



The Majorization Approach to SVM: The SVMmaj Package in R

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Abstract

Support Vector Machines (SVMs) have gained considerable popularity over the last two decades for binary classification. This paper concentrates on a recent optimization approach to SVMs, the SVM majorization approach, or **SVM-Maj** for short. This method is aimed at small and medium sized Support Vector Machine (SVM) problems, in which **SVM-Maj** performs well relative to other solvers. To obtain an SVM solution, most other solvers need to solve the dual problem. In contrast, **SVM-Maj** solves the primal SVM optimization iteratively thereby converging to the SVM solution. Furthermore, the simplicity of **SVM-Maj** makes it intuitively more accessible to the researcher than the state-of-art decomposition methods. Moreover, **SVM-Maj** can easily handle any well-behaved error function, while the traditional SVM solvers focus particularly on the absolute-hinge error. In this paper, the **SVM-Maj** approach is enhanced to include the use of different kernels, the standard way in the SVM literature for handling nonlinearities in the predictor space. In addition, we introduce the R package **SVMMaj** that implements this methodology. Amongst its features are the weighting of the error for individual objects in the training dataset, handling nonlinear prediction through monotone spline transformations and through kernels, and functions to do cross validation.

Keywords: Support Vector Machine, **SVM-Maj**, R, Majorization.

1. Introduction

For understanding what a support vector machine (SVM) is, consider the following data analysis problem: there are two groups of objects, say products of type A and type B, having

some common attributes such as color, price, weight, etc. The task of separating the two types of objects from each other is formally referred to as the binary classification task. Given the values for the attributes of a new object, we would like to assign this new object to a given group, or class. Such a binary classification task is dealt with routinely in medical, technical, economic, humanitarian, and other fields.

Numerous learning methods have been designed to solve the binary classification task, including Linear Discriminant Analysis, Binary Logistic Regression, Neural Networks, Decision Trees, Naive Bayes classifier, and others. In this paper, we focus on a method that has gained considerable popularity over the last two decades, called the Support Vector Machines (SVMs) classifier (Vapnik 1995). SVMs have emerged as one of the most popular and high-performing learning methods for classification. They have been successfully applied to areas ranging from bioinformatics (see, e.g., Furey *et al.* 2000; Guyon *et al.* 2002) to image recognition (see, e.g., Chapelle *et al.* 1999; Pontil and Verri 1998) and marketing (see, e.g., Cui and Curry 2005). In essence, SVMs divide two groups of objects from each other by building a hyperplane in the space of the predictor variables that separates them in an adequate way. The rapid success of SVMs can be attributed to a number of key qualities: robustness of results, avoiding overfitting, and the possibility to handle nonlinearities of the predictor variables easily through so-called kernel functions. In addition, the evaluation of an SVM model on test objects is relatively fast and simple. The SVM is formulated as a well-defined quadratic optimization problem that has a unique solution. Overfitting, that is, fitting an available training data-set too well, is avoided via a *penalty* term that suppresses too complex potential fits. Nonlinearities can be handled in two ways: (1) by a preprocessing step of the predictor variables, for example, by polynomial expansion or the use of splines (Groenen *et al.* 2007) and (2) by using the *kernel* trick that allows nonlinear solutions to be computed implicitly. Note that the use of kernels is very prominent in the SVM literature.

A variety of solvers for the SVM optimization task have been proposed in the literature. One of the initial ideas has been to apply general-purpose quadratic optimization solvers such as **LOQO** (Vanderbei 1994) and **MINOS** (Murtagh and Saunders 1998). One of the problems of such solvers is that they require the whole *kernel* matrix to be stored in memory, which is quadratic in the number of observations n . For small scale problems, this is not a problem, but for medium and large scale problems other methods are needed. One attempt to overcome the complete storage of the kernel matrix is by chunking (Boser *et al.* 1992; Osuna *et al.* 1997a). This method concentrates on a (working) subset of all training objects at a given iteration, effectively splitting the learning task into smaller subproblems that easily fit into the memory of a computer. Alternatively, direction search was proposed (Boser *et al.* 1992) that updates all unknown coefficients at each iteration in a certain feasible direction.

More recently, decomposition methods have established themselves as the mainstream technique for solving SVMs (Osuna *et al.* 1997b; Saunders *et al.* 1998; Joachims 1999). At each iteration, the decomposition method optimizes a subset of coefficients, and leaves the remaining coefficients unchanged. Solving a series of very simple optimization subproblems, this approach has proven to be one of the fastest for large scale SVM problems. The most popular decomposition method is the so-called Sequential Minimal Optimization (SMO) (Platt 1999), where only two coefficients are updated at each iteration, which can actually be done analytically. SMO is the basis of popular SVM solvers such as **LibSVM** (Chang and Lin 2001) and **SVMLight** (Joachims 1999), which has been implemented in the R packages **e1071** (Meyer *et al.* 2014) respectively **klaR** (Weihs *et al.* 2005). For the linear SVM case, alternative tech-

niques to the decomposition methods have recently been put forward, such as the cutting plane algorithm (Joachims 2006).

This paper concentrates on a recent optimization approach to solving SVMs (Groenen *et al.* 2007, 2008), referred to as the majorization approach to SVMs, or **SVM-Maj** for short. This method is aimed at small and medium sized SVM problems. An overview of some popular SVM solvers and some of their properties is given in Table 1. The other solvers are **LibSVM**, **SVMLight**, **SVM Torch** (Collobert and Bengio 2001), **mySVM** (Rüping 2000), **SVM-Perf** (Joachims 2006), and **LibLINEAR** (Fan *et al.* 2008).

| Properties | SVM-Maj | LIBSVM | SVMLight | SVM Torch | mySVM | SVM-Perf | LIBLINEAR |
|--|---------------|-----------------|----------------|------------|------------|------------|------------------|
| Nonlinear kernels | yes | yes | yes | yes | yes | no | no |
| Splines | yes | no | no | no | no | no | no |
| Suitable for large n | yes | yes | yes | yes | yes | no | yes |
| Suitable for large k | yes | yes | yes | no | yes | no | yes |
| Suitable for large n and large k | no | yes | yes | no | yes | no | |
| Dual approach | no | yes | yes | yes | yes | yes | no |
| Allows quadratic hinge | yes | yes* | no | no | yes | no | yes |
| Allows Huber hinge | yes | no | no | no | no | no | no |
| Allows k -fold cross val. | yes | yes | yes | no | yes | no | yes |
| Language | MATLAB, R | C++,Java | C, C++ | C++ | C | C++ | C, C++ |
| Gui interface or command line interface (cli) | MATLAB, R | <i>cli</i> | <i>cli</i> | <i>cli</i> | <i>cli</i> | <i>cli</i> | <i>cli</i> |
| Availability in R | SVMMaj | e1071 ** | klaR ** | no | no | no | LiblineaR |
| Multi-class problems | no | yes | yes | yes | no | yes | yes |

* after modification

** for non-linear kernels, the package **kernelab** can be used

Table 1: Comparison table of different SVM solvers available in 2015.

In this paper, the method of Groenen *et al.* (2008) is enhanced to the use of different kernels, the standard way in the SVM literature for handling nonlinearities in the predictor space. Moreover, we offer here a new special treatment for the case where the number of objects is less than the number of attributes. Three cases are distinguished for which **SVM-Maj** computes the solution efficiently: (1) the case with many more observations n than variables k , (2) the case with many variables k but medium sized n , and (3) the case that n is medium sized and the kernel space or the space of the variables is of lower rank than k or n . The case of large n is relatively more difficult for all SVM solvers, including **SVM-Maj**. This particularly holds when kernels are used. For this case, the alternative of introducing nonlinearity through splines in **SVM-Maj** can be used so that still for medium sized n , nonlinearity can be handled efficiently.

Among the advantages of the **SVM-Maj** approach are its intuitive optimization algorithm, its versatility, and the competitively fast estimation speed for medium sized problems. The majorization solver is an iterative algorithm with two easily tractable alternating steps that reveal the nature of solving the SVM optimization problem in an appealing way. The relative simplicity of **SVM-Maj** arguably makes it intuitively more accessible to the researcher than the state-of-art decomposition methods. Traditional SVM solvers focus particularly on the absolute-hinge error (the standard SVM error function), whereas the majorization algorithm has been designed to incorporate any well-behaved error function. This property can be viewed as a attractive feature of the majorization approach. The **SVM-Maj** package comes with the following in-built error functions: the classic absolute-hinge, Huber-hinge, and quadratic hinge. Furthermore, **SVM-Maj** solves the *primal* SVM optimization problem

even in the nonlinear case, in contrast to other solvers, which solve the *dual* problem. The advantage of solving the primal is that **SVM-Maj** converges to the optimal solution in each iterative step. In contrast, other methods solving the dual optimization problem need the dual problem to be fully converged to attain a solution.

The main aim of this paper is to introduce the **SVMMaj** package for R (R Development Core Team 2011). Its main features are: implementation of the **SVM-Maj** majorization algorithm for SVMs, handling of nonlinearity through splines and kernels, the ability to handle several error functions (among other the classic hinge, quadratic hinge and Huber hinge error).

In addition, **SVMMaj** is able to assign a fixed weight to each individual objects in a training dataset to receive different individual weights. In this way, the user can set importance of misclassifying the object by varying the individual weight. These weights can also be set per class. The **SVMMaj** package comes with a cross validation function to asses out-of-sample performance or evaluate meta parameters that come with certain SVM models.

This paper is organized as follows. First, Section 2 gives a brief introduction to SVMs. In Section 3, we describe the **SVM-Maj** algorithm and its update for each iteration is derived. Furthermore, Section 3 also discusses some computational efficiencies, and Section 4 presents the way nonlinearities are handled. Section 5 gives several detailed examples of how the **SVM-Maj** package can be used, and Section 6 concludes. The appendix gives technical derivations underlying the **SVM-Maj** algorithm.

2. Definitions

First of all, let us introduce some notations: n denotes the number of object; k denotes the number of attributes, \mathbf{X} is an $n \times k$ matrix containing the k attributes, without a column of ones to specify the intercept, \mathbf{y} is an $n \times 1$ vector with 1 if object i belongs to class 1 and -1 if it belongs to class -1 , r denotes the rank of matrix \mathbf{X} , and $\lambda > 0$ is the penalty parameter for the penalty term. The purpose of SVM is to produce a linear combination of predictor variables \mathbf{X} such that a positive prediction is classified to class $+1$ and a negative prediction to class -1 . Let β and α be parameters of the linear combination $\alpha + \mathbf{x}_i^\top \beta$. Then, for a given intercept α and vector with attribute weights β , the predicted class is given by

$$\hat{y}_i = \text{sign}(\mathbf{x}_i^\top \beta + \alpha) = \text{sign}(q_i + \alpha) = \text{sign}(\tilde{q}_i),$$

where $q_i = \mathbf{x}_i \beta$. Here, the term $\tilde{q}_i = q_i + \alpha$ is used to indicate the predicted score for object i , which also accounts for the intercept α .

