds to a gene. If byCondGroup is TRUE, then must also have columns cond and group.
times	Numeric vector of the times at which to calculate expected abundance for each row in featureMetadata.
sampleMetadata	data.table with columns sample, cond, and time. Either times or sampleMetadata must be provided, and the former takes precedence.
byCondGroup	Logical for whether to speed up the calculation by grouping by the columns cond and group. Primarily for internal use.

### Value

data.table derived from featureMetadata (but with more rows), with additional columns time and mu and possibly others. If sampling will use the negative binomial family, mu corresponds to log2 counts.

### See Also

[simphony\(\)](#), [getSampledAbund\(\)](#)

### Examples

```
library('data.table')  
featureMetadata = data.table(feature = c('feature_1', 'feature_2'),  
                             base = function(x) 0,  
                             amp = c(function(x) 0, function(x) 1),  
                             period = 24,  
                             phase = 0, rhyFunc = sin)
```

```
abundDt = getExpectedAbund(featureMetadata, times = 6:17)
```

---

getSampledAbund      *Sample abundance values*

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### Description

Sample feature abundance values from the given distributions. This function is used internally by [simphony\(\)](#), and should not usually need to be called directly.

### Usage

```
getSampledAbund(
  abundDt,
  logOdds = FALSE,
  family = c("gaussian", "negbinom", "bernoulli", "poisson"),
  inplace = FALSE
)
```

### Arguments

abundDt	data.table of expected abundance. If family is 'gaussian', required columns are feature, sample, mu, and sd. If family is 'negbinom', required columns are feature, sample, mu, dispFunc, cond, and group. If family is 'bernoulli' or 'poisson', required columns are feature, sample, and mu.
logOdds	Logical for whether mu corresponds to log-odds. Only used if family is 'bernoulli'.
family	Character string for the family of distributions from which to sample the abundance values. simphony will give a warning if it tries to sample from a distribution outside the region in which the distribution is defined: $\mu < 0$ for negative binomial and Poisson, and $\mu < 0$ or $\mu > 1$ for Bernoulli.
inplace	Logical for whether to modify abundDt in-place, adding a column abund containing the abundance values.

### Value

Matrix of abundance values, where rows correspond to features and columns correspond to samples.

### See Also

[simphony\(\)](#), [getExpectedAbund\(\)](#)

## Examples

```
library('data.table')
set.seed(6022)
abundDt = data.table(feature = 'feature_1', sample = c('sample_1', 'sample_2'),
                    mu = c(0, 5), sd = 1)
abundMat = getSampledAbund(abundDt)
```

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mergeSimData

*Merge abundance data, feature metadata, and sample metadata*

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## Description

Merge a simulation's abundance data, feature metadata, and sample metadata into one `data.table`. This function is useful for making plots using `ggplot2`.

## Usage

```
mergeSimData(simData, features = NULL)
```

## Arguments

`simData` List with the following elements, such as returned by [simphony\(\)](#):

- abundData** Matrix of abundance values, with rownames for features and column names for samples.
- sampleMetadata** `data.table` with columns `sample` and `cond`.
- featureMetadata** `data.table` with columns `feature` and `cond`.

`features` Character vector of features for which to get abundance data. If `NULL`, then all features.

## Value

`data.table`.

## See Also

[simphony\(\)](#)

## Examples

```
library('data.table')
featureGroups = data.table(amp = c(0, 1))
simData = simphony(featureGroups)
mergedSimData = mergeSimData(simData, simData$featureMetadata$feature[1:2])
```

simphony

*Simulate feature abundance data***Description**

Simulate experiments in which abundances of rhythmic and non-rhythmic features are measured at multiple timepoints in one or more conditions.

