Description  Factor analysis implementation for multiple data sources, i.e., for groups of variables. The whole data analysis pipeline is provided, including functions and recommendations for data normalization and model definition, as well as missing value prediction and model visualization. The model group factor analysis (GFA) is inferred with Gibbs sampling, and it has been presented originally by Virtanen et al. (2012), and extended in Klami et al. (2015) <DOI:10.1109/TNNLS.2014.2376974> and Bunte et al. (2016) <DOI:10.1093/bioinformatics/btw207>; for details, see the citation info.

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**Group factor analysis.**

**Description**

GFA does factor analysis for multiple data sets having matched observations, for exploratory or predictive data analysis.

**Details**

The posterior distribution of GFA model parameters can be inferred with function `gfa`, once the priors have been defined with `getDefaultOpts`. The priors are widely customizable, with two recommended setups: (i) dense group-sparse components (default; similar to package CCAGFA that provides variational Bayesian inference for the same model) and (ii) components interpretable as biclusters. It is recommended to preprocess the data with function `normalizeData`. Functions are provided for predicting missing data, choosing a prior for the residual noise, identifying robust components and visualizing the inferred model. A simple toy example of the pipeline is provided as demo(GFApipeline), and a more elaborate one as demo(GFAexample). Finally, the experiment presented in (Bunte, Leppaaho, Saarinen and Kaski: Sparse group factor analysis for biclustering of multiple data sources, Bioinformatics, 32(16):2457–2463, 2016) can be replicated with demo(GFAdream). Most of the computational complexity of the package is related to matrix operations, which can be parallelized inherently by using e.g. OpenBLAS libraries.

**Examples**

```r
# Data generation
X <- matrix(rnorm(20*3),20,3)  # Latent variables
W <- matrix(rnorm(30*3),30,3)  # Projection matrix
Y <- tcrossprod(X,W) + matrix(rnorm(20*30),20,30)  # Observations
Y <- sweep(Y, MARGIN=2, runif(30), "+")  # Feature means
Y <- list(Y[,1:10], Y[,11:30])  # Data grouping

# Model inference and visualization
norm <- normalizeData(Y, type="center")  # Centering
opts <- getDefaultOpt()  # Model options
# Fast runs for the demo, default options recommended in general
opts[c("iter.burnin", "iter.max")] <- c(500, 1000)
res <- gfa(norm$train, K=5, opts=opts)  # Model inference
rec <- reconstruction(res)  # Reconstruction
recOrig <- undoNormalizeData(rec, norm)  # ... to original space
vis <- visualizeComponents(res, Y, norm)  # Visualization
```
**getDefaultOpts**

A function for generating the default priors of GFA model

**Description**

`getDefaultOpts` returns the priors of GFA.

**Usage**

```r
getDefaultOpts(bicluster = FALSE)
```

**Arguments**

- `bicluster` Use binary sparsity priors in both the data modes? If FALSE (default), the components will be dense in the data sources, but group-sparse, i.e., each component is active in a (potentially different) subset of the data sources. If TRUE, binary sparsity is inferred for each data sample and feature, resulting in each component to be interpretable as a multi-source bicluster.

**Details**

This function returns options defining the model’s high-level structure (sparsity priors) and the model’s hyperparameters, defining uninformative priors. We recommend keeping these as provided, with one exception: if the uninformative prior of the noise residual (tau) seems to result in an overly complex model (no components become shut down even if the initial K is set high), risking overfitting, we recommend using function `informativeNoisePrior` to adjust the priors.

**Value**

A list with the following model options:

- `tauGrouped` If TRUE (default), data views have separate noise precisions, otherwise each feature has.
- `normalLatents` If TRUE, X will have a normal prior; if FALSE X, will have a spike-and-slab prior.
- `spikeW` Sparsity prior of W. "group"=group sparsity, "element"= element-wise sparsity with shared hyperparameter across views, "shared"= element-wise sparsity with no grouping.
- `ARDW` ARD prior type for W, determining the scale of the inferred components. "shared"=same scale for all the data sources, "grouped" (default)= separate scale for each data source, "element"=separate scale for each feature.
- `ARDLatent` ARD prior type for X: "shared" (default)=shared scale for all the samples, "element"=separate scale for each sample.
imputation Missing value imputation type: "Bayesian" (default)=proper Bayesian handling of missing values. "conservative"=missing values result in smaller parameter scale, which can be useful if tricky missing value structure causes exaggerated imputed values with the default setting (which can also be dealt with informative priors for alpha and beta).

