TrainSel Usage

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Introduction

In this section, we will illustrate the use of the package 'TrainSel'. We will use the data sets provided within the package under the object named 'WheatData' throughout this presentation. The original data was obtained from the webpage https://triticeaetoolbox.org/. The data contains the genomewide marker data (at 4670 markers) and a simulated trait data (phenotypic measurements are simulated using an infinitismall model) for 200 wheat varieties.

We can load the library and 'WheatData' using the following code:

```
library(TrainSel)
```

```
## Loading required package: cluster
```

```
data("WheatData")
```

Marker data is contained in the matrix object 'Wheat.M', a relationship matrix for the genotypes calculated from the marker matrix is in 'Wheat.K', and the plant height measurements are in 'Wheat.Y'. We can see the format of these data:

```
Wheat.M[1:5,1:5]
```

```
##       IWA1 IWA2 IWA3 IWA4 IWA5
## Line1    1    1   -1   -1   -1
## Line2    1    1    1   -1   -1
## Line3    1    1    1   -1   -1
## Line4    1    1    1    1   -1
## Line5    1    1    1   -1   -1
```

```
Wheat.K[1:5,1:5]
```

```
##            Line1      Line2      Line3      Line4      Line5
## Line1  1.9578361  0.8261588  0.7546713  0.5149389 -0.2697654
## Line2  0.8261588  2.0033376  0.5756170  0.5241991 -0.2315324
## Line3  0.7546713  0.5756170  1.9807687  0.7077443 -0.2888690
## Line4  0.5149389  0.5241991  0.7077443  2.2816612 -0.2645939
## Line5 -0.2697654 -0.2315324 -0.2888690 -0.2645939  1.8086996
```

```
Wheat.Y[1:5,]
```

```
##         id plant.height
## 1846 Line1     138.4471
## 250  Line2     122.5955
## 1541 Line3     134.7883
## 1516 Line4     121.4741
## 508  Line5     127.3920
```

Selection of a subset of genotypes for a phenotypic experiment in a single environment

Our aim is to build a predictive model for the plant height based on the genomewide marker data. The dataset contains the plant heights for all of these genotypes, however, for a moment, assume that we do not have the plant heights measurements for these 200 genotypes and currently only a subset of 160 candidate genotypes are available to be used in the phenotypic experiment. Furthermore, since measuring plant height for 160 candidate genotypes via a phenotypic experiment can be costly, we assume that we can only perform the phenotypic experiment with say a maximum of 50 training genotypes selected from the 160. Following this phenotypic experiment, we can use the available marker data and the measured height of these 50 genotypes to train a genomic prediction model to make inferences about the heights of the remaining 110 genotypes or any other set of genotypes that we have the same genomewide marker data, for example, the 40 genotypes that were not available for the phenotypic experiment.

Selection of a subset of genotypes for a homogeneous design in a single environment

The simplest use case for 'TrainSel' is the situation where phenotypic experiment will only performed in one homogeneous environment. In this case, our purpose is to select a subset of size 50 from the 160 available genotypes so that the genomic prediction models that are trained on this 50 has a good generalization performance.

We distinguish between two cases of optimal training set selection based on whether we seek that generalize well for a specific target set of genotypes (Targeted optimization) or not (Un-targeted optimization). Not all optimization criteria are sensitive to this distinction, however when it is so this is reflected in how the optimization criteria is calculated.

Un-targeted optimization There are many different statistics that can be used for the untargeted optimization with a homogeneous design in a single environment. The package 'TrainSel' is designed to be flexible to be used with any design criteria, however, this means that the users need to program their own optimization functions. Below are some example functions that should get started for writing your own:

D-optimality criterion D-optimality criterion is a model based design criterion. The underlying model for the D-optimality criterion is a linear model. For the problem of selection of a subset of genotypes for a homogeneous design in a single environment a linear model relating the genotypic data to phenotypic measurements in the training data can be expressed as

$$y = 1\mu + f(M)\beta + \epsilon,$$

where y is the n vector of phenotypic measurements in the training data, μ is a scalar parameter for the mean of the phenotypic measurements, M is the $n \times m$ the marker matrix for the n training genotypes, $f(M)$ is a genomic features matrix with dimensions $n \times q$, β is the q vector of effects of genomic features, and ϵ is the residual error vector of length n. We further assume that the elements of ϵ are independent and identically distributed with a normal distribution with zero mean and variance σ_e^2. Under this model the variance of the estimators for β is known to be proportional to $[f(M)'f(M)]^{-1}$. D-optimal selection of n training genotypes from N individuals in the candidate set involves minimizing the determinant of this matrix (or equivalently maximizing the log-determinant of $f(M)'f(M)$). The feature matrix $f(M)$ is usually the first q principal components matrix for the marker matrix M and for this measure to be defined q should be less than n.

```r
#We will use the first 30 principal components for this
Wheat.M_centered<-scale(Wheat.M, center=TRUE, scale=FALSE)
svdWheat.M_centered<-svd(Wheat.M_centered, nu=30, nv=30)

PC<-Wheat.M_centered%*%svdWheat.M_centered$v
dim(PC)
```

```
## [1] 200  30
```

```
dataDopt<-list(FeatureMat=PC)

DOPT<-function(soln, Data){
  Fmat<-Data[["FeatureMat"]]
  return(determinant(crossprod(Fmat[soln,]), logarithm=TRUE)$modulus)
}
```

