Package ‘bayesImageS’

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Type Package

Title Bayesian Methods for Image Segmentation using a Potts Model

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Description Various algorithms for segmentation of 2D and 3D images, such as computed tomography and satellite remote sensing. This package implements Bayesian image analysis using the hidden Potts model with external field prior of Moores et al. (2015) <doi:10.1016/j.csda.2014.12.001>. Latent labels are sampled using chequerboard updating or Swendsen-Wang. Algorithms for the smoothing parameter include pseudolikelihood, path sampling, the exchange algorithm, approximate Bayesian computation (ABC-MCMC and ABC-SMC), and the parametric functional approximate Bayesian (PFAB) algorithm. Refer to <doi:10.1007/s11222-014-9525-6> and <doi:10.1214/18-BA1130> for further details.

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https://mooresm.github.io/bayesImageS/

BugReports https://bitbucket.org/Azeari/bayesimages/issues

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Description

Bayesian methods for segmentation of 2D and 3D images, such as computed tomography and satellite remote sensing. This package implements image analysis using the hidden Potts model with external field prior. Latent labels are sampled using checkerboard updating or Swendsen-Wang. Algorithms for the smoothing parameter include pseudolikelihood, path sampling, the exchange algorithm, and approximate Bayesian computation (ABC-MCMC and ABC-SMC).

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References


**See Also**

vignette(package="bayesImageS")

---

**exactPotts**

*Calculate the distribution of the Potts model using a brute force algorithm.*

**Description**

**Warning:** this algorithm is $O(k^n)$ and therefore will not scale for $k^n > 2^{31} - 1$

**Usage**

```
exactPotts(neighbors, blocks, k, beta)
```

**Arguments**

- `neighbors` A matrix of all neighbours in the lattice, one row per pixel.
- `blocks` A list of pixel indices, dividing the lattice into independent blocks.
- `k` The number of unique labels.
- `beta` The inverse temperature parameter of the Potts model.

**Value**

A list containing the following elements:

- `expectation` The exact mean of the sufficient statistic.
- `variance` The exact variance of the sufficient statistic.
- `exp_PL` Pseudo-likelihood (PL) approximation of the expectation of $S(z)$.
- `var_PL` PL approx. of the variance of the sufficient statistic.
getBlocks 

Get Blocks of a Graph

Description
Obtain blocks of vertices of a 1D, 2D, or 3D graph, in order to use the conditional independence to speed up the simulation (chequerboard idea).

Usage
getBlocks(mask, nblock)

Arguments
mask a vector, matrix, or 3D array specifying vertices of a graph. Vertices of value 1 are within the graph and 0 are not.
nblock a scalar specifying the number of blocks. For a 2D graph nblock could be either 2 or 4, and for a 3D graph nblock could be either 2 or 8.

Details
The vertices within each block are mutually independent given the vertices in other blocks. Some blocks could be empty.

Value
A list with the number of components equal to nblock. Each component consists of vertices within the same block.

References

Examples
#Example 1: split a line into 2 blocks
getBlocks(mask=c(1,1,1,1,0,0,1,1,0), nblock=2)

#Example 2: split a 4x4 2D graph into 4 blocks in order
# to use the chequerboard idea for a neighbourhood structure
# corresponding to the second-order Markov random field.
getBlocks(mask=matrix(1, nrow=4, ncol=4), nblock=4)

#Example 3: split a 3x3x3 3D graph into 8 blocks
# in order to use the chequerboard idea for a neighbourhood
# structure based on the 18 neighbors definition, where the
# neighbors of a vertex comprise its available
getEdges

# adjacencies sharing the same edges or faces.
mask <- array(1, dim=rep(3,3))
getBlocks(mask, nblock=8)

---

getEdges

Get Edges of a Graph

Description

Obtain edges of a 1D, 2D, or 3D graph based on the neighbourhood structure.

Usage

getEdges(mask, neiStruc)

Arguments

- `mask`: a vector, matrix, or 3D array specifying vertices of a graph. Vertices of value 1 are within the graph and 0 are not.
- `neiStruc`: a scalar, vector of four components, or $3 \times 4$ matrix corresponding to 1D, 2D, or 3D graphs. It specifies the neighbourhood structure. See `getNeighbors` for details.

