Package 'vbmp'

November 12, 2026

Type Package

Title Variational Bayesian Multinomial Probit Regression

Version 1.80.0

Author Nicola Lama <nicola.lama@unina2.it>, Mark Girolami <girolami@dcs.gla.ac.uk>

Maintainer Nicola Lama <nicola.lama@unina2.it>

Description Variational Bayesian Multinomial Probit Regression with Gaussian Process Priors. It estimates class membership posterior probability employing variational and sparse approximation to the full posterior. This software also incorporates feature weighting by means of Automatic Relevance Determination.

License GPL (>= 2)

Suggests Biobase (>= 2.5.5), statmod

LazyLoad Yes

Depends R (>= 2.10)

URL http://bioinformatics.oxfordjournals.org/cgi/content/short/btm535v1

biocViews Classification

git_url https://git.bioconductor.org/packages/vbmp

git_branch RELEASE_3_23

git_last_commit 14204bf

git_last_commit_date 2026-04-28

Repository Bioconductor 3.23

Date/Publication 2026-11-11

Contents

BRCA12 2
covParams 3

lowerBound 3
plotDiagnostics 4
predClass 4
predError 5
predictCPP 5
predLik 6
vbmp 6

Index **11**

BRCA12 *BRCA tumour dataset*

Description

This data set gives the gene expression values of 30 breast cancer patients. Short-term primary fibroblast cultures were established from skin biopsies from 10 BRCA1 and 10 BRCA2 mutation carriers and 10 controls.

Usage

```
BRCA12
```

Format

`ExpressionSet` object containing 8080 genes x 30 pts. Case and controls are specified in `Target.class` of `phenoData`.

Source

The Institute of Cancer Research, Sutton, Surrey, UK

References

Zsofia Kote-Jarai et al. *Accurate Prediction of BRCA1 and BRCA2 Heterozygous Genotype Using Expression Profiling after Induced DNA Damage*, Clin Cancer Res 2006;12(13)

covParams *VBMP covariance functions parameters*

Description

Returns the value of the covariance functions parameters (theta).

Usage

```
covParams(obj)
```

Arguments

obj	an object inheriting from class VBMP.obj, usually the result of a call to vbmp

See Also

See Also as vbmp

lowerBound *VBMP Lower bound estimate*

Description

Returns the lower bound estimates for the VBMP fitted model.

Usage

```
lowerBound(obj)
```

Arguments

obj	an object inheriting from class VBMP.obj, usually the result of a call to vbmp

See Also

See Also as vbmp

plotDiagnostics *VBMP covariance diagnostics plot*

Description

plot the evolution of convergence diagnostics: lower-bound, predictive likelihood, out-of-bound test error and theta params (when inferred)

Usage

```
plotDiagnostics(obj)
```

Arguments

obj	an object inheriting from class VBMP.obj, usually the result of a call to vbmp

See Also

See Also as vbmp

predClass *VBMP Predicted class values*

Description

Predicted class targets of test dataset.

Usage

```
predClass(obj)
```

Arguments

obj	an object inheriting from class VBMP.obj, usually the result of a call to vbmp

See Also

See Also as vbmp

predError *Out-of-Sample VBMP Prediction error*

Description

Out-of-Sample Percent Prediction error estimate (0-1 error loss).

Usage

```
predError(obj)
```

Arguments

obj	an object inheriting from class VBMP.obj, usually the result of a call to vbmp

See Also

See Also as vbmp

predictCPP *VBMP predict functions parameters*

Description

Obtains estimates of class posterior probabilities from a fitted VBMP object

Usage

```
predictCPP(obj, X.TEST=NULL)
```

Arguments

obj	an object inheriting from class VBMP.obj, usually the result of a call to vbmp
X.TEST	optionally, matrix in which to look for variables with which to predict. If omitted, the fitted predictors are used.

See Also

See Also as vbmp

predLik *VBMP predictive likelihood estimate*

Description

Returns the predictive likelihood estimate for the VBMP fitted model.

Usage

```
predLik(obj)
```

Arguments

obj	an object inheriting from class VBMP.obj, usually the result of a call to vbmp

See Also

See Also as vbmp

vbmp *Variational Bayesian Multinomial Probit Regression with Gaussian Process Priors.*

Description

Used to fit a Multinomial Probit Regression model, specified by giving the matrix design X, the associated response variables t.class, kernel type and covariate scaling parameters. Covariance paramters can be inferred from the data.