In all of the following examples we will set the TrainSel algorithm parameters as follows: Number of iterations for the GA is 100, population size for GA is 30, and number of elite solutions at each iteration is 3. Depending on the size and complexity of the optimization problem we would like to adjust these parameters.

```
TSC<-TrainSelControl()
TSC$niterations=300
TSC$npop=300
TSC$nelite=10
```

```
TSOUTD<-TrainSel(Data=dataDopt,
           Candidates = list(1:160),
           setsizes = c(50),
           settypes = "UOS",
           Stat = DOPT, control=TSC)
```

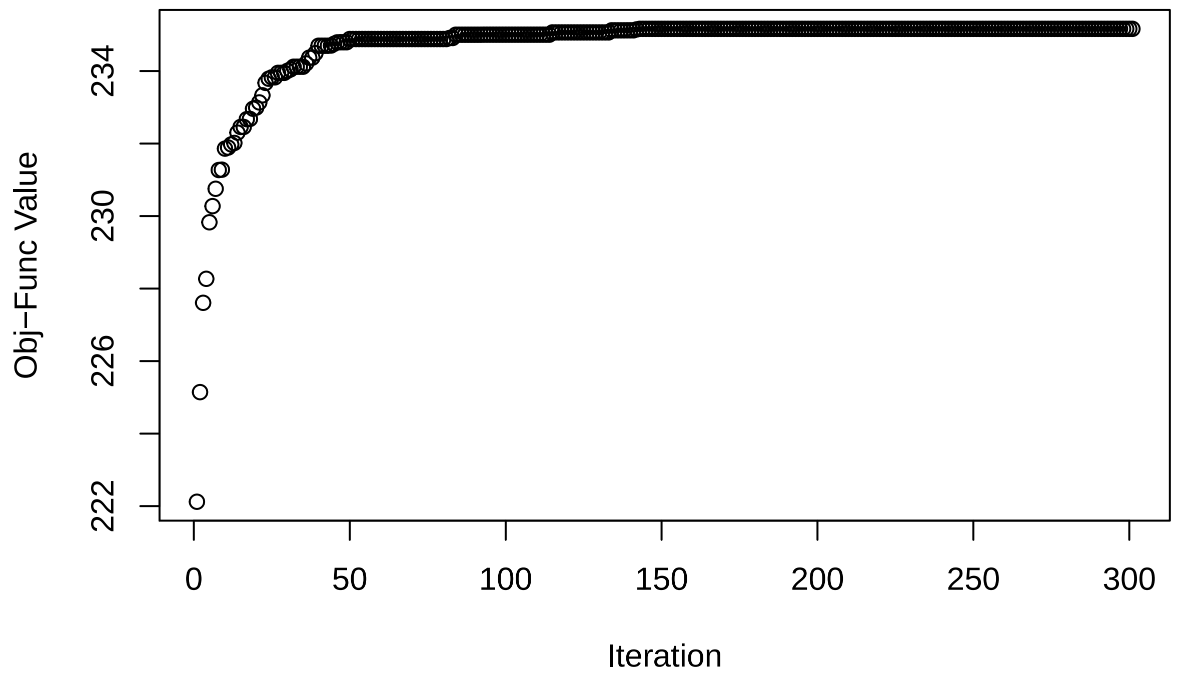
```
## Maximum number of iterations reached.
```

```
head(rownames(Wheat.M)[TSOUTD$BestSol_int])
```

```
## [1] "Line4"  "Line13" "Line15" "Line16" "Line17" "Line18"
```

Convergence should be checked after the algorithm finishes. We can do this by checking the path of the objective function through the iterations:

```
plot(TSOUTD$maxvec, xlab="Iteration",ylab="Obj-Func Value")
```



CDMEAN-optimality criterion CDMEAN-optimality criterion is also a model based criterion it is based on a G-BLUP mixed model. For the problem of selection of a subset of genotypes for a homogeneous design in a single environment, a G-BLUP model relating the genotypic data to phenotypic measurements in the training data can be expressed as

$$y = 1\mu + Zu + \epsilon$$

with μ a scalar parameter for the mean of the phenotypic measurements, Z the $n \times N$ design matrix for the N genotypes in the candidate set, $\epsilon \sim N_n(0, \sigma_e^2)$ independent of $u \sim N_q(0; \sigma_g^2 G)$.

For this model, the coefficient of determination matrix of $\widehat{u}$ for predicting u is given by

$$(GZ'PZG) \oslash G$$

where $P = V^{-1} - V^{-1}1(1'V^{-1}1)^{-1}1'V^{-1}$ is the projection matrix and $\oslash$ expresses the element-wise division.

The diagonals of this matrix are the coefficient of determination of the predictions for individual genotypes and the mean of these coefficient of determination values over the selected genotypes is called the CDMEAN-optimality criterion[1]. CDMEAN criterion takes values between 0 and 1 and the larger values are preferable. For the un-targeted optimization, the usual practice is to use CDMEAN that is calculated over the genotypes not included in the training set. We can program this objective function to be used in 'TrainSel' as follows:

```
# note that we are not using the target genotypes
dataCDMEANopt<-list(G=Wheat.K[1:160,1:160], lambda=1)

CDMEANOPT<-function(soln, Data){
  G<-Data[["G"]]
  lambda<-Data[["lambda"]]
```

[1]A risk averse approach would entail maximizing the minimum of selected diagonals.

```r
  Vinv<-solve(G[soln,soln]+lambda*diag(length(soln)))
  outmat<-(G[,soln]%*%(Vinv-(Vinv%*%Vinv)/sum(Vinv))%*%G[soln,])/G
  return(mean(diag(outmat[-soln,-soln])))
}

TSOUTCD<-TrainSel(Data=dataCDMEANopt,
           Candidates = list(1:160),
           setsizes = c(50),
           settypes = "UOS",
           Stat = CDMEANOPT, control=TSC)
```

```
## Maximum number of iterations reached.
```

```r
head(rownames(Wheat.M)[TSOUTCD$BestSol_int])
```

```
## [1] "Line4"  "Line5"  "Line6"  "Line11" "Line15" "Line17"
```

