

Package ‘shallot’

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Type Package

Title Random Partition Distribution Indexed by Pairwise Information

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Description Implementations are provided for the models described in the paper D. B. Dahl, R. Day, J. Tsai (2017) <DOI:10.1080/01621459.2016.1165103>. The Ewens, Ewens-Pitman, Ewens attraction, Ewens-Pitman attraction, and ddCRP distributions are available for prior and posterior simulation. Posterior simulation is based on a user-supplied likelihood. Supporting functions for partition estimation and plotting are also provided.

URL <https://github.com/dbdahl/shallot>

BugReports <https://github.com/dbdahl/shallot/issues>

Imports rscala (>= 3.2.3), commonsMath (>= 1.2), sdols (>= 1.7), stats

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R topics documented:

shallot-package	2
adj.rand.index	3
attraction	4
decay	5
enumerate.partitions	6
estimate.partition	7
mass	8
nsubsets	9
pairwise.proBABILITIES	11
partition.distribution	12

partition.pmf	13
permutation	14
process.samples	15
sample.partitions	16
sample.partitions.posterior	17
sampling.model	19

Index	22
--------------	-----------

shallot-package	<i>Random Partition Distribution Indexed by Pairwise Information</i>
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Description

This package implements models described in the paper [Dahl, D. B., Day, R., and Tsai, J. \(2017\), Random Partition Distribution Indexed by Pairwise Information, *Journal of the American Statistical Association*, accepted](#). The Ewens, Ewens-Pitman, Ewens attraction, Ewens-Pitman attraction, and ddCRP distributions are available for prior simulation. We hope in the future to add posterior simulation with a user-supplied likelihood. Supporting functions for partition estimation and plotting are also planned.

Author(s)

David B. Dahl <dahl@stat.byu.edu>

References

[Dahl, D. B., Day, R., and Tsai, J. \(2017\), Random Partition Distribution Indexed by Pairwise Information, *Journal of the American Statistical Association*, accepted. <DOI:10.1080/01621459.2016.1165103>](#)

See Also

[ewens.pitman.attraction](#), [sample.partitions](#), [estimate.partition](#)

Examples

```
data <- iris[,-ncol(iris)]
truth <- as.integer(iris[,ncol(iris)])
distance <- as.dist(as.matrix(dist(scale(data))+0.001))

decay <- decay.exponential(temperature(9.0, fixed=TRUE), distance)
permutation <- permutation(n.items=nrow(data), fixed = FALSE)
attraction <- attraction(permutation, decay)
mass <- mass(1.0, fixed = TRUE)
discount <- discount(0.2, fixed = TRUE)
distribution <- ewens.pitman.attraction(mass, discount, attraction)

raw <- sample.partitions(distribution, 500, parallel=FALSE)
samples <- process.samples(raw)
```

```
library(sdols)
pp <- expectedPairwiseAllocationMatrix(samples$labels)
est <- salso(pp)
conf <- confidence(est,pp)
plot(conf)
plot(conf,data=data)
```

adj.rand.index	<i>Adjusted Rand Index</i>
----------------	----------------------------

Description

This function calculates the adjusted Rand index between two clusterings/partitions.

Usage

```
adj.rand.index(c1, c2)
```

Arguments

c1	A vector containing cluster labels for a clustering/partition.
c2	A vector containing cluster labels for a clustering/partition.

Details

The [adj.rand.index](#) function takes as its input two clusterings/partitions in cluster label notation and computes the adjusted Rand index. The adjusted Rand index is at most 1.0 and large numbers indicate high similarity.

Value

A numeric vector of length one representing the adjusted Rand index between the two clusterings/partitions.

Author(s)

David B. Dahl <dahl@stat.byu.edu>

References

Hubert, L. and Arabie, P. (1985), Comparing partitions, *Journal of Classification*, **2**, 193-218.

See Also

[estimate.partition](#)

Examples

```
truth    <- c(1,1,2,2,2,1,3,3,3)
estimate <- c(1,2,2,2,2,1,2,3,3)
adj.rand.index(truth,estimate)
```

attraction	<i>Attraction</i>
------------	-------------------

Description

This function creates an attraction from a permutation and a decay in preparation for use in the [ewens.attraction](#), [ewens.pitman.attraction](#), and [ddcrp](#) functions. For details on each of these arguments, please see the links below.

