

# Package ‘oBGSelComp’

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**Type** Package  
**Title** oBGSelComp: overlapping Bayesian Group Selection for Compositional data  
**Version** 1.0  
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**Description** The oBGSelComp package implements an MCMC algorithm for a Bayesian hierarchical model for variable selection with a group structure in the context of correlated multivariate compositional response variables.  
**SystemRequirements** GSL (GNU Scientific Library)  
**License** GPL (>= 2.0)  
**Imports** sirt, gtools, AUC  
**RoxygenNote** 6.1.0  
**Encoding** UTF-8

## R topics documented:

oBGSelCompAlgo	1
SimulateData	3
<b>Index</b>	<b>4</b>

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oBGSelCompAlgo	<i>An MCMC algorithm to perform an overlapping Bayesian group selection for compositional response data.</i>
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## Description

The function implements an MCMC algorithm for a Bayesian model for compositional data using a Dirichlet model by allowing for straightforward incorporation of available high-dimensional covariate information within a log-linear regression framework. The method imposes prior distributions that account for the overlapping structure between groups.

## Usage

```
oBGSelCompAlgo(outcome=outcome,X=X,Pathway=Pathway,sample=10000,
burnin=1000,hyperprob=c(1,1),hypersig=c(5,0.01),hyperlamb=c(5,2), seed=1)
```

## Arguments

outcome	A compositional multivariate response of dimension $n \times q$
X	A set of covariate matrix of dimension $n \times p$ (e.g. gene expression)
Pathway	A binary pathway indicator matrix $P$ of dimension $K \times p$ where cell $(k, j)$ is 1 if the covariate $j$ belongs to group (or pathway) $k$ , and 0 otherwise.
sample	Total number of MCMC draws. It must be larger than burnin.
burnin	Number of draws to discard for burn-in
hyperprob	Hyperparameters of a beta(a,b) distribution, prior distribution of the probability of selecting groups
hypersig	Hyperparameters of an inverse gamma inv.gamma(a,b) distribution, prior distribution of the variance $\sigma_l^2$
hyperlamb	Hyperparameters of a gamma(a,b) distribution, prior distribution of the shrinkage parameter $\lambda_l$
seed	Random number are generated with seed=1 during the MCMC algorithm

## Details

The function will return two R objects, which can be assigned to a variable. To see the results, use the "\$" operator.

## Value

PostProbGrp	Marginal posterior probabilities of the group selection indicators, $Prob(\gamma_{lk} = 1)$
BetaSample	An MCMC sample of the regression effects $\beta_{lk}$

## References

Thierry Chekouo et al (2020), *A Bayesian Group Selection approach for the analysis of volumetric images of brain cancers and their genomic determinants*, submitted.

## See Also

[SimulateData](#)

## Examples

```
library(oBGSelComp)
## overlap groups (10 percent overlap)
dat=SimulateData(n=100,betaAbs=1,sig=.1,r2=0.5,propOverl=10,seed=1)
Res=oBGSelCompAlgo(outcome=dat$y,X=dat$X,Pathway=dat$Pathway,sample=10000,
burnin=1000,hyperprob=c(1,1),hypersig=c(4,0.01),hyperlamb=c(5,2), seed=1)
str(Res)
library(AUC)
q=4
AUC1=rep(0,q)
```

```

for (l in 1:q){
  AUC1[l]= auc(roc(Res$PostProbGrp[l,],as.factor(dat$GamKnown[l,])))
}
AUC1

```

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SimulateData

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*Generation of simulated data as explained in the reference manuscript.*


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## Description

This function generates compositional response and covariate data as described in the manuscript (see Section 5.2 in the manuscript).

## Usage

```
SimulateData(n=100,betaAbs=1,sig=.1,r2=0.5,propOverl=0,seed=1)
```

## Arguments

n	The number of subjects/samples
betaAbs	Effect values in absolute values of important features
sig	Value of the variance of latent values $\alpha$ 's given the feature set
r2	Variance value that represents correlation of features within pathways
propOverl	Proportion of overlap between "consecutive" groups. It can only take three values; 0, 10 and 50
seed	Seed to generate random numbers

## Details

The function will return three data matrices  $y$ ,  $X$ , Pathway and GamKnown which are respectively the compositional response data, the covariate matrix, the Pathway matrix indicator and the true gamma ( $\gamma(l,k)=1$  if pathway  $k$  is important for outcome  $l$ , and 0 otherwise)

## References

Thierry Chekouo et al (2020), *A Bayesian Group Selection approach for the analysis of volumetric images of brain cancers and their genomic determinants*, submitted.

## Examples

```

dat=SimulateData(n=100,betaAbs=1,sig=.1,r2=0.5,propOverl=0,seed=1)
str(dat)

```

# Index

oBGSelCompAlgo, [1](#)

SimulateData, [2](#), [3](#)