Maximin distance criterion Maximin distance criterion is a non-parametric design criteria. An optimal training set of size n from the N candidates is selected by maximizing the minimum [2] genetic distance among the training genotypes, so this is a space filling design. Next, we show how to program this criterion in R:

```r
dataMaximin<-list(DistMat=as.matrix(dist(Wheat.M_centered)))

MaximinOPT<-function(soln, Data){
  Dsoln<-Data[["DistMat"]][soln,soln]
  DsolnVec<-Dsoln[lower.tri(Dsoln,diag=FALSE)]
  return(min(DsolnVec))
}

TSOUTMaximin<-TrainSel(Data=dataMaximin,
           Candidates = list(1:160),
           setsizes = c(50),
           settypes = "UOS",
           Stat = MaximinOPT, control=TSC)
```

```
## Convergence Achieved
##  (no improv in the last 'minitbefstop' iters).
```

```r
head(rownames(Wheat.M)[TSOUTMaximin$BestSol_int])
```

```
## [1] "Line2"  "Line3"  "Line4"  "Line11" "Line15" "Line16"
```

Targeted optimization When the focus is on making inferences about the trait values for a known target set of genotypes is using genomic prediction, we can use what we call a targeted optimization criteria.

Mean PEV criterion based on linear model Dopt criterion is not sensitive to information about the target set of genotypes. Nevertheless, a related linear model based criteria called the mean prediction error variance (Mean PEV) can be used when the genotypic data for the target set is available. This criteria relates to the average prediction error variance of the predictions for the target set of genotypes using the linear model in Equation 1.

```r
##Target genotypes are in PC
dataPEVlm<-list(FeatureMat=PC, Target=161:200)
```

[2] We could also maximize the mean distance leading to Maximean criterion

```r
PEVlmOPT<-function(soln, Data){
  Fmat<-Data[["FeatureMat"]]
  targ<-Data[["Target"]]
  return(mean(diag(Fmat[targ,]%*%solve(crossprod(Fmat[soln,]))%*%t(Fmat[targ,]))))
}


TSOUTPEVlm<-TrainSel(Data=dataPEVlm,
           Candidates = list(1:160),
           setsizes = c(50),
           settypes = "UOS",
           Stat = PEVlmOPT, control=TSC)
```

```
## Maximum number of iterations reached.
```

```r
head(rownames(Wheat.M)[TSOUTPEVlm$BestSol_int])
```

```
## [1] "Line1"  "Line4"  "Line6"  "Line10" "Line12" "Line15"
```

```r

##This time the Target genotypes are in G
dataCDMEANTargetOpt<-list(G=Wheat.K, lambda=1, Target=161:200)

CDMEANOPTTarget<-function(soln, Data){
  G<-Data[["G"]]
  lambda<-Data[["lambda"]]
  targ<-Data[["Target"]]
  Vinv<-solve(G[soln,soln]+lambda*diag(length(soln)))
  outmat<-(G[,soln]%*%(Vinv-(Vinv%*%Vinv)/sum(Vinv))%*%G[soln,])/G
  return(mean(diag(outmat[targ,targ])))
}



TSOUTCDTarg<-TrainSel(Data=dataCDMEANTargetOpt,
           Candidates = list(1:160),
           setsizes = c(50),
           settypes = "UOS",
           Stat = CDMEANOPTTarget, control=TSC)
```

Targeted CDMEAN criterion

```
## Maximum number of iterations reached.
```

```r
head(rownames(Wheat.M)[TSOUTCDTarg$BestSol_int])
```

```
## [1] "Line8"  "Line13" "Line17" "Line22" "Line27" "Line28"
```

minimax criterion Minimize the maximum genomic distance of training genotypes to test genotypes.

```r
dataMiniMax<-list(DistMat=as.matrix(dist(Wheat.M_centered)))

MiniMaxOPT<-function(soln, Data){
  Dsoln<-Data[["DistMat"]][soln,161:200]
  DsolnVec<-max(c(unlist(Dsoln)))
  return(-(DsolnVec))
}

TSOUTMinimax<-TrainSel(Data=dataMiniMax,
           Candidates = list(1:160),
           setsizes = c(50),
           settypes = "UOS",
           Stat = MiniMaxOPT, control=TSC)
```

```
## Maximum number of iterations reached.
```

```r
head(rownames(Wheat.M)[TSOUTMinimax$BestSol_int])
```

```
## [1] "Line5"  "Line6"  "Line8"  "Line11" "Line13" "Line14"
```

Multiple Design Criterion Maximize the mean genomic distance of training genotypes at the same time minimize the mean distance to the target genotypes.