Usage

```
attraction(permutation, decay)
## S3 method for class 'shallot.attraction'
print(x, ...)
## S3 method for class 'shallot.attraction'
as.matrix(x, ...)
```

Arguments

permutation	An object of class <code>shallot.permutation</code> encoding the permutation of the items.
decay	An object of class <code>shallot.decay</code> detailing the transformation from distances to attractions.
x	An object of class <code>shallot.attraction</code> .
...	Currently ignored.

Value

An object of class `shallot.attraction`.

Author(s)

David B. Dahl <dahl@stat.byu.edu>

References

Dahl, D. B., Day, R., and Tsai, J. (2017), Random Partition Distribution Indexed by Pairwise Information, *Journal of the American Statistical Association*, accepted. <DOI:10.1080/01621459.2016.1165103>

See Also

[ddcrp](#), [decay](#), [ewens.attraction](#), [ewens.pitman.attraction](#), [permutation](#)

Examples

```
permutation <- permutation(n.items=50, fixed=FALSE)
decay <- decay.exponential(temperature(1.0), dist(scale(USArrests)))
attraction(permutation, decay)
```

decay	<i>Decay</i>
-------	--------------

Description

These functions specify the decay to map distances to attractions.

Usage

```
decay.reciprocal(temperature, distance)
decay.exponential(temperature, distance)
decay.subtraction(temperature, distance, multiplier = 1.01)
## S3 method for class 'shallot.decay'
print(x, ...)
```

Arguments

temperature	An object of class shallot.temperature.
distance	An object of class dist.
multiplier	An scalar greater than 1.0 to ensure that attractions from decay.subtraction are finite.
x	An object of class shallot.decay.
...	Currently ignored.

Details

There are currently three choices for decay functions: reciprocal, exponential, and subtraction.

The reciprocal decay maps a distance d to an attraction a as follows: $a = 1/d^t$, where t is the temperature.

The exponential decay maps a distance d to an attraction a as follows: $a = \exp(-t*d)$, where t is the temperature.

The subtract decay maps a distance d to an attraction a as follows: $a = (m-d)^t$, where t is the temperature and m is the maximum distance in distance multiplied by the supplied *multiplier*.

Author(s)

David B. Dahl <dahl@stat.byu.edu>

References

Dahl, D. B., Day, R., and Tsai, J. (2017), Random Partition Distribution Indexed by Pairwise Information, *Journal of the American Statistical Association*, accepted. <DOI:10.1080/01621459.2016.1165103>

See Also

[dist](#), [temperature](#), [attraction](#)

Examples

```
temp <- temperature(1.0)
distance <- dist(scale(USArrests))
decay1 <- decay.reciprocal(temp,distance)
decay2 <- decay.exponential(temp,distance)
decay3 <- decay.subtraction(temp,distance)
```

enumerate.partitions *Enumerate Partitions*

Description

This function enumerates all possible partitions for a given number of items.

Usage

```
enumerate.partitions(n.items)
```

Arguments

`n.items` An integer given then number of items to partition.

Details

This function returns an enumeration of the partition of `n.items` items.

Value

A matrix of cluster labels in which each row represents a clusterings.

Author(s)

David B. Dahl <dahl@stat.byu.edu>

See Also

[process.samples](#)

Examples

```
## Not run:  
example(shallot)  
  
## End(Not run)
```

estimate.partition	<i>Estimate Partition</i>
--------------------	---------------------------

Description

This function returns a partition that summarizes the partition distribution using the least-square clustering method (Dahl 2006), with extensions to perform greedy optimization and limit the number of subsets.

Usage

```
estimate.partition(x, pairwise.proBABILITIES = NULL,  
                  max.subsets = 0, max.scans = 0, parallel = TRUE)
```

Arguments

x	An object from the sample.partitions function.
pairwise.proBABILITIES	An object of class <code>shallot.pairwiseProbability</code> obtained from pairwise.proBABILITIES . If not supplied, it will be computed from x.
max.subsets	An integer limiting the number of subsets. Defaults to 0, which does not impose a constraint on the number of subsets.
max.scans	An integer controlling the greedy search. Defaults to 0, which disables the greedy search.
parallel	Should all of the CPU cores should be used? Defaults to TRUE.

