Hard

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double n = X.n_rows;
double p = X.n_cols;
double n_y = y.n_rows;
double n_beta = beta.n_rows;

// valid dimension

In [[https://web.stanford.edu/~hastie/glmnet/glmnet_alpha.html][here]] the author explains the detail of the loss function. The loss function of logistic regression is

$$- \Big\{ \frac{1}{N} \sum \left[y_i (\beta_0 + x_i^\top \beta) - \log(1 + e^{(\beta_0 + x_i^\top \beta)}) \right] \Big\} + \lambda \Big\{ \frac{(1 - \alpha)}{2} \|\beta\|_2^2 + \alpha \|\beta\|_1 \Big\}.$$

When $\alpha = 1$ we get what is required. Note that here $y_i \in \{0, 1\}$.

```
library(Rcpp)
library(RcppArmadillo)
library(inline)
library(ElemStatLearn)
library(testthat)
library(rbenchmark)
# Rcpp function
sourceCpp('C.cpp')
# The C code is as follow
#include <RcppArmadillo.h>
#include <assert.h>
// [[Rcpp::depends(RcppArmadillo)]]
using namespace Rcpp;
using namespace std;
using namespace arma;
int myassert(bool flag,char * info)
  {
  if (flag == 0){
    throw std::invalid_argument(info);
  }
  return 0;
};
// [[Rcpp::export]]
SEXP cpp_l(Mat<double> X,
              vec y,
              double beta_0,
              vec beta,
              double alpha,
              double lambda) {
```

```
myassert(n==n_y, "# of obs in X and y do not match!\n");
  myassert(p==n_beta, "# of features in X and beta do not match!\n")
  vec Xb = beta_0 + X*beta;
  double l = -accu(y\%Xb - log(1+exp(Xb)))/n;
  double Omega = lambda *accu((1-alpha)/2*beta%beta + alpha*abs(beta));
  return wrap(1+0mega);
}
# R implementation of the logistic loss function
# here y \setminus in \{0,1\}
r_l <- function(X,y,beta,beta_0,alpha,lambda){</pre>
  n \leftarrow dim(X)[1]
  Xb <- X%*%beta + beta_0
  1 \leftarrow -sum(y*Xb - log(1+exp(Xb)))/n
  Omega <- lambda*sum((1-alpha)/2*beta*beta + alpha*abs(beta))
  return(1+0mega)
}
# Start calculation
n <-10
p < -10
alpha <- 1;
lambda <- 1;</pre>
y < -c(1,2)
X \leftarrow matrix(c(1,2,3,4),2,2)
beta 0 <- 2
beta \leftarrow c(2,3)
a <- cpp_1(X,y,beta=beta,beta_0=beta_0,alpha,lambda)
b <- r_1(X,y,beta=beta,beta_0=beta_0,alpha,lambda)</pre>
all.equal(a,b)
## [1] TRUE
I also want to see how efficient C++ implementation is.
result <- benchmark(replications=rep(10000, 3),
                   cpp_1(X,y,beta=beta,beta_0=beta_0,alpha,lambda),
                     r_1(X,y,beta=beta,beta_0=beta_0,alpha,lambda),
                     columns=c('test', 'elapsed'))
print(result)
##
                                                             test elapsed
## 1 cpp_l(X, y, beta = beta, beta_0 = beta_0, alpha, lambda)
                                                                     0.15
## 3 cpp_1(X, y, beta = beta, beta_0 = beta_0, alpha, lambda)
                                                                     0.19
## 5 cpp_1(X, y, beta = beta, beta_0 = beta_0, alpha, lambda)
                                                                     0.21
                                                                     0.08
## 2
      r_1(X, y, beta = beta, beta_0 = beta_0, alpha, lambda)
      r_1(X, y, beta = beta, beta_0 = beta_0, alpha, lambda)
                                                                     0.08
      r_1(X, y, beta = beta, beta_0 = beta_0, alpha, lambda)
                                                                     0.06
```

Not very significant actually. Probably vectorization in R is already highly optimized. I should dive into the source code and then update this report.