Methods Comparison

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Contents

Chapter 1

Introduction

This vignette provides a comparison of the 12 variables selected by the 3 methods: coda_logistic_lasso, clr+logistic_lasso, selbal.

First, let us install and load the packages.

1.1 Packages installation and loading

```
#cran.packages = c('knitr','MASS','VennDiagram','gplots','glmnet')
#install.packages(cran.packages)
#devtools::install_github(repo = "UVic-omics/selbal")

library(knitr)
library(MASS)
library(VennDiagram)
library(gplots)
library(glmnet)
library(selbal)
```

1.2 Simulations

The way we simulate datasets.

1.3 Example datasets

We have two case studies.

1.3.1 Crohn disease data

```
load("./datasets/Crohn_data.rda")
dim(x_Crohn)
```

```
## [1] 975  48
```

The Crohn data have 975 samples and 48 taxa.

```
summary(y_Crohn)
```

```
##  CD  no
## 662 313
```

Among 975 samples, 662 samples are labeled as ‘CD’, the other 313 are labeled as ‘no’.

1.3.2 BEME day1 data

Chapter 2

Methods implementation

2.1 LOGISTIC LASSO

With linear constraint: $\sum \beta_j = 0$ (for $j > 1$)

```
# y: dependent variable, binary, vector of length n
# X: matrix of k covarites (positive values, taxa abundances in counts, proportions, intensities, ...),

coda_logistic_lasso<-function(y,X,lambda, maxiter=400, maxiter2=50, r=10,
                              tol=1.e-4, tol2=1.e-6){

  #install.packages("MASS")
  library(MASS)   # for the computation of the generalized inverse ginv()
#  library(tictoc)

  if (!is.numeric(y)){
    y<-as.numeric(y)-1
  }

  #source("functions_coda_logistic_lasso.R")

  # Transform initial data
  ztransformation(X)

  #initial values for beta
  #   p<<-ncol(X)   # p: number of covariates after filtering
  #   n<<-nrow(X);  # both defined on ztransformation function
  #beta_ini<-rep(1,p+1)/(p+1)  # uniform values
  beta_ini<-c(log(mean(y)/(1-mean(y))),rep(1/p,p))   # b0 related to mean(y) and uniform values for the

 #null deviance
  nulldev<-glm(y~1, family=binomial())[[10]]


  #initialization parameters

  k<-1
  epsilon<-0.1
```

```
beta_ant<-beta_ini
beta<-beta_ant
y_ant<-beta_ant
y_k<-y_ant
d_k<-y_ant
dev_explained_ant<-0


# Optimization with constraint
start_iter = Sys.time();
while((abs(epsilon)>tol)&(k<=maxiter)){
  #print(append("loop",k))
    k0<-0
    t_k<-10
    condition<-0.1
    while ((condition>0)&(k0<=maxiter2)){
      k0<-k0+1
      #print(append("k0",k0))
      d_k<-y_ant-t_k*grad_g(y_ant, z, y, n)

      # Soft thresholding:
      zproxi<-c(d_k[1],soft_thres(d_k[-1],lambda*t_k))

      # Projection:
      zproj<-projection(zproxi,p_c)

      # line search condition
      Gt<-(y_ant-zproj)/t_k
      condition<-g(y_ant-t_k*Gt,z, y, n)-g(y_ant,z, y, n)+t_k*t(grad_g(y_ant,z, y, n))%*%Gt-t_k/2*nor
      #print(append("condition",condition))
      #print(append("t_k",t_k))
      t_k<-t_k/2
    }
    beta<-zproj

    y_k<-beta+(k-1)/(k+r-1)*(beta-beta_ant)


    dev_explained<-1-(nrow(X)*2*g(beta,z, y, n)/nulldev)
    epsilon<-abs(dev_explained-dev_explained_ant)


    y_ant<-y_k
    beta_ant<-beta
    dev_explained_ant<-dev_explained
    k<-k+1
#print(append("epsilon",epsilon))

}
end_iter = Sys.time();
sprintf("iter time = %f",end_iter-start_iter)

#Projection of the optimal beta to fulfil the constraint sum(beta[j])=0, for j>1
```

```
  indx<-which(abs(zproxi)>tol2)
  if (abs(zproxi[1])>0) indx<-indx[-1]
  c0<-rep(1,(length(indx)))
  c0<-c0/sqrt(normSqr(c0))
  p_c0<-c0%*%t(c0)
  #beta1<-as.numeric(projection(beta[indx],p_c0))
  beta1<-projection(beta[indx],p_c0)
  #beta1
  beta_res<-c(beta[1],rep(0,p))
  beta_res[indx]<-beta1

  # print("beta coefficients:")
  # beta_res

  #print("taxa with non-zero coeff:")
  # selec<-colnames(z)[abs(beta_res)>0]

  #print("beta non-zero coefficients:")
  # beta_res[abs(beta_res)>0]

  #print("proportion of explained deviance")
  # dev_explained
  #print("proportion of explained deviance beta_res")

  dev_explained_beta_res<-1-(nrow(X)*2*g(beta_res,z, y, n)/nulldev)
  # dev_explained_beta_res


  results<-list(
     "number of iterations"=k,
       "number of selected taxa"=
         sum(abs(beta_res)>0)-1,
       "indices of taxa with non-zero coeff"=
        which(abs(beta_res)>0)-1,
       "taxa with non-zero coeff"=
       colnames(z)[abs(beta_res)>0],
       "beta non-zero coefficients"=
       beta_res[abs(beta_res)>0],
       "proportion of explained deviance"=
       dev_explained_beta_res,
     "betas"=
     beta_res)

  return(results)

} # END function coda_logistic_lasso
```

