Nearest Neighbor Autocovariates: With R Package

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Abstract

A fast R (R Development Core Team 2010) algorithm is given for computing the nearest neighbor autocovariates (Holmes and Adams 2003). These autocovariates may be used to select k for kNN classifiers using a maximum pseudolikelihood estimate for k. More general logistic regression and multinomial regression models may be developed using nearest neighbor autocovariates. Computation of nearest neighbor autocovariates and pseudolikelihood estimation of k are implemented in our **nnc** package (McLeod and Islam 2010).

Keywords: classification, k-nearest neighbors, logistic regression, multinomial regression, nearest neighbor autocovariates, nonlinearity.

1. Introduction

The k-nearest neighbor (kNN) classification algorithm is often considered among the most important methods in data mining (Wu and Kumar 2009; Hastie, Tibshirani, and Friedman 2009). The nearest neighbor autocovariates defined by Holmes and Adams (2003) allows one to determine the parameter k, the number of nearest neighbors in kNN, using maximum pseudolikelihood estimation. Furthermore, Holmes and Adams (2003) showed that by including several nearest neighbor autocovariates in a logistic or multilogistic model followed by a best subset or stepwise selection, a better model may be obtained that includes non-linear covariates along with the usual inputs. Empirical evidence presented in Holmes and Adams (2003, Section 3) suggests that this method works better than kNN by itself. Moreover, it was also found that the pseudolikelihood method tends to choose a larger value k for kNN than cross-validation methods¹. Even if kNN is used by itself, the pseudolikelihood method for choosing k seems to work better than leave-one-out cross-validation (Holmes and Adams 2003).

2. Nearest neighbor autocovariate for two classes

2.1. Pseudolikelihood function

Initially we consider the problem with two output² classes, denoted by $\{-1, 1\}$, and p inputs. Assume that there are n data values $\{y_i, x_i\}$, where $x_i \in \Re^p$, $y_i \in \{-1, 1\}$, i = 1, ..., n. The nearest neighbor autocovariate corresponding to the *i*th data value is defined by

$$z_i^{(k)} = \frac{1}{k} \sum_{\substack{\ell \sim i \\ \ell \sim i}} \{ \mathcal{I}(y_\ell = 1) - \mathcal{I}(y_\ell = -1) \},$$
(1)

where the summation is over the k-nearest neighbors of x_i in the set $x_1, x_2, \ldots, x_{i-1}, x_{i+1}, \ldots, x_n$ and \mathcal{I} is the indicator function. The autocovariate $z_i^{(k)} \in [-1, 1]$ represents the relative share of class 1's with respect to class -1's in the k nearest neighbors of x_i . Values of $z_i^{(k)}$ close to 1, indicate that 1's are more abundant in the kth order neighborhood of x_i while values of $z_i^{(k)}$ close to -1, indicate that -1's are more abundant.

The logistic regression model containing the covariates $z_i^{(k)}$ can be written as

$$\eta_{i} = \Pr(y_{i} = 1) \\ = \frac{\exp(\alpha_{k} z_{i}^{(k)})}{1 + \exp(\alpha_{k} z_{i}^{(k)})}.$$
(2)

For fixed k, the pseudolikelihood function for α_k is,

$$L_k(\alpha_k) = \prod_{i=1}^n \eta_i^{u_i} (1 - \eta_i)^{1 - u_i},$$
(3)

where $u_i = (z_i^{(k)} + 1)/2$. It is called a pseudolikelihood because the input, $z_i^{(k)}$, has been determined using the output, y_i . For fixed k, the maximum pseudolikelihood estimate, $\hat{\alpha}_k$, using the glm function for logistic regression is obtained. Holmes and Adams (2003) note that the predictions of the logistic regression defined in eqn (2) with $\alpha_k = \hat{\alpha}_k$ are identical to the predictions obtained from kNN with neighborhood size k.

Holmes and Adams (2003) suggest maximizing the profile pseudolikelihood,

$$\hat{k} = \operatorname*{argmax}_{k} L_{k}(\hat{\alpha}_{k}), \tag{4}$$

to obtain the optimal k, \hat{k} .

¹Larger k, corresponds to a more parsimonious model since there are few effective parameters

²Following Hastie *et al.* (2009) the response/explanatory variables are also called output/input variables respectively.

2.2. R algorithm

The nearest neighbor autocovariate is easily computed using the knn.cv function in the standard R package class. The knn.cv function implements leave-one-out cross-validation and, as a by-product, we may obtain \hat{y}_i , the leave-one-out prediction for the *i*th output and p_i , the proportion of votes for the winning class. Then $(p_ik - (k - p_ik))/k$ is the required autocovariate. The following script implements this computation for synth.tr, the training sample in the synthetic mixture dataset in MASS.

```
R> library("MASS")
R> library("class")
R> X <- synth.tr[, 1:2]
R> y <- 2 * synth.tr[, 3] - 1
R> k <- 10
R> ans <- knn.cv(train = X, cl = as.factor(y), k = k, prob = TRUE)
R> pr <- attr(ans, "prob")
R> yfit <- as.numeric(as.character(ans))
R> NumberOfVotesForWinner <- pr * k
R> NumberOfVotesForLoser <- k - NumberOfVotesForWinner
R> ConsensusProportion <- (NumberOfVotesForWinner - NumberOfVotesForLoser)/k
R> z <- yfit * ConsensusProportion
R> str(z)
```

The variable z displayed is the nearest neighbor autocovariate when k = 10. In general the nearest neighbor autocovariate for any k may be computed using the function nnc in our package nnc.