To find the optimal of the linear combination, we use the SVM loss function as a function of α and β to be minimized. The SVM loss function can be represented in several ways. Here, we follow the notation of Groenen *et al.* (2008) that allows for general error functions $f_1(\tilde{q}_i)$ and $f_{-1}(\tilde{q}_i)$. The goal of SVMs is to minimize the SVM loss function

$$\begin{aligned} L_{\text{SVM}}(\alpha, \beta) &= \sum_{i \in G_1} w_i f_1(\tilde{q}_i) + \sum_{i \in G_{-1}} w_i f_{-1}(\tilde{q}_i) + \lambda \beta^\top \beta \\ &= \text{Class 1 errors} + \text{Class -1 errors} + \text{Penalty for nonzero } \beta, \end{aligned}$$

over α and β , where G_1 and G_{-1} respectively denote the sets of class 1 and -1 objects, and w_i is a given nonnegative importance weight of observation i . Note that Groenen *et al.* (2008)

proved that minimizing $L_{\text{SVM}}(\alpha, \beta)$ is equivalent to minimizing the SVM error function in Vapnik (1995) and Burges (1998). Figure 1 and Table 2 contain different error functions that can be used, such as the classical hinge error standard in SVMs, the quadratic hinge, and the Huber hinge. Figure 1 plots the error functions as function value of \tilde{q}_i . All three hinge functions have the property that their error is only larger than zero if the predicted value $\tilde{q}_i < 1$ for class +1 objects and $\tilde{q}_i > -1$ for class -1 objects. The classic absolute hinge error is linear in \tilde{q}_i and is thus robust for outliers. However, it is also non-smooth at $\tilde{q}_i = 1$. The quadratic hinge is smooth but may be more sensitive to outliers. The Huber loss is smooth as well as robust. Those observations \mathbf{x}_i yielding zero errors do not contribute to the SVM solution and could therefore be removed without changing the SVM solution. The remaining observations \mathbf{x}_i that do have an error or have $|\tilde{q}_i| = 1$ determine the solution and are called support vectors, hence the name Support Vector Machine. Unfortunately, before the SVM solution is available it is unknown which of the observations are support vectors and which are not. Therefore, the SVM always needs all available data to obtain a solution.

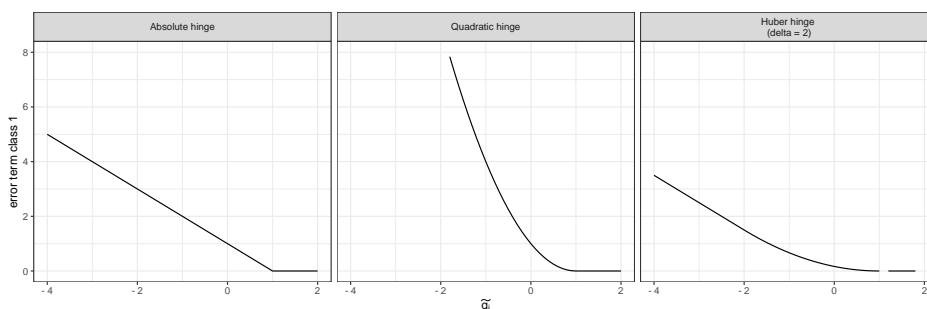


Figure 1: This figure shows the hinge error functions. Note that the error function is only nonzero if $\tilde{q} < 1$.

| Error function | $f_1(\tilde{q}_i)$ |
|-----------------|---|
| Absolute hinge | $\max(0, 1 - \tilde{q}_i)$ |
| Quadratic hinge | $\max(0, 1 - \tilde{q}_i)^2$ |
| Huber hinge | $\begin{cases} \frac{1}{2(\delta + 1)} \max(0, 1 - \tilde{q}_i)^2 & \tilde{q}_i > -\delta \\ \frac{(\delta - 1)}{2} - \tilde{q}_i & \tilde{q}_i \leq -\delta \end{cases}$ |

Table 2: Common error function used. The further \tilde{q}_i is from wrongly predicted, the higher its error. Note that $f_{-1}(\tilde{q}_i) = f_1(-\tilde{q}_i)$, therefore, only $f_1(\tilde{q}_i)$ is described below.

The weight w_i of observation i can be interpreted as the relative importance of the error of the observation. One can also assign the same weights for all observations in G_1 and different

weight for those in G_{-1} . Assigning weights per class is especially useful when one class is substantially larger than the other. By assigning a larger weight for the smaller subset, one can correct the dominance of the errors of the larger subset. For example, if there are n_1 objects in G_1 and n_{-1} objects in G_{-1} , then choosing

$$w_i = \begin{cases} (n_1 + n_{-1})/(2n_1) & i \in G_1 \\ (n_1 + n_{-1})/(2n_{-1}) & i \in G_{-1} \end{cases}$$

is one way to obtain equal weighting of the classes.

A more compact expression of L_{SVM} is obtained by exploiting the symmetric relation $f_{-1}(\tilde{q}_i) = f_1(-\tilde{q}_i) = f_1(y_i \tilde{q}_i)$. Then, the SVM loss function can be simplified into

$$\begin{aligned} L_{\text{SVM}}(\alpha, \beta) &= \sum_{i=1}^n w_i f_1(y_i \tilde{q}_i) + \lambda \beta^\top \beta \\ &= \text{Error} + \text{Penalty for nonzero } \beta. \end{aligned} \quad (1)$$

To minimize this function, we will use the **SVM-Maj** algorithm, discussed in the next section.

3. The SVM-Maj algorithm

The **SVMMaj** package minimizes the SVM loss function by using the **SVM-Maj** algorithm, that is based on the ideas of majorization (see, e.g., De Leeuw and Heiser 1980; De Leeuw 1994; Heiser 1995; Lange *et al.* 2000; Kiers 2002; Hunter and Lange 2004; Borg and Groenen 2005). Groenen *et al.* (2007, 2008) developed the algorithm for linear SVMs. Here, the **SVM-Maj** algorithm is extended to nonlinear situations that use a kernel matrix.

The **SVM-Maj** algorithm uses iterative majorization to minimize the loss function (1). The main point of this algorithm is to iteratively replace the original function $f(x)$ by an auxiliary function $g(x, \bar{x})$ at supporting point \bar{x} , for which the minimum can be easily computed. The auxiliary function, called the majorization function, has the properties that:

- the minimum x^* of $g(x, \bar{x})$ can be found easily, and
- $g(x, \bar{x})$ is always larger than or equal to the $f(x)$, and
- at the supporting point \bar{x} , $g(\bar{x}, \bar{x})$ is equal to $f(\bar{x})$.

Combining these properties gives the so-called sandwich inequality $f(x^*) \leq g(x^*, \bar{x}) \leq g(\bar{x}, \bar{x}) = f(\bar{x})$. That is, for each support point \bar{x} , we can find another point x^* of whose function value $f(x^*)$ is lower or equal to the former $f(\bar{x})$. Using this point x^* as the next iteration's support point and repeating the procedure, a next update can be obtained with a lower $f(x)$ value. This iterative process produces a series of function values that is non-increasing and generally decreasing. Note that this principle of majorization also works if the argument of f is a vector. Moreover, if f is strictly convex, as is the case with the SVM loss function, the updates converge to the minimum of the original function as the number of iterations increases.

The first step is to find the majorizing functions for the different hinge errors. The majorization function of the **SVM-Maj** algorithm is a quadratic function so that its minimum is obtained by setting the derivative to zero. Given the support point \bar{x} , a quadratic majorization function $g(x, \bar{x})$ can be written as

$$g(x, \bar{x}) = a(\bar{x})x^2 - 2b(\bar{x})x + o(\bar{x}). \quad (2)$$

As the parameter $o(\bar{x})$ is irrelevant for determining \hat{x} as it is constant for a given \bar{x} , we shall write o instead of $o(\bar{x})$ to indicate all terms that are not dependent on x in the majorizing function.

Conform Groenen *et al.* (2007, 2008), $f_1(y_i\tilde{q}_i)$ in (1) can be majorized by $g(\tilde{q}_i, \bar{q}_i, y_i) = a_i\tilde{q}_i^2 - 2b_i\tilde{q}_i + o_i$ with the parameters a_i , b_i , and o_i given in Table 3. As $f_1(y_i\tilde{q}_i) \leq g(\tilde{q}_i, \bar{q}_i, y_i)$, we can obtain the majorization function for the SVM loss function (1), using $\tilde{\mathbf{q}} = \mathbf{X}\boldsymbol{\beta} + \alpha\mathbf{1} = \mathbf{q} + \alpha\mathbf{1}$ and the support point $\bar{\mathbf{q}} = \bar{\alpha}\mathbf{1} + \bar{\mathbf{q}}$

$$\begin{aligned} L_{\text{SVM}}(\alpha, \boldsymbol{\beta}) &= \sum_i w_i f_1(y_i\tilde{q}_i) + \lambda\boldsymbol{\beta}^\top \boldsymbol{\beta} \\ &\leq \sum_i w_i g(\tilde{q}_i, \bar{q}_i, y_i) + \lambda\boldsymbol{\beta}^\top \boldsymbol{\beta} + o \\ &= \tilde{\mathbf{q}}^\top \mathbf{A}\tilde{\mathbf{q}} - 2\tilde{\mathbf{q}}^\top \mathbf{b} + \lambda\boldsymbol{\beta}^\top \boldsymbol{\beta} + o \\ &= (\alpha\mathbf{1} + \mathbf{q})^\top \mathbf{A}(\alpha\mathbf{1} + \mathbf{q}) - 2(\alpha\mathbf{1} + \mathbf{q})^\top \mathbf{b} + \lambda\boldsymbol{\beta}^\top \boldsymbol{\beta} + o \\ &= \text{Maj}(\alpha, \boldsymbol{\beta}), \end{aligned} \tag{3}$$

where \mathbf{A} is an $n \times n$ diagonal matrix with elements $w_i a_i$ and \mathbf{b} an $n \times 1$ vector with elements $w_i b_i$ (with a_i and b_i from Table 3). As $w_i > 0$ for all i , we can conclude that the diagonal matrix \mathbf{A} is positive definite, which implies that the majorization function is strictly quadratically convex, thereby guaranteeing a unique minimum of the majorizing function at the right hand side of (3). Groenen *et al.* (2008) showed in their article that the minimum of (3), that is, an update for the iteration process, can be computed as followed:

$$\left(\tilde{\mathbf{X}}^\top \mathbf{A} \tilde{\mathbf{X}} + \lambda \mathbf{J} \right) \begin{bmatrix} \alpha^+ \\ \boldsymbol{\beta}^+ \end{bmatrix} = \tilde{\mathbf{X}}^\top \mathbf{b}, \tag{4}$$

where $\tilde{\mathbf{X}} = \begin{bmatrix} \mathbf{1} & \mathbf{X} \end{bmatrix}$ and $\mathbf{J} = \begin{bmatrix} 0 & \mathbf{0}^\top \\ \mathbf{0} & \mathbf{I} \end{bmatrix}$. Appendix A shows the derivation of this update, while Algorithm 1 shows the steps taken by the **SVM-Maj** algorithm.

3.1. Computational efficiencies

Before we continue with the discussion of the extended options for the **SVM-Maj** algorithm, we will introduce a few modifications of the **SVM-Maj** algorithm to obtain computational efficiencies. One efficiency can be achieved by using the QR-decomposition on matrix \mathbf{X} to find a more efficient update. Another efficiency improvement can be obtained in case of using the quadratic or Huber hinge and the number of updates generally decreases when using a *relaxed update*. The algorithm is summarized in Algorithm 1 and the most important steps are discussed below and in the appendix.