2.2 LOGISTIC ELASTIC NET

```
##------------------------------------------------------------------
```

```
coda_logistic_elasticNet<-function(y,X,lambda, alpha=0.5, maxiter=1000, maxiter2=50, r=10,
                                   tol=1.e-4, tol2=1.e-6){

  #install.packages("MASS")
  library(MASS)   # for the computation of the generalized inverse ginv()
#  library(tictoc)

#  source("functions_coda_logistic_lasso.R")

  # Transform initial data
  ztransformation(X)

  #initial values for beta
  #beta_ini<-rep(1,p+1)/(p+1)  # uniform values
  beta_ini<-c(log(mean(y)/(1-mean(y))),rep(1/p,p))   # b0 related to mean(y) and uniform values for the

  #null deviance
  nulldev<-glm(y~1, family=binomial())[[10]]




  #initialization parameters

  k<-1
  epsilon<-0.1
  beta_ant<-beta_ini
  beta<-beta_ant
  y_ant<-beta_ant
  y_k<-y_ant
  d_k<-y_ant
  dev_explained_ant<-0
  # elastic parameters
  lambda=alpha*lambda;
  gamma=2*(1-alpha)/alpha;


  # Optimization with constraint
  start_iter = Sys.time()
  while((abs(epsilon)>tol)&(k<=maxiter)){
    #print(append("loop",k))
    k0<-0
    t_k<-10
    condition<-0.1
    while ((condition>0)&(k0<=maxiter2)){
      k0<-k0+1
      #print(append("k0",k0))
      d_k<-y_ant-t_k*grad_g(y_ant, z, y, n)

      # Soft thresholding:
      # zproxi<-c(d_k[1],soft_thres(d_k[-1],lambda*t_k))
      # zproxi = zproxi/(1+gamma*lambda);
```

```
    zproxi<-c(d_k[1],soft_thres(d_k[-1],lambda*t_k)/(1+gamma*lambda*t_k))


    # Projection:
    zproj<-projection(zproxi,p_c)

    # line search condition
    Gt<-(y_ant-zproj)/t_k
    condition<-g(y_ant-t_k*Gt,z, y, n)-g(y_ant,z, y, n)+t_k*t(grad_g(y_ant,z, y, n))%*%Gt-t_k/2*normS

    #print(append("condition",condition))
    #print(append("t_k",t_k))
    t_k<-t_k/2
  }
  beta<-zproj

  y_k<-beta+(k-1)/(k+r-1)*(beta-beta_ant)


  dev_explained<-1-(nrow(X)*2*g(beta,z, y, n)/nulldev)
  epsilon<-abs(dev_explained-dev_explained_ant)


  y_ant<-y_k
  beta_ant<-beta
  dev_explained_ant<-dev_explained
  k<-k+1
  #print(append("epsilon",epsilon))

}
end_iter = Sys.time()
sprintf("iter time = %f",end_iter - start_iter)


#Projection of the optimal beta to fulfil the constraint sum(beta[j])=0, for j>1
indx<-which(abs(zproxi)>tol2)
if (abs(zproxi[1])>0) indx<-indx[-1]
c0<-rep(1,(length(indx)))
c0<-c0/sqrt(normSqr(c0))
p_c0<-c0%*%t(c0)
#beta1<-as.numeric(projection(beta[indx],p_c0))
beta1<-projection(beta[indx],p_c0)
#beta1
beta_res<-c(beta[1],rep(0,p))
beta_res[indx]<-beta1

#print("beta coefficients:")
# beta_res

#print("taxa with non-zero coeff:")
# selec<-colnames(z)[abs(beta_res)>0]
#return(selec)
```

```
  #print("beta non-zero coefficients:")
  # beta_res[abs(beta_res)>0]

  #print("proportion of explained deviance")
  # dev_explained
  #print("proportion of explained deviance beta_res")

  dev_explained_beta_res<-1-(nrow(X)*2*g(beta_res,z, y, n)/nulldev)
  # dev_explained_beta_res


  results<-list("number of iterations"=k,
                "number of selected taxa"=
                  sum(abs(beta_res)>0)-1,
                "indices of taxa with non-zero coeff"=
                  which(abs(beta_res)>0)-1,
                "name of taxa with non-zero coeff"=
                  colnames(z)[abs(beta_res)>0],
                "beta non-zero coefficients"=
                  beta_res[abs(beta_res)>0],
                "proportion of explained deviance"=
                  dev_explained_beta_res,
                "betas"=
                  beta_res)

  return(results)

} # END function coda_logistic_ElasticNet
```

2.3 rangLambda

It provides a rang of lambda values corresponding to a given number of variables to be selected (numVar).