Details

There could be more than one way to define the same 3D neighbourhood structure for a graph (see Example 4 for illustration).

Value

A matrix of two columns with one edge per row. The edges connecting vertices and their corresponding first neighbours are listed first, and then those corresponding to the second neighbours, and so on and so forth. The order of neighbours is the same as in `getNeighbors`.

References


Examples

#Example 1: get all edges of a 1D graph.
mask <- c(0,0,rep(1,4),0,1,1,0,0)
getEdges(mask, neiStruc=2)

#Example 2: get all edges of a 2D graph based on neighbourhood structure
# corresponding to the first-order Markov random field.
mask <- matrix(1, nrow=2, ncol=3)
getEdges(mask, neiStruc=c(2,2,0,0))

#Example 3: get all edges of a 2D graph based on neighbourhood structure
# corresponding to the second-order Markov random field.
mask <- matrix(1, nrow=3, ncol=3)
getEdges(mask, neiStruc=c(2,2,2,2))

#Example 4: get all edges of a 3D graph based on 6 neighbours structure
# where the neighbours of a vertex comprise its available
# N,S,E,W, upper and lower adjacencies. To achieve it, there
# are several ways, including the two below.
mask <- array(1, dim=rep(3,3))
n61 <- matrix(c(2,2,0,0,
               0,2,0,0,
               0,0,0,0), nrow=3, byrow=TRUE)
n62 <- matrix(c(2,0,0,0,
               0,2,0,0,
               2,0,0,0), nrow=3, byrow=TRUE)
e1 <- getEdges(mask, neiStruc=n61)
e2 <- getEdges(mask, neiStruc=n62)
e1 <- e1[order(e1[,1], e1[,2]),]
e2 <- e2[order(e2[,1], e2[,2]),]
all(e1==e2)

#Example 5: get all edges of a 3D graph based on 18 neighbours structure
# where the neighbours of a vertex comprise its available
# adjacencies sharing the same edges or faces.
# To achieve it, there are several ways, including the one below.
n18 <- matrix(c(2,2,2,2,
               0,2,2,2,
               0,0,2,2), nrow=3, byrow=TRUE)
mask <- array(1, dim=rep(3,3))
getEdges(mask, neiStruc=n18)

getNeighbors

Get Neighbours of All Vertices of a Graph

Description

Obtain neighbours of vertices of a 1D, 2D, or 3D graph.
getNeighbors

Usage

getNeighbors(mask, neiStruc)

Arguments

mask a vector, matrix, or 3D array specifying vertices within a graph. Vertices of value 1 are within the graph and 0 are not.

neiStruc a scalar, vector of four components, or 3 \times 4 matrix corresponding to 1D, 2D, or 3D graphs. It gives the definition of neighbours of a graph. All components of neiStruc should be positive (\geq 0) even numbers. For 1D graphs, neiStruc gives the number of neighbours of each vertex. For 2D graphs, neiStruc[1] specifies the number of neighbours on vertical direction, neiStruc[2] horizontal direction, neiStruc[3] north-west (NW) to south-east (SE) diagonal direction, and neiStruc[4] south-west (SW) to north-east (NE) diagonal direction. For 3D graphs, the first row of neiStruc specifies the number of neighbours on vertical direction, horizontal direction and two diagonal directions from the 1-2 perspective, the second row the 1-3 perspective, and the third row the 2-3 perspective. The index to perspectives is represented with the leftmost subscript of the array being the smallest.

Details

There could be more than one way to define the same 3D neighbourhood structure for a graph (see Example 3 for illustration).

Value

A matrix with each row giving the neighbours of a vertex. The number of the rows is equal to the number of vertices within the graph and the number or columns is the number of neighbours of each vertex.

For a 1D graph, if each vertex has two neighbours, The first column are the neighbours on the left-hand side of corresponding vertices and the second column the right-hand side. For the vertices on boundaries, missing neighbours are represented by the number of vertices within a graph plus 1. When neiStruc is bigger than 2, The first two columns are the same as when neiStruc is equal to 2; the third column are the neighbours on the left-hand side of the vertices on the first column; the forth column are the neighbours on the right-hand side of the vertices on the second column, and so on and so forth. And again for the vertices on boundaries, their missing neighbours are represented by the number of vertices within a graph plus 1.