Efficient updates by using QR-decomposition

Usually, the loss function will be optimized by optimizing $\boldsymbol{\beta}$. However, when $k > n$, it is more efficient to optimize \mathbf{q} instead, as it has a lower dimensionality. In this situation, the dimensional space in which the optimal parameter values lies will be smaller and therefore it is more efficient and generally faster to compute an update. In case that $r = \text{rank}(\mathbf{X}) < \min(n, k)$, an even more efficient update exists. Moreover, in a higher dimensional space, one

| Error term | Parameters |
|-----------------|---|
| Absolute hinge | $a_i = \frac{1}{4} \max(1 - y_i \bar{q}_i , \epsilon)^{-1}$ $b_i = y_i a_i (1 + y_i \bar{q}_i - 1)$ $o_i = a_i (1 + y_i \bar{q}_i - 1)^2$ |
| Quadratic hinge | $a_i = 1$ $b_i = y_i a_i (1 + \max(y_i \bar{q}_i - 1, 0))$ $o_i = a_i (1 + \max(y_i \bar{q}_i - 1, 0))^2$ |
| Huber hinge | $a_i = \frac{1}{2} (k + 1)^{-1}$ $b_i = y_i a_i (1 + \max(y_i \bar{q}_i - 1, 0) + \min(y_i \bar{q}_i + k, 0))$ $o_i = a_i (1 + \max(y_i \bar{q}_i - 1, 0) + \min(y_i \bar{q}_i + k, 0))^2 + \min(y_i \bar{q}_i + k, 0)$ |

Table 3: Parameter values of a_i , b_i and o_i of the majorization function.

only needs a part of the space of β to find the optimal \mathbf{q} . The appendix discusses these issues more in detail and introduces efficient and consistent updates for **SVMMaj** for all possible situations. An overview of all efficient updates in each occasion can be found in Table 4.

Equation 4 optimizes β to optimize the loss function. However, in some cases, there exist an even more efficient update. Appendix A derives an efficient update for each of these cases by making use of the singular value decomposition (SVD)

$$\begin{array}{c} \mathbf{X} \\ (n \times k) \end{array} = \begin{array}{c} \mathbf{P} \\ (n \times r) \end{array} \begin{array}{c} \mathbf{\Lambda} \\ (r \times r) \end{array} \begin{array}{c} \mathbf{Q}^\top \\ (r \times k) \end{array}, \quad (5)$$

where $\mathbf{P}^\top \mathbf{P} = \mathbf{I}$ and $\mathbf{Q}^\top \mathbf{Q} = \mathbf{I}$ and $\mathbf{\Lambda}$ is a diagonal matrix. However, **SVMMaj** package uses the QR-decomposition to determine the rank of \mathbf{X} , as it is a computationally more efficient way to determine the rank of \mathbf{X} than doing so through the SVD-decomposition. Let the QR-decomposition of \mathbf{X}^\top be given by $\mathbf{X}^\top = \mathbf{VZ}^\top$ with $\mathbf{V}^\top \mathbf{V} = \mathbf{I}$ and \mathbf{Z} a lower triangular matrix. An additional QR-decomposition of \mathbf{Z} gives $\mathbf{Z} = \mathbf{UR}$ with $\mathbf{U}^\top \mathbf{U} = \mathbf{I}$ and \mathbf{R} an upper triangular matrix. Then we have

$$\begin{array}{c} \mathbf{X} \\ (n \times k) \end{array} = \begin{array}{c} \mathbf{U} \\ (n \times r) \end{array} \begin{array}{c} \mathbf{R} \\ (r \times r) \end{array} \begin{array}{c} \mathbf{V}^\top \\ (r \times k) \end{array}. \quad (6)$$

Note that matrices \mathbf{U} and \mathbf{V} are orthonormal matrices and therefore have the same properties as \mathbf{P} and \mathbf{Q} . Thus, we can replace matrices \mathbf{P} , $\mathbf{\Lambda}$ and \mathbf{Q} by respectively \mathbf{U} , \mathbf{R} and \mathbf{V} . The update (4) can then be computed through

$$(\tilde{\mathbf{Z}}^\top \mathbf{A} \tilde{\mathbf{Z}} + \lambda \mathbf{J}) \begin{bmatrix} \alpha^+ \\ \rho^+ \end{bmatrix} = \tilde{\mathbf{Z}}^\top \mathbf{b}, \quad (7)$$

where $\tilde{\mathbf{Z}} = \begin{bmatrix} \mathbf{1} & \mathbf{Z} \end{bmatrix} = \begin{bmatrix} \mathbf{1} & \mathbf{UR} \end{bmatrix}$ and where $\rho = \mathbf{V}^\top \beta$. Furthermore, β and \mathbf{q} can be derived from $\beta = \mathbf{V} \rho$ and $\mathbf{q} = \mathbf{Z} \rho = \mathbf{UR} \rho$. Note that in most cases, the decomposition of \mathbf{Z} is not necessary to perform, so that only a single QR-decomposition performance is needed.

Algorithm: SVM-Maj

input : $\mathbf{y} = n \times 1$ vector with class labels $+1$ and -1 ,
 $\mathbf{X} = n \times k$ matrix of explanatory variables ,
 $\lambda > 0$ the penalty parameter,
Hinge = {absolute,quadratic,huber} the hinge error function,
 $\delta > 0$ the Huber hinge parameter,
relax determining from which step to use the relaxed update (11),
method specifies whether $\boldsymbol{\rho}$ (using matrix decomposition) will be used or $\boldsymbol{\beta}$.

output: α_t , ($\boldsymbol{\rho}_t$ or $\boldsymbol{\beta}_t$)

$t = 0$;
Set ϵ to a small positive value;
Set ($\boldsymbol{\rho}_0$ or $\boldsymbol{\beta}_0$) and α_0 to random initial values;
Compute $L_0 = L_{\text{SVM}}(\alpha_0, \boldsymbol{\rho}_0)$ or $L_{\text{SVM}}(\alpha_0, \boldsymbol{\beta}_0)$ according to (1);
if *hinge* \neq *absolute* \mathcal{E} *method* = $\boldsymbol{\beta}$ **then**
| Find \mathbf{S} that solves (8);
else if *hinge* \neq *absolute* \mathcal{E} *method* = $\boldsymbol{\rho}$ **then**
| Find \mathbf{S} that solves (9);
end
while $t = 0$ or $(L_{t-1} - L_t)/L_t > \epsilon$ **do**
| $t = t + 1$;
| Compute a_i and b_i by Table 3;
| Set diagonal elements of \mathbf{A} to $w_i a_i$ and \mathbf{b} to $w_i b_i$;
| **if** *hinge* = *absolute* \mathcal{E} *method* = $\boldsymbol{\rho}$ **then**
| | Find α_t and $\boldsymbol{\rho}_t$ that solves (7): $\begin{bmatrix} \alpha_t \\ \boldsymbol{\rho}_t \end{bmatrix} = \tilde{\mathbf{Z}}^\top \mathbf{b}$;
| **else if** *hinge* = *absolute* \mathcal{E} *method* = $\boldsymbol{\beta}$ **then**
| | Find α_t and $\boldsymbol{\rho}_t$ that solves (4): $\begin{bmatrix} \alpha_t \\ \boldsymbol{\beta}_t \end{bmatrix} = \tilde{\mathbf{X}}^\top \mathbf{b}$;
| **else if** *hinge* \neq *absolute* \mathcal{E} *method* = $\boldsymbol{\rho}$ **then**
| | Find α_t and ($\boldsymbol{\rho}_t$ or $\boldsymbol{\beta}_t$) that solves: $\begin{bmatrix} \alpha^+ \\ \boldsymbol{\rho}^+ \end{bmatrix} = \mathbf{Sb}$
| **else if** *hinge* \neq *absolute* \mathcal{E} *method* = $\boldsymbol{\beta}$ **then**
| | Find α_t and ($\boldsymbol{\rho}_t$ or $\boldsymbol{\beta}_t$) that solves: $\begin{bmatrix} \alpha^+ \\ \boldsymbol{\beta}^+ \end{bmatrix} = \mathbf{Sb}$;
| **end**
| **if** $t \geq \text{relax}$ **then**
| | Replace $\alpha_t = 2\alpha_t - \alpha_{t-1}$;
| | Replace $\boldsymbol{\rho}_t = 2\boldsymbol{\rho}_t - \boldsymbol{\rho}_{t-1}$ or $\boldsymbol{\beta}_t = 2\boldsymbol{\beta}_t - \boldsymbol{\beta}_{t-1}$;
| **end**
| Compute $L_t = L_{\text{SVM}}(\alpha_t, \boldsymbol{\rho}_t)$ or $L_{\text{SVM}}(\alpha_t, \boldsymbol{\beta}_t)$ according to (1);
end

Algorithm 1: The SVM majorization algorithm

| Method | Situation |
|-----------------------|-------------------|
| β | $n \geq k, r = k$ |
| \mathbf{q} | $n \leq k, r = n$ |
| $\boldsymbol{\theta}$ | $r < \min(n, k)$ |

Table 4: An overview of the most efficient updates for each situation.

As this decomposition is already performed to determine the rank of \mathbf{X} , it is efficient to use update (7) in all three cases distinguished in Table 4. Nevertheless, in case n and k are both very large, it may be more efficient not to perform a matrix decomposition at all to avoid unnecessary computations. Instead, one can use update (4).

Quadratic and Huber hinge

For the quadratic and Huber hinge, the parameters a_i does not depend on the support point $\bar{\mathbf{q}}$, which means that the matrix \mathbf{A} remain fixed during the algorithm steps. In fact, the parameters a_i are the same for all i , that is, $a_i = a$ for all i . Therefore, extra computational efficiency can be obtained by solving the linear system

$$(a\tilde{\mathbf{X}}^\top \tilde{\mathbf{X}} + \lambda \mathbf{J})\mathbf{S} = \tilde{\mathbf{X}}^\top, \quad (8)$$

or, when using QR-decomposition,

$$(a\tilde{\mathbf{Z}}^\top \tilde{\mathbf{Z}} + \lambda \mathbf{J})\mathbf{S} = \tilde{\mathbf{Z}}^\top, \quad (9)$$

so that the original update (7) can be simplified into

$$\begin{bmatrix} \alpha^+ \\ \boldsymbol{\rho}^+ \end{bmatrix} = \mathbf{S}\mathbf{b}, \quad (10)$$

so that in each iteration the update can be obtained by a single matrix multiplication instead of solving a linear system.

Computational efficiency by the relaxed updates

The parameter updates obtained by (7) find the minimum of the majorization function in (3). This guarantees that the next update will always be better than the previous point. However, it turns out that often the updates converge faster when making the update twice as long by using a relaxed update (De Leeuw and Heiser 1980):

$$\boldsymbol{\theta}_{t+1}^* = \boldsymbol{\theta}_{t+1} + (\boldsymbol{\theta}_{t+1} - \boldsymbol{\theta}_t) = 2\boldsymbol{\theta}_{t+1} - \boldsymbol{\theta}_t. \quad (11)$$

This relaxation is most effective when **SVMMaj** has already performed several iterations. Preliminary experimentation revealed that this is the case when at least 20 iterations without relaxed updates have been performed. Therefore, we will implement (11) after 20 iterations to increase model estimation efficiency.

4. Nonlinearities

In the previous sections, we have only discussed the **SVM-Maj** algorithm for the linear case. However, often a better prediction can be obtained by allowing for nonlinearity of the predictor variables. Therefore, one might consider to use nonlinearity in the model estimation. In the **SVMMaj** package, two different implementation of nonlinearity can be used: I-splines and kernels. One can choose one of these implementation, or both of them.