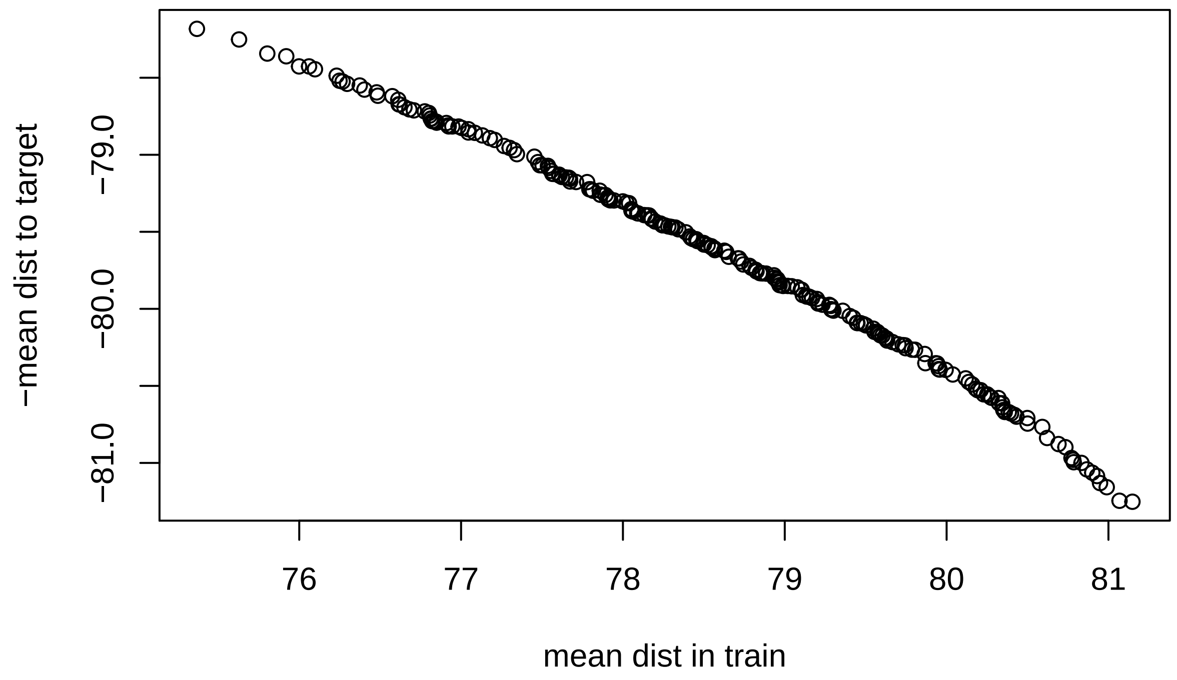
```r
dataMultOpt<-list(DistMat=as.matrix(dist(Wheat.M_centered)))

MultOPT<-function(soln, Data){
  D<-Data[["DistMat"]]
  Dsoln<-D[soln,161:200]
  DsolnVec1<- -mean(c(unlist(Dsoln)))
  Dsoln2<-D[soln,soln]
  DsolnVec2<-mean(c(unlist(Dsoln2)))
  return(c(DsolnVec2,DsolnVec1))
}
TSOUTMultOPt<-TrainSel(Data=dataMultOpt,
           Candidates = list(1:160),
           setsizes = c(50),
           settypes = "UOS",
           Stat = MultOPT, nStat=2, control=TSC)
```

```
## Maximum number of iterations reached.
```

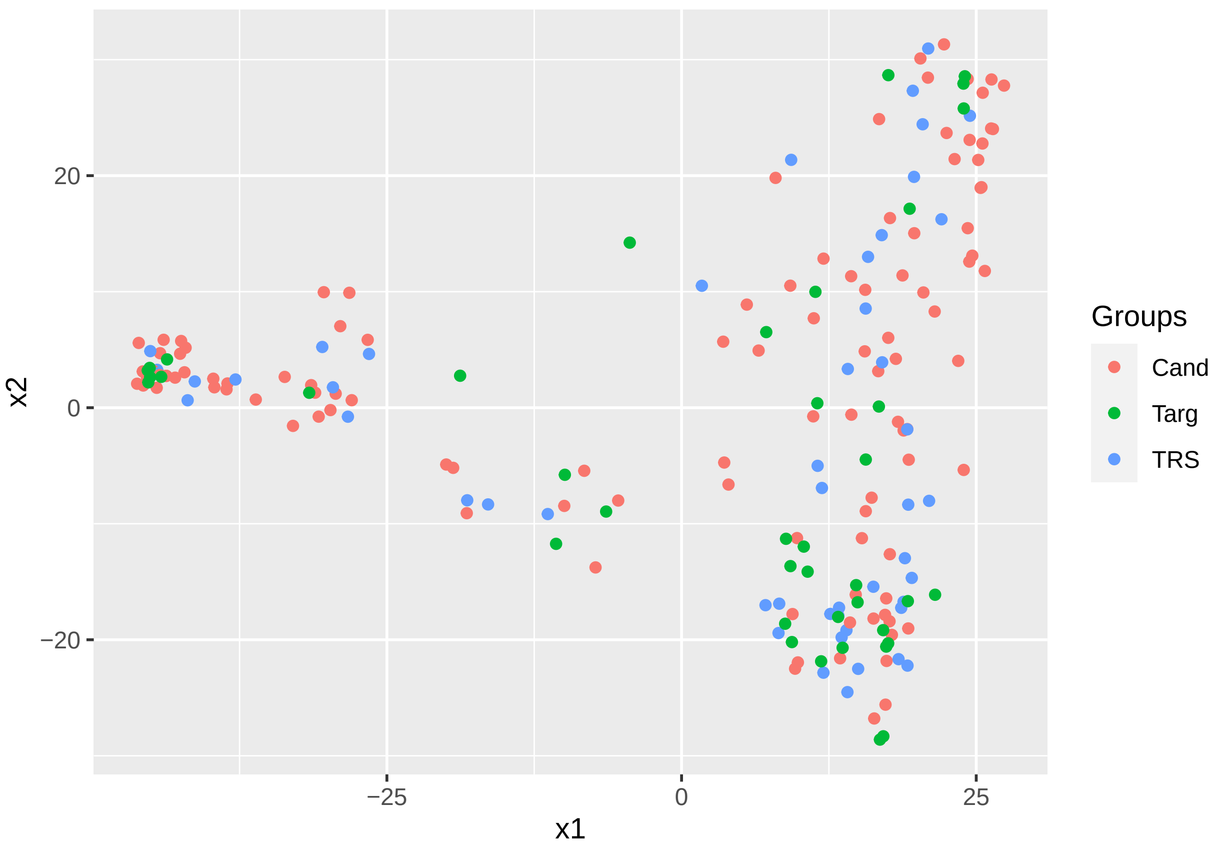
Plot the frontier solutions:

```r
FrontierSols<-t(TSOUTMultOPt$BestVal)
plot(FrontierSols, xlab="mean dist in train",
     ylab="-mean dist to target")
```



```
Solns<-which((FrontierSols[,1]>=79) & (FrontierSols[,2]>= -80))# subset of solutions
Selected<-TSOUTMultOPt$BestSol_int[, Solns[1]]

Groups<-rep("Cand",200)
Groups[161:200]<-"Targ"
Groups[Selected]<-"TRS"
PlotData<-data.frame(x1=PC[,1], x2=PC[,2], Groups=factor(Groups))
library(ggplot2)
p<-ggplot(PlotData, aes(x=x1,y=x2, color=Groups))+geom_point()
p
```