The default initial lambda is lambdaIni=1.

```
##-----------------------------------------------------------------

rangLambda <- function(y,X,numVar, lambdaIni =1){
  lambdaB = lambdaIni;
  lambdaA = 0;
  #lambda=0.5*(lambdaB+lambdaA);
  lambda=lambdaIni;
  results <- coda_logistic_lasso(y,X,lambda, maxiter = 100);
  numVarAct = results[[2]];
  if (numVarAct > numVar){
    lambda=lambda+0.5;
    #lambda=lambda+1;
    lambdaB =lambda;
  }else{
    lambdaB =lambda;
  }
  nIter=1;
  presentLambda = NULL;
```

```
  presentnumVar = NULL;
  presentLambda[nIter] = lambda;
  presentnumVar[nIter] = numVarAct;
  numvarA=ncol(X);
  numvarB=numVarAct;
  print(c(lambdaA, lambdaB, numvarA, numvarB))
  diffNvar = abs(numvarB-numvarA);
  while ((diffNvar>1) & (abs(numVarAct-numVar)>0) & (nIter < 6)){
    nIter=nIter+1;
    lambda=0.5*(lambdaB+lambdaA);
    results <- coda_logistic_lasso(y,X,lambda, maxiter = 100);
    numVarAct = results[[2]];
    if (numVarAct < numVar) {
      lambdaB = lambda;
      numvarB = numVarAct;
    }else{
      lambdaA = lambda;
      numvarA = numVarAct;
    }
    presentLambda[nIter] = lambda;
    presentnumVar[nIter] = numVarAct;
    diffNvar = abs(numvarB-numvarA);
    print(c(lambdaA, lambdaB, numvarA, numvarB))
  }
  indx=which(presentnumVar >= 0);
  results = list( 'rang lambdas'=c(lambdaA,lambdaB), 'num selected variables'=c(numvarA,numvarB))
  return(results);
}
```

2.4 Soft thresholding

http://www.simonlucey.com/soft-thresholding/

```
soft_thres<-function(b, lambda){
  x<-rep(0,length(b))
  # Set the threshold
  th = lambda/2;

  #First find elements that are larger than the threshold
  k <- which(b > th)
  x[k] <- b[k] - th

  # Next find elements that are less than abs
  k <-which(abs(b) <= th)
  x[k] <- 0

  # Finally find elements that are less than -th
  k <-which(b < -th)
  x[k] = b[k] + th

  return(x)
}
```

2.5 Other functions

```
##---------------------------------------------------------------------

norm1<-function(x){
  return(sum(abs(x)))
}

normSqr<-function(x){
  return(sum(x^2))
}


ztransformation<-function(X){
  p<<-ncol(X)   # p: number of covariates after filtering
  n<<-nrow(X);
  # log transformation Z=log(X)
  z<-log(X)

  # z=matrix of covariates: add a first column of 1's for beta0
  z<-cbind(rep(1,nrow(z)),z)
  z<-as.matrix(z)

  # c=linear constraint sum(betas)=0 (except beta0)
  c<-c(0,rep(1,ncol(X)))
  c<-c/sqrt(sum(c^2))
  c<-as.matrix(c)
  p_c<<-c%*%t(c)

  # z transformation (centering) for improvement of optimization
  # this transformation does not affect the estimation since the linear predictor is the same
  z<<-(z-(z%*%p_c))
  colnames(z)<<-c("beta0",colnames(X))

  return(z)

}

A<-function(x){
  y<-log(1+exp(x))
  return(y)
}


mu_beta<-function(x, Z){
  zetabybeta<-Z%*%x
  res<-rep(1,length(zetabybeta))
  indzb<-which(zetabybeta<=100)
  res[indzb]<-exp(zetabybeta[indzb])/(1+exp(zetabybeta[indzb]))
  return(res)
}

g<-function(x,Z,Y,n){
```

```
  res<- (t(Y))%*%Z%*%x
  res<-res-sum(log(1+exp(Z%*%x)))
  res<- as.vector((-res)/n)
  return(res)
}

h<-function(x, lambda){
  lambda*norm1(x)
}

grad_g<-function(x, Z, Y, n){
  res<- (t(Y-mu_beta(x,Z)))%*%Z
  res<- as.vector((-res)/n)
  return(res)
}


# Projection

projection<-function(x, M){
  if (ncol(M)*nrow(M)>0){
    res<-x-ginv(M)%*%M%*%x
  } else {res<-rep(0,length(x))}
  return(res)
}


F<-function(x,t_k,d_k){
  lambda*t_k*norm1(x[-1])+normSqr(d_k-x)/2
}

F2<-function(x,Z,Y,n,lambda){
  g(x,Z,Y,n)+lambda*norm1(x[-1])
}

trapezInteg <- function(x,y) {
# Compute AUC using trapezoid numerical method
  n = length(x);
  sumArea = 0;
  for (i in 1:(n-1)){
    h=x[i+1]-x[i];
    if (abs(h) > 1.e-7){
      sumArea = sumArea + 0.5*(y[i+1]+y[i])*h;
    }else{
      sumArea = sumArea;
    }
  }
  return(sumArea)
}
```