Value

A partition as a vector of cluster labels.

Author(s)

David B. Dahl <dahl@stat.byu.edu>

References

Dahl, D. B., Day, R., and Tsai, J. (2017), Random Partition Distribution Indexed by Pairwise Information, *Journal of the American Statistical Association*, accepted. <DOI:10.1080/01621459.2016.1165103>

Dahl, D. B. (2006), Model-Based Clustering for Expression Data via a Dirichlet Process Mixture Model, in *Bayesian Inference for Gene Expression and Proteomics*, Kim-Anh Do, Peter Mueller, Marina Vannucci (Eds.), Cambridge University Press.

See Also

[sample.partitions](#), [process.samples](#), [plot.partition](#), [adj.rand.index](#)

Examples

```
## Not run:
example(shallot)

## End(Not run)
```

mass

Mass, Discount, and Temperature Parameters

Description

These functions set the mass, discount, and temperature parameters and, in the case of them being random, specify the parameters of their distribution.

Usage

```
mass(..., fixed = TRUE)
discount(..., fixed = TRUE)
temperature(..., fixed = TRUE)
## S3 method for class 'shallot.mass'
print(x, ...)
## S3 method for class 'shallot.discount'
print(x, ...)
## S3 method for class 'shallot.temperature'
print(x, ...)
```

Arguments

...	A number greater than 0.0 representing the value of the mass, discount, or temperature parameters. Or, in the case of them being random, a vector of two numbers representing either: i. the shape and rate parameters of the gamma distribution for the mass or temperature, or ii. the shape parameters of the beta distribution for the discount. This argument is currently ignored for the associated print functions.
x	An object from the mass , discount , or temperature functions.
fixed	If TRUE, the parameter is fixed. If FALSE, the parameter value is samples from either: i. a gamma distribution for the mass or temperature, or ii. a beta distribution for the discount.

Details

If no parameters are specified, the mass parameter defaults to 1.2, the discount parameter defaults to 0.05, the temperature parameter defaults to 3.0. If the mass parameter is random, the default shape and rate parameters of the gamma distribution are 2.5 and 2, respectively. If the discount parameter is random, the default shape parameters of the beta distribution are 1.0 and 1.0. If the temperature parameter is random, the default shape and rate parameters of the gamma distribution are 2 and 0.5, respectively.

Value

An object of class `shallot.mass`, `shallot.discount`, or `shallot.temperature`.

Author(s)

David B. Dahl <dahl@stat.byu.edu>

Examples

```
mass()
mass(1.0)
mass(1.4, fixed=FALSE)
mass(0.5, 1, fixed=FALSE)
discount()
discount(0.2)
discount(1, 3, fixed=FALSE)
temperature()
temperature(2)
temperature(2, 4, fixed=FALSE)
```

nsubsets

Number of Subsets

Description

These functions either sample the number of subsets for supported partition distributions or computes probabilities, means, and variances of these distributions.

Usage

```
nsubsets.random(x, n.samples)
nsubsets.probability(x, n.subsets)
nsubsets.average(x)
nsubsets.variance(x)
```

Arguments

<code>x</code>	An object of class <code>shallot.distribution</code> .
<code>n.samples</code>	An integer containing the number of samples.
<code>n.subsets</code>	An integer containing the number of subsets.
<code>...</code>	Currently ignored.

Value

The `nsubsets.random` function returns a vector of random samples of the number of subsets in the distribution `x`.

The `nsubsets.probability` function returns the probability that the number of subsets is `n.subsets` in the distribution `x`. Depending on the number of items and the value of `n.subsets`, this function can be computationally intensive.

The `nsubsets.average` and `nsubsets.variance` functions return the mean and variances, respectively, of the number of subsets in the distribution `x`.