2.3. Application to synthetic mixture dataset

When using the glm function, it is more convenient to work with the deviance. We use the nnc function to plot the deviance for various k.



Figure 1: Deviance for pseudo-logistic regression and mle for k.

The result $\hat{k} = 66$ agrees with computation reported by Holmes and Adams (2003) for this dataset.

3. Nearest neighbor autocovariate for multiclass case

In the multiclass case we have Q classes, $\mathfrak{C}_1, \mathfrak{C}_2, \ldots, \mathfrak{C}_Q$ and the multiclass autocovariate for class $j = 2, \ldots, Q$, is defined by,

$$z_{i,j}^{(k)} = \frac{1}{k} \sum_{\substack{k \\ \ell \sim i}} \{ \mathcal{I}(y_\ell = \mathfrak{C}_j) - \mathcal{I}(y_\ell = \mathfrak{C}_1) \},$$
(5)

where i = 1, ..., n and $z_{i,j}^{(k)} \in [-1, 1]$. So the autocovariate, $z_{i,j}^{(k)}$, has the interpretation as the relative proportion of \mathfrak{C}_j to \mathfrak{C}_1 in a neighborhood of size k about the *i*th data point. The k nearest neighbors excluding the *i*th data point itself are used. Positive values of $z_{i,j}^{(k)}$ indicate \mathfrak{C}_j is more frequent than \mathfrak{C}_1 . Similarly, negative values of $z_{i,j}^{(k)}$ indicate \mathfrak{C}_1 is more numerous than \mathfrak{C}_j .

The multiclass autocovariate $z_{i,j}^{(k)}$ may be computed conveniently in R using two passes of the algorithm for computing autocovariates with two classes. Two new response or output vectors are defined. For both output vectors, the class values corresponding to \mathfrak{C}_1 are set to -1 and for the *j*th autocovariate, the values corresponding to \mathfrak{C}_j are set to 1. In the first output vector, values corresponding to all other classes set to -1 and in the second output vector these values are set to 1. The nnc algorithm for binary classes using each of these output vectors as response variables is used to obtain two autocovariate vectors. The average of these two vectors produced by nnc is the required *j*th multiclass autocovariate, $z_{i,j}^{(k)}$, $i = 1, \ldots, n$. Doing this for $j = 2, \ldots, Q$, produces all Q - 1 autocovariates.

The code snippet below illustrates how this works for the built-in dataset iris.

```
R> k <- 17
R> X <- iris[, 1:4]
R> Y <- iris[, 5]
R > n <- length(Y)
R > y < - numeric(n)
R> classes <- unique(Y)
R> Q <- length(classes)
R > ind1 <- Y == classes[1]
R> y[ind1] <- -1
R > z < - matrix(numeric(n * (Q - 1)), nrow = n)
R> for (j in 2:Q) {
      indk <- Y == classes[j]</pre>
+
      indOther <- !(ind1 | indk)</pre>
+
      v[indk] <- 1
+
      y[indOther] <- -1
+
      zA \leftarrow nnc(X = X, Y = y, k = k)
      y[indOther] <- 1
+
      zB <- nnc(X, y, k)
+
      z[, j - 1] <- (zA + zB)/2
+
+ }
R> tail(z, 5)
```

	[,1]	[,2]
[146,]	0.05882353	0.9411765
[147,]	0.23529412	0.7647059
[148,]	0.05555556	0.9444444
[149,]	0.0000000	1.0000000
[150,]	0.17647059	0.8235294

The last 5 values for the nearest neighbor autocovariate corresponding to $z_{i,j}^{(k)}$, $i = 146, \ldots, 150$, j = 2, 3 and k = 17 are displayed.

As a further check, we have implemented the nearest neighbor autocovariate computation for the multiclass case in Mathematica (Wolfram Research, Inc 2008). This algorithm uses the definition in eqn (5) directly so the resulting algorithmic details are completely different but the numerical results agree with our R function nnc. This Mathematica package is included along with sample output in the documentation with our R package nnc. Setting,

$$\eta_{i,j} = \Pr(y_i = \mathfrak{C}_j) \\ = \frac{\exp(\alpha_j z_{i,j}^{(k)})}{\sum_{j=1}^{Q} \exp(\alpha_j z_{i,j}^{(k)})},$$
(6)

where we set $\alpha_1 = 0$ and $z_{i,1} = 0, i = 1, ..., n$. We see that the model has the form of a multinomial regression (Hastie *et al.* 2009). In R, for fixed k, maximum pseudolikelihood estimates for $\alpha_2, ..., \alpha_Q$ may be obtained using the **multinom** function in the package **nnet**.³ Using the pseudo maximum likelihood estimates for $\alpha_2, ..., \alpha_Q$ the model in eqn (6) gives identical predictions as the kNN algorithm with parameter k (Holmes and Adams 2003).