Splines are piecewise polynomial functions of a specified variable. The **SVMMaj** package can transform each explanatory variable into I-splines (Ramsay 1988). This transformation will split the original predictor variable \mathbf{x}_j into a number of spline bases gathered in the matrix \mathbf{B}_j . After specifying the interior knots k_s that define the boundaries of the pieces and the degree d_s of the polynomials, one can transform the variable \mathbf{x}_j into the basis \mathbf{B}_j of a size of $n \times (d_s + k_s)$. This spline basis \mathbf{B}_j will then be used as a set of $(d_s + k_s)$ variables to find a linear separating plane of a higher dimension. The piecewise polynomial transformation of variable \mathbf{x}_j can then be obtained through computing the linear combination of the spline bases $\mathbf{B}_j \boldsymbol{\gamma}_j$ with the initially unknown weights $\boldsymbol{\gamma}_j$. Then, all spline bases \mathbf{B}_j and weights $\boldsymbol{\gamma}_j$ are gathered in $\mathbf{B} = [\mathbf{B}_1, \mathbf{B}_2, \dots, \mathbf{B}_k]$ and $\boldsymbol{\beta}^\top = [\boldsymbol{\gamma}_1^\top, \boldsymbol{\gamma}_2^\top, \dots, \boldsymbol{\gamma}_k^\top]$. Note that here we use I-splines as they have the property that if multiplied by positive weights, there is a guaranteed monotone relation with the original variable \mathbf{x}_j . This property can aid the interpretation of the weights as $\boldsymbol{\beta}$ can be split into a vector of positive and one of negative weights.

It is also possible to map the matrix \mathbf{X} differently into a higher dimensional space through so-called kernels. Let us map the explanatory variables of observation i , that is, \mathbf{x}_i into $\phi(\mathbf{x}_i)$ with mapping function $\phi: \mathcal{R}^k \rightarrow \mathcal{R}^m$. Furthermore, let us denote $k_{ij} = \phi(\mathbf{x}_i)^\top \phi(\mathbf{x}_j)$ as the inner product of the transformed vectors of \mathbf{x}_i and \mathbf{x}_j . Then, the *kernel matrix* \mathbf{K} is denoted as the inner product matrix with value k_{ij} in row i and column j . Note that the kernel matrix always is of size $n \times n$ and $\mathbf{K} = \boldsymbol{\Phi} \boldsymbol{\Phi}^\top$ with row i equal to $\phi(\mathbf{x}_i)^\top$. Using this property, we can summarize the mapping of \mathbf{X} even when $m \rightarrow \infty$ into a matrix of finite size, even if $m \rightarrow \infty$. This method is also known as the ‘kernel trick’.

We will now show that this kernel matrix \mathbf{K} can be used to find an efficient majorization update. Then the matrix $\boldsymbol{\Phi}$ is used instead of \mathbf{X} to derive the majorization update. Let us perform the QR-decomposition on $\boldsymbol{\Phi}$ analogous to (6), that is

$$\begin{array}{ccccccc} \boldsymbol{\Phi} & = & \mathbf{U} & \mathbf{R} & \mathbf{V}^\top & = & \mathbf{Z} & \mathbf{V}^\top, \\ (n \times m) & & (n \times r) & (r \times r) & (r \times m) & & (n \times r) & (r \times m) \end{array} \quad (12)$$

where r denotes the rank of $\boldsymbol{\Phi}$ satisfying $r \leq \min(n, m) = n \ll \infty$. Note that the update (7) does not require \mathbf{V} . Moreover, the relation between $\boldsymbol{\Phi}$ and \mathbf{K} can be given by $\mathbf{K} = \boldsymbol{\Phi} \boldsymbol{\Phi}^\top$. Using decomposition (12) yields

$$\mathbf{K} = \boldsymbol{\Phi} \boldsymbol{\Phi}^\top = (\mathbf{Z} \mathbf{V}^\top)(\mathbf{V} \mathbf{Z}^\top) = \mathbf{Z} \mathbf{Z}^\top. \quad (13)$$

As \mathbf{Z} is a lower triangular matrix, it can be obtained by performing a Cholesky decomposition on \mathbf{K} . Therefore, without actually computing the mapped space $\boldsymbol{\Phi}$, it is still possible to perform **SVM-Maj** by using the kernel matrix \mathbf{K} .

There is a wide variety of available kernels to obtain nonlinearity of the predictors. Table 5 shows some important examples of often used kernel functions.

| Type of kernel | Kernel function $\phi(\mathbf{x}_i)^\top \phi(\mathbf{x}_j)$ |
|---------------------------|--|
| linear | $\mathbf{x}_i^\top \mathbf{x}_j$ |
| homogeneous polynomial | $(\text{scale } \mathbf{x}_i^\top \mathbf{x}_j)^{\text{degree}}$ |
| nonhomogeneous polynomial | $(\text{scale } \mathbf{x}_i^\top \mathbf{x}_j + 1)^{\text{degree}}$ |
| radial basis function | $\exp(-\text{sigma} \mathbf{x}_i - \mathbf{x}_j ^2)$ |
| Laplace | $\exp(-\text{sigma} \mathbf{x}_i - \mathbf{x}_j)$ |

Table 5: Table of some examples of kernel functions, which can be used in the **SVMMaj** package.

As \mathbf{V} is usually unknown, β cannot be calculated. Nevertheless, it is still possible to predict the class labels of an unseen sample \mathbf{X}_2 . Using $\mathbf{q} = \Phi\beta$ and (12), we can derive

$$\begin{aligned}
\beta &= \mathbf{V}\rho \\
&= \mathbf{V}(\mathbf{R}^\top \mathbf{U}^\top \mathbf{U}(\mathbf{R}^\top)^{-1})\rho \\
&= (\mathbf{V}\mathbf{R}\mathbf{U}^\top)\mathbf{U}(\mathbf{R}^\top)^{-1}\rho \\
&= \Phi^\top \mathbf{U}(\mathbf{R}^\top)^{-1}\rho.
\end{aligned}$$

The predicted values of an unseen test sample \mathbf{X}_2 are

$$\mathbf{q}_2 = \Phi_2\beta = \Phi_2\Phi^\top \mathbf{U}(\mathbf{R}^\top)^{-1}\rho = \mathbf{K}_2\mathbf{U}(\mathbf{R}^\top)^{-1}\rho, \quad (14)$$

where Φ_2 and Φ are denoted as the transformed matrix of respectively \mathbf{X}_2 and \mathbf{X} into the high dimensional space and \mathbf{K} denotes the kernel matrix $\Phi_2\Phi^\top$.

5. The **SVMMaj** package in R

The **SVM-Maj** algorithm for the Support Vector Machine (SVM) is implemented in the **SVMMaj** package in R. Its main functions are `svmmaj`, which estimates the SVM, and `svmmajcrossval`, which performs a grid search of k -fold cross validations using **SVM-Maj** to find the combination of input values, (such as λ and degree in the case of a polynomial kernel) giving the best prediction performance.

The `svmmaj` function requires the $n \times k$ attribute matrix \mathbf{X} and the $n \times 1$ vector \mathbf{y} with class labels. Apart from the data objects, other parameter input values can be given as input to tune the model: `lambda`, `hinge`, `weights.obs`, `scale` and parameters for nonlinearities and settings of the algorithm itself. Table 6 shows the arguments of function `svmmaj` and its default values. For example,

```
R> svmmaj(X, y, lambda = 2, hinge = "quadratic", scale = "interval")
```

runs the SVM model with $\lambda = 2$, using a *quadratic* hinge and for each attribute, the values are scaled to the interval [0,1].

The function `svmmajcrossval` uses the same parameter input values and additionally the parameters to be used as grid points of the k -fold cross validation. These parameters should be given in the list object `search.grid`, e.g.,

| Parameter | Values | Description |
|----------------------------|--|---|
| <code>lambda</code> | scalar | Nonnegative penalty parameter of the penalty term. Default value is 1. |
| <code>hinge</code> | 'absolute',* 'quadratic', 'huber', vector | Specifies the hinge error term: = Use the absolute hinge error. = Use the quadratic hinge error. = Use the Huber hinge error. Vector with the nonnegative weight for the residual of each object or class, which can either be a vector of length 2 to specify the weights for each class, or a vector of length <code>length(y)</code> giving the weights for each object i . Default value is <code>c(1,1)</code> =Rescales all variables in <code>X</code> to have zero mean and standard deviation equal to 1. =Rescales all variables in <code>X</code> to be in the range [0, 1]. =No scaling is done. |
| <code>scale</code> | 'zscore', 'interval', 'none',* | In case of a linear kernel, <code>decomposition=FALSE</code> will not perform a decomposition at all and uses update 4 instead. |
| <code>decomposition</code> | logical | |
| <code>spline.knots</code> | integer | Number of interior knots of the spline which is equal to one less than the number of adjacent intervals. Default value is 0, which corresponds with a single interval. |
| <code>spline.degree</code> | integer | Degree of the spline basis. Default value is 1, representing the linear case. |
| <code>kernel</code> | | The kernel function of package <code>kernelLab</code> , which specifies which kernel type to be used. Possible kernels and its parameter values are among others: = The linear kernel: <code>k(x, x') = <x, x'></code> . = The polynomial kernel: <code>k(x, x') = (scale <x, x'> + offset) ^ degree</code> . = The Gaussian Radial Basis Function (RBF) kernel: <code>k(x, x') = exp(-sigma x - x' ^ 2)</code> . = The Laplacian kernel: <code>k(x, x') = exp(-sigma x - x')</code> . |
| <code>kernel.sigma</code> | 1 | Kernel parameter <code>sigma</code> used in the RBF and Laplacian kernel. |
| <code>kernel.degree</code> | 1 | Kernel parameter <code>degree</code> used in the polynomial kernel. |
| <code>kernel.scale</code> | 1 | Kernel parameter <code>scale</code> used in the polynomial kernel. |
| <code>kernel.offset</code> | 0 | Kernel parameter <code>offset</code> used in the polynomial kernel. |
| <code>convergence</code> | double | Specifies the convergence criterion of the algorithm. Default value is <code>3e-7</code> |
| <code>print.step</code> | logical | <code>print.step=TRUE</code> shows the progress of the iteration. Default value is <code>FALSE</code> . |
| <code>initial.point</code> | vector | Initial values <code>[c0 rho]</code> (see Algorithm 1) to be used in the SVM-Maj algorithm, the length of the vector equals the rank of explanatory matrix <code>X</code> plus one. |
| <code>increase.step</code> | integer | The iteration level from where the relaxed update (11) will be used. Default value is 20. |
| <code>na.action</code> | <code>na.action</code> | Specifies which <code>na.action</code> object will be used to handle missing values. Default is omit observations with missing values. |

Table 6: Parameter input values of `svmmaj`. The default settings are marked with *

```
R> svmmajcrossval(X, y, search.grid = list(lambda = c(1, 2, 4)))
```

performs a cross validation of X and y with as grid points $\lambda = 1, 2, 4$.

As an example, we use the `AusCredit` data set of the `libsvm` data sets (Chang and Lin 2001), which is included in the **SVMMaj** package. This data set consists of in total 690 credit requests, 307 of which are classified as positive and 383 as negative. These classifications are stored in `AusCredit$y` with class label `Rejected` to represent the negative responses, and label `Accepted` for the positive responses. In total, 14 attributes of each applicant has been stored as explanatory variables in `AusCredit$X`. Due to confidentiality, the labels of all explanatory variables are not available. Moreover, the observations in the data set `AusCredit` is split into `AusCredit.tr`, consisting the first 400 observations, and `AusCredit.te`, with the remaining 290 observations. `AusCredit.tr` will be used to estimate the model, while the `AusCredit.te` is used to analyze the prediction performances.

