

Package ‘BayesBrainMap’

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Type Package

Title Estimate Brain Networks and Connectivity with Population-Derived Priors

Version 0.3.1

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Description Implements Bayesian brain mapping with population-derived priors, including the original model described in Mejia et al. (2020) <[doi:10.1080/01621459.2019.1679638](https://doi.org/10.1080/01621459.2019.1679638)>, the model with spatial priors described in Mejia et al. (2022) <[doi:10.1080/10618600.2022.2104289](https://doi.org/10.1080/10618600.2022.2104289)>, and the model with population-derived priors on functional connectivity described in Mejia et al. (2025) <[doi:10.1093/biostatistics/kxaf022](https://doi.org/10.1093/biostatistics/kxaf022)>. Population-derived priors are based on templates representing established brain network maps, for example derived from independent component analysis (ICA), parcellations, or other methods. Model estimation is based on expectation-maximization or variational Bayes algorithms. Includes direct support for 'CIFTI', 'GIFTI', and 'NIFTI' neuroimaging file formats.

Depends R (>= 3.6.0)

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Additional_repositories <https://inla.r-inla-download.org/R/testing>

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Imports abind, fMRITools (>= 0.8.0), foreach, Matrix, matrixStats, methods, pesel, SQUAREM, stats, utils

Suggests ciftiTools (>= 0.13.2), excursions, RNifti, oro.nifti, gifti, ggplot2, parallel, doParallel, knitr, rmarkdown, INLA, testthat (>= 3.0.0)

URL <https://github.com/mandymejia/BayesBrainMap>

BugReports <https://github.com/mandymejia/BayesBrainMap/issues>

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bdiag_m2

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bdiag_m2	<i>Bdiag m2</i>
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Description

Bdiag m2

Usage

bdiag_m2(mat, N)

Arguments

mat	a k x k 'matrix'
N	how many times to repeat mat

Value

a sparse ($Nk \times Nk$) matrix of class "dgCMatrix".

BrainMap	<i>BrainMap</i>
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Description

Deprecated: This function is deprecated. Use [fit_BBM](#) instead.

Usage

BrainMap(...)

Arguments

...	See fit_BBM
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Chol_samp_fun	<i>Cholesky-based FC sampling</i>
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Description

Cholesky-based FC sampling

Usage

```
Chol_samp_fun(Chol_vals, p, M, chol_diag, chol_offdiag, Chol_mat_blank)
```

Arguments

Chol_vals	Matrix of Cholesky factorizations (upper triangular values) for all prior sessions (nN*nM x nChol)
p	Pivot/reordering applied to FC matrices prior to Cholesky factorization
M	Number of samples to draw
chol_diag	Indices of diagonal upper triangular elements
chol_offdiag	Indices of off-diagonal upper triangular elements
Chol_mat_blank	A nLxnL matrix indexing the upper triangular elements

EM_BBM.spatial	<i>EM Algorithms for Bayesian brain maps</i>
----------------	--

Description

EM Algorithms for Bayesian brain maps

Usage

```
EM_BBM.spatial(
  prior_mean,
  prior_var,
  meshes,
  BOLD,
  theta0,
  C_diag,
  H,
  Hinv,
  maxiter = 100,
  usePar = FALSE,
  epsilon = 0.001,
  reduce_dim = TRUE,
  verbose = FALSE
```

```

)

EM_BBM.independent(
    prior_mean,
    prior_var,
    BOLD,
    theta0,
    C_diag,
    H,
    Hinv,
    maxiter = 100,
    epsilon = 0.001,
    reduce_dim = FALSE,
    usePar = FALSE,
    verbose
)

```

Arguments

prior_mean	($V \times Q$ matrix) mean maps for each network in the prior, where Q is the number of networks, $V = nvox$ is the number of data locations.
prior_var	($V \times Q$ matrix) between-subject variance maps for each network in prior
meshes	NULL for spatial independence model, otherwise a list of objects of class "BBM_mesh" containing the triangular mesh (see make_mesh) for each brain structure.
BOLD	($V \times Q$ matrix) dimension-reduced fMRI data
theta0	(list) initial guess at parameter values: A ($Q \times Q$ mixing matrix), nu0_sq (residual variance from first level) and (for spatial model only) kappa (SPDE smoothness parameter for each network map)
C_diag	($Q \times 1$) diagonal elements of matrix proportional to residual variance.
H, Hinv	For dimension reduction of the spatial Bayesian brain map model, which assumes that all networks have the same smoothness parameter, κ
maxiter	Maximum number of EM iterations. Default: 100.
usePar	Parallelize the computation? Default: FALSE. Can be the number of cores to use or TRUE, which will use the number available minus two. Not yet implemented for spatial Bayesian brain map.
epsilon	Smallest proportion change between iterations. Default: 0.001.
reduce_dim	Reduce the temporal dimension of the data using PCA? Default: TRUE for the spatial EM algorithm, and FALSE for the independent EM algorithm.
verbose	If TRUE, display progress of algorithm. Default: FALSE.

Details

EM_BBM.spatial implements the expectation-maximization (EM) algorithm described in Mejia et al. (2019+) for estimating the subject-level networks and unknown parameters in the Bayesian brain map model with spatial priors on subject effects.

In both models, if original fMRI timeseries has covariance $\sigma^2 I_T$, the prewhitened timeseries achieved by premultiplying by (QxT) matrix H from PCA has diagonal covariance $\sigma^2 HH'$, so C_diag is $diag(HH')$.

Value

A list: theta (list of final parameter estimates), subjNet_mean (estimates of subject-level networks), subjNet_var (variance of subject-level networks, for non-spatial model) or subjNet_cov (covariance matrix of subject-level networks, for spatial model – note that only diagonal and values for neighbors are computed), and success (flag indicating convergence (TRUE) or not (FALSE))

engagements	<i>engagements</i>
-------------	--------------------

Description

Deprecated: This function is deprecated. Use [id_engagements](#) instead.

Usage

engagements(...)

Arguments

... See [id_engagements](#)

estimate.ESS	<i>Estimation of effective sample size</i>
--------------	--

Description

Estimation of effective sample size

Usage

estimate.ESS(mesh, Y, ind = NULL, trace = FALSE)

Arguments

- | | |
|-------|--|
| mesh | INLA mesh |
| Y | data |
| ind | index of the data locations in the mesh |
| trace | If TRUE, a formula based on the trace is used, otherwise the inverse correlation is used |

Details

The functions computes the effective sample size as $trace(Q^{-1})/trace(Q * Q)$ as in Bretherton et al. (1999), Journal of Climate.

