Package: bpgmm (via r-universe)

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Type Package

Title Bayesian Model Selection Approach for Parsimonious Gaussian Mixture Models

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Imports methods (>= 3.5.1), mcmcse (>= 1.3-2), pgmm (>= 1.2.3), mvtnorm (>= 1.0-10), MASS (>= 7.3-51.1), parallel, Rcpp (>= 1.0.1), gtools (>= 3.8.1), label.switching (>= 1.8), fabMix (>= 5.0), mclust (>= 5.4.3)

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Description Model-based clustering using Bayesian parsimonious Gaussian mixture models. MCMC (Markov chain Monte Carlo) are used for parameter estimation. The RJMCMC (Reversible-jump Markov chain Monte Carlo) is used for model selection. GREEN et al. (1995) <doi:10.1093/biomet/82.4.711>.

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URL https://github.com/YaoxiangLi/bpgmm, https://yaoxiangli.github.io/bpgmm/, https://doi.org/10.1007/s00357-021-09391-8

BugReports https://github.com/YaoxiangLi/bpgmm/issues

Encoding UTF-8

RoxygenNote 7.3.2

Suggests knitr, rmarkdown, testthat

LinkingTo Rcpp, RcppArmadillo

VignetteBuilder knitr

NeedsCompilation yes

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`constraint_to_model` *Convert PGMM Constraint Codes to Paper Model Names*

Description

The paper represents the eight PGMM covariance structures with three-letter model names. Each letter is either ‘C‘ for constrained or ‘U‘ for unconstrained. The letters indicate whether the loading matrix is shared across clusters, whether the noise covariance is shared across clusters, and whether the noise covariance is isotropic within clusters.

Usage

```
constraint_to_model(constraint)
```

Arguments

`constraint`	Integer or numeric vector of length three with entries ‘0‘ or ‘1‘. ‘1‘ maps to ‘C‘; ‘0‘ maps to ‘U‘.

Value

A character scalar, one of ‘CCC‘, ‘CCU‘, ‘CUC‘, ‘CUU‘, ‘UCC‘, ‘UCU‘, ‘UUC‘, or ‘UUU‘.

model_to_constraint *Convert PGMM Paper Model Names to Constraint Codes*

Description

Convert PGMM Paper Model Names to Constraint Codes

Usage

```
model_to_constraint(model)
```

Arguments

model	Character scalar naming one of the eight PGMM covariance structures: 'CCC', 'CCU', 'CUC', 'CUU', 'UCC', 'UCU', 'UUC', or 'UUU'.

Value

Integer vector of length three. '1' means constrained and '0' means unconstrained.

pgmm_rjmcmc *Bayesian Model-Based Clustering with Parsimonious Gaussian Mixture Models*

Description

Carries out model-based clustering using parsimonious Gaussian mixture models. MCMC is used for parameter estimation and RJMCMC is used for model selection.

Usage

```
pgmm_rjmcmc(
  X,
  m_init,
  m_range,
  q_new,
  delta = 2,
  ggamma = 2,
  burn = 20,
  niter = 1000,
  constraint = c(0, 0, 0),
  d_vec = c(1, 1, 1),
  s_vec = c(1, 1, 1),
  m_step = 0,
  v_step = 0,
  split_combine = 0,
  verbose = TRUE
)
```

Arguments

X	the observation matrix with variables in rows and observations in columns.
m_init	the number of initial clusters.
m_range	the allowed range for the number of clusters.
q_new	the number of latent factors for a new cluster.
delta	scalar hyperparameter for the noise covariance prior
ggamma	scalar hyperparameter used in covariance-structure proposals
burn	the number of burn-in iterations
niter	the number of posterior sampling iterations
constraint	initial PGMM covariance constraint. Use a three-letter model label such as '"CCC"' or '"UUU"', or a numeric vector of length three with binary entries. For example, 'c(1, 1, 1)' is 'CCC', the fully constrained model, and 'c(0, 0, 0)' is 'UUU', the fully unconstrained model.
d_vec	a vector of hyperparameters with length three, shape parameters for alpha1, alpha2 and bbeta respectively
s_vec	a vector of hyperparameters with length three, rate parameters for alpha1, alpha2 and bbeta respectively
m_step	indicator for RJMCMC model selection on the number of clusters.
v_step	indicator for RJMCMC model selection on covariance structures.
split_combine	indicator for using split/combine moves in the cluster-number RJMCMC step.
verbose	logical; if 'TRUE', print iteration progress.