Example 1 *Train the SVM-model using the data set of Australian credit requests to classify the creditibility of the applicant.*

The command

```
R> library("SVMMaj")
```

loads the **SVMMaj** package into R. In this example, we will use the components X and y in the training set `AusCredit.tr`, which consists of explanatory variables respectively class labels of 400 credit requests, to train the model. Afterwards, the characteristics of the remaining 290 requests, which has been stored into component X of test set `AusCredit.te`, are used to predict the classification of the applicant. Using the actual class labels, `AusCredit.te$y`, the out of sample prediction performance is analyzed by comparing the ones with the predicted using the SVM model as estimated with `AusCredit.tr`. Running the SVM on the training data is done as follows.

```
R> model <- svmmaj(AusCredit.tr$X, AusCredit.tr$y, lambda = 100)
R> model
```

Model:

| | |
|---------------------------|----------|
| update method | svd |
| attribute dimension | 400 14 |
| degrees of freedom | 14 |
| number of iterations | 40 |
| loss value | 300.6324 |
| number of support vectors | 359 |

As a result, the trained model will be returned as an `svmmaj`-object. The `print` method of this object shows which update method is used, the number of iterations before convergence, the found minimum loss value and the number of support vectors. In case no kernel is used, the matrix Z from update (7) is obtained through the QR-decomposition shown in (6) by default. In case a nonlinear kernel is used, Z is being calculated through the Cholesky decomposition (13). One can choose not to perform a decomposition when using a nonlinear kernel by

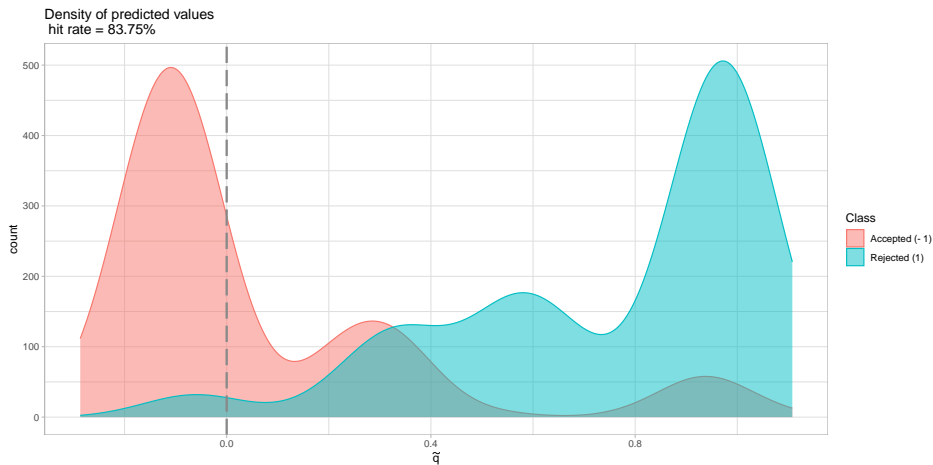


Figure 2: This figure shows the distribution of predicted values \tilde{q} of the two classes of Example 1, which can be obtained through the `plot()` method. These densities are created by the `density` function. This function specifies beforehand the bandwidth value to plot the density, which is shown on top of the graph.

specifying `decomposition = FALSE`. Then the original update (4) will be used. A graph of the distribution of the predicted values \tilde{q} for each class can be plotted via the `plot()` method using the `density` function of R, see Figure 2. The distribution shows that the majority of the **Accepted** class (-1) respondents received predicted \tilde{q}_i close to -1 and only a few close to $+1$. The same holds for the **Rejected** class ($+1$) respondents showing that the majority of respondents are correctly classified. A more detailed description of the model can be requested by using the `summary()` method.

```
R> summary(model)
```

Call:

```
svmmaj.default(X = AusCredit.tr$X, y = AusCredit.tr$y, lambda = 100)
```

Settings:

| | |
|----------------|----------|
| lambda | 100 |
| hinge error | absolute |
| spline basis | no |
| type of kernel | linear |

Data:

| | |
|-------------------------------|-------------------|
| class labels | Accepted Rejected |
| rank of X | 14 |
| number of predictor variables | 14 |
| number of objects | 400 |
| omitted objects | 0 |

Model:

| | |
|---------------------------|----------|
| update method | svd |
| number of iterations | 40 |
| loss value | 300.6324 |
| number of support vectors | 359 |

Confusion matrix:

| | | | |
|--------------|-----------------|----------|-------|
| | Predicted(yhat) | | |
| Observed (y) | Accepted | Rejected | Total |
| Accepted | 122 | 57 | 179 |
| Rejected | 8 | 213 | 221 |
| Total | 130 | 270 | 400 |

Classification Measures:

| | |
|----------------------------------|-------|
| hit rate | 0.837 |
| weighted hit rate | 0.838 |
| misclassification rate | 0.163 |
| weighted missclassification rate | 0.162 |

| | | | |
|----------|-------|--------|-----------|
| | TP | FP | Precision |
| Accepted | 0.682 | 0.3184 | 0.938 |
| Rejected | 0.964 | 0.0362 | 0.789 |

The **Settings** segment describes the parameter settings used to estimate the model. In this example, the scales of the explanatory variables have not been changed and a linear model is specified because no spline or nonlinear kernel is used. Furthermore, the penalty term of the loss function consists of an absolute hinge, with a penalty parameter λ of 1. In the **Data** segment, the properties of the input data are shown: the labels of each class, the rank of the explanatory variable matrix **X** (in case of using I-splines, this will be the rank of the resulting spline bases) and the size of the data (the number of objects and number of predictor variables). **SVMMaj** has the possibility to handle missing values through a specified **na.action**-object. In case observations with missing values are omitted, the number of omitted observations will also be printed in this segment. The **Model** segment summarizes the trained model as a result of the **SVM-Maj** algorithm: it specifies which update has been used, the number of iterations needed to obtain this model, the optimal loss value and the number of support vectors. The classification performance of the model on the data used to estimate can be found in the last segment, **Classification table**, where the confusion matrix is followed by measured *true positive (TP)*, *false positive (FP)* and *precision* below. True positive of a class denotes the proportion of objects of that class that are being predicted correctly, whereas false positive denotes proportion of the incorrectly predicted objects of a class. The precision of a class is the proportion of correctly predicted objects of the class among all objects predicted to be classified as that class.

Next, we would like to test how well the estimated SVM model predicts an unseen sample: the 290 objects in **AusCredit.te\$X** is used as hold-out sample. This is done through the **predict()** method.

```
R> predict(model, AusCredit.te$X)
```

Prediction frequencies:

| | Accepted | Rejected |
|-----------|----------|----------|
| frequency | 85 | 205 |

Confusion matrix:

| | Predicted(yhat) | | |
|--------------|-----------------|----------|-------|
| Observed (y) | Accepted | Rejected | Total |
| Accepted | 85 | 0 | 85 |
| Rejected | 0 | 205 | 205 |
| Total | 85 | 205 | 290 |

Classification Measures:

| | |
|------------------------|---|
| hit rate | 1 |
| misclassification rate | 0 |

| | TP | FP | Precision |
|----------|----|----|-----------|
| Accepted | 1 | 0 | 1 |
| Rejected | 1 | 0 | 1 |

If the actual class labels are known, one can include this object in the method to show the prediction performance:

```
R> predict(model, AusCredit.te$X, AusCredit.te$y)
```

Prediction frequencies:

| | Accepted | Rejected |
|-----------|----------|----------|
| frequency | 85 | 205 |

Confusion matrix:

| | Predicted(yhat) | | |
|--------------|-----------------|----------|-------|
| Observed (y) | Accepted | Rejected | Total |
| Accepted | 76 | 52 | 128 |
| Rejected | 9 | 153 | 162 |
| Total | 85 | 205 | 290 |

Classification Measures:

| | |
|----------------------------------|------|
| hit rate | 0.79 |
| weighted hit rate | 0.79 |
| misclassification rate | 0.21 |
| weighted missclassification rate | 0.21 |

| | TP | FP | Precision |
|----------|-------|--------|-----------|
| Accepted | 0.594 | 0.4062 | 0.894 |
| Rejected | 0.944 | 0.0556 | 0.746 |

The classification measures of this unseen sample prediction are similar to these of the in-sample predictions, which mean that this model has no problem of overfitting. Moreover, average hit rate of 85% indicates that this model predicts the objects quite well. Note the difference in true positive value between the classes; it appears that this model predicts classes in class Accepted slightly better than the other class.

To show a the distribution of \hat{q} for all applicants or, if the actual class labels are given, for each class, the argument `show.plot=TRUE` can be included, which result into a figure as in Figure 3.

Prediction frequencies:

| | Accepted | Rejected |
|-----------|----------|----------|
| frequency | 85 | 205 |

Confusion matrix:

| | Predicted(yhat) | | |
|--------------|-----------------|----------|-------|
| Observed (y) | Accepted | Rejected | Total |
| Accepted | 76 | 52 | 128 |
| Rejected | 9 | 153 | 162 |
| Total | 85 | 205 | 290 |

Classification Measures:

| | |
|----------------------------------|------|
| hit rate | 0.79 |
| weighted hit rate | 0.79 |
| misclassification rate | 0.21 |
| weighted missclassification rate | 0.21 |

| | TP | FP | Precision |
|----------|-------|--------|-----------|
| Accepted | 0.594 | 0.4062 | 0.894 |
| Rejected | 0.944 | 0.0556 | 0.746 |

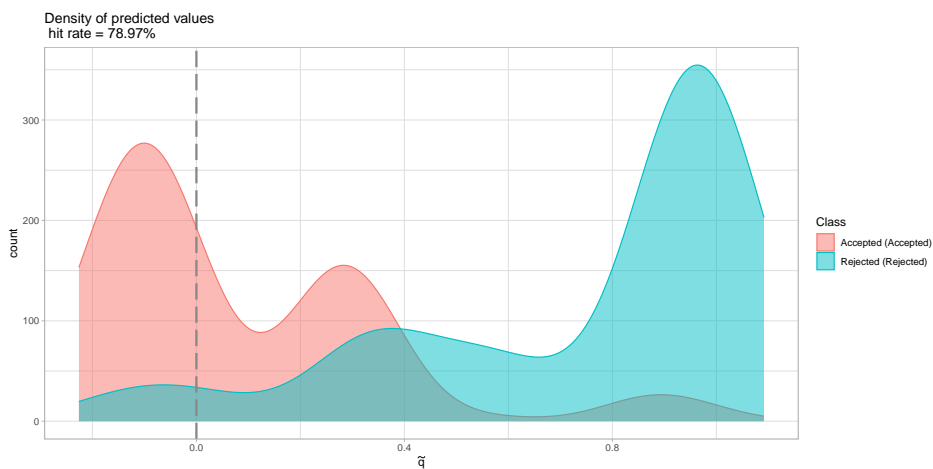


Figure 3: Densities of the predictions in \hat{q} split by class.


```

+           search.grid = list(lambda = 10^seq(4, -4)),
+           hinge = "absolute", convergence = 1e-4)
R> model <- svmmaj(
+           voting.tr$X, voting.tr$y, hinge = "absolute",
+           lambda = results.absolute$param.opt$lambda)
R> q.absolute <- predict(model, voting.te$X, voting.te$y)