Since multinom prints convergence information and since we need to call this function many times, it is useful to use sink, as in the code snippet below to omit unnecessary output.

```
R> library("nnet")
R> kmax <- 50
R> d <- numeric(kmax)
R> for (k in 1:kmax) {
+
      z \leftarrow nnc(X = X, Y = Y, k = k)
      sink("junk.txt")
+
      d[k] <- multinom(Y ~ z)$deviance</pre>
+
      sink()
+
+ }
R> unlink("junk.txt")
R> khat <- which.min(d)
R> plot(d, xlab = "k", ylab = "deviance")
R> points(khat, d[khat], col = "blue", pch = 16, cex = 1.5)
R> title(sub = bquote(hat(k) == .(khat)))
```

³ The function multinom seems to have better convergence properties in the non-penalized case than glmnet. The non-penalized case is obtained by setting the argument lambda=0 in glmnet.



Figure 2: Estimate for the k parameter in kNN for iris dataset. Fisher linear discriminant analysis uses 5 parameters for this problem, the kNN-pseudolikelihood method produces $\hat{k} = 18$ which is equivalent to about $\nu \approx 8$ effective parameters.

Our function nnc handles the multiclass case and we have also implemented a function khat that uses the profile pseudolikelihood to estimate k. When Q = 2, the profile pseudolikelihood is obtained using glm and for Q > 2, multinom is used.

In the vignette accompanying our R package **nnc**, we provide a script for a cross-validation comparison of Fisher linear discriminant analysis and kNN for the iris dataset. The delete-d cross-validation method with 10^4 randomly chosen test samples was used. The computations took about 27 minutes on a Mac Pro running eight threads. The observed misclassification rates are 0.18088 and 0.01978 for kNN and Fisher linear discriminant analysis respectively. It was not surprising the Fisher linear discriminant analysis outperformed kNN for this dataset since an exploratory analysis of the iris dataset does not suggest nonlinearity is an issue. More details are given in the vignette.

4. Application to logistic regression

Holmes and Adams (2003) suggest including nearest neighbor autocovariates as inputs in logistic regression models to allow for nonlinear effects. By using these autocovariates corresponding to various size neighborhoods, we can incorporate a greater range of nonlinear effects than simply using one neighborhood.

To illustrate this method, we use the kyphosis data that is included in the **rpart** library. The output is a binary indicator of the presence or absence of the condition after treatment and there are three inputs, Age, Number and Start. First we estimate k for pure kNN and we find $\hat{k} = 8$.

```
R> library("rpart")
R> X <- kyphosis[, 2:4]
R> Y <- kyphosis[, 1]
R> kHat <- khat(X = X, Y = Y, plot = FALSE)
R> kHat
```

[1] 8

This result suggests using the first eight autocovariates as additional inputs. We fit with a linear logistic regression followed by stagewise model selection using the AIC criterion.

```
R> Z <- sapply(1:8, function(k) nnc(X = X, Y = Y, k = k))
R> dimnames(Z)[[2]] <- paste("z", 1:8, sep = "")
R> kdf <- data.frame(Z, kyphosis)
R> ans <- glm(Kyphosis ~ ., family = binomial(link = "logit"), data = kdf)
R> step(ans, trace = 0)$coefficients
```

 clintercept)
 z1
 z5
 z6
 z7
 z8

 -4.12166880
 -2.35111478
 11.07409030
 -11.07094427
 -6.80680382
 9.85025556

 Age
 Number
 Start

 0.02371589
 0.90752239
 -0.39572491

Instead of using the built-in R function step for stagewise optimization, an exhaustive best subset approach using bestglm (McLeod and Xu 2009) is available when the number of inputs is not too large.

```
R> library("bestglm")
R> Xy <- data.frame(X, Z, Kyphosis = as.numeric(Y) - 1)
R> ans <- bestglm(Xy = Xy, family = binomial(link = "logit"), IC = "AIC")</pre>
```

Morgan-Tatar search since family is non-gaussian.

R> ans\$BestModel\$coefficients

2	z1	Start	Number	Age	(Intercept)
11.0740903	-2.35111478	-0.39572491	0.90752239	0.02371589	-4.12166880
			z8	z7	z6
			9.85025556	-6.80680382	-11.07094427

In this case the exhaustive subset method produced the same answer.

It might be even better to use a regularization approach for logistic and multinomial regression as is implemented in the R package **glmnet** (Friedman, Hastie, and Tibshirani 2010b,a). This method can not only handle a large number of inputs but it also produces even better predictions. Recent work with non-concave penalty methods for regularization is also very promising (Fan and Li 2001; Zhang 2010).

Nearest neighbor autocovariates may easily be incorporated into multinomial regression as well as many types of classification algorithms (Islam 2008). In particular, Islam (2008) showed that nearest neighbor autocovariates could be used to improve predictions with regularized discriminant analysis in microarray data (Guo, Hastie, and Tibshirani 2007).

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