Usage

```
vbmp(X, t.class, X.TEST, t.class.TEST, theta, control = list())
```

Arguments

X	Feature matrix for parameter 'estimation'
t.class	Target values, integer number used for class labels.
X.TEST	Feature matrix to compute out-of-sample (test) prediction errors and likelihoods
t.class.TEST	Target values for test data
theta	The covariance function parameters (e.g. scaling coefficients for each dimension)
control	A list of control parameters. See Details

Details

In this implementation a single covariance function is shared across all classes. Compute the predictive posteriors on the test set and the associated likelihood and test errors at each iteration.

The control argument is a list that can supply any of the following components:

InfoLevel 0 to suppress tracing (> 0 to print different levels of monitoring information)

sFILE.TRACE File name where to redirect output (default NULL)

bThetaEstimate if covariance parameter estimation switched on. Defaults to FALSE (switched off)

sKernelType Kernel function used in training and predicting. Currently implemented kernels are Gaussian (`"gauss"`), Cauchy (`"cauchy"`), Laplace (`"laplace"`), Polynomial (`"poly"`), Homogeneous polynomial (`"hpoly"`), 'Thin-plate' spline (`"tps"`), 'linear' spline (`"lsp"`) and Inner product(`"iprod"`). Defaults to `"gauss"`.

maxIts Maximum number of variational EM steps to take. Defaults to 50.

Thresh Convergence threshold on marginal likelihood lowerbound. Defaults to 1e-4.

method Integral computation method: "quadrature" (Gaussian quadrature) or "classic"(simple sampler). Defaults to "quadrature".

nNodesQuad Number of nodes used for quadrature. Defaults to 49.

nSampsTG Number of samples used in obtaining mean of truncated Gaussian. Defaults to 1000.

nSampsIS Number of samples used in the importance sampler. Defaults to 1000.

nSmallNo Small number used to prevent numerical problems (ill-conditioned covariance matrix). Defaults to 1e-10.

parGammaTau,parGammaSigma The location and scale parameters of the Gamma prior over covaraince params. Default to 1e-6.

bMonitor TRUE to collect monitor convergence diagnostics at each iteration. Defaults to FALSE.

bPlotFitting TRUE to plot test performance results at each iteration during model estimation (if TRUE it forces bMonitor to TRUE). Defaults to FALSE.

Value

`vbmp` returns an object of class "VBMP.obj". An object of class "VBMP.obj" is a list containing at least the following components:

`Kc`	Number of classes
`Ptest`	Matrix of multinomial class predictive posterior probabilities for the test data
`X`	Feature matrix
`invPHI`	Inverse of the Kernel matrix
`Y`	Matrix of auxiliary variables
`M`	Matrix of GP random variables
`theta`	covariance kernel hyperparameters (estimates computed during model fitting, if inferred
`sKernelType`	Kernel function used in training and predicting

Test.Err	Out-of-Sample Percent Prediction error estimates computed during model fitting (0-1 error loss).
PL	Predictive Likelihood estimates computed during model fitting
LOWER.BOUND	Lower bound estimates computed during model fitting

Author(s)

N Lama <nicola.lama@unina2.it>, MA Girolami <girolami@dcs.gla.ac.uk>

References

Girolami M, Rogers S, *Variational Bayesian Multinomial Probit Regression with Gaussian Process Priors*, Neural Computation 18, 1790-1817 (2006). Lama N, Girolami M *vbmp: Variational Bayesian Multinomial Probit Regression for multi-class classification in R*, Bioinformatics 24(1):135-136 (2008). http://bioinformatics.oxfordjournals.org/cgi/content/short/btm535v1