Chapter 3

CODA_LOGISTIC_LASSO

3.1 Crohn disease data

```
y<-y_Crohn
summary(y)
```

```
##  CD  no
## 662 313
```

y is the binary outcome, can be numerical (values 0 and 1), factor (2 levels) or categorical (2 categories)

```
x<-x_Crohn
```

x is the matrix of microbiome abundances, either absolute abundances (counts) or relative abundances (proportions);

x should not be the matrix of log(counts) or log(proportions). The method itself performs the log-transformation of the abundances.

```
dim(x)
```

```
## [1] 975  48
```

The rows of x are individuals/samples, the columns are taxa

```
rangLambda(y,x,numVar=12, lambdaIni =0.15)
```

```
## [1]  0.00  0.65 48.00 17.00
## [1]  0.000  0.325 48.000  2.000
## [1]  0.1625  0.3250 12.0000  2.0000
```

```
## $`rang lambdas`
## [1] 0.1625 0.3250
##
## $`num selected variables`
## [1] 12  2
```

It provides a rang of lambda values corresponding to a given number of variables to be selected (numVar).

The default initial lambda is lambdaIni=1.

```
results_codalasso<-coda_logistic_lasso(y,x,lambda=0.19)
```

lambda is the penalization parameter: the larger the value of lambda the fewer number of variables will be selected.

```
results_codalasso
```

```
## $`number of iterations`
## [1] 23
##
## $`number of selected taxa`
## [1] 11
##
## $`indices of taxa with non-zero coeff`
##  [1]  0  2  5  9 19 27 31 32 33 39 40 48
##
## $`taxa with non-zero coeff`
##  [1] "beta0"                          "g__Parabacteroides"
##  [3] "f__Peptostreptococcaceae_g__" "g__Eggerthella"
##  [5] "g__Dialister"                   "o__Lactobacillales_g__"
##  [7] "g__Prevotella"                  "g__Roseburia"
##  [9] "g__Lachnospira"                 "g__Streptococcus"
## [11] "g__Aggregatibacter"             "g__Bilophila"
##
## $`beta non-zero coefficients`
##  [1] -1.0023255478 -0.0057464016  0.0202907034 -0.0184875313 -0.0992393846
##  [6] -0.0159418386 -0.0030842274  0.2530005235 -0.0085670215 -0.0818265310
## [11] -0.0406982632  0.0002999724
##
## $`proportion of explained deviance`
## [1] 0.1542276
##
## $betas
##  [1] -1.0023255478  0.0000000000 -0.0057464016  0.0000000000  0.0000000000
##  [6]  0.0202907034  0.0000000000  0.0000000000  0.0000000000 -0.0184875313
## [11]  0.0000000000  0.0000000000  0.0000000000  0.0000000000  0.0000000000
## [16]  0.0000000000  0.0000000000  0.0000000000  0.0000000000 -0.0992393846
## [21]  0.0000000000  0.0000000000  0.0000000000  0.0000000000  0.0000000000
## [26]  0.0000000000  0.0000000000 -0.0159418386  0.0000000000  0.0000000000
## [31]  0.0000000000 -0.0030842274  0.2530005235 -0.0085670215  0.0000000000
## [36]  0.0000000000  0.0000000000  0.0000000000  0.0000000000 -0.0818265310
## [41] -0.0406982632  0.0000000000  0.0000000000  0.0000000000  0.0000000000
## [46]  0.0000000000  0.0000000000  0.0000000000  0.0002999724
```

```
selected_codalasso<-results_codalasso[[4]][-1]

columns_selected_codalasso<-results_codalasso[[3]][-1]

#coef<-results[[5]][-1]

write.csv(data.frame(columns_selected_codalasso,selected_codalasso),"./Generated_datasets/results_codala
```

