

# Package ‘BLSM’

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**Title** Bayesian Latent Space Model

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**Description** Provides a Bayesian latent space model for complex networks, either weighted or unweighted. Given an observed input graph, the estimates for the latent coordinates of the nodes are obtained through a Bayesian MCMC algorithm. The overall likelihood of the graph depends on a fundamental probability equation, which is defined so that ties are more likely to exist between nodes whose latent space coordinates are close. The package is mainly based on the model by Hoff, Raftery and Handcock (2002) <[doi:10.1198/016214502388618906](https://doi.org/10.1198/016214502388618906)> and contains some extra features (e.g., removal of the Procrustean step, weights implemented as coefficients of the latent distances, 3D plots).

The original code related to the above model was retrieved from <[https://www.stat.washington.edu/people/pdhoff/Code/hoff\\_raftery\\_handcock\\_2002\\_jasa/](https://www.stat.washington.edu/people/pdhoff/Code/hoff_raftery_handcock_2002_jasa/)>.

Users can inspect the MCMC simulation, create and customize insightful graphical representations or apply clustering techniques.

**Depends** R (>= 3.3.0)

**Imports** Rcpp (>= 0.12.4)

**Suggests** rgl (>= 0.98.1)

**LinkingTo** Rcpp, RcppEigen

**License** GPL (>= 2)

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alpha_up	<i>Update step for the <math>\alpha</math> variable</i>
----------	---

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### Description

Accept/reject the proposal for the  $\alpha$  model variable

### Usage

alpha\_up(Y, lpz, W, alpha, adelta, a\_a, a\_b)

### Arguments

Y	Adjacency matrix of the observed network
lpz	Matrix containing the negative square root of the Euclidean distances between latent positions
W	BLSM Weights matrix of the observed network
alpha	Model variable $\alpha$
adelta	The uniform proposal for $\alpha$ is defined on the $[-adelta, +adelta]$ interval
a_a	Shape parameter of the Gamma prior distribution for $\alpha$ . The value is usually set to 1, so the prior is actually an exponential distribution.
a_b	Rate parameter of the Gamma prior distribution for $\alpha$ .

### Value

Updated value of the  $\alpha$  variable

## Description

R package allowing the computation of a Bayesian Latent Space Model for complex networks.

Latent Space Models are characterized by the presence of unobservable variables (latent coordinates) that are used to compute the likelihood of the observed networks. Their goal is to map the observed network in the latent space by meeting specific probabilistic requirements, so that the estimated latent coordinates can then be used to describe and characterize the original graph.

In the BLSM package framework, given a network characterized by its adjacency  $Y$  matrix, the model assigns a binary random variable to each tie:  $Y_{ij}$  is related to the tie between nodes  $i$  and  $j$  and its value is 1 if the tie exists, 0 otherwise.

The model assumes the independence of  $Y_{ij}|x_i, x_j, \alpha$ , where  $x_i$  and  $x_j$  are the coordinates of the nodes in the multidimensional latent space and  $\alpha$  is an additional parameter such that  $\text{logit}(P(Y_{ij} = 1)) = \alpha - \|x_i - x_j\|$ .

The latent space coordinates are estimated by following a MCMC procedure that is based on the overall likelihood induced by the above equation.

Due to the symmetry of the distance, the model leads to more intuitive outputs for undirected networks, but the functions can also deal with directed graphs.

If the network is weighted, i.e. to each tie is associated a positive coefficient, the model's probability equation becomes  $\text{logit}(P(Y_{ij} = 1)) = \alpha - W_{ij}\|x_i - x_j\|$ , where  $W_{ij}$  denotes the weight related to link existing between  $x_i$  and  $x_j$ . This means that even non existing links should have a weight, therefore the matrix used in the computation isn't the original weights matrix but actually a specific "BLSM weights" matrix that contains positive coefficients for all the possible pairs of nodes. When dealing with weighted networks, please be careful to pass a "BLSM weights" matrix as input # (please refer to [example\\_weights\\_matrix](#) for more detailed information and a valid example).

The output of the model allows the user to inspect the MCMC simulation, create insightful graphical representations or apply clustering techniques to better describe the latent space. See [estimate\\_latent\\_positions](#) or [plot\\_latent\\_positions](#) for further information.

## References

P. D. Hoff, A. E. Raftery, M. S. Handcock, Latent Space Approaches to Social Network Analysis, Journal of the American Statistical Association, Vol. 97, No. 460, (2002), pp. 1090-1098.

A. Donizetti, A Latent Space Model Approach for Clustering Complex Network Data, Master's Thesis, Politecnico di Milano, (2017).

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dst	<i>Geodesic distance</i>
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### Description

Evaluate geodesic distance (shortest path) between all pairs of nodes in the network.