iter.max The total number of Gibbs sampling steps (default 5000).

iter.saved The number of saved posterior samples (default 100).

iter.burnin The number of burn-in samples (default 2500).

init.tau The initial noise precision. High values imply initializing the model with an adequate number of components. Default 1000.

sampleZ When to start sampling spike and slab parameters (default: Gibbs sample 1).

prior.alpha_0t The shape parameter of tau’s prior (default 10).

prior.beta_0t The rate parameter of tau’s prior (default 10).

prior.alpha_0 The shape parameter of alpha’s prior (default 10).

prior.beta_0 The rate parameter of alpha’s prior (default 01).

prior.alpha_0X The shape parameter of beta’s prior (default 10).

prior.beta_0X The rate parameter of beta’s prior (default 1).

prior.beta Bernoulli prior for the spike-and-slab prior of W (counts for 1s and 0s; default c(1,1)).

prior.betaX Bernoulli prior for the possible spike-and-slab prior of X (default c(1,1)).

verbose The verbosity level. 0=no printing, 1=moderate printing, 2=maximal printing (default 1).

convergenceCheck Check for the convergence of the data reconstruction, based on the Geweke diagnostic (default FALSE).

save.posterior A list determining which parameters’ posterior samples are saved (default: X, W and tau).

Examples

#Given pre-specified data collection Y and component number K
opts <- getDefaultOpts(bicluster=FALSE)
opts$normalLatents <- FALSE #Binary sparsity for each sample and data source
## Not run: model <- gfa(Y,opts,K)

---

gfa Gibbs sampling for group factor analysis

Description

gfa returns posterior samples of group factor analysis model.
Usage

gfa(Y, opts, K = NULL, projection = NULL, filename = "")

Arguments

Y Either
  1. Data sources with co-occurring samples: a list of data matrices, where Y[[m]]
     is a numeric $N \times D_m$ matrix, or
  2. Data sources paired in two modes (some data sources share the samples of
     the first data source, and some share its features): A list with two elements
     structured as 1. The data collections Y[[1]] and Y[[2]] should be connected
     by sharing their first data source, i.e. Y[[1]][[1]] should equal the transpose
     of Y[[2]][[1]].

NOTE: The data features should have roughly zero mean and unit variance.
If this is not the case, preprocessing with function normalizeData is recom-
     mended.

opts List of model options; see function getDefaultOpts.

K The number of components (i.e. latent variables). Recommended to be set some-
    what higher than the expected component number, so that the sampler can de-
    termine the model complexity by shutting down excessive components. High
    values result in high CPU time. Default: half of the minimum of the sample size
    and total data dimensionality.

projection Fixed projections. Only intended for sequential prediction use via function
    sequentialGfaPrediction. Default: NULL.

filename A string. If provided, will save the sampling chain to this file every 100 itera-
    tions. Default ",", inducing no saving.

Details

GFA allows factor analysis of multiple data sources (i.e. data sets). The priors of the model can be
set to infer bicluster structure from the data sources; see getDefaultOpts. Missing values (NAs)
are inherently supported. They will not affect the model parameters, but can be predicted with
function reconstruction, based on the observed values of the corresponding sample and feature.
The association of a data source to each component is inferred based on the data. Letting only a
subset of the components to explain a data source results in the posterior identifying relationships
between any subset of the data sources. In the extreme cases, a component can explain relationships
within a single data source only ("structured noise"), or across all the data sources.

Value

A list containing the model parameters - in case of pairing in two modes, each element is a list of
length 2; one element for each mode. For most parameters, the final posterior sample is provided to
aid in initial checks; all the posterior samples should be used for model analysis. The list elements
are:

w The loading matrix (final posterior sample); $D \times K$ matrix.

x The latent variables (final sample); $N \times K$ matrix.
informativeNoisePrior

Z The spike-and-slab parameters (final sample); $D \times K$ matrix.
r The probability of slab in Z (final sample).
$rz$ The probability of slab in the spike-and-slab prior of X (final sample).
tau The noise precisions (final sample); D-element vector.
alpha The precisions of the projection weights W (final sample); $D \times K$ matrix.
beta The precisions of the latent variables X (final sample); $N \times K$ matrix.
groups A list denoting which features belong to each data source.
D Data dimensionalities; M-element vector.
K The number of components inferred. May be less than the initial K.