3.2 BEME day1 data

Chapter 4

CLR_LOGISTIC_LASSO

4.1 Crohn disease data

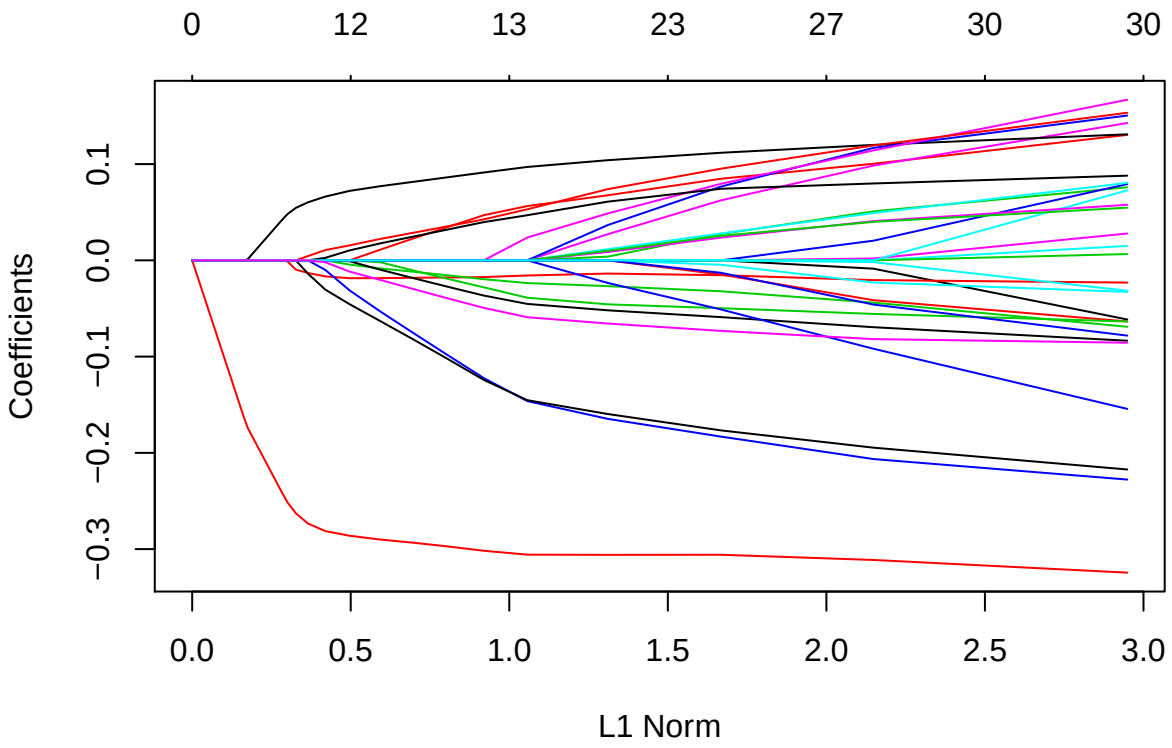
```
y<-y_Crohn_numeric
```

glmnet() requires y to be numeric.

```
x<-as.matrix(x_Crohn)

# CLR transformation Z=log(x)
z<-log(x)
clrx<- apply(z,2,function (x) x-rowMeans(z))
#rowMeans(clrx)

clrlasso <- glmnet(clrx, y, standardize=FALSE , alpha=1,family="binomial", lambda=seq(0.015,2,0.01))
plot(clrlasso)
```




```
print(clrlasso)
```

```
##
## Call:  glmnet(x = clrx, y = y, family = "binomial", alpha = 1, lambda = seq(0.015,      2, 0.01), sta
##
##         Df      %Dev Lambda
##   [1,]  0 1.769e-15  1.995
##   [2,]  0 1.769e-15  1.985
##   [3,]  0 1.769e-15  1.975
##   [4,]  0 1.769e-15  1.965
##   [5,]  0 1.769e-15  1.955
##   [6,]  0 1.769e-15  1.945
##   [7,]  0 1.769e-15  1.935
##   [8,]  0 1.769e-15  1.925
##   [9,]  0 7.783e-15  1.915
##  [10,]  0 1.769e-15  1.905
##  [11,]  0 1.769e-15  1.895
##  [12,]  0 1.769e-15  1.885
##  [13,]  0 1.769e-15  1.875
##  [14,]  0 1.769e-15  1.865
##  [15,]  0 1.769e-15  1.855
##  [16,]  0 1.769e-15  1.845
##  [17,]  0 1.769e-15  1.835
##  [18,]  0 1.769e-15  1.825
##  [19,]  0 1.769e-15  1.815
##  [20,]  0 1.769e-15  1.805
##  [21,]  0 7.783e-15  1.795
##  [22,]  0 1.769e-15  1.785
##  [23,]  0 1.769e-15  1.775
##  [24,]  0 1.769e-15  1.765
```

```
##  [25,]  0 1.769e-15  1.755
##  [26,]  0 1.769e-15  1.745
##  [27,]  0 1.769e-15  1.735
##  [28,]  0 1.769e-15  1.725
##  [29,]  0 1.769e-15  1.715
##  [30,]  0 1.769e-15  1.705
##  [31,]  0 1.769e-15  1.695
##  [32,]  0 1.769e-15  1.685
##  [33,]  0 7.783e-15  1.675
##  [34,]  0 1.769e-15  1.665
##  [35,]  0 1.769e-15  1.655
##  [36,]  0 1.769e-15  1.645
##  [37,]  0 1.769e-15  1.635
##  [38,]  0 1.769e-15  1.625
##  [39,]  0 1.769e-15  1.615
##  [40,]  0 1.769e-15  1.605
##  [41,]  0 1.769e-15  1.595
##  [42,]  0 1.769e-15  1.585
##  [43,]  0 1.769e-15  1.575
##  [44,]  0 1.769e-15  1.565
##  [45,]  0 7.783e-15  1.555
##  [46,]  0 1.769e-15  1.545
##  [47,]  0 1.769e-15  1.535
##  [48,]  0 1.769e-15  1.525
##  [49,]  0 1.769e-15  1.515
##  [50,]  0 1.769e-15  1.505
##  [51,]  0 1.769e-15  1.495
##  [52,]  0 1.769e-15  1.485
##  [53,]  0 1.769e-15  1.475
##  [54,]  0 1.769e-15  1.465
##  [55,]  0 1.769e-15  1.455
##  [56,]  0 1.769e-15  1.445
##  [57,]  0 7.783e-15  1.435
##  [58,]  0 1.769e-15  1.425
##  [59,]  0 1.769e-15  1.415
##  [60,]  0 1.769e-15  1.405
##  [61,]  0 1.769e-15  1.395
##  [62,]  0 1.769e-15  1.385
##  [63,]  0 1.769e-15  1.375
##  [64,]  0 1.769e-15  1.365
##  [65,]  0 1.769e-15  1.355
##  [66,]  0 1.769e-15  1.345
##  [67,]  0 1.769e-15  1.335
##  [68,]  0 1.769e-15  1.325
##  [69,]  0 7.783e-15  1.315
##  [70,]  0 1.769e-15  1.305
##  [71,]  0 1.769e-15  1.295
##  [72,]  0 1.769e-15  1.285
##  [73,]  0 1.769e-15  1.275
##  [74,]  0 1.769e-15  1.265
##  [75,]  0 1.769e-15  1.255
##  [76,]  0 1.769e-15  1.245
##  [77,]  0 1.769e-15  1.235
##  [78,]  0 1.769e-15  1.225
```

```