Selection of a subset of genotypes for an known design in a single environment

In certain cases, we are looking for conducting a phenotypic experiment with n training genotypes selected out of N candidate genotypes but in addition, we also have a particular blocking structure and environmental covariates involved in the design of the experiment. Suppose the matrix E is the $n \times p$ environmental covariates matrix. For instance, this matrix could be the design matrix for a row-column blocking within the environment. We assume still that we want make inferences about the genomic values after accounting for these covariates. In this case, the order in which the genotpes are positioned in the environment will be important. Perhaps, we would like to use similar genotypes in genotypes in dissimilar blocks and also we would like to observe as genetically distant genotypes within similar blocks.

Un-targeted optimization

D-optimality criterion with environmental covariates D-optimality criterion can be easily adopted for this purpose. FIrts we write the model as

$$y = E\beta_{env} + f(M)\beta_f + \epsilon$$

where y is the n vector of phenotypic measurements in the training data, E is the $n \times p$ design matrix for the environmental covariates, β_{env} is the p vector of the effects of the environmental covariates, M is the $n \times m$ the marker matrix for the n training genotypes, $f(M)$ is a genomic features matrix with dimensions $n \times q$, β_f is the q vector of effects of genomic features, and ϵ is the residual error vector of length n. We further assume that the elements of ϵ are independent and identically distributed with a normal distribution with zero mean and variance σ_e^2. Under this model the variance of the estimators for β is known to be proportional to $[f(M)'(I - E(E'E)^{-1}E')f(M)]^{-1}$. D-optimal selection of n training genotypes from N individuals in the candidate set involves minimizing the determinant of this matrix (or equivalently maximizing the log-determinant of $f(M)'(I - E(E'E)^{-1}E')f(M)$). The matrix $(I - E(E'E)^{-1}E')$ is the projection matrix to the orthogonal space of column space of E.

```r
E<-data.frame(expand.grid(row=paste("row",1:5, sep="_"),
                          col=paste("col",1:10, sep="_")))
E$row<-as.factor(E$row)
E$col<-as.factor(E$col)


DesignE<-model.matrix(~row+col+row*col, data=E)

P<-diag(nrow(DesignE))-DesignE%*%solve(crossprod(DesignE))%*%t(DesignE)

dataDoptEnv<-list(FeatureMat=PC, Projection=P)

DOPTwithE<-function(soln, Data){
  Fmat<-Data[["FeatureMat"]]
  P<-Data[["Projection"]]
  return(determinant(crossprod(P%*%Fmat[soln,]), logarithm=TRUE)$modulus)
}

TSOUTDwithE<-TrainSel(Data=dataDoptEnv,
           Candidates = list(1:160),
           setsizes = c(50),
           settypes = "OS",
           Stat = DOPTwithE, control=TSC)
```

```
## Maximum number of iterations reached.
```

```r
TSOUTDwithE$BestSol_int #order of this is important
```

```
##  [1]   4 142  95  19  61  78 117  71  43 133  90 132 128  41  69 110 131  42  15
## [20] 160  25  70 101 112  97  83  45 108 159  17 154 149 146  18  35 124  47 158
## [39]  31 139  13  93 105  53 140 148  16  81 156  62
```

```r
head(rownames(Wheat.M)[TSOUTDwithE$BestSol_int])
```

```
## [1] "Line4"   "Line142" "Line95"  "Line19"  "Line61"  "Line78"
```

```r
E$GID<-rownames(Wheat.M)[TSOUTDwithE$BestSol_int]
###Here is the final design
head(E)
```

```
##     row   col     GID
## 1 row_1 col_1   Line4
## 2 row_2 col_1 Line142
## 3 row_3 col_1  Line95
## 4 row_4 col_1  Line19
## 5 row_5 col_1  Line61
## 6 row_1 col_2  Line78
```

CDMEAN-optimality criterion with environmental covariates We can also use environmental covariates with the CDMEAN-optimality criterion. In ordor to do this we first need to add the environmental covariates into the G-BLUP model. This model is written as

$$y = E\beta_{env} + +Zu + \epsilon$$

with E is the $n \times p$ design matrix for the environmental covariates, β_{env} is the p vector of the effects of the environmental covariates, Z is the $n \times N$ design matrix for the N genotypes in the candidate set, $\epsilon \sim N_n(0, \sigma_e^2)$ is independent of $u \sim N_q(0; \sigma_g^2 G)$.