### Usage

```
dst(M)
```

### Arguments

M	Input adjacency matrix
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### Value

Matrix containing all the pairwise geodesic distances

### Examples

```
dst(example_adjacency_matrix)
```

---

estimate_latent_positions	<i>BLSM simulation</i>
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### Description

Core function of the BLSM package: run a simulation to obtain the positions of the network nodes in the latent space for each sampled iteration.

The positions are simulated accordingly to the model assumptions, please refer to [BLSM](#) for further information. The output of the function can be used to retrieve and compare specific iterations, observe their evolution or simply compute the average positions (more details in the descriptions and examples below).

### Usage

```
estimate_latent_positions(Y, W, procrustean = TRUE, k = 2, alpha = 2,
  nscan = 8 * 10^5, burn_in = 5 * 10^5, odens = 10^3, zdelta = 1,
  z_norm_prior_mu = 0, z_norm_prior_sd = 10, adelta = 0.3,
  a_exp_prior_a = 1, a_exp_prior_b = 1, dynamic_plot = FALSE,
  dynamic_circles = FALSE, ...)
```

**Arguments**

Y	Adjacency matrix of the network
W	(Optional) BLSM Weight matrix of the network
procrustean	Boolean to include/exclude (TRUE/FALSE) the Procrustean Transform step in the algorithm. Set TRUE by default.
k	Space dimensionality
alpha	Starting value of the $\alpha$ variable
nscan	Number of iterations
burn_in	Burn-in value (starting iterations to be discarded)
odens	Thinning: only 1 iteration every odens will be sampled and stored in the output
zdelta	Standard deviation of the Gaussian proposal for latent positions
z_norm_prior_mu	Mean of the Gaussian prior distribution for latent positions
z_norm_prior_sd	Standard deviation of the Gaussian prior distribution for latent positions
adelta	The uniform proposal for $\alpha$ is defined on the $[-adelta, +adelta]$ interval
a_exp_prior_a	Shape parameter of the Gamma prior distribution for $\alpha$ . As the value is usually set to 1 the prior is an exponential distribution.
a_exp_prior_b	Rate parameter of the Gamma prior distribution for $\alpha$ .
dynamic_plot	Boolean to plot dynamically the simulated positions (one update every odens iterations)
dynamic_circles	Boolean to add circles of radius $\alpha$ to the dynamic plots
...	Additional parameters that can be passed to <a href="#">plot_latent_positions</a>

**Value**

Returns a "BLSM object" (blsm\_obj), i.e. a list containing:

- Alpha  $\alpha$  values from the sampled iterations
- Likelihood Log-likelihood values from the sampled iterations
- Iterations Latent space coordinates from the sampled iterations. Latent positions are stored in a 3D array whose dimensions are given by (1: number of nodes, 2: space dimensionality, 3: number of iterations). In the non-Procrustean framework the latent distances are given instead of the positions: another 3D array is returned, whose dimensions are given by (1: number of nodes, 2: number of nodes, 3: number of iterations). The command needed in order to get the average values over the iterations for either the positions or the distances is `rowMeans(blsm_obj$Iterations, dims=2)` (see example below).
- StartingPositions Latent space coordinates right after the initialization step. In the non-Procrustean framework starting distances are given instead.
- Matrix Original matrices of the network (adjacency and BLSM weights)
- Parameters List of parameters specified during the call to [estimate\\_latent\\_positions](#)

## Examples

```
## Not run:
# Procrustean version followed by clustering
blsm_obj = estimate_latent_positions(example_adjacency_matrix,
                                   burn_in = 3*10^4, nscan = 10^5, dynamic_plot = TRUE)

avg_latent_positions = rowMeans(blsm_obj$Iterations, dims=2)
h_cl = hclust(dist(avg_latent_positions), method="complete")
n = 3
latent_space_clusters = cutree(h_cl, k=n)
print(latent_space_clusters)
plot(avg_latent_positions, col=rainbow(n)[latent_space_clusters], pch=20)

# Non-Procrustean version followed by clustering
blsm_obj_2 = estimate_latent_positions(example_adjacency_matrix, procrustean=FALSE,
                                     burn_in = 3*10^4, nscan = 10^5)
avg_latent_distances = rowMeans(blsm_obj_2$Iterations, dims=2)
h_cl = hclust(as.dist(avg_latent_distances), method="complete")
n = 3
latent_space_clusters_2 = cutree(h_cl, k=n)
print(latent_space_clusters_2)

# Weighted network
blsm_obj_3 = estimate_latent_positions(example_adjacency_matrix, example_weights_matrix,
                                     burn_in = 10^5, nscan = 2*10^5, dynamic_plot = TRUE)

## End(Not run)
```

---

example\_adjacency\_matrix

*Example Adjacency Matrix*

---

## Description

Adjacency matrix of a 10 nodes random network for testing purposes

## Usage

```
example_adjacency_matrix
```

## Format

A binary adjacency matrix representing links between nodes.