See Also

See Also as predictCPP, covParams, lowerBound, predError, predLik, predClass

Examples

```
## ------------------------------------------------------------------------
## EXAMPLE 1 - Theta estimate with synthetic data
## ------------------------------------------------------------------------
## Samples of 2-D data points drawn from three nonlinearly separable
## classes which take the form of two annular rings and one zero-centered
## Gaussian are used in this little illustrative example.
genSample <- function(n, noiseVar=0) {
    ## class 1 and 2 (x ~ U(0,1))
    u <- 4. * matrix(runif(2*n), nrow=n, ncol=2) - 2.;
    i <- which(((u[, 1]^2 + u[, 2]^2) > .1) & ((u[, 1]^2 + u[, 2]^2) < .5) );
    j <- which(((u[, 1]^2 + u[, 2]^2) > .6) & ((u[, 1]^2 + u[, 2]^2) < 1) );
    X <- u[c(i, j),];
    t.class <- c(rep(1, length(i)),rep(2, length(j)));
    ## class 3 (x ~ N(0,1))
    x <- 0.1 * matrix(rnorm(2*length(i)), ncol=2, nrow=length(i) );
    k <- which((x[, 1]^2 + x[, 2]^2) < 0.1);
    X <- rbind(X, x[k, ]);
    t.class <- c(t.class, rep(3, length(k)));
    ## add random coloumns
   if (noiseVar>0) X <- cbind(X, matrix(rnorm(noiseVar*nrow(X)), ncol=noiseVar, nrow=nrow(X)));
    structure( list( t.class=t.class, X=X), class="MultiNoisyData");
}

set.seed(123); ## Init random number generator

## Generate training and test samples as an independent
## test set to assess out-of-sample prediction error
## and predictive likelihoods.
nNoisyInputs <- 0;       ## number of additional noisy input parameters
```

```
Ntest <- Ntrain <- 500;  ## sample sizes
dataXt.train <- genSample(Ntrain, nNoisyInputs);
dataXt.test  <- genSample(Ntest,  nNoisyInputs);

## Not run:
 theta <- runif(ncol(dataXt.train$X));
 res <- vbmp( dataXt.train$X, dataXt.train$t.class,
        dataXt.test$X, dataXt.test$t.class, theta,
         control=list(bThetaEstimate = T,
         bPlotFitting=T, maxIts=50));

## End(Not run)

## set theta params (previously estimated)
theta <- c(0.09488309, 0.16141604);
## Fit the vbmp
res <- vbmp( dataXt.train$X, dataXt.train$t.class,
        dataXt.test$X, dataXt.test$t.class, theta,
        control=list(maxIts=5));
## print out-of-sample error estimate
predError(res);

## Not run:
## ------------------------------------------------------------
## EXAMPLE 2 - BRCA12 genomic data
## ------------------------------------------------------------
## Leave-one-out (LOO) cross-validation prediction error of the probabilistic
## Gaussian process classifier used in Zsofia Kote-Jarai et al.
## Clin Cancer Res 2006;12(13);3896-3901

  if(any(installed.packages()[,1]=="Biobase")) {
    library("Biobase");
    data("BRCA12");
    brca.y <- BRCA12$Target.class;
    brca.x <- t(exprs(BRCA12));
  } else {
    print("Deprecated.....");
   load(url("http://www.dcs.gla.ac.uk/people/personal/girolami/pubs_2005/VBGP/BRCA12.RData"));
    brca.y <- as.numeric(BRCA12$y);
    brca.x <- as.matrix(BRCA12[,-1]);
  }

  sKernelType <- "iprod";  ## Covariance function type
  Thresh <- 1e-8;  ## Iteration threshold
  InfoLevel <- 1;
  theta <- rep(1.0, ncol(brca.x));
  ITER.THETA <- 24;
  n     <- nrow(brca.x) ;
  Kfold <- n; # number of folds , if equal to n then LOO
  samps <- sample(rep(1:Kfold, length=n), n, replace=FALSE);
  res   <- rep(NA, n);
  print(paste("LOO crossvalidation started...... (",n,"steps)"));
  for (x in 1:Kfold) {
```

```
        cat(paste(x,", ",sep="")); flush.console();
        resX <- vbmp( brca.x[samps!=x,], brca.y[samps!=x],
                      brca.x[samps==x,], brca.y[samps==x],
                      theta,  control=list(bThetaEstimate=F,
                      bPlotFitting=F, maxIts=ITER.THETA,
                      sKernelType=sKernelType, Thresh=Thresh));
        res[samps==x] <- predClass(resX);
    }
    print("(end)");
    print(paste("Crossvalidated error rate", round(sum(res!=brca.y)/n,2)));

## End(Not run)
```

Index

∗ **datasets**
BRCA12, 2
∗ **models**
vbmp, 6
∗ **utilities**
covParams, 3
lowerBound, 3
plotDiagnostics, 4
predClass, 4
predError, 5
predictCPP, 5
predLik, 6

BRCA12, 2

covParams, 3, *8*

lowerBound, 3, *8*

plotDiagnostics, 4
predClass, 4, *8*
predError, 5, *8*
predictCPP, 5, *8*
predLik, 6, *8*

vbmp, *3–6*, 6