##   [79,]  0 1.769e-15  1.215
##   [80,]  0 1.769e-15  1.205
##   [81,]  0 7.783e-15  1.195
##   [82,]  0 1.769e-15  1.185
##   [83,]  0 1.769e-15  1.175
##   [84,]  0 1.769e-15  1.165
##   [85,]  0 1.769e-15  1.155
##   [86,]  0 1.769e-15  1.145
##   [87,]  0 1.769e-15  1.135
##   [88,]  0 1.769e-15  1.125
##   [89,]  0 1.769e-15  1.115
##   [90,]  0 1.769e-15  1.105
##   [91,]  0 1.769e-15  1.095
##   [92,]  0 1.769e-15  1.085
##   [93,]  0 7.783e-15  1.075
##   [94,]  0 1.769e-15  1.065
##   [95,]  0 1.769e-15  1.055
##   [96,]  0 1.769e-15  1.045
##   [97,]  0 1.769e-15  1.035
##   [98,]  0 1.769e-15  1.025
##   [99,]  0 1.769e-15  1.015
##  [100,]  0 1.769e-15  1.005
##  [101,]  0 1.769e-15  0.995
##  [102,]  0 1.769e-15  0.985
##  [103,]  0 1.769e-15  0.975
##  [104,]  0 1.769e-15  0.965
##  [105,]  0 7.783e-15  0.955
##  [106,]  0 1.769e-15  0.945
##  [107,]  0 1.769e-15  0.935
##  [108,]  0 1.769e-15  0.925
##  [109,]  0 1.769e-15  0.915
##  [110,]  0 1.769e-15  0.905
##  [111,]  0 1.769e-15  0.895
##  [112,]  0 1.769e-15  0.885
##  [113,]  0 1.769e-15  0.875
##  [114,]  0 1.769e-15  0.865
##  [115,]  0 1.769e-15  0.855
##  [116,]  0 1.769e-15  0.845
##  [117,]  0 7.783e-15  0.835
##  [118,]  0 1.769e-15  0.825
##  [119,]  0 1.769e-15  0.815
##  [120,]  0 1.769e-15  0.805
##  [121,]  0 1.769e-15  0.795
##  [122,]  0 1.769e-15  0.785
##  [123,]  0 1.769e-15  0.775
##  [124,]  0 1.769e-15  0.765
##  [125,]  0 1.769e-15  0.755
##  [126,]  0 1.769e-15  0.745
##  [127,]  0 1.769e-15  0.735
##  [128,]  0 1.769e-15  0.725
##  [129,]  0 7.783e-15  0.715
##  [130,]  0 1.769e-15  0.705
##  [131,]  0 1.769e-15  0.695
##  [132,]  0 1.769e-15  0.685
```

```
## [133,]  0 1.769e-15  0.675
## [134,]  0 1.769e-15  0.665
## [135,]  0 1.769e-15  0.655
## [136,]  0 1.769e-15  0.645
## [137,]  0 1.769e-15  0.635
## [138,]  0 1.769e-15  0.625
## [139,]  0 1.769e-15  0.615
## [140,]  0 1.769e-15  0.605
## [141,]  0 7.783e-15  0.595
## [142,]  0 1.769e-15  0.585
## [143,]  0 1.769e-15  0.575
## [144,]  0 1.769e-15  0.565
## [145,]  0 1.769e-15  0.555
## [146,]  0 1.769e-15  0.545
## [147,]  0 1.769e-15  0.535
## [148,]  0 1.769e-15  0.525
## [149,]  0 1.769e-15  0.515
## [150,]  0 1.769e-15  0.505
## [151,]  0 1.769e-15  0.495
## [152,]  0 1.769e-15  0.485
## [153,]  0 7.783e-15  0.475
## [154,]  0 1.769e-15  0.465
## [155,]  0 1.769e-15  0.455
## [156,]  0 1.769e-15  0.445
## [157,]  0 1.769e-15  0.435
## [158,]  0 1.769e-15  0.425
## [159,]  0 1.769e-15  0.415
## [160,]  0 1.769e-15  0.405
## [161,]  0 1.769e-15  0.395
## [162,]  0 1.769e-15  0.385
## [163,]  1 1.275e-03  0.375
## [164,]  1 7.497e-03  0.365
## [165,]  1 1.355e-02  0.355
## [166,]  1 1.944e-02  0.345
## [167,]  1 2.517e-02  0.335
## [168,]  1 3.074e-02  0.325
## [169,]  1 3.615e-02  0.315
## [170,]  1 4.141e-02  0.305
## [171,]  1 4.651e-02  0.295
## [172,]  1 5.146e-02  0.285
## [173,]  1 5.626e-02  0.275
## [174,]  1 6.091e-02  0.265
## [175,]  1 6.541e-02  0.255
## [176,]  1 6.976e-02  0.245
## [177,]  1 7.396e-02  0.235
## [178,]  1 7.802e-02  0.225
## [179,]  2 8.230e-02  0.215
## [180,]  2 8.806e-02  0.205
## [181,]  2 9.359e-02  0.195
## [182,]  2 9.891e-02  0.185
## [183,]  2 1.040e-01  0.175
## [184,]  2 1.089e-01  0.165
## [185,]  2 1.135e-01  0.155
## [186,]  3 1.181e-01  0.145
```

```
## [187,]  3 1.240e-01  0.135
## [188,]  5 1.319e-01  0.125
## [189,]  8 1.422e-01  0.115
## [190,] 10 1.557e-01  0.105
## [191,] 12 1.711e-01  0.095
## [192,] 12 1.860e-01  0.085
## [193,] 12 1.999e-01  0.075
## [194,] 12 2.125e-01  0.065
## [195,] 13 2.256e-01  0.055
## [196,] 20 2.457e-01  0.045
## [197,] 23 2.683e-01  0.035
## [198,] 27 2.910e-01  0.025
## [199,] 30 3.162e-01  0.015
```

```
clrlasso_coef<-coef(clrlasso,s=0.10)
sum(abs(clrlasso_coef)>0)
```

```
## [1] 13
```

```
selected_clrlasso<-which(as.numeric(abs(coef(clrlasso, s=0.1)))>0)[-1];
```