**Usage**

```
simphony(
  featureGroupsList,
  fracFeatures = NULL,
  nFeatures = 10,
  timepointsType = c("auto", "specified", "random"),
  timeRange = c(0, 48),
  interval = 2,
  nReps = 1,
  timepoints = NULL,
  nSamplesPerCond = NULL,
  rhyFunc = sin,
  dispFunc = NULL,
  logOdds = FALSE,
  family = c("gaussian", "negbinom", "bernoulli", "poisson")
)
```

**Arguments**

featureGroupsList

data.frame or data.table (for a single condition) or list of data.frames or data.tables (for multiple conditions), where each row corresponds to a group of features to simulate. The following columns are all optional:

**fracFeatures** Fraction of simulated features to allocate to each group. Defaults to  $1/(\text{number of groups})$ .

**rhyFunc** Function to generate rhythmic abundance. Must have a period of  $2\pi$ . Defaults to sin.

**amp** Amplitude of rhythm. Defaults to 0. Corresponds to multiplicative term in front of rhyFunc. Can be numeric (constant over time) or a function (time-dependent). See vignette for examples.

**period** Period of rhythm. Defaults to 24.

**phase** Phase of rhythm, in the same units as period. Defaults to 0. Corresponds to an additive term in rhyFunc.

**base** Baseline abundance, i.e., abundance when rhyFunc term is 0. Depending on family, defaults to 0 ('gaussian'), 8 ('negbinom', mean log2 counts), 0 ('bernoulli' with logOdds as TRUE), 0.5 ('bernoulli' if logOdds as FALSE), or 1 ('poisson'). Can be numeric (constant over time) or a function (time-dependent). See vignette for examples.

	<b>sd</b> Standard deviation of sampled abundance values. Defaults to 1. Only used if family is 'gaussian'.
	<b>dispFunc</b> Function to calculate dispersion of sampled abundance values, given expected abundance in counts. Only used if family is 'negbinom'.
fracFeatures	Fraction of simulated features to allocate to each group. Defaults to 1/(number of groups). Only used if the first featureGroupsList data.frame lacks a fracFeatures column.
nFeatures	Integer for the total number of features to simulate.
timepointsType	Character string for how to set the timepoints for the simulation. Must be 'auto' (default), 'specified', or 'random'.
timeRange	Numeric vector for the range of timepoints to use for the simulation. Defaults to c(0, 48). Only used if timepointsType is 'auto' or 'random'.
interval	Number for the amount of time between consecutive timepoints, in the same units as period. The first timepoint is 0. Only used if timepointsType is 'auto'.
nReps	Integer for the number of replicates per timepoint. Only used if timepointsType is 'auto'.
timepoints	Numeric vector of exact timepoints to simulate, including any replicates. Only used if timepointsType is 'specified'.
nSamplesPerCond	Integer for the number of samples per condition, which will be randomly uniformly spaced between 0 and period and different for each condition. Only used if timepointsType is 'random'.
rhyFunc	Function to generate rhythmic abundance. Must have a period of $2\pi$ . Defaults to sin. Only used if a data.frame in featureGroupsList lacks a rhyFunc column.
dispFunc	Function to calculate dispersion of sampled abundance values, given expected abundance in counts. Defaults to defaultDispFunc. Only used if family is 'negbinom' and a data.frame in featureGroupsList lacks a dispFunc column.
logOdds	Logical for whether the rhythmic function corresponds to log-odds. Only used if family is 'bernoulli'.
family	Character string for the family of distributions from which to sample the abundance values. simphony will give a warning if it tries to sample from a distribution outside the region in which the distribution is defined: $\mu < 0$ for negative binomial and Poisson, and $\mu < 0$ or $\mu > 1$ for Bernoulli.

## Value

List with the following elements:

**abundData** Matrix of abundance values (counts, if family is 'negbinom'), with features as rownames and samples as colnames.

**sampleMetadata** data.table with one row per sample.

**featureMetadata** data.table with one row per feature per condition. Columns amp and base are functions of time. Columns amp0 and base0 are numeric and correspond to the amplitude and baseline abundance at time 0, respectively.