For this model, the coefficient of determination matrix of $\widehat{u}$ for predicting u is given by

$$(GZ'PZG) \oslash G$$

where $P = V^{-1} - V^{-1}E(E'V^{-1}E)^{-1}E'V^{-1}$ is the projection matrix and $\oslash$ expresses the element-wise division.

```
dataCDMEANoptwithEnv<-list(G=Wheat.K[1:160,1:160],E=DesignE, lambda=1)

CDMEANOPTwithEnv<-function(soln, Data){
  G<-Data[["G"]]
  E<-Data[["E"]]

  lambda<-Data[["lambda"]]
  Vinv<-solve(G[soln,soln]+lambda*diag(length(soln)))
  outmat<-(G[,soln]%*%
             (Vinv-Vinv%*%E%*%solve(t(E)%*%Vinv%*%E)%*%t(E)
              %*%Vinv)%*%G[soln,])/G
  return(mean(diag(outmat[-soln,-soln])))
}


TSOUTCDwithENV<-TrainSel(Data=dataCDMEANoptwithEnv,
           Candidates = list(1:160),
           setsizes = c(50),
           settypes = "OS",
           Stat = CDMEANOPTwithEnv, control=TSC)
```

```
## Convergence Achieved
##  (no improv in the last 'minitbefstop' iters).
```

```
E$GID<-rownames(Wheat.M)[TSOUTCDwithENV$BestSol_int]
###Here is the final design
head(E)
```

```
##     row   col     GID
## 1 row_1 col_1 Line126
## 2 row_2 col_1  Line66
## 3 row_3 col_1  Line88
## 4 row_4 col_1 Line100
## 5 row_5 col_1 Line146
## 6 row_1 col_2 Line148
```

Targeted optimization and allowing for replicates We can also do targeted optimization in this case with minimal change to the last code:

```
dataCDMEANoptwithEnvTarget<-list(G=Wheat.K,E=DesignE,Target=161:200, lambda=1)

CDMEANOPTwithEnvTarget<-function(soln, Data){
  G<-Data[["G"]]
  E<-Data[["E"]]
  targ<-Data[["Target"]]
  lambda<-Data[["lambda"]]
  Vinv<-solve(G[soln,soln]+lambda*diag(length(soln)))
  outmat<-(G[,soln]%*%
             (Vinv-Vinv%*%E%*%solve(t(E)%*%Vinv%*%E)%*%t(E)%*%Vinv)
           %*%G[soln,])/G
  return(mean(diag(outmat[targ,targ])))
}



TSOUTCDwithENVTarg<-TrainSel(Data=dataCDMEANoptwithEnvTarget,
           Candidates = list(1:160),
           setsizes = c(50),
           settypes = "OMS",
           Stat = CDMEANOPTwithEnvTarget, control=TSC)
```

```
## Convergence Achieved
##  (no improv in the last 'minitbefstop' iters).
```

```
E$GID<-rownames(Wheat.M)[TSOUTCDwithENVTarg$BestSol_int]
###Here is the final design
head(E)
```

```
##     row   col    GID
## 1 row_1 col_1  Line93
## 2 row_2 col_1   Line6
## 3 row_3 col_1 Line120
## 4 row_4 col_1  Line82
## 5 row_5 col_1  Line43
## 6 row_1 col_2 Line121
```

Design for a phenotypic experiment in multiple environments

In practice, most genomic selection experiments are performed over multiple environments. Designing genomic selection over multiple environments means we would like to choose training genotypes to use in each of these environments and for genomic selection the distribution of the alleles within and between the different environments can be arranged optimally for obtaining better generalization performance.

Using CDMEAN-optimality criterion for genomic selection experiment design in multiple environments As before, we first need to state the underlying model. For multi-environmental trials, a commonly used genomic prediction model is the multi-environmental G-BLUP model. Suppose we have 3 environments, in Environment 1 we can accommodate 30 genotypes in a 6-rows 5-columns design, in Environment 2 we can accommodate 20 genotypes in a 4-rows 5-columns design, and in Environment 3 we can accommodate 50 genotypes in an unknown homogeneous design. We assume that the genomic covariance of the environments is (proportionally) equal to the matrix

$$V_g = \begin{pmatrix} 1.0 & .7 & .5 \\ .7 & 1.2 & .8 \\ .5 & .8 & 1.5 \end{pmatrix}$$

We assume that the residual errors in these environments are correlated with the following covariance matrix

$$V_e = \begin{pmatrix} 1.0 & 0 & 0 \\ 0 & 1.5 & 0 \\ 0 & 0 & 1.0 \end{pmatrix}.$$

We can express the model for the training data as follows:

$$\begin{pmatrix} y_1 \\ y_2 \\ y_3 \end{pmatrix} = E\beta_{env} + \begin{pmatrix} Z_1u_1 \\ Z_2u_2 \\ Z_3u_3 \end{pmatrix} + \begin{pmatrix} Z_1\epsilon_1 \\ Z_2\epsilon_2 \\ Z_3\epsilon_3 \end{pmatrix}$$

where E is the $n \times p$ design matrix for the environmental covariates, β_{env} is the p vector of the effects of the environmental covariates, y_i is an n_i vector and Z_i is the $n_i \times N$ design matrix for the N genotypes in the candidate set in environment i for $i = 1, 2, 3$. In addition, we assume $(\epsilon_1, \epsilon_2, \epsilon_3) \sim N_{N\times 3}(0, I_N, V_e)$ is independent of $(u_1, u_2, u_3) \sim N_{N\times 3}(0; G, V_g)$. This means that the vectorized form of these matrices $\epsilon = vec(\epsilon_1, \epsilon_2, \epsilon_3)$ and $u = vec(u_1, u_2, u_3)$ are independently distributed as $N_{3N}(0, V_e \otimes I_N)$ and $N_{3N}(0, V_g \otimes G)$.