Value

Estimate of the effective sample size

estimate_nu	<i>Universally estimate IW dof parameter nu based on method of moments, so that no empirical variance is under-estimated</i>
-------------	--

Description

Universally estimate IW dof parameter nu based on method of moments, so that no empirical variance is under-estimated

Usage

estimate_nu(var_FC, mean_FC)

Arguments

var_FC	Empirical between-subject variance of covariance matrices (QxQ)
mean_FC	Empirical mean of covariance matrices (QxQ)

Value

estimate for nu

estimate_nu_matrix	<i>Estimate IW dof parameter nu based on method of moments</i>
--------------------	--

Description

Estimate IW dof parameter nu based on method of moments

Usage

estimate_nu_matrix(var_FC, mean_FC)

Arguments

var_FC	Empirical between-subject variance of covariance matrices (QxQ)
mean_FC	Empirical mean of covariance matrices (QxQ)

Value

QxQ matrix of estimates for nu

estimate_prior	<i>Estimate prior</i>
----------------	-----------------------

Description

Estimate prior for Bayesian brain mapping based on fMRI data

Usage

```
estimate_prior(
  BOLD,
  BOLD2 = NULL,
  template,
  mask = NULL,
  inds = NULL,
  drop_first = 0,
  nuisance = NULL,
  scrub = NULL,
  TR = NULL,
  hpf = NULL,
  GSR = FALSE,
  scale_by = c("mean", "sd", "none"),
  scale_sm_FWHM = 4,
  scale_sm_surfl = NULL,
  scale_sm_surfr = NULL,
  Q2 = 0,
  Q2_max = NULL,
  covariates = NULL,
  brainstructures = "all",
  resamp_res = NULL,
  keep_S = FALSE,
  keep_FC = FALSE,
  FC = TRUE,
  FC_nPivots = 100,
  FC_nSamp = 50000,
  FC_updateA = FALSE,
  varTol = 1e-06,
  maskTol = 0.1,
  missingTol = 0.1,
  usePar = FALSE,
  wb_path = NULL,
  verbose = TRUE
)
```

```
estimate_prior.cifti(  
  BOLD,  
  BOLD2 = NULL,  
  template,  
  mask = NULL,  
  inds = NULL,  
  drop_first = 0,  
  nuisance = NULL,  
  scrub = NULL,  
  TR = NULL,  
  hpf = NULL,  
  GSR = FALSE,  
  scale_by = c("mean", "sd", "none"),  
  scale_sm_FWHM = 4,  
  scale_sm_surfl = NULL,  
  scale_sm_surfr = NULL,  
  Q2 = 0,  
  Q2_max = NULL,  
  covariates = NULL,  
  brainstructures = "all",  
  resamp_res = NULL,  
  keep_S = FALSE,  
  keep_FC = FALSE,  
  FC = TRUE,  
  FC_nPivots = 100,  
  FC_nSamp = 50000,  
  FC_updateA = FALSE,  
  varTol = 1e-06,  
  maskTol = 0.1,  
  missingTol = 0.1,  
  usePar = FALSE,  
  wb_path = NULL,  
  verbose = TRUE  
)
```

```
estimate_prior.gifti(  
  BOLD,  
  BOLD2 = NULL,  
  template,  
  mask = NULL,  
  inds = NULL,  
  drop_first = 0,  
  nuisance = NULL,  
  scrub = NULL,  
  TR = NULL,  
  hpf = NULL,  
  GSR = FALSE,
```

```

scale_by = c("mean", "sd", "none"),
scale_sm_FWHM = 4,
scale_sm_surfl = NULL,
scale_sm_surfr = NULL,
Q2 = 0,
Q2_max = NULL,
covariates = NULL,
brainstructures = "all",
resamp_res = NULL,
keep_S = FALSE,
keep_FC = FALSE,
FC = TRUE,
FC_nPivots = 100,
FC_nSamp = 50000,
FC_updateA = FALSE,
varTol = 1e-06,
maskTol = 0.1,
missingTol = 0.1,
usePar = FALSE,
wb_path = NULL,
verbose = TRUE
)

```

```

estimate_prior.nifti(
  BOLD,
  BOLD2 = NULL,
  template,
  mask = NULL,
  inds = NULL,
  drop_first = 0,
  nuisance = NULL,
  scrub = NULL,
  TR = NULL,
  hpf = NULL,
  GSR = FALSE,
  scale_by = c("mean", "sd", "none"),
  scale_sm_FWHM = 4,
  scale_sm_surfl = NULL,
  scale_sm_surfr = NULL,
  Q2 = 0,
  Q2_max = NULL,
  covariates = NULL,
  brainstructures = "all",
  resamp_res = NULL,
  keep_S = FALSE,
  keep_FC = FALSE,
  FC = TRUE,
  FC_nPivots = 100,

```

```

FC_nSamp = 50000,
FC_updateA = FALSE,
varTol = 1e-06,
maskTol = 0.1,
missingTol = 0.1,
usePar = FALSE,
wb_path = NULL,
verbose = TRUE
)

```

Arguments

BOLD, BOLD2	Vector of subject-level fMRI data in one of the following formats: CIFTI file paths, "xifti" objects, GIFTI file paths, "gifti" objects, NIFTI file paths, "nifti" objects, or $V \times T$ numeric matrices, where V is the number of data locations and T is the number of timepoints. If BOLD2 is provided it must be in the same format as BOLD; BOLD will be the test data and BOLD2 will be the retest data. BOLD2 should be the same length as BOLD and have the same subjects in the same order. If BOLD2 is not provided, BOLD will be split in half; the first half will be the test data and the second half will be the retest data.
template	Group-level template: either a group ICA (GICA), or a parcellation. A GICA should be provided as a format compatible with BOLD, or a (vectorized) numeric matrix ($V \times Q$). Its columns will be centered. A parcellation must be in CIFTI format for use with CIFTI BOLD data (other formats to be implemented in the future). The parcellation should have the same locations as the BOLD and one column, with integer values indicating the parcel to which each location belongs to. Each parcel is modeled as a brain map; instead of the first step of dual regression, the medial timecourse of each parcel is used.
mask	Required if the entries of BOLD are NIFTI file paths or "nifti" objects, optional for other formats. For NIFTI, this is a binary array of the same spatial dimensions as the fMRI data, with TRUE corresponding to in-mask voxels. For other formats, a logical vector.
inds	Numeric indices of the networks in template to include in the prior. If NULL, use all of the original networks (default). If inds is provided, the networks not included will be removed after calculating dual regression, not before. This is because removing the networks prior to dual regression would leave unmodelled signals in the data, which could bias the priors.
drop_first	(Optional) Number of volumes to drop from the start of each BOLD session. Default: 0.
nuisance	(Optional) Nuisance matrices to regress from the BOLD data. Should be a list of matrices, with time along the rows and nuisance signals along the columns, where each entry corresponds to a BOLD session; or, if BOLD2 is provided, should be a length-2 list of such lists with the first sublist corresponding to BOLD and