**experMetadata** List of arguments that were passed to simphony.

### See Also

[defaultDispFunc\(\)](#), [getExpectedAbund\(\)](#), [getSampledAbund\(\)](#), [mergeSimData\(\)](#)

### Examples

```
library('data.table')

# Simulate data for features having one of three sets of rhythmic parameters.
featureGroups = data.table(amp = c(0, 1, 1), phase = c(0, 0, 6),
                           rhyFunc = c(cos, cos, sin))
simData = simphony(featureGroups)

# Simulate data for an experiment with specified timepoints and replicates.
featureGroups = data.table(amp = c(0, 1))
simData = simphony(featureGroups, timepointsType = 'specified',
                   timepoints = c(0, 2, 2, 4, 12, 16, 21))

# Simulate data for an experiment with random timepoints between 0 and 24.
featureGroups = data.table(amp = c(0, 2))
simData = simphony(featureGroups, timepointsType = 'random',
                   timeRange = c(0, 24), nSamplesPerCond = 20)

# Simulate data with time-dependent rhythm amplitude or baseline abundance
featureGroups = data.table(amp = c(function(x) 1, function(x) 2^(-x / 24)),
                           base = c(function(x) x / 12, function(x) 0))
simData = simphony(featureGroups)

# Simulate data for features whose rhythmicity varies between two conditions.
featureGroupsList = list(
  data.table(amp = c(1, 2, 2), phase = c(0, -3, 0), period = c(24, 24, 22)),
  data.table(amp = c(3, 2, 2), phase = c(0, 3, 0), period = c(24, 24, 26)))
simData = simphony(featureGroupsList)

# Simulate data from a negative binomial distribution with a higher variance.
featureGroups = data.table(amp = 1, base = 6:8)
dispFunc = function(x) 3 * defaultDispFunc(x)
simData = simphony(featureGroups, family = 'negbinom', dispFunc = dispFunc)

# Simulate data at high temporal resolution from a Poisson distribution that
# alternates between two states.
featureGroups = data.table(amp = 1, base = 0,
                           rhyFunc = function(x) ifelse(x %% (2 * pi) < pi, 0.5, 4))

simData = simphony(featureGroups, timeRange = c(0, 24 * 4), interval = 0.1,
                   nReps = 1, family = 'poisson')
```



```

# Simulate data for 100 features, half non-rhythmic and half rhythmic, with
# amplitudes for rhythmic features sampled from a log-normal distribution.
nFeatures = 100
rhyFrac = 0.5
nRhyFeatures = round(rhyFrac * nFeatures)
rhyAmps = exp(rnorm(nRhyFeatures, mean = 0, sd = 0.25))
fracFeatures = c(1 - rhyFrac, rep(rhyFrac / nRhyFeatures, nRhyFeatures))
featureGroups = data.table(amp = c(0, rhyAmps), fracFeatures = fracFeatures)
simData = simphony(featureGroups, nFeatures = nFeatures)

# Simulate data for 100 rhythmic features, with baseline log2 expected counts
# and residual log dispersion sampled from distributions whose parameters
# were estimated, using DESeq2 and fitdistrplus, from circadian RNA-seq data
# from mouse liver (PRJNA297287).
nFeatures = 100
baseLog2Counts = rnorm(nFeatures, mean = 8.63, sd = 2.73)
dispFactors = exp(rnorm(nFeatures, sd = 0.819))
dispFuncs = sapply(dispFactors, function(z) {function(x) defaultDispFunc(x) * z})
featureGroups = data.table(base = baseLog2Counts, dispFunc = dispFuncs, amp = 1)
simData = simphony(featureGroups, nFeatures = nFeatures, family = 'negbinom')

```

---

splitDiffFeatureGroups

*Split differential featureGroups*


---

## Description

Split a diffFeatureGroups data.frame into a list of two featureGroups data.frames, which can then be passed to [simphony\(\)](#).

## Usage

```
splitDiffFeatureGroups(diffFeatureGroups, checkValid = TRUE)
```

## Arguments

diffFeatureGroups	data.frame with optional columns meanBase, dBase, meanSd, dSd, meanAmp, dAmp, meanPhase, and dPhase describing the changes in abundance between two conditions. Each row corresponds to a group of features.
checkValid	Logical for whether to only return rows for which both amplitudes are greater than or equal to zero and both standard deviations are greater than zero.

## Value

List of two data.tables with possible columns base, sd, amp, and phase, depending on the columns in diffFeatureGroups.

**See Also**[simphony\(\)](#)**Examples**

```
dGroups = data.frame(meanAmp = c(1, 1, 1, 1), dAmp = c(1, 1, 2, 2),  
                    meanPhase = c(0, 0, 0, 0), dPhase = c(0, 3, 0, 3))  
featureGroups = splitDiffFeatureGroups(dGroups)
```

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