

vbmp

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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	<i>VBMP covariance functions parameters</i>
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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	<i>VBMP Lower bound estimate</i>
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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	<i>Out-of-Sample VBMP Prediction error</i>
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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](#)

predLik	<i>VBMP predictive likelihood estimate</i>
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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](#)

predictCPP

VBMP predict functions parameters

Description

Obtains estimates of class posterior probabilities from a fitted VBMP object

Usage

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

Arguments

<code>obj</code>	an object inheriting from class <code>VBMP</code> . <code>obj</code> , usually the result of a call to <code>vbmp</code>
<code>X.TEST</code>	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](#)

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 parameters can be inferred from the data.

Usage

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

Arguments

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

<code>Kc</code>	Number of classes
<code>Ptest</code>	Matrix of multinomial class predictive posterior probabilities for the test data
<code>X</code>	Feature matrix
<code>invPHI</code>	Inverse of the Kernel matrix
<code>Y</code>	Matrix of auxiliary variables
<code>M</code>	Matrix of GP random variables
<code>theta</code>	covariance kernel hyperparameters (estimates computed during model fitting, if inferred)
<code>sKernelType</code>	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

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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 columns
  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 <- "iproduct"; ## 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)
```

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