```

5.2. Hinge functions

SVMMaj allows using the quadratic hinge or the Huber hinge instead of the standard absolute hinge. An important advantage of the quadratic hinge is that it has the potential to be computationally much more efficient than the absolute hinge. Let us perform a similar cross validation on the `voting` data set using the quadratic hinge by

```

R> results.quadratic <- svmmajcrossval(
+           voting.tr$X, voting.tr$y,
+           search.grid = list(lambda = 10^seq(4, -2, length.out = 10)),
+           hinge = "quadratic", convergence = 1e-4)
R> model <- svmmaj(
+           voting.tr$X, voting.tr$y, hinge = "quadratic",
+           lambda = results.quadratic$param.opt$lambda)
R> q.quadratic <- predict(model, voting.te$X, voting.te$y)

```

A summary of the results of these examples can be found in Table 7. Figure 4 shows the hit rate of the cross validation using different lambda values. It can be seen that both hinges have similar out-of-sample predictive power. It is also clear that per iteration, the quadratic hinge is much faster than the absolute hinge. The effect of the increased computational efficiency of the quadratic hinge is in this example canceled by a large increase of the number of iterations as it requires more iterations to converges.

| | Absolute | Quadratic |
|-----------------------|----------|-----------|
| CPU-time (sec) | 1.23 | 1.63 |
| Mean no. of iter | 211.64 | 839.73 |
| CPU-time (per iter) | 0.01 | 0.00 |
| Optimal p | -0.80 | 0.40 |
| Hit rate (average TP) | 0.55 | 0.55 |

Table 7: Results of the fivefold cross validation estimation using the `svmcrossval` function. CPU-time is the time in CPU seconds needed to perform fivefold cross validation and Optimal p the value of which 10^p returns the best hit rate in the cross validation. Mean no. of iterations denotes the average value of the sum of the number of iterations per lambda-value. CPU-time per iter is the mean computation time needed to perform one iteration. Hit rate is the average TP value by predicting the class labels of the holdout sample of 134 congress men using the first 300 congress men as sample of estimation.

5.3. Nonlinearities

The package **SVMMaj** can also implement nonlinearity in the model. One can choose to


```

+                               scale = "interval", search.grid = list(lambda = 10^seq(
+                               hinge = "quadratic", spline.knots = 5, spline.degree =
+                               weights.obs = list(positive = 2, negative = 1))
R> model.spline <- svmmaj(
+                               diabetes.tr$X, diabetes.tr$y,
+                               scale = "interval", lambda = results.spline$param.opt$lambda,
+                               spline.knots = 5, spline.degree = 2, hinge = "quadratic",
+                               weights.obs = list(positive = 2, negative = 1))
R> predict(
+   model.spline, diabetes.te$X, diabetes.te$y,
+   weights = list(positive = 2, negative = 1))

```

Prediction frequencies:

| | negative | positive |
|-----------|----------|----------|
| frequency | 91 | 77 |

Confusion matrix:

| | Predicted(yhat) | | |
|--------------|-----------------|----------|-------|
| Observed (y) | negative | positive | Total |
| negative | 80 | 28 | 108 |
| positive | 11 | 49 | 60 |
| Total | 91 | 77 | 168 |

Classification Measures:

| | |
|----------------------------------|-------|
| hit rate | 0.768 |
| weighted hit rate | 0.781 |
| misclassification rate | 0.232 |
| weighted missclassification rate | 0.219 |

| | TP | FP | Precision |
|----------|-------|-------|-----------|
| negative | 0.741 | 0.259 | 0.879 |
| positive | 0.817 | 0.183 | 0.636 |

The optimal λ for the model using I-splines can be found in `results.spline$param.opt`, which is 10^1 . This λ value equals the penalty value which will give the lowest misclassification rate in the cross-validation. One of the advantages of using splines to handle nonlinear prediction is the possibility to show the effect of a variable by plotting its estimated transformation. Figure 5 shows these plots of the splines per variable, which can be used for interpretation of the effects of each individual variable. In this figure, one can clearly see nonlinear effects in most variables. For example, the *diabetes pedigree* (x_7) shows a positive relation with respect to female patients with **positive** results, but with a diminishing returns to scale. On the other hand, *Age* (x_8) has a reverse *v*-shape: respondents who are around 40 are more likely to have diabetes. Overall, *glucose concentration* (x_2) and *BMI* (x_6) have the largest effect on the class prediction when its values are large.

Kernel

Another way of implementing nonlinearity in the model by using a kernel. In this example, we will use the Radial Basis Function in our model training. To find the optimal λ and σ values we performed a five fold cross validation with the grids: $\lambda = 10^{-6}, 10^{-5} \dots 10^4, 10^5, 10^6$ and $\sigma = 2^{-5}, 2^{-4} \dots 2^4, 2^5$ by the following commands.

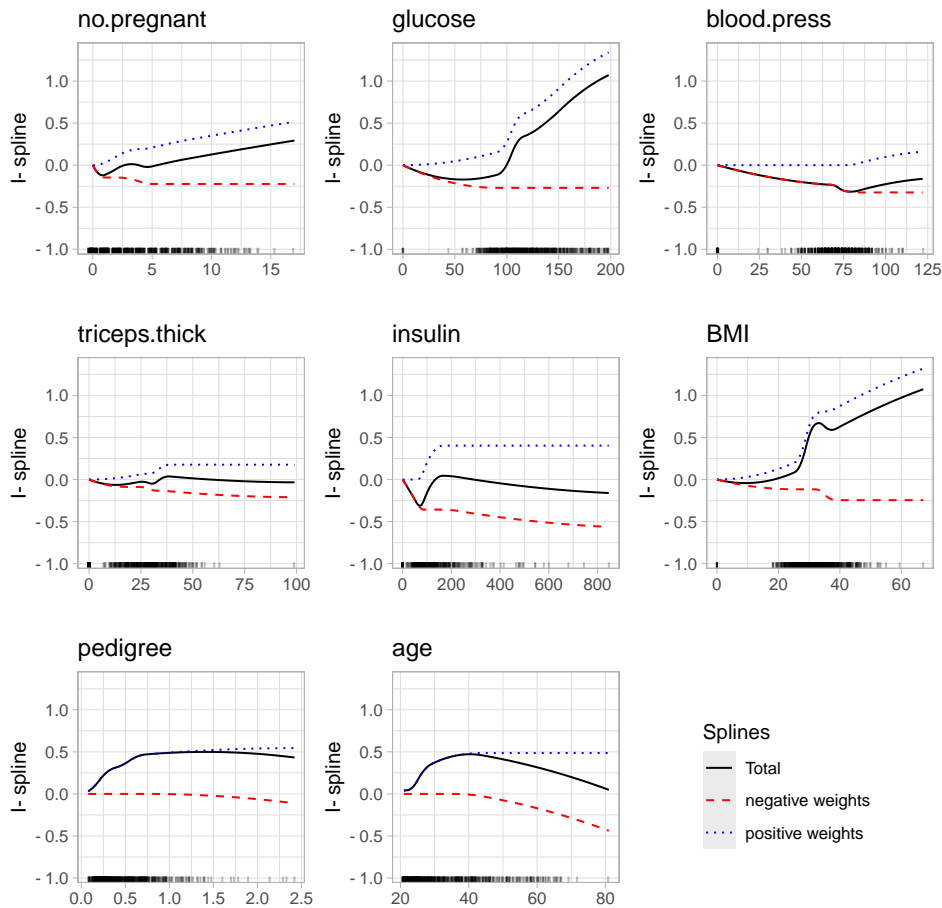


Figure 5: The spline plots of each of 8 variables used to predict the result of a test for diabetes among females of Pima Indian heritages. This model has been performed with `lambda = 10` and the spline basis with 5 inner knots and a degree of 2. Each graph denotes the loss term of the corresponding variable with different values. The higher the predicted value \tilde{q} , the higher the probability of positive test.

```
R> library(kernlab)
R> results.kernel <- svmmajcrossval(
+     diabetes.tr$X, diabetes.tr$y,
+     scale = "interval",
+     search.grid = list(
+         kernel.sigma = 2^seq(-4, 4, by = 2),
```

```

+           lambda = 10^seq(-4, 4, by = 2)
+           ), hinge = "quadratic", kernel = rbfdot,
+           weights.obs = list(positive = 2, negative = 1),
+           options = list(convergence = 1e-4))
R> model.kernel <- svmmaj(
+           diabetes.tr$X, diabetes.tr$y,
+           scale = "interval", lambda = results.kernel$param.opt$lambda,
+           kernel.sigma = results.kernel$param.opt$kernel.sigma,
+           kernel = rbfdot, hinge = "quadratic",
+           weights.obs = list(positive = 2, negative = 1))
R> predict(
+           model.kernel, diabetes.te$X, diabetes.te$y,
+           weights = list(positive = 2, negative = 1))

```

Prediction frequencies:

| | negative | positive |
|-----------|----------|----------|
| frequency | 127 | 41 |

Confusion matrix:

| | Predicted(yhat) | | |
|--------------|-----------------|----------|-------|
| Observed (y) | negative | positive | Total |
| negative | 99 | 9 | 108 |
| positive | 28 | 32 | 60 |
| Total | 127 | 41 | 168 |

Classification Measures:

| | |
|----------------------------------|-------|
| hit rate | 0.780 |
| weighted hit rate | 0.715 |
| misclassification rate | 0.220 |
| weighted missclassification rate | 0.285 |

| | TP | FP | Precision |
|----------|-------|--------|-----------|
| negative | 0.917 | 0.0833 | 0.78 |
| positive | 0.533 | 0.4667 | 0.78 |

Observing the prediction results, we can see that the model using I-splines has a higher TP-value of female persons having **positive** result in diabetes as well as the hit rate (average TP-value) suggesting that for these data the I-spline transformation is better able to pick up the nonlinearities in the predictor variables than the radial basis kernel.

6. Discussion

This paper introduces the R-package **SVMMaj**. This package implements the **SVM-Maj** algorithm of (Groenen *et al.* 2007, 2008) with the addition of nonlinear models with kernels. One of the advantages of the **SVM-Maj** approach is the competitively fast training speed for

medium sized problems. Furthermore, it allows individual objects in a training dataset to receive different individual weight.

Another advantage of **SVM-Maj** is the possibility to use different loss functions, besides the commonly used absolute hinge. In this package, the absolute hinge, quadratic hinge and Huber hinge has been implemented. Nevertheless, this can be expanded to any other error function $f(q)$ that satisfies the following condition: the second derivative of its function has a bounded maximum, so that a quadratic majorization function can be found. If in addition $f(q)$ is convex, then the overall loss function (3) is strictly convex, so that the the **SVM-Maj** algorithm is guaranteed to stop at the global minimum.