The indices of selected variables (abs(coef)>0)

```
selected_clrlasso<-selected_clrlasso-1
taxa_id<-colnames(x_Crohn)[selected_clrlasso]

write.csv(data.frame(selected_clrlasso,taxa_id),"./Generated_datasets/results_clrlasso_Crohn12.csv")
```

4.2 BEME day1 data

Chapter 5

Selbal: selection of balances

5.1 Crohn disease data

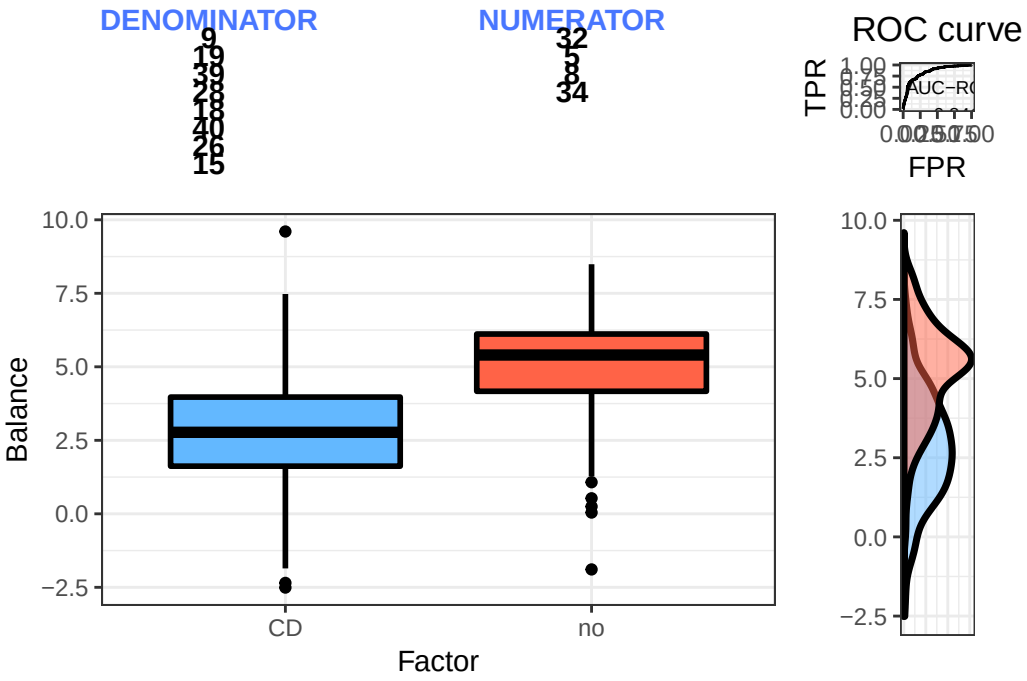
```
y<-y_Crohn
```

For binary outcomes (logistic regression), selbal requires y to be factor.