Author(s)

David B. Dahl <dahl@stat.byu.edu>

References

Dahl, D. B., Day, R., and Tsai, J. (2017), Random Partition Distribution Indexed by Pairwise Information, *Journal of the American Statistical Association*, accepted. <DOI:10.1080/01621459.2016.1165103>

See Also

[partition.distribution](#)

Examples

```
pd <- ewens.pitman.attraction(
  mass(1),
  discount(0.05),
  attraction(permutation(n.items=50, fixed=FALSE),
    decay.exponential(temperature(1.0), dist(scale(USArrests))))))
mean(nsubsets.random(pd, 1000))
nsubsets.average(pd)

pde <- ewens(mass(1), 50)
nsubsets.variance(pde)
nsubsets.probability(pde, 4)
```

`pairwise.proBABILITIES`*Pairwise Probabilities*

Description

These functions relate to the pairwise probabilities that two items are clustered together, i.e., belong to the same subset in a partition.

Usage

```
pairwise.proBABILITIES(x, parallel = TRUE)
## S3 method for class 'shallot.pairwiseProbability'
print(x, ...)
## S3 method for class 'shallot.pairwiseProbability'
as.matrix(x, ...)
```

Arguments

<code>x</code>	An object of class <code>shallot.samples.raw</code> when supplied to <code>pairwise.proBABILITIES</code> or an object of class <code>shallot.pairwiseProbability</code> when supplied to <code>print</code> and <code>as.matrix</code> .
<code>parallel</code>	Should all of the CPU cores should be used? Defaults to TRUE.
<code>...</code>	Currently ignored.

Details

`pairwise.proBABILITIES` calculates the pairwise probabilities that two items are clustered together, i.e., belong to the same subset in a partition.

`as.matrix` converts the results of `pairwise.proBABILITIES` to an R matrix.

Value

The `pairwise.proBABILITIES` function returns an object of class `shallot.pairwiseProbability`.

The `as.matrix` function returns a square matrix.

Author(s)

David B. Dahl <dahl@stat.byu.edu>

See Also

[sample.partitions](#), [process.samples](#), [estimate.partition](#)

Examples

```
## Not run:
example(shallot)

## End(Not run)
```

partition.distribution

Distribution

Description

These functions specify the Ewens, Ewens-Pitman, Ewens attraction, Ewens-Pitman attraction, and ddCRP distributions which would then be used in the [sample.partitions](#) function.

Usage

```
ewens(mass,n.items,names = paste0("c", 1:n.items))
## S3 method for class 'shallot.distribution.ewens'
print(x, ...)
ewens.pitman(mass,discount,n.items,names = paste0("c", 1:n.items))
## S3 method for class 'shallot.distribution.ewensPitman'
print(x, ...)
ewens.attraction(mass, attraction)
## S3 method for class 'shallot.distribution.ewensAttraction'
print(x, ...)
ewens.pitman.attraction(mass, discount, attraction)
## S3 method for class 'shallot.distribution.ewensPitmanAttraction'
print(x, ...)
ddcrp(mass, attraction)
## S3 method for class 'shallot.distribution.ddcrp'
print(x, ...)
```

Arguments

mass	An object of class shallot.mass.
discount	An object of class shallot.discount.
attraction	An object of class shallot.attraction.
n.items	An integer containing the number of items to partition.
names	A character vector containing the names of the items. The default names are of the form “c1”, “c2”, etc.
x	An object of class shallot.distribution.
...	Currently ignored.

Value

An object of class `shallot.distribution`.

Author(s)

David B. Dahl <dahl@stat.byu.edu>

References

Dahl, D. B., Day, R., and Tsai, J. (2017), Random Partition Distribution Indexed by Pairwise Information, *Journal of the American Statistical Association*, accepted. <DOI:10.1080/01621459.2016.1165103>

See Also

[mass](#), [discount](#), [attraction](#), [sample.partitions](#)

Examples

```
pd1 <- ewens(mass(1),50)

decay <- decay.exponential(temperature(1.0),dist(scale(USArrests)))
attraction <- attraction(permutation(n.items=50, fixed=FALSE), decay)
pd2 <- ewens.pitman.attraction(mass(1), discount(0.05), attraction)

pd3 <- ddcrp(mass(1), attraction)
```

partition.pmf

Obtain the Probability Mass Function of a Partition Distribution

Description

This function returns the probability mass function (pmf) of a partition distribution.

Usage

```
partition.pmf(x)
```

Arguments

`x` An object of class `shallot.distribution` obtained, for example, from the [ewens.pitman.attraction](#) function.