	the second sublist corresponding to BOLD2. If NULL, do not remove any nuisance signals. Nuisance regression is performed in a simultaneous regression with any spike regressors from scrub and DCT bases from hpf. Note that the nuisance matrices should be provided with timepoints matching the original BOLD and BOLD2 irregardless of drop_first. Nuisance matrices will be truncated automatically if drop_first>0.
scrub	(Optional) Numeric vectors of integers giving the indices of volumes to scrub from the BOLD data. (List the volumes to remove, not the ones to keep.) Should be a list of such vectors, where each entry corresponds to a BOLD session; or, if BOLD2 is provided, should be a length-2 list of such lists with the first sublist corresponding to BOLD and the second sublist corresponding to BOLD2. If NULL (default), do not scrub. Scrubbing is performed within a nuisance regression by adding a spike regressor to the nuisance design matrix for each volume to scrub. Note that indices are counted beginning with the first index in the BOLD session irregardless of drop_first. The indices will be adjusted automatically if drop_first>0.
TR	The temporal resolution of the data, i.e. the time between volumes, in seconds. TR is required for detrending with hpf.
hpf	The frequency at which to apply a highpass filter to the data during pre-processing, in Hertz. Default: NULL (disabled). If the data has not already been highpass filtered, a recommended filter value is .01 Hz. The highpass filter serves to detrend the data, since low-frequency variance is associated with noise. Highpass filtering is accomplished by nuisance regression of discrete cosine transform (DCT) bases. Note the TR argument is required for highpass filtering. If TR is not provided, an error will be raised if hpf is set.
GSR	Center BOLD across columns (each image)? This is equivalent to performing global signal regression. Default: FALSE.
scale_by	Scale the BOLD at each voxel based on either its "mean" (default), or its "sd". Mean scaling cannot be used if the BOLD have already been de-meanned.
scale_sm_FWHM	Full width at half maximum (FWHM) for smoothing the estimates of scale across brain locations (see scale_by), to reduce the variance of the estimates. Set to 0 to disable smoothing, or Inf for "global" smoothing (estimate and use one measure of scale across the entire brain). Otherwise, for "local" smoothing, this should be a positive number. Note that local smoothing is only available for surface data input (CIFTI or GIFTI BOLD). Default: local smoothing with a FWHM of 4.
scale_sm_surfl, scale_sm_surfr	Required only for "local" smoothing (see scale_sm_FWHM). To smooth the scale estimates, provide the surface geometries along which to smooth, as GIFTI geometry files or ciftiTools "surf" objects. The resolutions should match with the BOLD data. To create a "surf" object from data, see make_surf. If not provided, the fs_LR "midthickness" surfaces will be used.

Q2, Q2_max	Obtain dual regression estimates after denoising? Denoising is based on modeling and removing nuisance ICs. It may result in a cleaner estimate for smaller datasets, but it may be unnecessary (and time-consuming) for larger datasets. Set Q2 to control denoising: use a positive integer to specify the number of nuisance ICs, NULL to have the number of nuisance ICs estimated by PESEL, or zero (default) to skip denoising. If <code>is.null(Q2)</code>, use Q2_max to specify the maximum number of nuisance ICs that should be estimated by PESEL. Q2_max must be less than $T * .75 - Q$ where T is the minimum number of timepoints in each fMRI scan and Q is the number of networks in the template. If NULL (default), Q2_max will be set to $T * .50 - Q$, rounded.
covariates	Subjects by variables numeric matrix of covariates to take into account for model estimation. Column names should give the name of each variable. Default: NULL (no covariates). NOTE: Not implemented yet.
brainstructures	Only applies if the entries of BOLD are CIFTI file paths. This is a character vector indicating which brain structure(s) to obtain: "left" (left cortical surface), "right" (right cortical surface) and/or "subcortical" (subcortical and cerebellar gray matter). Can also be "all" (obtain all three brain structures). Default: <code>c("all")</code>.
resamp_res	Only applies if the entries of BOLD are CIFTI file paths. Resample the data upon reading it in? Default: NULL (no resampling).
keep_S	Keep the DR estimates of S? If FALSE (default), do not save the DR estimates and only return the priors. If TRUE, the DR estimates of S are returned too. If a single file path, save the DR estimates as an RDS file at that location rather than returning them.
keep_FC	Keep the DR estimates of the FC <code>cor(A)</code>? If FALSE (default), do not save the DR estimates and only return the priors. If TRUE, the DR estimates of <code>cor(A)</code> and its Cholesky factor are returned too. If a single file path, save the DR estimates as an RDS file at that location rather than returning them.
FC	Include the functional connectivity prior? Default: TRUE.
FC_nPivots	Number of pivots to use in Cholesky-based FC prior estimation. Set to zero to skip Cholesky-based FC prior estimation. Default: 100.
FC_nSamp	Number of FC matrix samples to generate across all pivots. This should be a multiple of FC_nPivots.
FC_updateA	Update the timecourses before computing FC? Default: FALSE. Only applies if FC.
varTol	Tolerance for variance of each data location. For each scan, locations which do not meet this threshold are masked out of the analysis. Default: $1e-6$. Variance is calculated on the original data, before any normalization.
maskTol	For computing the dual regression results for each subject: tolerance for number of locations masked out due to low variance or missing values. If more than this many locations are masked out, a subject is skipped without calculating dual regression. maskTol can be specified either as a proportion of the number of

	locations (between zero and one), or as a number of locations (integers greater than one). Default: .1, i.e. up to 10 percent of locations can be masked out. If BOLD2 is provided, masks are calculated for both scans and then the intersection of the masks is used, for each subject.
missingTol	For computing the variance decomposition across all subjects: tolerance for number of subjects masked out due to low variance or missing values at a given location. If more than this many subjects are masked out, the location's value will be NA in the priors. missingTol can be specified either as a proportion of the number of locations (between zero and one), or as a number of locations (integers greater than one). Default: .1, i.e. up to 10 percent of subjects can be masked out at a given location.
usePar, wb_path	Parallelize the DR computations over subjects? Default: FALSE. Can be the number of cores to use or TRUE, which will use the number on the PC minus two. If the input data is in CIFTI format, the wb_path must also be provided.
verbose	Display progress updates? Default: TRUE.

Details

All fMRI data (entries in BOLD and BOLD2, and template) must be in the same spatial resolution.

Value

A list: the prior and var_decomp with entries in matrix format; the mask of locations without prior values due to too many low variance or missing values; the function params such as the type of scaling and detrending performed; the dat_struct which can be used to convert prior and var_decomp to "xifti" or "nifti" objects if the BOLD format was CIFTI or NIFTI data; and DR results if isTRUE(keep_S) and/or isTRUE(keep_FC).