Details

The 'constraint' argument follows the three-letter PGMM model notation used in Lu, Li, and Love (2021). The first entry indicates whether loading matrices are shared across clusters, the second whether noise covariance matrices are shared across clusters, and the third whether the noise covariance is isotropic within each cluster. Use [model_to_constraint()] to convert model names such as 'CCC', 'CCU', 'CUC', 'CUU', 'UCC', 'UCU', 'UUC', and 'UUU' into the numeric vector used internally.

Value

A list of posterior samples with snake_case fields: 'tau_samples', 'psi_samples', 'mean_samples', 'lambda_samples', 'factor_score_samples', 'allocation_samples', 'constraint_samples', 'alpha1_samples', 'alpha2_samples', 'beta_samples', and 'active_cluster_samples'.

`pgmm_rjmcmc_chains` *Run Multiple Independent Bayesian PGMM Chains*

Description

Runs independent ‘pgmm_rjmcmc()‘ chains, optionally in parallel. This is the safest way to use multiple CPU cores because each MCMC iteration depends on the previous state, while independent chains can be evaluated concurrently.

Usage

```
pgmm_rjmcmc_chains(
  X,
  m_init,
  m_range,
  q_new,
  delta = 2,
  ggamma = 2,
  burn = 20,
  niter = 1000,
  constraint = c(0, 0, 0),
  d_vec = c(1, 1, 1),
  s_vec = c(1, 1, 1),
  m_step = 0,
  v_step = 0,
  split_combine = 0,
  verbose = FALSE,
  chains = 2,
  cores = min(chains, available_cores()),
  seed = NULL
)
```

Arguments

`X`	the observation matrix with variables in rows and observations in columns.
`m_init`	the number of initial clusters.
`m_range`	the allowed range for the number of clusters.
`q_new`	the number of latent factors for a new cluster.
`delta`	scalar hyperparameter for the noise covariance prior
`ggamma`	scalar hyperparameter used in covariance-structure proposals
`burn`	the number of burn-in iterations
`niter`	the number of posterior sampling iterations
`constraint`	initial PGMM covariance constraint. Use a three-letter model label such as ‘"CCC"‘ or ‘"UUU"‘, or a numeric vector of length three with binary entries. For example, ‘c(1, 1, 1)‘ is ‘CCC‘, the fully constrained model, and ‘c(0, 0, 0)‘ is ‘UUU‘, the fully unconstrained model.

d_vec	a vector of hyperparameters with length three, shape parameters for alpha1, alpha2 and bbeta respectively
s_vec	a vector of hyperparameters with length three, rate parameters for alpha1, alpha2 and bbeta respectively
m_step	indicator for RJMCMC model selection on the number of clusters.
v_step	indicator for RJMCMC model selection on covariance structures.
split_combine	indicator for using split/combine moves in the cluster-number RJMCMC step.
verbose	logical; if 'TRUE', print iteration progress.
chains	positive integer giving the number of independent chains.
cores	positive integer giving the number of worker processes to use. Values greater than 'chains' are reduced to 'chains'.
seed	optional integer seed used to generate deterministic per-chain seeds.

Value

A list with one fitted 'pgmm_rjmcmc()' result per chain. The result has class 'bpgmm_rjmcmc_chains' and stores the per-chain seeds in the 'chain_seeds' attribute.

`summarize_pgmm_rjmcmc` *Summarize RJMCMC Samples from a Bayesian PGMM Fit*

Description

Summarizes posterior samples from [pgmm_rjmcmc()] into the modal allocation, posterior counts for the number of clusters, posterior counts for the eight PGMM covariance-constraint models, and optionally the adjusted Rand index against a known reference partition.

Usage

```
summarize_pgmm_rjmcmc(fit, true_cluster = NULL)
```

Arguments

fit	Result list from [pgmm_rjmcmc()].
true_cluster	Optional true or reference cluster allocation.

Value

A list with 'allocation', 'n_clusters', 'n_constraints', and optionally 'ari'.

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