and the following elements:

posterior the posterior samples of, by default, X, W and tau.
cost The likelihood of all the posterior samples.
aic The Akaike information criterion of all the posterior samples.
opts The options used for the GFA model.
conv An estimate of the convergence of the model’s reconstruction based on Geweke diagnostic. Values significantly above 0.05 imply a non-converged model, and hence the need for a longer sampling chain.
time The CPU time (in seconds) used to sample the model.

informativeNoisePrior Informative noise residual prior

Description

informativeNoisePrior returns an informative noise prior for GFA, for a given data collection. The function sets the noise residual parameters such that the expected proportion of variance explained is for all variables and groups (in contrast to being proportional to their original scale). Recommended e.g. when the data is 'small n, large p', and the standard prior from getDefaultOpts seems to overfit the model by not shutting off any component with high initial K.

Usage

informativeNoisePrior(Y, opts, noiseProportion = 0.5, conf = 1)

Arguments

Y The data. For details, see function gfa.
opts Model options. See function getDefaultOpts for details. If option tauGrouped is TRUE (default), each data source is given equal importance (feature importance may vary within each source). If it is FALSE, each feature is given equal importance.
normalizeData

noiseProportion
proportion of total variance to be explained by noise. Suggested to lie between 0.01 and 0.99.

conf
Confidence in the prior, relative to confidence in the data. Suggested to lie between 0.01 and 100.

Value
The input model options (opts) with an updated residual noise prior, corresponding to the elements prior.alpha_0t and prior.beta_0t.

Examples
#Given data collection Y
opts <- getDefaultOpts()
## Not run: opts <- informativeNoisePrior(Y,opts,0.2,1)
## Not run: res <- gfa(Y,opts=opts)

normalizeData Normalize data to be used by GFA

Description
normalizeData is used to transform a data collection into a normalized form suitable for GFA. This function does two things: 1. It centers each variable. GFA assumes zero-mean data, as it models variances. 2. It normalizes the scales of variables and/or variable groups. Features with higher variance will affect the model structure more; if this is not desired, the normalization should be done. In GFA it is additionally possible to normalize the importance of variable groups (data sources), in addition or instead of individual variables. Finally, the total variance of data is normalized for numerical reasons. This is particularly important if no other normalization is done. NOTE: the function assumes continuous-valued data. If some features are e.g. binary with only a small portion of 1s, we do not recommend centering them.

Usage
normalizeData(train, test = NULL, type = "scaleOverall")

Arguments

train a training data set. For a detailed description, see parameter Y in gfa.
test a test dataset. Should be provided if sequential prediction is used later.
type Specifies the type of normalization to do. Mean-centering of the features is performed in all the cases, and option "center" does not perform any scaling. Option "scaleOverall" (default) uses a single parameter to scale the variance of the whole data collection to 1, while "scaleSources" scales each data source to have variance 1. Finally, "scaleFeatures" performs z-normalization, i.e. assigns the variance of each feature to 1.
**reconstruction**

**Value**

A list containing the following elements:

- **train** Normalized training data.
- **test** Normalized test data for sequential prediction (if provided as input).
- **trainMean** Feature-wise means of the training data sources.
- **trainSd** Feature-wise/overall standard deviations of the training data sources.

---

**reconstruction**  
*Full data reconstruction based on posterior samples*

**Description**

reconstruction returns the full data reconstruction based on given posterior samples.

**Usage**

reconstruction(res, average = TRUE)

**Arguments**

- **res** The sampled model from function gfa
- **average** If TRUE (default), averages the reconstruction over the posterior predictive samples. If set to FALSE, the output may require a large amount of memory. In case of large input data, we recommend acquiring the posterior predictive samples for subsets of data at a time, based on this implementation.

**Value**

The data reconstruction, a numeric $N \times \sum_{m=1}^{M} D_m$ matrix, if average is TRUE (default). Otherwise, the reconstruction is a $N \times \sum_{m=1}^{M} D_m \times N_{post}$ array, with posterior samples in the third dimension. If the input data has been paired in two modes, the output will be a list of length 2, one element corresponding to each mode.
robustComponents

Robust GFA components

Description

robustComponents analyzes a collection of sampling chains and returns robust components.