For a 2D graph, the index to vertices is column-wised. For each vertex, the order of neighbours are as follows. First are those on the vertical direction, second the horizontal direction, third the NW to SE diagonal direction, and forth the SW to NE diagonal direction. For each direction, the neighbours of every vertex are arranged in the same way as in a 1D graph.

For a 3D graph, the index to vertices is that the leftmost subscript of the array moves the fastest. For each vertex, the neighbours from the 1-2 perspective appear first and then the 1-3 perspective and finally the 2-3 perspective. For each perspective, the neighbours are arranged in the same way as in a 2D graph.
References


Examples

#Example 1: get all neighbours of a 1D graph.
mask <- c(0,0,rep(1,4),0,1,0,0,1,1,1)
getNeighbors(mask, neiStruct=2)

#Example 2: get all neighbours of a 2D graph based on neighbourhood structure
# corresponding to the second-order Markov random field.
mask <- matrix(1, nrow=2, ncol=3)
getNeighbors(mask, neiStruct=c(2,2,2,2))

#Example 3: get all neighbours of a 3D graph based on 6 neighbours structure
# where the neighbours of a vertex comprise its available
# N,S,E,W, upper and lower adjacencies. To achieve it, there
# are several ways, including the two below.
mask <- array(1, dim=rep(3,3))
n61 <- matrix(c(2,2,0,0,
0,2,0,0,
0,0,0,0), nrow=3, byrow=TRUE)
n62 <- matrix(c(2,0,0,0,
0,2,0,0,
2,0,0,0), nrow=3, byrow=TRUE)
n1 <- getNeighbors(mask, neiStruct=n61)
n2 <- getNeighbors(mask, neiStruct=n62)
n1 <- apply(n1, 1, sort)
n2 <- apply(n2, 1, sort)
all(n1==n2)

#Example 4: get all neighbours of a 3D graph based on 18 neighbours structure
# where the neighbours of a vertex comprise its available
# adjacencies sharing the same edges or faces.
# To achieve it, there are several ways, including the one below.

n18 <- matrix(c(2,2,2,2,
0,2,2,2,
0,0,2,2), nrow=3, byrow=TRUE)
mask <- array(1, dim=rep(3,3))
getNeighbors(mask, neiStruct=n18)

---

gibbsGMM

Fit a mixture of Gaussians to the observed data.
**gibbsNorm**

**Description**
Fit a mixture of Gaussians to the observed data.

**Usage**
```
gibbsGMM(y, niter = 1000, nburn = 500, priors = NULL)
```

**Arguments**
- `y`: A vector of observed pixel data.
- `niter`: The number of iterations of the algorithm to perform.
- `nburn`: The number of iterations to discard as burn-in.
- `priors`: A list of priors for the parameters of the model.

**Value**
A matrix containing MCMC samples for the parameters of the mixture model.

**Examples**
```
y <- rnorm(100, mean=5, sd=2)
res.norm <- gibbsNorm(y, priors=list(mu=0, mu.sd=1e6, sigma=1e-3, sigma.nu=1e-3))
summary(res.norm$mu[501:1000])
summary(res.norm$sigma[501:1000])
```

**gibbsNorm**

*Fit a univariate normal (Gaussian) distribution to the observed data.*

**Description**
Fit a univariate normal (Gaussian) distribution to the observed data.

**Usage**
```
gibbsNorm(y, niter = 1000, priors = NULL)
```

**Arguments**
- `y`: A vector of observed pixel data.
- `niter`: The number of iterations of the algorithm to perform.
- `priors`: A list of priors for the parameters of the model.

**Value**
A list containing MCMC samples for the mean and standard deviation.

**Examples**
```
y <- rnorm(100, mean=5, sd=2)
res.norm <- gibbsNorm(y, priors=list(mu=0, mu.sd=1e6, sigma=1e-3, sigma.nu=1e-3))
summary(res.norm$mu[501:1000])
summary(res.norm$sigma[501:1000])
```
initSedki

Initialize the ABC algorithm using the method of Sedki et al. (2013)

Description

Initialize the ABC algorithm using the method of Sedki et al. (2013)

Usage

initSedki(y, neighbors, blocks, param = list(npart = 10000),
  priors = NULL)

Arguments

y A vector of observed pixel data.
neighbors A matrix of all neighbours in the lattice, one row per pixel.
blocks A list of pixel indices, dividing the lattice into independent blocks.
param A list of options for the ABC-SMC algorithm.
priors A list of priors for the parameters of the model.