Use summary to print a description of the prior results, and for CIFTI-format data use plot to plot the prior mean and variance estimates. Use [export_prior](#) to save the priors to individual RDS, CIFTI, or NIFTI files (depending on the BOLD format).

Examples

```
nT <- 21
nV <- 140
nQ <- 6
mU <- matrix(rnorm(nV*nQ), nrow=nV)
mS <- mU %*% diag(seq(nQ, 1)) %*% matrix(rnorm(nQ*nT), nrow=nQ)
BOLD <- list(B1=mS, B2=mS, B3=mS)
BOLD <- lapply(BOLD, function(x){x + rnorm(nV*nT, mean = 100, sd=.05)})
template <- mU
estimate_prior(BOLD=BOLD, template=mU, FC_nSamp=2000, scale_sm_FWHM=Inf)

## Not run:
estimate_prior(
  run1_cifti_fnames, run2_cifti_fnames,
  gICA_cifti_fname, brainstructures="all",
  scale_sm_FWHM=Inf, TR=0.71, Q2=NULL, varTol=10,
  usePar=FALSE
```

```
)
## End(Not run)
```

export_prior

Export prior

Description

Export the priors (mean, variance, and FC) as separate files for visualization or processing outside of BayesBrainMap.

Usage

```
export_prior(x, out_fname = NULL, var_method = c("non-negative", "unbiased"))
```

Arguments

x	The result of estimate_prior
out_fname	Use NULL (default) to just return the prior objects directly. Otherwise, use a character vector of length 3 or 4 of file path(s) to save the output to: the mean prior, the variance prior, the variance decomposition, and the FC prior if present, in that order. If one file name is provided, it will be appended with "_mean.[file_ext]" for the prior mean map, "_var.[file_ext]" for the prior variance map, "_varDecomp.rds" for the variance decomposition, and "_FC.rds" where [file_ext] will be "dscalar.nii" for CIFTI input, "nii" for NIFTI input, and "rds" for data input.
var_method	"non-negative" (default) or "unbiased"

Value

If is.null(out_fname), the priors in data matrix, "xifti", or "nifti" format, to match the format of the original BOLD data. Otherwise, the paths to the new files specified by out_fname. If prior includes functional connectivity components, the FC prior and its mean and variance will be included.

Examples

```
## Not run:
tm <- estimate_prior(cii1_fnames, cii2_fnames, gICA_fname, usePar=FALSE)
export_prior(tm, out_fname="my_prior", var_method="unbiased")

## End(Not run)
```

fit_BBM

*Bayesian brain mapping***Description**

Fit Bayesian brain mapping model using variational Bayes (VB) or expectation-maximization (EM).

Usage

```
fit_BBM(
  BOLD,
  prior,
  var_method = c("non-negative", "unbiased"),
  scale_by = c("prior", "mean", "sd", "none"),
  scale_sm_FWHM = "prior",
  scale_sm_surfl = NULL,
  scale_sm_surfr = NULL,
  nuisance = NULL,
  scrub = NULL,
  drop_first = 0,
  hpf = "prior",
  TR = NULL,
  GSR = "prior",
  Q2 = "prior",
  Q2_max = "prior",
  covariates = NULL,
  brainstructures = "prior",
  mask = NULL,
  varTol = "prior",
  spatial_model = NULL,
  resamp_res = NULL,
  rm_mwall = TRUE,
  reduce_dim = FALSE,
  method_FC = c("VB1", "VB2", "none"),
  maxiter = 100,
  miniter = 3,
  epsilon = 0.001,
  kappa_init = 0.2,
  usePar = TRUE,
  PW = FALSE,
  seed = 1234,
  doMLE = TRUE,
  verbose = TRUE
)
```

Arguments

BOLD	Vector of subject-level fMRI data in one of the following formats: CIFTI file paths, "xifti" objects, NIFTI file paths, "nifti" objects, or $V \times T$ numeric matrices, where V is the number of data locations and T is the number of time-points. If multiple BOLD data are provided, they will be independently centered, scaled, detrended (if applicable), and denoised (if applicable). Then they will be concatenated together followed by computing the initial dual regression estimate.
prior	Prior estimates in a format compatible with BOLD, from estimate_prior .
var_method	Which calculation of the prior variance to use: "non-negative" (default) or "unbiased". The unbiased prior variance is based on the assumed mixed effects/ANOVA model, whereas the non-negative prior variance adds to it to account for greater potential between-subjects variation. (The prior mean is the same for either choice of var_method.)
scale_by	Scale the BOLD at each voxel based on either its "mean" or its "sd", or "none" for no scaling if the data has already been scaled. Default: "prior", to use the same option that was used for estimation of the prior.
scale_sm_FWHM	Full width at half maximum (FWHM) for smoothing the estimates of scale across brain locations (see scale_by), to reduce the variance of the estimates. Set to 0 to disable smoothing, or Inf for "global" smoothing (estimate one measure of scale across the entire brain). Otherwise, for "local" smoothing, this should be a positive number. Note that local smoothing is only available for surface data input (CIFTI or GIFTI BOLD). Default: "prior", to use the same option used for estimation of the prior.
scale_sm_surfl, scale_sm_surfr	Required only for "local" smoothing (see scale_sm_FWHM). To smooth the scale estimates, provide the surface geometries along which to smooth, as GIFTI geometry files or ciftiTools "surf" objects. The resolutions should match with the BOLD data. To create a "surf" object from data, see make_surf. If not provided, the fs_LR "midthickness" surfaces will be used.
nuisance	(Optional) Signals to regress from the data, given as a numeric matrix with the same number of rows as there are volumes in the BOLD data. If multiple BOLD sessions are provided, this argument can be a list to use different nuisance regressors for different sessions. Nuisance regression is performed as a first step, before centering, scaling, and denoising. An intercept column will automatically be added to nuisance. If NULL, no extra nuisance signals will be regressed from the data, but a nuisance regression will still be used if warranted by scrub or hpf.
scrub	(Optional) A numeric vector of integers giving the indices of volumes to scrub from the BOLD data. (List the volumes to remove, not the ones to keep.) If multiple BOLD sessions are provided, this argument can be a list to remove different volumes for different sessions. Scrubbing is performed within nuisance regression by adding a spike regressor to the nuisance design matrix for each volume to scrub. If NULL (default), do not scrub.