A. Efficient updates for SVM-Maj

Recall that the relationship between \mathbf{q} and β can be written as

$$\mathbf{q} = \mathbf{X}\beta. \quad (15)$$

In some situations, different values of β may lead to the same \mathbf{q} , when deriving \mathbf{q} from β . In other situations, the opposite could happen, that is, several values of \mathbf{q} may result into the same β value. Thus, there is not always a one-to-one mapping of \mathbf{q} to β and the reverse. Therefore, one should take these possible situations into account when performing iterative majorization. To illustrate this, we will use the singular value decomposition (SVD) of \mathbf{X} :

$$\begin{matrix} \mathbf{X} & = & \mathbf{P} & \Lambda & \mathbf{Q}^\top, \\ (n \times k) & & (n \times r) & (r \times r) & (r \times k) \end{matrix}, \quad (16)$$

where \mathbf{P} and \mathbf{Q} are orthonormal matrices which satisfy $\mathbf{P}^\top \mathbf{P} = \mathbf{I}$ and $\mathbf{Q}^\top \mathbf{Q} = \mathbf{I}$ and Λ is a diagonal matrix. The relationship between \mathbf{q} and β can then be written as:

$$\mathbf{q} = \mathbf{X}\beta = \mathbf{P}\Lambda\mathbf{Q}^\top\beta, \quad (17)$$

$$\begin{matrix} \mathbf{P}^\top \mathbf{q} & = & \Lambda & \mathbf{Q}^\top \beta. \\ (r \times 1) & & (r \times r) & (r \times 1) \end{matrix}. \quad (18)$$

Let us first examine the left part of the equation. \mathbf{q} can be written as a combination of two orthogonal vectors, a projection of \mathbf{q} on \mathbf{P} and a projection on its complement $(\mathbf{I} - \mathbf{P}\mathbf{P}^\top)$, that is,

$$\mathbf{q} = \mathbf{P}\mathbf{P}^\top \mathbf{q} + (\mathbf{I} - \mathbf{P}\mathbf{P}^\top) \mathbf{q} = \mathbf{q}_B + \mathbf{q}_N. \quad (19)$$

Multiplying both sides with \mathbf{P}^\top gives

$$\begin{aligned} \mathbf{P}^\top \mathbf{q} &= \mathbf{P}^\top (\mathbf{q}_B + \mathbf{q}_N) \\ &= \mathbf{P}^\top \mathbf{q}_B + \mathbf{P}^\top (\mathbf{I} - \mathbf{P}\mathbf{P}^\top) \mathbf{q} \\ &= \mathbf{P}^\top \mathbf{q}_B + (\mathbf{P}^\top - \mathbf{P}^\top) \mathbf{q} \\ &= \mathbf{P}^\top \mathbf{q}_B + \mathbf{0} \\ &= \mathbf{P}^\top \mathbf{q}_B. \end{aligned}$$

In other words, the left part of (18) is only dependent of \mathbf{q}_B . When $r = n$, $\mathbf{P}\mathbf{P}^\top$ equals \mathbf{I} and thus, $\mathbf{q} = \mathbf{q}_B + \mathbf{q}_N = \mathbf{q}_B + (\mathbf{I} - \mathbf{I})\mathbf{q} = \mathbf{q}_B$. In this case there is always an unique solution of

$$\mathbf{P}^\top \mathbf{q} = \Lambda \theta, \text{ for any } \theta \in \mathfrak{R}^r. \quad (20)$$

However, when $r < n$, $\mathbf{P}\mathbf{P}^\top = \mathbf{I}$ does not hold and there are infinitely many solutions to (20) so that an one-to-one relationship of \mathbf{q} and $\boldsymbol{\beta}$ in (15) is lost indeed.

Similarly, $\boldsymbol{\beta}$ can be written as $\boldsymbol{\beta} = \mathbf{Q}\mathbf{Q}^\top\boldsymbol{\beta} + (\mathbf{I} - \mathbf{Q}\mathbf{Q}^\top)\boldsymbol{\beta} = \boldsymbol{\beta}_B + \boldsymbol{\beta}_N$, and $\mathbf{Q}^\top\boldsymbol{\beta} = \mathbf{Q}^\top(\boldsymbol{\beta}_B + \boldsymbol{\beta}_N) = \mathbf{Q}^\top\boldsymbol{\beta}_B$. If $r < k$ then there is no unique solution to $\mathbf{Q}^\top\boldsymbol{\beta} = \boldsymbol{\theta}$ with $\boldsymbol{\theta} \in \mathfrak{R}^r$. Note that $\boldsymbol{\beta}_B$ and $\boldsymbol{\beta}_N$ are independent to each other and that

$$\boldsymbol{\beta}_N^\top\boldsymbol{\beta}_B = \boldsymbol{\beta}_B^\top\boldsymbol{\beta}_N = \boldsymbol{\beta}^\top(\mathbf{Q}\mathbf{Q}^\top)(\mathbf{I} - \mathbf{Q}\mathbf{Q}^\top)\boldsymbol{\beta} = 0, \quad (21)$$

as $\mathbf{Q}\mathbf{Q}^\top(\mathbf{I} - \mathbf{Q}\mathbf{Q}^\top) = \mathbf{0}$.

As a result, we have to take care that a proper relation between $\boldsymbol{\beta}$ and \mathbf{q} is retained, when more efficient updates are derived. In the next section, we will examine three different situations and introduce the optimization method by optimizing the parameters which has the lowest dimension, that is, $\min(r, n, k)$. In this way, it can be assured that \mathbf{q}_N and $\boldsymbol{\beta}_N$ are both zero vectors. Subsequently, we will discuss the use of each optimization method in each situation.

A.1. $\boldsymbol{\beta}$ -method: Full rank and more objects than variables ($n > k$ and $r = k$)

When the number of variables is smaller than the number of objects, and if \mathbf{X} is of full rank, then $\mathbf{Q}\mathbf{Q}^\top = \mathbf{I}$ and each $\boldsymbol{\beta}$ will give an unique \mathbf{q} . As $\dim(\boldsymbol{\beta}) < \dim(\mathbf{q})$, it is most efficient to optimize the loss function through $\boldsymbol{\beta}$. The majorization function can as follows be written as a function of $\boldsymbol{\beta}$.

$$\text{Maj}(\boldsymbol{\beta}, \alpha) = (\alpha\mathbf{1} + \mathbf{X}\boldsymbol{\beta})^\top \mathbf{A}(\alpha\mathbf{1} + \mathbf{X}\boldsymbol{\beta}) - 2(\alpha\mathbf{1} + \mathbf{X}\boldsymbol{\beta})^\top \mathbf{b} + \lambda\boldsymbol{\beta}^\top\boldsymbol{\beta} + o. \quad (22)$$

To derive an update, we set the first derivatives of (22) with respect to $\boldsymbol{\beta}$ and α to zero, which yields

$$\begin{aligned} \mathbf{1}^\top \mathbf{A}(\mathbf{1}\alpha + \mathbf{X}\boldsymbol{\beta}) &= \mathbf{1}^\top \mathbf{b} \\ \mathbf{X}^\top \mathbf{A}(\mathbf{1}\alpha + \mathbf{X}\boldsymbol{\beta}) + \lambda\boldsymbol{\beta} &= \mathbf{X}^\top \mathbf{b}, \end{aligned}$$

or in matrix form,

$$\begin{bmatrix} \mathbf{1}^\top \mathbf{A} \mathbf{1} & \mathbf{1}^\top \mathbf{A} \mathbf{X} \\ \mathbf{X}^\top \mathbf{A} \mathbf{1} & \mathbf{X}^\top \mathbf{A} \mathbf{X} + \lambda \mathbf{I} \end{bmatrix} \begin{bmatrix} \alpha \\ \boldsymbol{\beta} \end{bmatrix} = \begin{bmatrix} \mathbf{1}^\top \mathbf{b} \\ \mathbf{X}^\top \mathbf{b} \end{bmatrix}.$$

Using the fact that $\alpha_0\mathbf{1} + \mathbf{X}\boldsymbol{\beta} = \begin{bmatrix} \mathbf{1} & \mathbf{X} \end{bmatrix} \begin{bmatrix} \alpha \\ \boldsymbol{\beta} \end{bmatrix}$, an update of both $\boldsymbol{\beta}$ and α_0 can be derived by solving the linear system

$$\left(\begin{bmatrix} \mathbf{1}^\top \\ \mathbf{X}^\top \end{bmatrix} \mathbf{A} \begin{bmatrix} \mathbf{1} & \mathbf{X} \end{bmatrix} + \lambda \begin{bmatrix} 0 & \mathbf{0}^\top \\ \mathbf{0} & \mathbf{I} \end{bmatrix} \right) \begin{bmatrix} \alpha^+ \\ \boldsymbol{\beta}^+ \end{bmatrix} = \begin{bmatrix} \mathbf{1}^\top \mathbf{b} \\ \mathbf{X}^\top \mathbf{b} \end{bmatrix},$$

or, in compact form

$$\left(\tilde{\mathbf{X}}^\top \mathbf{A} \tilde{\mathbf{X}} + \lambda \mathbf{J} \right) \begin{bmatrix} \alpha^+ \\ \boldsymbol{\beta}^+ \end{bmatrix} = \tilde{\mathbf{X}}^\top \mathbf{b}, \quad (23)$$

where $\tilde{\mathbf{X}} = \begin{bmatrix} \mathbf{1} & \mathbf{X} \end{bmatrix}$ and $\mathbf{J} = \begin{bmatrix} 0 & \mathbf{0}^\top \\ \mathbf{0} & \mathbf{I} \end{bmatrix}$.

To prove that the the linear system (23) has a unique solution under the assumption that $\mathbf{X} \neq \mathbf{0}$, we will show that the matrix $\tilde{\mathbf{X}}^\top \mathbf{A} \tilde{\mathbf{X}} + \lambda \mathbf{J}$ is positive definite. Let us examine the following equation

$$\begin{aligned} \begin{bmatrix} \alpha & \beta^\top \end{bmatrix} \left(\tilde{\mathbf{X}}^\top \mathbf{A} \tilde{\mathbf{X}} + \lambda \mathbf{J} \right) \begin{bmatrix} \alpha \\ \beta \end{bmatrix} &= \begin{bmatrix} \alpha & \beta \end{bmatrix} \tilde{\mathbf{X}}^\top \mathbf{A} \tilde{\mathbf{X}} \begin{bmatrix} \alpha \\ \beta \end{bmatrix} + \lambda \begin{bmatrix} \alpha & \beta^\top \end{bmatrix} \mathbf{J} \begin{bmatrix} \alpha \\ \beta \end{bmatrix} \\ &= (\alpha \mathbf{1} + \mathbf{X} \beta)^\top \mathbf{A} (\alpha \mathbf{1} + \mathbf{X} \beta) + \lambda \beta^\top \beta. \end{aligned} \quad (24)$$

From this equation, we can see that (24) equals the sum of two positive values. Furthermore, the right part $\lambda \beta^\top \beta$ of the equation equals zero only if $\beta = \mathbf{0}$, whereas the left part will be zero only when $(\alpha \mathbf{1} + \mathbf{X} \beta) = \mathbf{0}$. As both equations only hold when $\alpha = 0$ and $\beta = \mathbf{0}$, we know that the matrix $\tilde{\mathbf{X}}^\top \mathbf{A} \tilde{\mathbf{X}} + \lambda \mathbf{J}$ is positive definite.