If y is numeric selbal implements linear regression.

```
x<-x_Crohn
colnames(x)<-(1:ncol(x))

selbal_Crohn<-selbal(x = x, y = y, logt=T, maxV=12)
```




```
selected_selbal<-as.numeric(c(selbal_Crohn[[6]][,1],selbal_Crohn[[6]][,2]))
```

```
## Warning: NAs introduced by coercion
```

```
id.na<-which(is.na(selected_selbal))
selected_selbal<-selected_selbal[-id.na]
selected_selbal<-as.character(selected_selbal)

columns_selected_selbal<-which(colnames(x)%in% selected_selbal)
taxa_id<-colnames(x_Crohn)[columns_selected_selbal]

write.csv(data.frame(columns_selected_selbal, taxa_id),"./Generated_datasets/results_selbal_Crohn12.csv
```

5.2 BEME day1 data

Chapter 6

Concordance of variables selected by the three methods

6.1 Crohn disease data

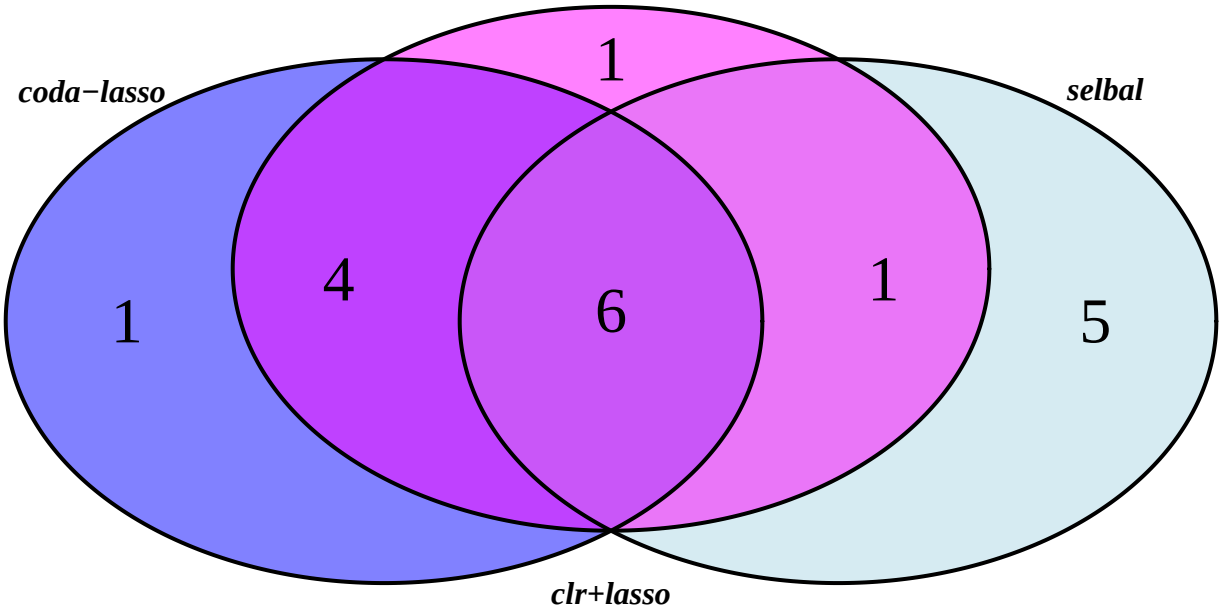
```
d_selbal<-read.csv("./Generated_datasets/results_selbal_Crohn12.csv", header = T)
d_clrlasso<-read.csv("./Generated_datasets/results_clrlasso_Crohn12.csv", header = T)
d_codalasso<-read.csv("./Generated_datasets/results_codalasso_Crohn12.csv", header = T)

#(d_selbal[,2], d_clrlasso[,2], d_codalasso[,2])

taxa_selected<-list(d_clrlasso[,2], d_codalasso[,2], d_selbal[,2])
taxa.id_selected<-list(d_clrlasso[,3], d_codalasso[,3], d_selbal[,3])


venn.plot <- venn.diagram(taxa_selected , NULL, fill=c("magenta", "blue", "lightblue"),
                          alpha=c(0.5,0.5,0.5), cex = 2, cat.fontface=4,
                          category.names=c("clr+lasso", "coda-lasso", "selbal"),
                          main="Concordance of selected taxa for Crohn data")
grid.draw(venn.plot)
```

Concordance of selected taxa for Crohn data




```
taxa.id <- venn(taxa.id_selected, show.plot=FALSE)
taxa <- venn(taxa_selected, show.plot=FALSE)

inters_taxa.id <- attr(taxa.id,"intersections")
inters_taxa <- attr(taxa,"intersections")

lapply(inters_taxa, head)
```

```
## $A
## [1] "10"
##
## $B
## [1] "27"
##
## $C
## [1] "15" "18" "26" "28" "34"
##
## $`A:B`
## [1] "2"  "31" "33" "48"
##
## $`A:C`
## [1] "8"
##
## $`A:B:C`
## [1] "5"  "9"  "19" "32" "39" "40"
```

```
lapply(inters_taxa.id, head)
```

```
## $A
```

```
## [1] "g__Faecalibacterium"
##
## $B
## [1] "o__Lactobacillales_g__"
##
## $C
## [1] "g__Blautia"           "g__Dorea"             "g__Oscillospira"
## [4] "g__Adlercreutzia"     "o__Clostridiales_g__"
##
## $`A:B`
## [1] "g__Parabacteroides" "g__Prevotella"      "g__Lachnospira"
## [4] "g__Bilophila"
##
## $`A:C`
## [1] "g__Bacteroides"
##
## $`A:B:C`
## [1] "f__Peptostreptococcaceae_g__" "g__Eggerthella"
## [3] "g__Dialister"                 "g__Roseburia"
## [5] "g__Streptococcus"             "g__Aggregatibacter"
```

6.2 BEME day1 data