drop_first	(Optional) Number of volumes to drop from the start of each BOLD session. Default: 0.
TR, hpf	These arguments control detrending. TR is the temporal resolution of the data, i.e. the time between volumes, in seconds; hpf is the frequency of the high-pass filter, in Hertz. Detrending is performed via nuisance regression of DCT bases. Default: "prior" to use the values from the prior. Set hpf to 0 to disable the high-pass filter. Be sure to set the correct TR if it's different for the new data compared to the data used in estimate_prior. Note that if multiple BOLD sessions are provided, their TR and hpf must be the same; both arguments accept only one value.
GSR	Center BOLD across columns (each image)? This is equivalent to performing global signal regression. Default: "prior", to use the same option used for estimation of the prior.
Q2, Q2_max	Denoise the BOLD data? Denoising is based on modeling and removing nuisance ICs. It may result in a cleaner estimate for smaller datasets, but it may be unnecessary (and time-consuming) for larger datasets. Set Q2 to control denoising: use a positive integer to specify the number of nuisance ICs, NULL to have the number of nuisance ICs estimated by PESEL, or zero to skip denoising. If is.null(Q2), use Q2_max to specify the maximum number of nuisance ICs that should be estimated by PESEL. Q2_max must be less than $T * .75 - Q$ where T is the number of timepoints in BOLD and Q is the number of networks in the prior. If NULL, Q2_max will be set to $T * .50 - Q$, rounded. The defaults for both arguments is "prior", to use the same option used for estimation of the prior.
covariates	Numeric vector of covariates to take into account for model estimation. Names should give the name of each variable. The covariates must match those of the prior. Default: NULL (no covariates). NOTE: Not implemented yet.
brainstructures	Only applies if the entries of BOLD are CIFTI file paths. This is a character vector indicating which brain structure(s) to obtain: "left" (left cortical surface), "right" (right cortical surface) and/or "subcortical" (subcortical and cerebellar gray matter). Can also be "all" (obtain all three brain structures). Default: "prior" to use the same brainstructures present in the prior).
mask	Required only if the entries of BOLD are NIFTI file paths or "nifti" objects. This is a binary array of the same spatial dimensions as the fMRI data, with TRUE corresponding to in-mask voxels.
varTol	Tolerance for variance of each data location. For each scan, locations which do not meet this threshold are masked out of the analysis. Default: "prior" to use the same brainstructures present in the prior). Variance is calculated on the original data, before any normalization. Set to 0 to avoid removing locations due to low variance.
spatial_model	Should spatial modeling be performed? If NULL, assume spatial independence. Otherwise, provide meshes specifying the spatial priors assumed on each independent component. Each should represent a brain structure, between which spatial independence can be assumed.

If BOLD represents CIFTI-format data, `spatial_model` should give the left and right cortex surface geometries (whichever one(s) are being used) as "surf" objects or GIFTI surface geometry file paths. Spatial modeling is not yet available for the subcortex. This argument can also be TRUE, in which case spatial modeling will be performed with the surfaces included in the first entry of BOLD if it is a "xifti" object, or if those are not present available, the default inflated surfaces from `ciftiTools`.

If BOLD represents NIFTI-format data, spatial modeling is not yet available.

If BOLD is a numeric matrix, `spatial_model` should be a list of meshes (see [make_mesh](#)).

<code>resamp_res</code>	Only applies if BOLD represents CIFTI-format data. The target resolution for resampling (number of cortical surface vertices per hemisphere). For spatial modelling, a value less than 10000 is recommended for computational feasibility. If NULL (default), do not perform resampling.
<code>rm_mwall</code>	Only applies if BOLD represents CIFTI-format data. Should medial wall (missing data) locations be removed from the mesh? If TRUE, faster computation but less accurate estimates at the boundary of wall.
<code>reduce_dim</code>	Reduce the temporal dimension of the data using PCA? Default: TRUE. Skipping dimension reduction will slow the model estimation, but may result in more accurate results. Ignored for FC prior ICA
<code>method_FC</code>	Variational Bayes (VB) method for FC prior ICA model: "VB1" (default) uses a conjugate Inverse-Wishart prior for the $\text{cor}(A)$; "VB2" draws samples from $p(\text{cor}(A))$ to emulate the population distribution using a combination of Cholesky, SVD, and random pivoting. "none" Uses standard prior ICA without FC prior
<code>maxiter</code>	Maximum number of EM or VB iterations. Default: 100.
<code>miniter</code>	Minimum number of EM or VB iterations. Default: 3.
<code>epsilon</code>	Smallest proportion change between iterations. Default: .001.
<code>kappa_init</code>	Starting value for kappa. Default: 0.2.
<code>usePar</code>	Parallelize the computation? Default: TRUE. Can be the number of cores to use or TRUE, which will use the number available minus two.
<code>PW</code>	Prewhiten to account for residual autocorrelation? Default: FALSE. Only affects FC prior ICA models.
<code>seed</code>	(Only applicable for FC calculation and if PW) Seed to use for computing temporal effective sample size (ESS) to correct sums over t . If NULL, do not change the seed. Default: 1234.
<code>doMLE</code>	If TRUE. Will calculate and return MLE map based on BBM temporal mixing matrix estimate. Default: TRUE
<code>verbose</code>	If TRUE, display progress of algorithm

Value

A (spatial) prior ICA object, which is a list containing: `subjNet_mean`, the $V \times L$ estimated independent components $\mathbf{S}$; `subjNet_se`, the standard errors of $\mathbf{S}$; the mask of locations without prior values due to too many low variance or missing values; the nuisance design matrix or matrices if applicable; and the function params such as the type of scaling and detrending performed.

If BOLD represented CIFTI or NIFTI data, subjNet_mean and subjNet_se will be formatted as "xifti" or "nifti" objects, respectively.

Examples

```
## Not run:
tm <- estimate_prior(cii1_fnames, cii2_fnames, gICA_fname, usePar=FALSE)
fit_BBM(newcii_fname, tm, spatial_model=TRUE, resamp_res=2000, usePar=FALSE)

## End(Not run)
```

id_engagements

Engagements of (spatial) Bayesian brain mapping

Description

Identify areas of engagement in each network from the result of (spatial) Bayesian brain mapping.