Value

A function that takes a partition (as a vector in cluster label notation) and returns the probability — or, if `log=TRUE`, the log of the probability — of the supplied partition.

Author(s)

David B. Dahl <dahl@stat.byu.edu>

Examples

```
## Not run:
example(shallot)

## End(Not run)
```

permutation

Permutation

Description

These function define a permutation for subsequent use.

Usage

```
permutation(..., n.items = NULL, fixed = TRUE)
## S3 method for class 'shallot.permutation'
print(x, ...)
```

Arguments

...	For the function permutation , a permutation of the integers 1, 2,... n, where n is the length of the vector. For the function print.shallot.permutation , this is ignored.
n.items	An optional argument provided instead of ... to request a random partition. The argument fixed must be FALSE.
x	An object of class shallot.permutation.
fixed	Should the permutation be fixed?

Details

A valid permutation of length n is an integer vector of length n containing each integer 1, 2,... n only once.

Value

An object of class shallot.permutation.

Author(s)

David B. Dahl <dahl@stat.byu.edu>

References

Dahl, D. B., Day, R., and Tsai, J. (2017), Random Partition Distribution Indexed by Pairwise Information, *Journal of the American Statistical Association*, accepted. <DOI:10.1080/01621459.2016.1165103>

See Also

[attraction](#)

Examples

```
## Demonstrate permutation.  
permutation(c(3, 1, 2, 5, 4))  
permutation(c(3, 1, 2, 5, 4), fixed=FALSE)  
permutation(n.items=5, fixed=FALSE)
```

process.samples	<i>Process Sampled Partitions</i>
-----------------	-----------------------------------

Description

This function extracts the partitions from the results of the [sample.partitions](#) function.

Usage

```
process.samples(x)
```

Arguments

x An object from the [sample.partitions](#) function.

Details

This function extracts the sampled partitions from the results of the [sample.partitions](#) function.

Value

A list containing a matrix of cluster labels in which each row represents a clustering. The list also contains sampled model parameters if `sample.parameter` is not NULL.

Author(s)

David B. Dahl <dahl@stat.byu.edu>

See Also

[sample.partitions](#)

Examples

```
## Not run:  
example(shallot)  
  
## End(Not run)
```

sample.partitions *Sample Partitions from Partition Distributions*

Description

This function samples partitions from the Ewens, Ewens-Pitman, Ewens attraction, Ewens-Pitman attraction, and ddCRP distributions.

Usage

```
sample.partitions(x, n.draws, parallel = TRUE)  
## S3 method for class 'shallot.samples.raw'  
print(x, ...)
```

Arguments

x	An object of class shallot.distribution obtained, for example, from the ewens.pitman.attraction function.
n.draws	An integer representing the desired number of samples. Due to parallelization, slightly more samples may be returned.
parallel	Should sampling be done in parallel by simultaneously using all CPU cores?
...	Currently ignored.

Value

An object of class shallot.samples.raw which can be subsequently be used in [process.samples](#), [pairwise.proBABILITIES](#), [estimate.partition](#),

Note

If this function is interrupted by the user, the computation engine will be broken and subsequent calls to package functions may fail until a new R session is started.

Author(s)

David B. Dahl <dahl@stat.byu.edu>

See Also

[partition.distribution](#), [process.samples](#), [pairwise.proBABILITIES](#), [estimate.partition](#)
[sample.partitions.posterior](#)

Examples

```
## Not run:
example(shallot)

## End(Not run)
```

```
sample.partitions.posterior
```

Sample Partitions from Posterior Distribution of Partition

Description

This function samples partitions from the posterior distribution of a partition based on a user-supplied likelihood and the following prior partition distributions: Ewens, Ewens-Pitman, Ewens attraction, Ewens-Pitman attraction, and ddCRP distributions.