Usage

robustComponents(models, corThr = 0.9, matchThr = 0.5)

Arguments

- **models**: Either a vector containing the file names, where the models are saved as 'res', or a list containing the models.
- **corThr**: How close two components are required to be, in terms of correlation, in order to match them.
- **matchThr**: How big proportion of the chains need to contain the component to include it in the robust components.

Details

The function returns the effects (i.e. reconstructions) of robust components to the data level. It is useful for a thorough model interpretation, accumulating power over several sampling chains by comparing them in the observation space (as opposed to the latent space). The function is needed for this task, as the extreme multi-modality of factor analysis prohibits efficient sampling techniques that would result in a posterior estimate converging to the true posterior in practice. The function uses a heuristic correlation-based procedure to analyze which components occur frequently in GFA sampling chains.

Value

A list with the following elements (when input data are paired in two modes, the returned list is of length 2, containing the following elements for each mode):

- **Krobust**: The number of robust components found with the given thresholds.
- **effect**: The component effect in the data space; and array of size $N \times \sum_{m=1}^{M} D_m \times Krobust$.
- **indices**: The corresponding component indices; a \(\text{length}(models) \times Krobust\) matrix. Negative indices denote the closest component in the corresponding repetition, having no components above the threshold.
- **cor**: The correlations of the components matched to this robust component; a matrix of size \(\text{length}(models) \times Krobust\). The correlations are reported relative to the first repetition with this component observed.
**Examples**

```r
X <- matrix(rnorm(10*2),10,2)
W <- matrix(rnorm(15*2),15,2)
Y <- tcrossprod(X,W) + matrix(rnorm(10*15),10,15)
opts <- getDefaultOpts() #Default options
#Fast runs for the demo, default options recommended in general
opts[c("iter.burnin", "iter.max")]<- c(500, 1000)
res <- list()
for(i in 1:4) res[[i]] <- gfa(list(Y[,1:6], Y[,7:15]), opts=opts,K=3)
rob <- robustComponents(res)
```

**sequentialGfaPrediction**

*Sequential prediction of new samples from observed data views to unobserved*

**Description**

sequentialGfaPrediction returns predictions for unobserved data sources of a new set of data samples.

**Usage**

`sequentialGfaPrediction(Y, model)`

**Arguments**

- **Y**
  - The new data samples, in a similar format as in function `gfa`

- **model**
  - The sampled model from function `gfa`, with `model$opts$predict` being a logical vector with the length matching the length of `Y`, describing which data views will be predicted (TRUE), and which have been observed (FALSE).

**Value**

A list containing the predictions, with the observed data sources empty. Additionally, sampling MSE is given as element 'mse', and likelihood as 'cost'.
undoNormalizeData  

A function for returning predictions into the original data space

**Description**

undoNormalizeData returns the predictions on normalized data acquired from `normalizeData` into the original data space.

**Usage**

undoNormalizeData(pred, normalization)

**Arguments**

- `pred` The predictions acquired from `reconstruction`.
- `normalization` The output list obtained from `normalizeData`.

**Value**

The predictions in the original data space.

visualizeComponents  

Visualize GFA components

**Description**

visualizeComponents illustrates the factorization inferred by GFA, averaging over the posteriors of the parameters, if they have been stored.

**Usage**

visualizeComponents(
    model,
    Y = NULL,
    norm = NULL,
    mode = 1,
    showAll = TRUE,
    hclust = FALSE,
    topK = 3,
    topFeatures = NA,
    topSamples = NA
)
visualizeComponents

Arguments

- **model**: The learned GFA model.
- **Y**: The used input data to be plotted, if supplied. Default NULL.
- **norm**: The normalization acquired from `normalizeData`, if applied. If provided, the reconstruction is shown in the original data space. Default NULL.
- **mode**: Determines which mode to visualize in case of pairing in two modes (default: 1).
- **showAll**: Show the full predictions and factorizations? May be cumbersome for large data. Default TRUE.
- **hclust**: Order features and samples based on hierarchical clustering? Default FALSE.
- **topK**: Number of strongest components visualized in the data space. Default 3.
- **topFeatures**: How many most relevant features to show for the data space visualizations? Default NA, showing all the features.
- **topSamples**: How many most relevant samples to show for the data space visualizations? Default NA, showing all the samples.

Value

A list containing the matrices that have been visualized.
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