Variational Bayesian Multinomial Probit Regression for Gaussian Process multi-class classification

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Introduction

The vbmp package implements multinomial probit regression with Gaussian Process priors and 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.

For more detailed description of classification using multinomial-probit regression model with Gaussian Process priors, refer to Girolami and Rogers (2006).

To illustrate the potential of the method, a couple of examples are presented on a synthetic toy dataset and on literature data from the breast cancer study by Kote-Jarai et al. (2006)

The vbmp function

The vbmp function carries out multi-class classification training and testing. The control parameter list provides optional control settings. The default Gaussian Process covariance functions are radial basis-style functions but other choice are possible. Whether or not to infer the scale parameter of the covariance functions is an option (bThetaEstimate=T). The target values t.class and t.class.TEST can be factors or integer values in 1:n where n is the number of classes.

The synthetic toy dataset

In this illustrative example dataset is composed of uniformly distributed 2-D data points drawn from 3 nonlinearly separable classes which take the form of two annular rings and one zero-centered bivariate Gaussian with spherical covariance matrix (see Fig. 1). Four additional random noise parameters were added to the dataset

Gaussian kernel functions were adopted with scale parameter inferred by the vbmp method using vague hyperpriors (Gamma prior over covariance params defaults to $10^{-6}$). Monitor diagnostics are depicted in figure 2 where the progress of Automatic Relevance Detection (ARD) Neal (1998) is evident with the four irrelevant features are effectively removed from the model.
Define a function to generate the dataset:

```r
set.seed(123)

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```r
defineSample <- function(n, noiseVar = 0) {
  n <- 10
  nt <- round(n/3, 0)
  u <- 4 * matrix(runif(2 * KF * n), nrow = KF * n, ncol = 2) - 2
  i <- which(((u[, 1]^2 + u[, 2]^2) > 0.1) & ((u[, 1]^2 + u[, 2]^2) < 0.5))
  j <- which(((u[, 1]^2 + u[, 2]^2) > 0.6) & ((u[, 1]^2 + u[, 2]^2) < 1))
  X <- u[c(sample(i, nt), sample(j, nt)), ]
  t.class <- c(rep(1, nt), rep(2, nt))
  x <- 0.1 * matrix(rnorm(2 * KF * length(i)), ncol = 2, nrow = length(i) * KF)
  k <- which(((x[, 1]^2 + x[, 2]^2) < 0.1)
  nt <- n - 2 * nt
  X <- rbind(X, x[sample(k, nt), ])
  t.class <- c(t.class, rep(3, nt))
  if (noiseVar > 0)
    X <- cbind(X, matrix(rnorm(noiseVar * n), ncol = noiseVar, nrow = nrow(X)))
  structure(list(t.class = t.class, X = X), class = "MultiNoisyData")
```

Set the number of additional noisy input parameters:

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nNoisyInputs <- 4

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Set the sample sizes:

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Ntrain <- 100
Ntest <- Ntrain * 5

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Generate training and test samples independently:

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dataXtTrain <- genSample(Ntrain, nNoisyInputs)
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Initialization of scale covariance function and of the maximum number of iterations:

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theta <- rep(1, ncol(dataXtTrain$X))
max.train.iter <- 12

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Train, test and plot monitors

```r
library(vbmp)
res <- vbmp(dataXtTrain$X, dataXtTrain$t.class, dataXtTest$X,
+ dataXtTest$t.class, theta, control = list(bThetaEstimate = T,
+ bMonitor = T, maxIts = max.train.iter))
Figure 1: Scatter plot of the first two dimensions of the toy dataset. Classes are identified by different colors

Print the out-of-sample prediction error

> predError(res)

[1] 0.028
> plotDiagnostics(res)

Figure 2: Monitor diagnostics for the evolution of: posterior means for the Gaussian kernel scale parameters (top-left), lower bound on the marginal likelihood (top-right), predictive likelihood (bottom-left) and out-of-sample accuracy (0/1-error loss)
Breast cancer dataset

The dataset consist of 8080 genes and 30 samples from three classes of individual with specific gene mutations. As reported in Kote-Jarai et al. (2006) using a linear inner product covariance function the Leave-One-Out error is zero which improves on an SVM multiclass classifier adopted by Kote-Jarai et al. (2006).

```r
> library("Biobase")
> data("BRCA12")
> brca.y <- BRCA12$Target.class
> brca.x <- t(exprs(BRCA12))

Define a function to set up the target class predictor during cross-validation. It uses linear inner product covariance function and 24 training iterations and sets iteration threshold to $10^{-8}$. Initialize all theta values to 1 and, in this case, it is not necessarily to run the importance sampler to obtain the weightings in the features.

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```r
> predictVBMP <- function(x) {
+   sKernelType <- "iprod"
+   Thresh <- 1e-08
+   theta <- rep(1, ncol(brca.x))
+   max.train.iter <- 24
+   resX <- vbmp(brca.x[!x, ], brca.y[!x], brca.x[!x], brca.y[!x],
+     theta, control = list(bThetaEstimate = F, bPlotFitting = F,
+     maxIts = max.train.iter, sKernelType = sKernelType,
+     Thresh = Thresh))
+   predClass(resX)
+ }
```

In the following code, Kfold is the number of cross validation folds and it is set equal to n, the number of pts in the dataset, in order to obtain the Leave-One-Out approach. res collects the predicted targets.

```r
> n <- nrow(brca.x)
> Kfold <- n
> samps <- sample(rep(1:Kfold, length = n), n, replace = FALSE)
> res <- rep(NA, n)
> print(paste("Crossvalidation started...... (", n, "steps )"))
[1] "Crossvalidation started...... ( 30 steps )"

```r
> for (x in 1:Kfold) {
+   cat(paste(x, ", " ifelse(x%%10 == 0, ",n", ""), sep = ""))
+   flush.console()
+   res[samps == x] <- predictVBMP(samps == x)
+ }
```

1, 2, 3, 4, 5, 6, 7, 8, 9, 10,
11, 12, 13, 14, 15, 16, 17, 18, 19, 20,
21, 22, 23, 24, 25, 26, 27, 28, 29, 30,
The Cross-validated error rate can be finally evaluated:

\[ CVerrorRate <- \text{round}(\text{sum}(\text{res} \neq \text{brca.y})/n, 2) \]

References