Usage

```
sample.partitions.posterior(partition, sampling.model, partition.model,
  n.draws, massRWSD = 0.5, discountRWSD = 0.1,
  k = min(length(partition), 25), temperatureRWSD = 0.5,
  progress.bar = interactive())
```

Arguments

partition	An object of class <code>shallot.distribution.data</code>
sampling.model	An object of class <code>shallot.distribution.data</code> obtained from the sampling.model function.
partition.model	An object of class <code>shallot.distribution</code> obtained, for example, from the ewens.pitman.attraction function.
n.draws	An integer representing the desired number of samples.
massRWSD	The standard deviation of the random walk proposal for updating the mass parameter.
discountRWSD	The standard deviation of the random walk proposal for updating the discount parameter.
k	The number of items to shuffle when proposing an update for the permutation.
temperatureRWSD	The standard deviation of the random walk proposal for updating the temperature parameter.
progress.bar	Should a progress bar be shown while sampling?

Value

An object of class `shallot.samples.raw` which can be subsequently be used in [process.samples](#), [pairwise.probabilities](#), [estimate.partition](#),

Note

If this function is interrupted by the user, the computation engine will be broken and subsequent calls to package functions may fail until a new R session is started.

Author(s)

David B. Dahl <dahl@stat.byu.edu>

See Also

[partition.distribution](#), [process.samples](#), [pairwise.probabilities](#), [estimate.partition](#)
[sample.partitions](#)

Examples

```

1+2
#\donttest{
#mass <- mass(1.0, fixed=TRUE)
#discount <- discount(0.05, fixed=TRUE)
#distance <- dist(scale(USArrests[1:9,]))
#if ( min(distance[upper.tri(distance)],na.rm=TRUE) == 0 )
# stop("Oops, distances must be strictly positive.")
#
#n.items <- attr(distance,"Size")
#permutation <- permutation(n.items=n.items, fixed=FALSE)
#temperature <- temperature(2, fixed=TRUE)
#attraction <- attraction(permutation,decay.exponential(temperature,distance))
#partition.distribution <- ewens.pitman.attraction(mass, discount, attraction)
#
### Model inputs.
#data <- c(-1.48, -1.40, -1.16, -1.08, -1.02, 0.14, 0.51, 0.53, 0.78)
#sigma <- 0.1
#mu0 <- 0.0
#sigma0 <- 1.0
#
### Derived values.
#s2 <- sigma * sigma
#s02 <- sigma0 * sigma0
#s02Inv <- 1.0 / s02
#c <- -1.0 / (2.0 * s2)
#
### Sampling model of Neal (JCGS, 2009)
### Function to perform an MCMC update of the parameter.
#sample.parameter <- function(indices=scalaType("D1"), parameter=scalaType("D0")) {
# sum <- sum(data[indices])
# variance <- 1 / (s02Inv + length(indices) / s2)
# mean <- variance * (mu0 / s02 + sum / s2)
# rnorm(1, mean, sqrt(variance))
#}
#
#library(rscala)
#s <- shallot:::s

```

```

#sample.parameter.compiled <- s(data=data,mu0=mu0,s2=s2,s02=s02,s02Inv=s02Inv) ^ sample.parameter
#
#
### Function to evaluate the likelihood contribution for an observation.
#log.density <- function(i=scalaType("D0"), indices=scalaType("D1"), parameter=scalaType("D0")) {
# resid <- data[i] - parameter
# c * resid * resid
#}
#
#log.density.compiled <- s(data=data,c=c) ^ log.density
#
#sampling.model <- sampling.model(sample.parameter, log.density)
#
### Perform posterior sampling.
#initial.partition <- rep(1,length(data))
#n.draws <- 10
#raw <- sample.partitions.posterior(initial.partition,sampling.model,partition.distribution,
#                                 massRWS=3,temperatureRWS=1,n.draws)
#samples.format1 <- process.samples(raw)
#parameterMatrix <- t(sapply(seq_len(n.draws), function(i) {
#  unlist(samples.format1$parameters[[i]])[samples.format1$labels[i,]]
#}))
#
#tail(samples.format1$hyperparameters)
#
### Shrinkage to group means?
#plot(data,apply(parameterMatrix,2,mean))
#abline(a=0,b=1)
#
#samples.format1$hyperparameters
#
### Post processing to find the partition estimate.
#library(sdols)
#pp <- expectedPairwiseAllocationMatrix(samples.format1$labels)
#est <- salso(pp)
#plot(confidence(est,pp))
#\dontshow{
#rscala::scalaDisconnect(shallot::s)
#}
#}

```

Description

These functions set the mass, discount, and temperature parameters and, in the case of them being random, specify the parameters of their distribution.