Value

A matrix containing SMC samples for the parameters of the Potts model.

References


mcmcpotts

Fit the hidden Potts model using a Markov chain Monte Carlo algorithm.

Description

Fit the hidden Potts model using a Markov chain Monte Carlo algorithm.

Usage

mcmcpotts(y, neighbors, blocks, priors, mh, niter = 55000,
  nburn = 5000, truth = NULL)
Arguments

- **y**: A vector of observed pixel data.
- **neighbors**: A matrix of all neighbors in the lattice, one row per pixel.
- **blocks**: A list of pixel indices, dividing the lattice into independent blocks.
- **priors**: A list of priors for the parameters of the model.
- **mh**: A list of options for the Metropolis-Hastings algorithm.
- **niter**: The number of iterations of the algorithm to perform.
- **nburn**: The number of iterations to discard as burn-in.
- **truth**: A matrix containing the ground truth for the pixel labels.

Value

A matrix containing MCMC samples for the parameters of the Potts model.

Description

Simulate pixel labels using chequerboard Gibbs sampling.

Usage

```r
mcmcpottsnodata(beta, k, neighbors, blocks, niter = 1000, random = TRUE)
```

Arguments

- **beta**: The inverse temperature parameter of the Potts model.
- **k**: The number of unique labels.
- **neighbors**: A matrix of all neighbors in the lattice, one row per pixel.
- **blocks**: A list of pixel indices, dividing the lattice into independent blocks.
- **niter**: The number of iterations of the algorithm to perform.
- **random**: Whether to initialize the labels using random or deterministic starting values.

Value

A list containing the following elements:

- **alloc**: An n by k matrix containing the number of times that pixel i was allocated to label j.
- **z**: An (n+1) by k matrix containing the final sample from the Potts model after niter iterations of chequerboard Gibbs.
- **sum**: An niter by 1 matrix containing the sum of like neighbors, i.e. the sufficient statistic of the Potts model, at each iteration.
Examples

# Swendsen-Wang for a 2x2 lattice
neigh <- matrix(c(5,2,5,3, 1,5,5,4, 5,4,1,5, 3,5,2,5), nrow=4, ncol=4, byrow=TRUE)
blocks <- list(c(1,4), c(2,3))
res.Gibbs <- mcmcpottsNoData(0.7, 3, neigh, blocks, niter=200)
res.Gibbs$z
res.Gibbs$sum[200]

---

**Simulation from the Potts model using single-site Gibbs updates.**

---

**Description**

100 iterations of Gibbs sampling for a 500 × 500 lattice with \( \beta = 0.22 \) and \( k = 2 \).

**Usage**

res

**Format**

A list containing 7 variables.

**See Also**

mcmcpotts

---

**Simulation from the Potts model using single-site Gibbs updates.**

---

**Description**

100 iterations of Gibbs sampling for a 500 × 500 lattice with \( \beta = 0.44 \) and \( k = 2 \).

**Usage**

res2

**Format**

A list containing 7 variables.

**See Also**

mcmcpotts
Simulation from the Potts model using single-site Gibbs updates.

Description
100 iterations of Gibbs sampling for a $500 \times 500$ lattice with $\beta = 0.88$ and $k = 2$.

Usage
res3

Format
A list containing 7 variables.

See Also
mcmcPotts

Simulation from the Potts model using single-site Gibbs updates.

Description
100 iterations of Gibbs sampling for a $500 \times 500$ lattice with $\beta = 1.32$ and $k = 2$.

Usage
res4

Format
A list containing 7 variables.

See Also
mcmcPotts
Simulation from the Potts model using single-site Gibbs updates.

Description
5000 iterations of Gibbs sampling for a 500 × 500 lattice with \( \beta = 1.32 \) and \( k = 2 \).

Usage
res5

Format
A list containing 4 variables.

See Also
mcmcpottsnodata

smcPotts
Fit the hidden Potts model using approximate Bayesian computation with sequential Monte Carlo (ABC-SMC).

Description
Fit the hidden Potts model using approximate Bayesian computation with sequential Monte Carlo (ABC-SMC).