Usage

```
id_engagements(
  bMap,
  u = NULL,
  z = 2,
  alpha = 0.01,
  type = c(">", "abs >", "<", "!="),
  method_p = c("BH", "bonferroni"),
  verbose = FALSE,
  which.nets = NULL,
  deviation = FALSE
)
```

Arguments

bMap	Fitted (spatial) Bayesian brain map from fit_BBM .
u, z	Set a threshold value for engagement? A threshold value can be specified directly with u, or a z-score-like threshold in terms of standard deviations (the SD of values in the mean prior) can be specified with z. Only one type of threshold can be used. Default: z=2. Set both u and z to NULL to not use a threshold. Either u or z can also be a vector to test multiple thresholds at once, as long as type is not "!=" (to ensure the engagement regions are successive subsets).
alpha	Significance level for hypothesis testing. Default: 0.01.
type	Type of region: ">" (default), "abs >", "<", or "!=". "abs >" tests for magnitude by taking the absolute value and then testing if they are greater than...

method_p	If the input is a "bMap.[format]" model object, the type of multiple comparisons correction to use for p-values, or NULL for no correction. Default: "BH" (Benjamini & Hochberg, i.e. the false discovery rate). Another option is "bonferroni" correction. See <code>help(p.adjust)</code> for the full list of options. Note that multiple comparisons will account for data locations, but not networks.
verbose	If TRUE, display progress of algorithm. Default: FALSE.
which.nets	Indices of networks for which to identify engagements. If NULL (default), use all networks.
deviation	If TRUE identify significant deviations from the prior mean, rather than significant areas of engagement. Default: FALSE.

Value

A list containing engagement maps for each network, the joint and marginal PPMs for each network, masks of regions meeting the threshold(s) if provided, and the parameters used for computing engagement. If the input represented CIFTI- or NIFTI-format data, then the engagements maps will be formatted accordingly.

Use `summary` to obtain information about the engagements results. For CIFTI-format engagements, use `plot` to visualize the engagement maps.

Examples

```
## Not run:
id_engagements(fit_BBM_result, alpha=.05, deviation=TRUE)

## End(Not run)
```

IW_var	<i>Compute theoretical Inverse-Wishart variance of covariance matrix elements</i>
--------	---

Description

Compute theoretical Inverse-Wishart variance of covariance matrix elements

Usage

```
IW_var(nu, p, xbar_ij, xbar_ii, xbar_jj)
```

Arguments

nu	Inverse Wishart degrees of freedom parameter
p	Matrix dimension for IW distribution
xbar_ij	Empirical mean of covariance matrices at element (i,j)
xbar_ii	Empirical mean of covariance matrices at the ith diagonal element
xbar_jj	Empirical mean of covariance matrices at the jth diagonal element

Value

Theoretical IW variance for covariance element (i,j)

IW_var_cor	<i>Compute theoretical Inverse-Wishart variance of correlation matrix elements</i>
------------	--

Description

Compute theoretical Inverse-Wishart variance of correlation matrix elements

Usage

```
IW_var_cor(nu, p, xbar_ij)
```

Arguments

nu	Inverse Wishart degrees of freedom parameter
p	Matrix dimension for IW distribution
xbar_ij	Empirical mean of covariance matrices at element (i,j)

Value

Theoretical IW variance for correlation element (i,j)

lik	<i>Compute likelihood in SPDE model for ESS estimation</i>
-----	--

Description

Compute likelihood in SPDE model for ESS estimation

Usage

```
lik(theta, Y, G, C, ind = NULL)
```

Arguments

theta	Value of hyperparameters
Y	Data vector
G	SPDE G matrix
C	SPDE C matrix
ind	Indices of data locations in the mesh

Value

Log likelihood value

plot.bMap.cifti	<i>Plot fit_BBM estiamte</i>
-----------------	------------------------------

Description

Plot fit_BBM estiamte

Usage

```
## S3 method for class 'bMap.cifti'
plot(x, what = c("maps", "FC"), stat = c("mean", "se"), ...)
```

Arguments

x	The result of fit_BBM with CIFTI data
what	The "maps" (default) on the brain, or the "FC" matrix. If both are desired, use two separate plot calls to first plot the maps and then plot the FC. If "FC", the default color scale will be from blue (-1) to red (1). This can be changed with the colFUN argument to plot_FC_gg .
stat	"mean" (default) or "se". Note that for the FC, only the mean estimate is available, not the SE.
...	Additional arguments to view_xifti if what=="maps", or plot_FC_gg if what=="FC".

Value

The plot

plot.bMap.matrix	<i>Plot prior</i>
------------------	-------------------

Description

This feature is not supported yet.

Usage

```
## S3 method for class 'bMap.matrix'
plot(x, ...)
```

Arguments

x	The result of fit_BBM with NIFTI data
...	Additional arguments

Value

Nothing, because an error is raised.

plot.bMap.nifti	<i>Plot prior</i>
-----------------	-------------------

Description

Plot prior

Usage

```
## S3 method for class 'bMap.nifti'
plot(
  x,
  stat = c("mean", "se"),
  plane = c("axial", "sagittal", "coronal"),
  n_slices = 9,
  slices = NULL,
  ...
)
```

Arguments

x	The result of <code>fit_BBM</code> with NIFTI data
stat	"mean" (default), "se"
plane, n_slices, slices	Anatomical plane and which slice indices to show. Default: 9 axial slices.
...	Additional arguments

Value

The plot

plot.bMap_eng.cifti	<i>Plot engagements</i>
---------------------	-------------------------

Description

Plot engagements

Usage

```
## S3 method for class 'bMap_eng.cifti'
plot(
  x,
  stat = c("engaged", "pvals", "pvals_adj", "tstats", "se", "thresholded"),
  test_level = NULL,
  ...
)
```

Arguments

x	The engagements from <code>id_engagements.cifti</code>
stat	"engaged" (default), "pvals", "pvals_adj", "tstats", "vars", or "thresholded".
test_level	If stat is not "engaged" or thresholded, which test level should be used? See <code>dimnames(x\$engaged_mat)[[3]]</code> for the test levels. If NULL (default), the first test level will be used.
...	Additional arguments to <code>view_xifti</code>

Value

The engagements plot

<code>plot.prior.cifti</code>	<i>Plot prior</i>
-------------------------------	-------------------

Description

Plot prior

Usage

```
## S3 method for class 'prior.cifti'
plot(
  x,
  what = c("maps", "FC"),
  stat = c("mean", "sd", "var"),
  var_method = c("non-negative", "unbiased"),
  FC_method = c("empirical", "IW", "Chol", "none"),
  ...
)
```

Arguments

x	The prior from <code>estimate_prior.cifti</code>
what	The "maps" (default) on the brain, or the "FC" matrix. If both are desired, use two separate plot calls to first plot the maps and then plot the FC. If "FC", the default color scale will be from blue (-1) to red (1). This can be changed with the <code>colFUN</code> argument to plot_FC_gg .
stat	Which prior statistic to plot: the "mean" (default), "sd" for the square root of the variance template, or "var" for the variance template.
var_method	"non-negative" (default) or "unbiased", for the variance estimate of the maps. Note that FC variance estimates are always non-negative.
FC_method	If <code>what=="FC"</code> : empirical ("emp") (default), Inverse-Wishart ("IW"), or Cholesky ("Chol").
...	Additional arguments to view_xifti if <code>what=="maps"</code> , or plot_FC_gg if <code>what=="FC"</code> .