In our case $n_1 = 30, n_2 = 20, n_3 = 50$, and $n = n_1 + n_2 + n_3 = 100$. Here is how you can approach this problem using 'TrainSel':

```
Vg=matrix(c(1.0 , .7 , .5 , .7 , 1.2 ,.8 , .5 , .8 , 1.5), 3,3)
Ve=matrix(c(1.0, 0,0  , 0,1.5,0 , 0,0,1.0), 3,3)
rownames(Vg)<-colnames(Vg)<-rownames(Ve)<-colnames(Ve)<-paste("E",1:3, sep="")
G<-kronecker(Vg, Wheat.K, make.dimnames = TRUE)
R<-kronecker(Ve, diag(nrow(Wheat.K)), make.dimnames = TRUE)
#### Note the shape of G (same as R)
head(rownames(G))
```

```
## [1] "E1:Line1" "E1:Line2" "E1:Line3" "E1:Line4" "E1:Line5" "E1:Line6"
```

```
tail(rownames(G))
```

```
## [1] "E3:Line195" "E3:Line196" "E3:Line197" "E3:Line198" "E3:Line199"
## [6] "E3:Line200"
```

```
dim(G)
```

```
## [1] 600 600
```

By examining the shape of the G matrix above we see that the candidate set are on the 1st through 160th, 200th through 360th and,400th through 560th rows and columns of this matrix. We want to use 30 from 1 through 160, 20 from 200 through 360 and 50 from 400 through 560. The first two sets are ordered and last one is unordered. We are also going to assume duplicates within an environment are not allowed.

Design Matrix for the environments is obtained below. I am assuming no interaction effects between rows and columns.

```
E1<-(expand.grid(row=paste("row",1:6, sep="_"),
                 col=paste("col",1:5, sep="_")))


E2<-(expand.grid(row=paste("row",1:4, sep="_"),
                 col=paste("col",1:5, sep="_")))


E3<-data.frame(row=paste("row",rep(1,50),sep="_"),
               col=paste("col",rep(1,50), sep="_"))



EnvData<-data.frame(Env=c(rep("E1", 30), rep("E2", 20),rep("E3", 50)),
                 rbind(E1,E2,E3))
DesignE<-model.matrix(~Env+Env/(row+col), data=EnvData)
DesignE<-DesignE[,colSums(DesignE)>0]
```

```
## This is the names of the fixed effects design matrix
colnames(DesignE)
```

```
##  [1] "(Intercept)"    "EnvE2"          "EnvE3"          "EnvE1:rowrow_2"
##  [5] "EnvE2:rowrow_2" "EnvE1:rowrow_3" "EnvE2:rowrow_3" "EnvE1:rowrow_4"
##  [9] "EnvE2:rowrow_4" "EnvE1:rowrow_5" "EnvE1:rowrow_6" "EnvE1:colcol_2"
## [13] "EnvE2:colcol_2" "EnvE1:colcol_3" "EnvE2:colcol_3" "EnvE1:colcol_4"
## [17] "EnvE2:colcol_4" "EnvE1:colcol_5" "EnvE2:colcol_5"
```

```
dataCDMEANoptwithEnvME<-list(G=G,R=R, E=DesignE)
Target<-c(161:200, 361:400,561:600)
# we will exclude these since we assume nontargeted
CDMEANOPTwithEnvME<-function(soln, Data){
  G<-Data[["G"]]
  R<-Data[["R"]]
  E<-Data[["E"]]
  Vinv<-solve(G[soln,soln]+R[soln,soln])
  outmat<-(G[,soln]
           %*%(Vinv-Vinv%*%E%*%solve(t(E)%*%Vinv%*%E)%*%t(E)%*%Vinv)
           %*%G[soln,])/G
  return(mean(diag(outmat[-c(soln, Target),-c(soln, Target)])))
  #returning the mean CD on the remaining GIDs
  #(1:200 after deleting Target and the training.)
}


TSOUTCDwithENVME<-TrainSel(Data=dataCDMEANoptwithEnvME,
           Candidates = list(1:160, 201:360,401:560),
           setsizes = c(30,20,50),
           settypes = c("OS","OS","UOS"),
           Stat = CDMEANOPTwithEnvME, control=TSC)
```

```
## Maximum number of iterations reached.
```

```
##Putting GIDs in the design #first 30 are Env1
E1$GID<-rownames(G)[TSOUTCDwithENVME$BestSol_int[1:30]]
###Here is the final design for env 1
head(E1)
```

```
##     row   col       GID
## 1 row_1 col_1   E1:Line5
## 2 row_2 col_1 E1:Line156
## 3 row_3 col_1  E1:Line79
## 4 row_4 col_1  E1:Line12
## 5 row_5 col_1  E1:Line57
## 6 row_6 col_1  E1:Line39
```

```
##second 20 are Env2

E2$GID<-rownames(G)[TSOUTCDwithENVME$BestSol_int[31:50]]
###Here is the final design for env 2
head(E2)
```

```
##     row   col       GID
## 1 row_1 col_1  E2:Line21
## 2 row_2 col_1  E2:Line71
## 3 row_3 col_1  E2:Line78
## 4 row_4 col_1  E2:Line80
## 5 row_1 col_2 E2:Line137
## 6 row_2 col_2  E2:Line48
```

```
##Last 50 are Env3
E3$GID<-rownames(G)[TSOUTCDwithENVME$BestSol_int[51:100]]
###Here is the final design for env 3
head(E3)
```

```
##     row   col       GID
## 1 row_1 col_1  E3:Line4
## 2 row_1 col_1  E3:Line6
## 3 row_1 col_1 E3:Line11
## 4 row_1 col_1 E3:Line16
## 5 row_1 col_1 E3:Line17
## 6 row_1 col_1 E3:Line19
```