Usage
smcPotts(y, neighbors, blocks, param = list(npart = 10000, nstat = 50),
          priors = NULL)

Arguments

y
A vector of observed pixel data.

neighbors
A matrix of all neighbors in the lattice, one row per pixel.

blocks
A list of pixel indices, dividing the lattice into independent blocks.

param
A list of options for the ABC-SMC algorithm.

priors
A list of priors for the parameters of the model.

Value
A matrix containing SMC samples for the parameters of the Potts model.
**sufficientStat**

*Calculate the sufficient statistic of the Potts model for the given labels.*

**Description**

Calculate the sufficient statistic of the Potts model for the given labels.

**Usage**

`sufficientStat(labels, neighbors, blocks, k)`

**Arguments**

- `labels`: A matrix of pixel labels.
- `neighbors`: A matrix of all neighbors in the lattice, one row per pixel.
- `blocks`: A list of pixel indices, dividing the lattice into independent blocks.
- `k`: The number of unique labels.

**Value**

The sum of like neighbors.

**swNoData**

*Simulate pixel labels using the Swendsen-Wang algorithm.*

**Description**

The algorithm of Swendsen & Wang (1987) forms clusters of neighbouring pixels, then updates all of the labels within a cluster to the same value. When simulating from the prior, such as a Potts model without an external field, this algorithm is very efficient.

**Usage**

`swNoData(beta, k, neighbors, blocks, niter = 1000, random = TRUE)`

**Arguments**

- `beta`: The inverse temperature parameter of the Potts model.
- `k`: The number of unique labels.
- `neighbors`: A matrix of all neighbors in the lattice, one row per pixel.
- `blocks`: A list of pixel indices, dividing the lattice into independent blocks.
- `niter`: The number of iterations of the algorithm to perform.
- `random`: Whether to initialize the labels using random or deterministic starting values.
Value

A list containing the following elements:

alloc  An n by k matrix containing the number of times that pixel i was allocated to label j.

z  An (n+1) by k matrix containing the final sample from the Potts model after niter iterations of Swendsen-Wang.

sum  An niter by 1 matrix containing the sum of like neighbors, i.e. the sufficient statistic of the Potts model, at each iteration.

References


Examples

```r
# Swendsen-Wang for a 2x2 lattice
neigh <- matrix(c(5,2,5,3, 1,5,5,4, 5,4,1,5, 3,5,2,5), nrow=4, ncol=4, byrow=TRUE)
blocks <- list(c(1,4), c(2,3))
res.sw <- swNoData(0.7, 3, neigh, blocks, niter=200)
res.sw$z
res.sw$sum[200]
```

synth  Simulation from the Potts model using Swendsen-Wang.

Description

Simulations for a 500 × 500 lattice for fixed values of the inverse temperature parameter, β.

Usage

synth

Format

A list containing 5 variables:

- 0.22 simulations for β = 0.22
- 0.44 simulations for β = 0.44
- 0.88 simulations for β = 0.88
- 1.32 simulations for β = 1.32
- tm time taken by the simulations

See Also

swNoData
TestResample

Test the residual resampling algorithm.

Description

Test the residual resampling algorithm.

Usage

testResample(values, weights, pseudo)

Arguments

values A vector of SMC particles.
weights A vector of importance weights for each particle.
pseudo A matrix of pseudo-data for each particle.

Value

A list containing the following elements:

beta A vector of resampled particles.
wtx The new importance weights, after resampling.
pseudo A matrix of pseudo-data for each particle.
idx The indices of the parents of the resampled particles.

References

Index

*Topic datasets
  res, 12
  res2, 12
  res3, 13
  res4, 13
  res5, 14
  synth, 16
*Topic spatial
  getBlocks, 4
  getEdges, 5
  getNeighbors, 6
bayesImageS, 2
bayesImageS-package (bayesImageS), 2
exactPotts, 3
getBlocks, 4
getEdges, 5
getNeighbors, 6
gibbsGMM, 8
gibbsNorm, 9
initSedki, 10
mcmcPotts, 10, 12, 13
mcmcPottsNoData, 11, 14
res, 12
res2, 12
res3, 13
res4, 13
res5, 14
smcPotts, 14
sufficientStat, 15
swNoData, 15, 16
synth, 16
testResample, 17