Value

The plot

plot.prior.gifti	<i>Plot prior</i>
------------------	-------------------

Description

Plot prior

Usage

```
## S3 method for class 'prior.gifti'
plot(
  x,
  what = c("maps", "FC"),
  stat = c("mean", "sd", "var"),
  var_method = c("non-negative", "unbiased"),
  FC_method = c("empirical", "IW", "Chol", "none"),
  ...
)
```

Arguments

x	The prior from estimate_prior.gifti
what	The "maps" (default) on the brain, or the "FC" matrix. If both are desired, use two separate plot calls to first plot the maps and then plot the FC. If "FC", the default color scale will be from blue (-1) to red (1). This can be changed with the colFUN argument to plot_FC_gg .
stat	Which prior statistic to plot: the "mean" (default), "sd" for the square root of the variance template, or "var" for the variance template.
var_method	"non-negative" (default) or "unbiased", for the variance estimate of the maps. Note that FC variance estimates are always non-negative.
FC_method	If what=="FC": empirical ("empirical") (default), Inverse-Wishart ("IW"), or Cholesky ("Chol").
...	Additional arguments to view_xifit if what=="maps", or plot_FC_gg if what=="FC".

Value

The plot

plot.prior.matrix	<i>Plot prior</i>
-------------------	-------------------

Description

Plot prior

Usage

```
## S3 method for class 'prior.matrix'
plot(x, ...)
```

Arguments

x	The prior from estimate_prior.matrix
...	Additional arguments

Value

The plot

plot.prior.nifti	<i>Plot prior</i>
------------------	-------------------

Description

Based on oro.nifti::image.

Usage

```
## S3 method for class 'prior.nifti'
plot(
  x,
  what = c("maps", "FC"),
  stat = c("mean", "sd", "var"),
  FC_method = c("empirical", "IW", "Chol", "none"),
  var_method = c("non-negative", "unbiased"),
  plane = c("axial", "sagittal", "coronal"),
  n_slices = 9,
  slices = NULL,
  ...
)
```

Arguments

x	The prior from estimate_prior.nifti
what	The "maps" (default) on the brain, or the "FC" matrix. If both are desired, use two separate plot calls to first plot the maps and then plot the FC. If "FC", the default color scale will be from blue (-1) to red (1). This can be changed with the colFUN argument to plot_FC_gg .
stat	Which prior statistic to plot: the "mean" (default), "sd" for the square root of the variance template, or "var" for the variance template.
FC_method	If what=="FC": empirical ("empirical") (default), Inverse-Wishart ("IW"), or Cholesky ("Chol").
var_method	"non-negative" (default) or "unbiased", for the variance estimate of the maps. Note that FC variance estimates are always non-negative.
plane, n_slices, slices	Anatomical plane and which slice indices to show. Default: 9 axial slices.
...	Additional arguments to oro.nifti::image if what=="maps", or plot_FC_gg if what=="FC".

Details

Consider using struct_prior to obtain the 3D volumes to plot with a different viewer function (e.g. from oro.nifti) if desired.

Value

The plot

pw_estimate	<i>Estimate residual autocorrelation for prewhitening</i>
-------------	---

Description

Estimate residual autocorrelation for prewhitening

Usage

```
pw_estimate(A, ar_order, aic = FALSE)
```

Arguments

A	Estimated A matrix (T x Q)
ar_order, aic	Order of the AR model used to prewhiten the data at each location. If !aic (default), the order will be exactly ar_order. If aic, the order will be between zero and ar_order, as determined by the AIC.

Value

Estimated AR coefficients and residual variance at every vertex

summary.bMap.cifti	<i>Summarize a "bMap.cifti" object</i>
--------------------	--

Description

Summary method for class "bMap.cifti"

Usage

```
## S3 method for class 'bMap.cifti'
summary(object, ...)

## S3 method for class 'summary.bMap.cifti'
print(x, ...)

## S3 method for class 'bMap.cifti'
print(x, ...)
```

Arguments

object	Object of class "bMap.cifti".
...	further arguments passed to or from other methods.
x	The result of <code>fit_BBM</code> with CIFTI data

Value

A list summarizing of the results of the BrainMap analysis.
 Nothing, invisibly.
 Nothing, invisibly.

summary.bMap.matrix	<i>Summarize a "bMap.matrix" object</i>
---------------------	---

Description

Summary method for class "bMap.matrix"

Usage

```
## S3 method for class 'bMap.matrix'
summary(object, ...)

## S3 method for class 'summary.bMap.matrix'
print(x, ...)

## S3 method for class 'bMap.matrix'
print(x, ...)
```

Arguments

object	Object of class "bMap.matrix".
...	further arguments passed to or from other methods.
x	The prior from estimate_prior.cifti

Value

A list summarizing of the results of the BrainMap analysis.

Nothing, invisibly.

Nothing, invisibly.

summary.bMap.nifti	<i>Summarize a "bMap.nifti" object</i>
--------------------	--

Description

Summary method for class "bMap.nifti"

Usage

```
## S3 method for class 'bMap.nifti'
summary(object, ...)

## S3 method for class 'summary.bMap.nifti'
print(x, ...)

## S3 method for class 'bMap.nifti'
print(x, ...)
```

Arguments

object	Object of class "bMap.nifti".
...	further arguments passed to or from other methods.
x	The prior from estimate_prior.cifti

Value

A list summarizing of the results of the BrainMap analysis.

Nothing, invisibly.

Nothing, invisibly.

summary.bMap_eng.cifti

Summarize a "bMap_eng.cifti" object

Description

Summary method for class "bMap_eng.cifti"

Usage

```
## S3 method for class 'bMap_eng.cifti'
summary(object, ...)

## S3 method for class 'summary.bMap_eng.cifti'
print(x, ...)

## S3 method for class 'bMap_eng.cifti'
print(x, ...)
```

Arguments

object	Object of class "bMap_eng.cifti".
...	further arguments passed to or from other methods.
x	The engagements from id_engagements.cifti

Value

A list summarizing the data and results for the engagements analysis.
 Nothing, invisibly.
 Nothing, invisibly.

summary.bMap_eng.matrix

Summarize a "bMap_eng.matrix" object

Description

Summary method for class "bMap_eng.matrix"

Usage

```
## S3 method for class 'bMap_eng.matrix'
summary(object, ...)

## S3 method for class 'summary.bMap_eng.matrix'
print(x, ...)

## S3 method for class 'bMap_eng.matrix'
print(x, ...)
```

Arguments

object	Object of class "bMap_eng.matrix".
...	further arguments passed to or from other methods.
x	The engagements from id_engagements

Value

A list summarizing the data and results for the engagements analysis.

Nothing, invisibly.