---

example\_blsm\_obj      *Example BLSM object*

---

### Description

BLSM object obtained by applying the Procrustean version of the latent space model to the unweighted network whose adjacency matrix is [example\\_adjacency\\_matrix](#). Further details concerning the simulation are contained in the BLSM object itself.

### Usage

```
example_blsm_obj
```

### Format

BLSM object (blsm\_obj), i.e. a list containing:

- Alpha  $\alpha$  values from the sampled iterations
- Likelihood Log-likelihood values from the sampled iterations
- Iterations Latent space coordinates from the sampled iterations. Latent positions are stored in a 3D array whose dimensions are given by (1: number of nodes, 2: space dimensionality, 3: number of iterations). In the non-Procrustean framework the latent distances are given instead of the positions: another 3D array is returned, whose dimensions are given by (1: number of nodes, 2: number of nodes, 3: number of iterations). The command needed in order to get the average values over the iterations for either the positions or the distances is `rowMeans(blsm_obj$Iterations, dims=2)` (see example below).
- StartingPositions Latent space coordinates right after the initialization step. In the non-Procrustean framework starting distances are given instead.
- Matrix Original matrices of the network (adjacency and BLSM weights)
- Parameters List of parameters specified during the call to [estimate\\_latent\\_positions](#)

---

example\_weights\_matrix  
*Example Weights Matrix*

---

### Description

"BLSM weights" matrix of a 10 nodes random network for testing purposes

### Usage

```
example_weights_matrix
```

**Format**

A matrix containing positive weights for all pairs of nodes.

Given a couple of nodes, a weight expresses the importance of the distance between the coordinates associated to the two nodes in the latent space in terms of the overall likelihood of the graph. For this reason, even missing links must have a coefficient, otherwise the relative positioning of disconnected nodes would have no effect at all on the graph likelihood.

The exact probability equation is described in [BLSM](#), as well as the notation used.

A few examples:

- for unweighted networks, the "BLSM weights" matrix has all the values set to 1.
- if two nodes share a strong connection, then the weight coefficient should be greater than 1 so that their positions in the latent space will be closer than they would be in an unweighted framework.
- if two nodes share a weak connection, a coefficient smaller than 1 will allow the latent coordinates to be pretty far from each other even though the nodes are connected.

---

 lpY

*Network log-likelihood*


---

**Description**

Compute the log-likelihood of the whole observed network based on the latent positions estimates and the model assumptions. See [BLSM](#) for more information.

**Usage**

```
lpY(Y, lpz, alpha, W)
```

**Arguments**

Y	Adjacency matrix of the observed network
lpz	Matrix containing the negative square root of the Euclidean distances between latent positions (output of <a href="#">lpz_dist</a> )
alpha	Model variable $\alpha$
W	BLSM Weights matrix of the observed network

**Value**

Log-likelihood of the observed network



---

lpYNODE                      *Network log-likelihood for individual updates*

---

### Description

Compute the log-likelihood of the whole observed network based on the latent positions estimates and the model assumptions. The function follows almost the same approach as [lpY](#), but it is more suitable for the individual updates occurring during the simulation.

### Usage

```
lpYNODE(Y, Z, alpha, node, diag, W)
```

### Arguments

Y	Adjacency matrix of the observed network
Z	Latent positions matrix
alpha	Model variable $\alpha$
node	Specific node in the network corresponding to the latent coordinate which will be used as reference
diag	Diagonal from $t(Z) \% \% Z$ matrix, passed to speed up the process.
W	BLSM Weights matrix of the observed network

### Value

Log-likelihood of the observed network

---

lpz\_dist                      *Distance between latent positions*

---

### Description

Compute the square root of the Euclidean distances between latent positions and return them with a negative sign.

### Usage

```
lpz_dist(Z)
```

### Arguments

Z	Latent positions matrix. The matrix size must be $(n, k)$ , where $n$ and $k$ denote respectively the number of nodes in the network and the latent space dimensionality.
---	---

**Value**

Matrix containing the negative square root of the Euclidean distances between latent positions

**Examples**

```
pos = matrix(rnorm(20), ncol=2)
lpz_dist(pos)
```

---

lpz_distNODE	<i>lpz_dist optimized for individual updates</i>
--------------	--

---

**Description**

Compute the square root of the Euclidean distances between a specific coordinate in the latent space and all the others. The function follows almost the same approach as [lpz\\_dist](#), but it is more suitable for the individual updates occurring during the simulation.

**Usage**

```
lpz_distNODE(Z, node, diag)
```

**Arguments**

Z	Latent positions matrix
node	Specific node in the network corresponding to the latent coordinate which will be used as reference
diag	Diagonal from $t(Z) \%* \% Z$ matrix, passed to speed up the process.