Usage

```
sampling.model(sample.parameter, log.density)
```

Arguments

sample.parameter

A function taking two arguments with names `indices` and `parameter` having default values `c()` and `NULL`, respectively. With those default values, the function should return a sample from the centering distribution as an **R** object of any type. Otherwise, `indices` is a vector of integers indicating the cluster elements and `parameter` is the current value of the parameter for the cluster, and the function should return an updated value for the cluster parameter based on a valid MCMC update.

log.density

A function taking three arguments with names `i`, `indices`, and `parameter` and returning a double giving the log of the likelihood contribution of item `i` to a clustering with members `indices` and parameter `parameter`.

Value

An object of class `shallot.distribution.data`.

Author(s)

David B. Dahl <dahl@stat.byu.edu>

Examples

```
## Model inputs.
data <- c(-1.48, -1.40, -1.16, -1.08, -1.02, 0.14, 0.51, 0.53, 0.78)
sigma <- 0.1
mu0 <- 0.0
sigma0 <- 1.0

## Derived values.
s2 <- sigma * sigma
s02 <- sigma0 * sigma0
s02Inv <- 1.0 / s02
c <- -1.0 / (2.0 * s2)

## Sampling model of Neal (JCGS, 2009)
## Function to perform an MCMC update of the parameter.
sample.parameter <- function(indices=c(), parameter=NULL) {
  sum <- sum(data[indices])
  variance <- 1 / (s02Inv + length(indices) / s2)
  mean <- variance * (mu0 / s02 + sum / s2)
  rnorm(1, mean=mean, sd=sqrt(variance))
}

## Function to evaluate the likelihood contribution for an observation.
log.density <- function(i, indices, parameter) {
  resid <- data[i] - parameter
```

```
      c * resid * resid
    }

sm <- sampling.model(sample.parameter, log.density)
sm
```

Index

*Topic **package**

- shallot-package, 2
- adj.rand.index, 3, 3, 8
- as.matrix, 11
- as.matrix.shallot.attraction (attraction), 4
- as.matrix.shallot.pairwiseProbability (pairwise.proBABILITIES), 11
- attraction, 4, 6, 13, 15
- ddcrp, 4
- ddcrp (partition.distribution), 12
- decay, 4, 5
- discount, 8, 13
- discount (mass), 8
- dist, 6
- enumerate.partitions, 6
- estimate.partition, 2, 3, 7, 11, 16–18
- ewens (partition.distribution), 12
- ewens.attraction, 4
- ewens.pitman.attraction, 2, 4, 13, 16, 17
- mass, 8, 8, 13
- nsubsets, 9
- nsubsets.average, 10
- nsubsets.probability, 10
- nsubsets.random, 10
- nsubsets.variance, 10
- pairwise.proBABILITIES, 7, 11, 11, 16–18
- partition.distribution, 10, 12, 16, 18
- partition.pmf, 13
- permutation, 4, 14, 14
- plot.partition, 8
- print, 11
- print.shallot.attraction (attraction), 4
- print.shallot.decay (decay), 5
- print.shallot.discount (mass), 8
- print.shallot.distribution.ddcrp (partition.distribution), 12
- print.shallot.distribution.ewens (partition.distribution), 12
- print.shallot.distribution.ewensAttraction (partition.distribution), 12
- print.shallot.distribution.ewensPitman (partition.distribution), 12
- print.shallot.distribution.ewensPitmanAttraction (partition.distribution), 12
- print.shallot.mass (mass), 8
- print.shallot.pairwiseProbability (pairwise.proBABILITIES), 11
- print.shallot.permutation, 14
- print.shallot.permutation (permutation), 14
- print.shallot.samples.raw (sample.partitions), 16
- print.shallot.temperature (mass), 8
- process.samples, 6, 8, 11, 15, 16–18
- sample.partitions, 2, 7, 8, 11–13, 15, 16, 18
- sample.partitions.posterior, 16, 17
- sampling.model, 17, 19
- shallot (shallot-package), 2
- shallot-package, 2
- temperature, 6, 8
- temperature (mass), 8