Nothing, invisibly.

```
summary.bMap_eng.nifti
```

Summarize a "bMap_eng.nifti" object

Description

Summary method for class "bMap_eng.nifti"

Usage

```
## S3 method for class 'bMap_eng.nifti'
summary(object, ...)

## S3 method for class 'summary.bMap_eng.nifti'
print(x, ...)

## S3 method for class 'bMap_eng.nifti'
print(x, ...)
```

Arguments

object	Object of class "bMap_eng.nifti".
...	further arguments passed to or from other methods.
x	The engagements from id_engagements

Value

A list summarizing the data and results for the engagements analysis.

Nothing, invisibly.

Nothing, invisibly.

summary.prior.cifti	<i>Summarize a "prior.cifti" object</i>
---------------------	---

Description

Summary method for class "prior.cifti"

Usage

```
## S3 method for class 'prior.cifti'
summary(object, ...)

## S3 method for class 'summary.prior.cifti'
print(x, ...)

## S3 method for class 'prior.cifti'
print(x, ...)
```

Arguments

object	Object of class "prior.cifti".
...	further arguments passed to or from other methods.
x	The prior from estimate_prior.cifti

Value

A list summarizing the prior: data dimensions, options used for prior estimation, etc.

Nothing, invisibly.

Nothing, invisibly.

summary.prior.gifti	<i>Summarize a "prior.gifti" object</i>
---------------------	---

Description

Summary method for class "prior.gifti"

Usage

```
## S3 method for class 'prior.gifti'
summary(object, ...)

## S3 method for class 'summary.prior.gifti'
print(x, ...)

## S3 method for class 'prior.gifti'
print(x, ...)
```

Arguments

object	Object of class "prior.gifti".
...	further arguments passed to or from other methods.
x	The prior from estimate_prior.gifti

Value

A list summarizing the prior: data dimensions, options used for prior estimation, etc.
 Nothing, invisibly.
 Nothing, invisibly.

summary.prior.matrix	<i>Summarize a "prior.matrix" object</i>
----------------------	--

Description

Summary method for class "prior.matrix"

Usage

```
## S3 method for class 'prior.matrix'
summary(object, ...)

## S3 method for class 'summary.prior.matrix'
print(x, ...)

## S3 method for class 'prior.matrix'
print(x, ...)
```

Arguments

object	Object of class "prior.matrix".
...	further arguments passed to or from other methods.
x	The prior from estimate_prior.cifti

Value

A list summarizing the prior: data dimensions, options used for prior estimation, etc.

Nothing, invisibly.

Nothing, invisibly.

summary.prior.nifti	<i>Summarize a "prior.nifti" object</i>
---------------------	---

Description

Summary method for class "prior.nifti"

Usage

```
## S3 method for class 'prior.nifti'
summary(object, ...)

## S3 method for class 'summary.prior.nifti'
print(x, ...)

## S3 method for class 'prior.nifti'
print(x, ...)
```

Arguments

object	Object of class "prior.nifti".
...	further arguments passed to or from other methods.
x	The prior from estimate_prior.nifti

Value

A list summarizing the prior: data dimensions, options used for prior estimation, etc.

Nothing, invisibly.

Nothing, invisibly.

UpdateTheta_BBM

*Parameter Estimates in EM Algorithm for Bayesian brain map***Description**

Parameter Estimates in EM Algorithm for Bayesian brain map

Usage

```

UpdateTheta_BBM(
  prior_mean,
  prior_var,
  meshes,
  BOLD,
  theta,
  C_diag,
  H,
  Hinv,
  s0_vec,
  D,
  Dinv_s0,
  verbose = FALSE,
  return_MAP = FALSE,
  update = c("all", "kappa", "A")
)

UpdateTheta_iBM(
  prior_mean,
  prior_var,
  BOLD,
  theta,
  C_diag,
  H,
  Hinv,
  update_nu0sq = TRUE,
  return_MAP = FALSE,
  verbose = TRUE
)

```

Arguments

prior_mean	$(V \times Q)$ matrix) mean maps for each network in prior
prior_var	$(V \times Q)$ matrix) between-subject variance maps for each network in prior
meshes	NULL for spatial independence model, otherwise a list of objects of class "BBM_mesh" containing the triangular mesh (see make_mesh) for each brain structure.
BOLD	$(V \times Q)$ matrix) dimension-reduced fMRI data

theta	(list) current parameter estimates
C_diag	($Q \times 1$) diagonal elements of residual covariance after dimension reduction
H, Hinv	For dimension reduction
s0_vec	Vectorized prior means
D	Sparse diagonal matrix of prior standard deviations
Dinv_s0	The inverse of D times s0_vec
verbose	If TRUE, display progress of algorithm. Default: FALSE.
return_MAP	If TRUE. return the posterior mean and precision of the latent fields instead of the parameter estimates. Default: FALSE.
update	Which parameters to update. Either "all", "A" or "kappa".
update_nu0sq	For non-spatial model: updating nu0sq is recommended if dimension reduction was not performed, and is not recommended if it was.

Value

An updated list of parameter estimates, theta, OR if return_MAP=TRUE, the posterior mean and precision of the latent fields

var_sq_err	<i>Compute the error between empirical and theoretical variance of covariance matrix elements</i>
------------	---

Description

Compute the error between empirical and theoretical variance of covariance matrix elements

Usage

```
var_sq_err(nu, p, var_ij, xbar_ij, xbar_ii, xbar_jj)
```

Arguments

nu	Inverse Wishart degrees of freedom parameter
p	Matrix dimension for IW distribution
var_ij	Empirical between-subject variance of covariance matrices at element (i,j)
xbar_ij	Empirical mean of covariance matrices at element (i,j)
xbar_ii	Empirical mean of covariance matrices at the ith diagonal element
xbar_jj	Empirical mean of covariance matrices at the jth diagonal element

Value

Squared difference between the empirical and theoretical IW variance of covariance matrices at element (i,j)

`var_sq_err_constrained`*Compute the overall error between empirical and theoretical variance of CORRELATION matrix elements*

Description

Compute the overall error between empirical and theoretical variance of CORRELATION matrix elements

Usage

```
var_sq_err_constrained(nu, p, var, xbar, M = 10000)
```

Arguments

<code>nu</code>	Inverse Wishart degrees of freedom parameter
<code>p</code>	Matrix dimension for IW distribution
<code>var</code>	Empirical between-subject variances of CORRELATION matrix (upper triangle)
<code>xbar</code>	Empirical mean of CORRELATION matrix (upper triangle)
<code>M</code>	Penalty to assign if theoretical variance is smaller than empirical variance

Value

Sum of squared difference between the empirical and theoretical IW variance of CORRELATION matrix, but with constraint that theoretical variances must not be smaller than empirical variances

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