**Value**

Vector containing the negative square root of the Euclidean distances between latent positions

---

mlpY	<i>Network (positive) log-likelihood</i>
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---

**Description**

Compute the (positive) log-likelihood of the whole observed network based on the latent positions estimates and the model assumptions. The inputs are slightly different from those of [lpY](#), so the function basically applies some preprocessing before calling [lpY](#) and returning its value with the opposite sign.

**Usage**

```
mlpY(avZ, Y, W)
```

**Arguments**

avZ	Vector containing the $\alpha$ value and the latent positions
Y	Adjacency matrix of the observed network
W	BLSM Weights matrix of the observed network

**Value**

Log-likelihood of the observed network

---

plot\_latent\_positions *Base BLSM plot function*

---

**Description**

Plot latent positions from a Procrustean simulation.

**Usage**

```
plot_latent_positions(blsm_obj, colors, points_size = 0.1,
  labels_point_size = 5, labels_point_color = "yellow",
  labels_text_size = 1, labels_text_color = "blue", circles_2D = FALSE)
```

**Arguments**

blsm_obj	BLSM object obtained through <a href="#">estimate_latent_positions</a>
colors	(Optional) Colors of the simulated coordinate points in the latent space. Internal default colors are used if the argument is missing.
points_size	Size of the coordinate points
labels_point_size	Size of the label points
labels_point_color	Color of the label points
labels_text_size	Text size in the label points
labels_text_color	Text color in the label points
circles_2D	Plot circles of radius $\alpha$ (see the model's main variables) centered around the label points

**Examples**

```
plot_latent_positions(example_blsm_obj, labels_point_color = "black", labels_text_color = "black")

plot_latent_positions(example_blsm_obj, circles_2D = TRUE)
```

---

plot\_traceplots\_acf     *BLSM traceplots and ACF*

---

### Description

Traceplots and autocorrelation functions for the  $\alpha$  variable and a selected node (or pair of nodes in the non-Procrustean framework).

### Usage

```
plot_traceplots_acf(blsm_obj, chosen_node = 1, coordinate = 1,
  chosen_pair = c(1, 2))
```

### Arguments

blsm_obj	BLSM object obtained through <a href="#">estimate_latent_positions</a>
chosen_node	Specified node for traceplot and autocorrelation function (Procrustean framework)
coordinate	Specified coordinate dimension from the n-dimensional latent space
chosen_pair	Specified pair of nodes for traceplot and autocorrelation function (non-Procrustean framework)

### Examples

```
plot_traceplots_acf(example_blsm_obj, chosen_node=3, coordinate=1)

## Not run:
# Run the simulation without Procrustean step
blsm_obj = estimate_latent_positions(example_adjacency_matrix, procrustean = FALSE,
  burn_in = 3*10^4, nscan = 10^5)

# Plot
plot_traceplots_acf(blsm_obj, chosen_pair=c(2,5))

## End(Not run)
```

---

proc\_crr     *Procrustean corresponding positions*

---

### Description

Given a set of starting coordinates, the function returns the Procrustean Transform of the initial points that minimizes the sum of squared positional difference from a set of reference coordinates. The (Euclidean) distances between a candidate configuration and the reference are evaluated by considering the couples of corresponding points.

The reference configuration must be centered at the origin.

**Usage**

```
proc_crr(Z, Z0)
```

**Arguments**

Z                    set of initial coordinates to be transformed  
 Z0                   set of reference coordinates centered at the origin

**Value**

Set of coordinates minimizing the distance between the initial configuration and the reference one

**Examples**

```
# Create configuration and center it at the origin
pos_ref = matrix(runif(20), ncol=2)
pos_ref = t(t(pos_ref)-colMeans(pos_ref))

# Create a new configuration by adding a perturbation to the previous one
pos = pos_ref + matrix(rnorm(20, mean=1, sd=0.1), ncol=2)

# Compute the Procrustean Transform and inspect the results
proc_pos = proc_crr(pos, pos_ref)
plot(pos_ref, col="blue", pch=20, xlim=c(-1,3), ylim=c(-1,3))
points(pos, col="red", pch=20)
points(proc_pos, col="purple", pch=20)
```

---

 Z\_up

---

*Update step for the latent positions*


---

**Description**

Accept/reject the proposals for the latent positions

**Usage**

```
Z_up(Y, Z, W, alpha, zdelta, mu_z, sd_z)
```

**Arguments**

Y                    Adjacency matrix of the observed network  
 Z                    Latent positions matrix  
 W                    BLSM Weights matrix of the observed network  
 alpha                Model variable  $\alpha$   
 zdelta               Standard deviation of the Gaussian proposal for latent positions  
 mu\_z                 Mean of the Gaussian prior distribution for latent positions  
 sd\_z                 Standard deviation of the Gaussian prior distribution for latent positions

**Value**

Updated latent positions matrix

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