An update of \mathbf{q} can be calculated by $\mathbf{q}^+ = \mathbf{X} \beta^+$. Note that \mathbf{q}_N necessarily equals zero, as

$$\mathbf{q}_N = (\mathbf{I} - \mathbf{P} \mathbf{P}^\top) \mathbf{q} = (\mathbf{I} - \mathbf{P} \mathbf{P}^\top) \mathbf{P} \mathbf{A} \mathbf{Q}^\top \beta = (\mathbf{P} - \mathbf{P} \mathbf{P}^\top \mathbf{P}) \mathbf{A} \mathbf{Q}^\top \beta = \mathbf{0}.$$

A.2. q-method: Full rank and less objects than variables ($n < k$ and $r = n$)

When $k > n$, or more general $k > r$, we know that there are no unique solutions to $\mathbf{q} = \mathbf{X} \beta$ and that $\mathbf{X} \beta = \mathbf{X}(\beta_B + \beta_N) = \mathbf{X} \beta_B$, that is, \mathbf{q} is not dependent of β_N . Consider the penalty term $\lambda \beta^\top \beta$. As $\mathbf{Q} \mathbf{Q}^\top (\mathbf{I} - \mathbf{Q} \mathbf{Q}^\top) = \mathbf{0}$, the penalty term can be simplified as

$$\lambda \beta^\top \beta = \lambda (\beta_B + \beta_N)^\top (\beta_B + \beta_N) = \lambda \beta_B^\top \beta_B + \lambda \beta_N^\top \beta_N$$

Moreover, as $\lambda \beta_N^\top \beta_N \geq 0$ and \mathbf{q} does not depend on β_N , β_N can be set to zero, with the result that $\beta = \beta_B$. Nevertheless, when the number of variables k is larger than the number of objects n , and when \mathbf{X} is of full rank, that is $r = k$, then $\mathbf{P} \mathbf{P}^\top = \mathbf{I}$ and each \mathbf{q} will give an unique β . As $\dim(\mathbf{q}) < \dim(\beta)$, it is most efficient to optimize the loss function through \mathbf{q} . β can then be derived using (18), that is,

$$\beta = \mathbf{Q} \mathbf{A}^{-1} \mathbf{P}^\top \mathbf{q} = \mathbf{Q} \mathbf{A} \mathbf{P}^\top \mathbf{P} \mathbf{A}^{-2} \mathbf{P}^\top \mathbf{q} = \mathbf{X}^\top (\mathbf{X} \mathbf{X}^\top)^{-1} \mathbf{q},$$

using the fact that $(\mathbf{X} \mathbf{X}^\top) (\mathbf{P} \mathbf{A}^{-2} \mathbf{P}^\top) (\mathbf{X} \mathbf{X}^\top) = (\mathbf{P} \mathbf{A}^2 \mathbf{P}) (\mathbf{P} \mathbf{A}^{-2} \mathbf{P}^\top) (\mathbf{P} \mathbf{A}^2 \mathbf{P}) = (\mathbf{P} \mathbf{A}^2 \mathbf{P})$. Note that β does not depend on \mathbf{q}_N , as $\beta = \mathbf{Q} \mathbf{A}^{-1} \mathbf{P}^\top \mathbf{q} = \mathbf{Q} \mathbf{A}^{-1} \mathbf{P}^\top \mathbf{q}_B$. The penalty term $\lambda \beta^\top \beta$ can then be written as

$$\begin{aligned} \lambda \beta^\top \beta &= \lambda (\mathbf{X}^\top (\mathbf{X} \mathbf{X}^\top)^{-1} \mathbf{q})^\top (\mathbf{X}^\top (\mathbf{X} \mathbf{X}^\top)^{-1} \mathbf{q}) \\ &= \lambda \mathbf{q}^\top (\mathbf{X} \mathbf{X}^\top)^{-1} \mathbf{X} \mathbf{X}^\top (\mathbf{X} \mathbf{X}^\top)^{-1} \mathbf{q} = \lambda \mathbf{q}^\top (\mathbf{X} \mathbf{X}^\top)^{-1} \mathbf{q} = \lambda \mathbf{q}^\top \mathbf{K}^{-1} \mathbf{q}, \end{aligned}$$

where $\mathbf{K} = \mathbf{X} \mathbf{X}^\top = \mathbf{P} \mathbf{A}^2 \mathbf{P}^\top$.

Therefore, the majorization function can as follows be written as a function of \mathbf{q} .

$$\text{Maj}(\beta, \alpha) = (\alpha \mathbf{1} + \mathbf{q})^\top \mathbf{A} (\alpha \mathbf{1} + \mathbf{q}) - 2(\alpha \mathbf{1} + \mathbf{q})^\top \mathbf{b} + \lambda \mathbf{q}^\top \mathbf{K}^{-1} \mathbf{q}. \quad (25)$$

The first-order conditions of (25) are

$$\begin{aligned} \mathbf{1}^\top \mathbf{A} (\mathbf{1} \alpha + \mathbf{q}) &= \mathbf{1}^\top \mathbf{b}, \\ \mathbf{A} (\mathbf{1} \alpha + \mathbf{q}) + \lambda \mathbf{K}^{-1} \mathbf{q} &= \mathbf{b}. \end{aligned}$$

Using $\begin{bmatrix} \mathbf{1} & \mathbf{I} \end{bmatrix} \begin{bmatrix} \alpha & \mathbf{q} \end{bmatrix} = \mathbf{1}\alpha + \mathbf{q} = \tilde{\mathbf{q}}$, the parameters \mathbf{q} and α can be updated by deriving

$$\left(\begin{bmatrix} \mathbf{1}^\top \\ \mathbf{I} \end{bmatrix} \mathbf{A} \begin{bmatrix} \mathbf{1} & \mathbf{I} \end{bmatrix} + \lambda \begin{bmatrix} 0 & \mathbf{0}^\top \\ \mathbf{0} & \mathbf{K}^{-1} \end{bmatrix} \right) \begin{bmatrix} \alpha^+ \\ \mathbf{q}^+ \end{bmatrix} = \begin{bmatrix} \mathbf{1}^\top \mathbf{b} \\ \mathbf{b} \end{bmatrix},$$

or, in compact form

$$(\tilde{\mathbf{I}}^\top \mathbf{A} \tilde{\mathbf{I}} + \lambda \mathbf{L}) \begin{bmatrix} \alpha^+ \\ \mathbf{q}^+ \end{bmatrix} = \tilde{\mathbf{I}}^\top \mathbf{b}, \quad (26)$$

where $\tilde{\mathbf{I}} = \begin{bmatrix} \mathbf{1} & \mathbf{I} \end{bmatrix}$ and $\mathbf{L} = \begin{bmatrix} 0 & \mathbf{0}^\top \\ \mathbf{0} & \mathbf{K}^{-1} \end{bmatrix}$.

Similar to (23), we can show that $(\tilde{\mathbf{I}}^\top \mathbf{A} \tilde{\mathbf{I}} + \lambda \mathbf{L})$ is positive definite and thus (26) can always be solved.

Also, the corresponding update for β , which is

$$\beta^+ = \mathbf{Q} \mathbf{\Lambda}^{-1} \mathbf{P}^\top \mathbf{q} = \mathbf{X} (\mathbf{X} \mathbf{X}^\top)^{-1} \mathbf{q}, \quad (27)$$

equals β_B , as

$$\beta_N = (\mathbf{I} - \mathbf{Q} \mathbf{Q}^\top) \beta = (\mathbf{I} - \mathbf{Q} \mathbf{Q}^\top) \mathbf{Q} \mathbf{\Lambda}^{-1} \mathbf{P}^\top \mathbf{q} = (\mathbf{Q} - \mathbf{Q} \mathbf{Q}^\top \mathbf{Q}) \mathbf{\Lambda}^{-1} \mathbf{P}^\top \mathbf{q} = \mathbf{0}.$$

A.3. θ -method: Rank is smaller than either n or k ($r < \min(n, k)$)

When $r < \min(n, k)$, the interdependence of \mathbf{q} and \mathbf{X} can be summarized in an $r \times 1$ vector $\boldsymbol{\theta} = \mathbf{Q}^\top \beta = \mathbf{\Lambda}^{-1} \mathbf{P}^\top \mathbf{q}$ from (18). As \mathbf{q}_N and β_N are not of interest, it is efficient to optimize the loss function by $\boldsymbol{\theta}$. β will then be calculated through $\beta = \mathbf{Q} \boldsymbol{\theta}$, which will assure that $\beta = \mathbf{Q} \boldsymbol{\theta} = \mathbf{Q} \mathbf{Q}^\top \beta = \beta_B$, in a similar way, it can be shown that $\mathbf{q} = \mathbf{q}_B$. Using the fact that $\mathbf{q} = \mathbf{X} \beta = \mathbf{P} \mathbf{\Lambda} \mathbf{Q}^\top \beta = \mathbf{P} \mathbf{\Lambda} \boldsymbol{\theta}$ and $\boldsymbol{\theta}^\top \boldsymbol{\theta} = \beta^\top \mathbf{Q} \mathbf{Q}^\top \beta = \beta_B^\top \beta_B = \beta^\top \beta$, the majorization function can be written as

$$\text{Maj}(\beta, \alpha) = (\alpha \mathbf{1} + \mathbf{P} \mathbf{\Lambda} \boldsymbol{\theta})^\top \mathbf{A} (\alpha \mathbf{1} + \mathbf{P} \mathbf{\Lambda} \boldsymbol{\theta}) - 2(\alpha \mathbf{1} + \mathbf{P} \mathbf{\Lambda} \boldsymbol{\theta})^\top \mathbf{b} + \lambda \boldsymbol{\theta}^\top \boldsymbol{\theta}, \quad (28)$$

with the first-order condition

$$\begin{aligned} \mathbf{1}^\top \mathbf{A} (\alpha \mathbf{1} + \mathbf{P} \mathbf{\Lambda} \boldsymbol{\theta}) &= \mathbf{1}^\top \mathbf{b} \\ \mathbf{\Lambda} \mathbf{P}^\top \mathbf{A} (\alpha \mathbf{1} + \mathbf{P} \mathbf{\Lambda} \boldsymbol{\theta}) + \lambda \mathbf{I} \boldsymbol{\theta} &= \mathbf{\Lambda} \mathbf{P}^\top \mathbf{b}. \end{aligned}$$

Using $\begin{bmatrix} \mathbf{1} & \mathbf{P} \mathbf{\Lambda} \end{bmatrix} \begin{bmatrix} \alpha & \boldsymbol{\theta} \end{bmatrix} = \mathbf{1} \alpha_0 + \mathbf{P} \mathbf{\Lambda} \boldsymbol{\theta} = \tilde{\mathbf{q}}$, the parameters $\boldsymbol{\theta}$ and α_0 can be updated by deriving

$$\left(\begin{bmatrix} \mathbf{1}^\top \\ \mathbf{\Lambda} \mathbf{P}^\top \end{bmatrix} \mathbf{A} \begin{bmatrix} \mathbf{1} & \mathbf{P} \mathbf{\Lambda} \end{bmatrix} + \lambda \begin{bmatrix} 0 & \mathbf{0}^\top \\ \mathbf{0} & \mathbf{I} \end{bmatrix} \right) \begin{bmatrix} \alpha^+ \\ \boldsymbol{\theta}^+ \end{bmatrix} = \begin{bmatrix} \mathbf{1}^\top \mathbf{b} \\ \mathbf{\Lambda} \mathbf{P}^\top \mathbf{b} \end{bmatrix},$$

or, in compact form

$$(\tilde{\mathbf{P}}^\top \mathbf{A} \tilde{\mathbf{P}} + \lambda \mathbf{J}) \begin{bmatrix} \alpha^+ \\ \boldsymbol{\theta}^+ \end{bmatrix} = \tilde{\mathbf{P}}^\top \mathbf{b}, \quad (29)$$

where $\tilde{\mathbf{P}} = \begin{bmatrix} \mathbf{1} & \mathbf{P} \mathbf{\Lambda} \end{bmatrix}$.

The advantage of this method is that $r \leq \min(n, k)$, which means that it restricts to the space of which the relationship between \mathbf{q} and β is described. Moreover, it is assured that the dimension of θ is the lowest of three (that is, $r \leq \min(n, k)$), and thus it is most efficient and consistent algorithm. However, this method requires the SVD or the QR decomposition to be computed, which may need much computational time in case n and k are large. Therefore, one should consider the alternatives when the matrix \mathbf{X} is of full rank, that is when $r = \min(n, k)$.

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