Implementing a penalty function for the total number of genotypes in the experiment

Suppose we want to restrict the total number of unique genotypes used in the above multi-environmental design to between 80 and 90. We can use a penalty function approach to impose this constraint: A penalty function forces the optimization algorithm to find desired solutions by assigning the points that don't satisfy the constraints values that is small with respect to the values of the optimization criteria (the size of this value might depend on how far the solutions are from satisfying the constrains), if the constraints are satisfied then the then the penalty functions returns zero.

```
PenaltyFunction<-function(soln){
  soln1<-soln[1:30]
  soln2<-soln[31:50]-200
  soln3<-soln[51:100]-400
  numuniquegeno<-length(unique(c(soln1,soln2,soln3)))
  if( (numuniquegeno<80) |  (90<numuniquegeno)){
    return(min(numuniquegeno-80, 90-numuniquegeno))
     } else {
    return(0)
    }
}
```

```
CDMEANOPTwithEnvMEwithPenalty<-function(soln, Data){
  penalty<-PenaltyFunction(soln)
  if (penalty==0){
  G<-Data[["G"]]
  R<-Data[["R"]]
  E<-Data[["E"]]
  Vinv<-solve(G[soln,soln]+R[soln,soln])
  outmat<-(G[,soln]
         %*%(Vinv-Vinv%*%E%*%solve(t(E)%*%Vinv%*%E)%*%t(E)%*%Vinv)
         %*%G[soln,])/G
  return(mean(diag(outmat[-c(soln, Target),-c(soln, Target)])))
  } else {return(penalty)}
}



TSOUTCDwithENVMEwithPenalty<-TrainSel(Data=dataCDMEANoptwithEnvME,
           Candidates = list(1:160, 201:360,401:560),
           setsizes = c(30,20,50),
           settypes = c("OS","OS","UOS"),
           Stat = CDMEANOPTwithEnvMEwithPenalty, control=TSC)
```

```
## Maximum number of iterations reached.
```

```
E1$GID<-rownames(G)[TSOUTCDwithENVMEwithPenalty$BestSol_int[1:30]]
###Here is the final design for env 1
head(E1)
```

```
##     row   col        GID
## 1 row_1 col_1  E1:Line21
## 2 row_2 col_1  E1:Line99
## 3 row_3 col_1 E1:Line148
## 4 row_4 col_1 E1:Line102
## 5 row_5 col_1 E1:Line157
## 6 row_6 col_1 E1:Line158
```

```
E2$GID<-rownames(G)[TSOUTCDwithENVMEwithPenalty$BestSol_int[31:50]]
###Here is the final design for env 2
head(E2)
```

```
##     row   col        GID
## 1 row_1 col_1  E2:Line57
## 2 row_2 col_1 E2:Line116
## 3 row_3 col_1  E2:Line25
## 4 row_4 col_1 E2:Line137
## 5 row_1 col_2  E2:Line84
## 6 row_2 col_2  E2:Line19
```

```
E3$GID<-rownames(G)[TSOUTCDwithENVMEwithPenalty$BestSol_int[51:100]]
###Here is the final design for env 3
head(E3)
```

```
##     row   col       GID
## 1 row_1 col_1  E3:Line4
## 2 row_1 col_1  E3:Line5
## 3 row_1 col_1  E3:Line6
## 4 row_1 col_1  E3:Line9
## 5 row_1 col_1 E3:Line11
## 6 row_1 col_1 E3:Line16
```

Other usage examples in plant breeding

'TrainSel' can be adopted to be used in optimization of problems other than the design of training populations for genomic prediction. The following examples demonstrate use of the package in some mixed integer optimization problems related to plant breeding.

Unsupervised Variable Selection

In some cases, we are interested in a subset of markers that represent the information contained in the all of the available markers. We can use the distance correlation measure between the marker data with all of the markers and the marker data with a selected set of markers to aid us in this process. We want to maximize the distance correlation measure for a given set of markers of size say 100. You can do this with the following code:

```r
library(energy)
dataVarSel<-list(dist(Wheat.M_centered), Wheat.M_centered)
funVarSel<-function(soln,Data){
out<-bcdcor(Data[[1]],dist(Data[[2]][,soln]))
return(out)
}

TSOUTVarSel<-TrainSel(Data=dataVarSel,
           Candidates = list(1:ncol(Wheat.M_centered)),
           setsizes = c(100),
           settypes = c("UOS"),
           Stat = funVarSel, control=TSC)
```

```
## Maximum number of iterations reached.
```

```r
#to check convergence
#plot(TSOUTVarSel$maxvec, "Distance Correlation")
AnchorMarkers<-TSOUTVarSel$BestSol_int
```

Optimal parental proportions and the Pareto front

In this example we want to select 10 parents out of the 40 genotypes in the target set and provide parental proportions for those 10 parents so that the mean GEBVs (estimated using a model based on the anchor markers) for the progeny of these parents mixed in these proportions would be maximized and inbreeding of the progeny is minimized.

We first need to estimate the marker effects. In this example we will only use the anchor markers, and the model is trained on all 160 candidate genotypes.

```r
library(EMMREML)
```

```
## Loading required package: Matrix
```

```r
mixedmodelout<-emmreml(y=Wheat.Y[1:160,2],
                       X=matrix(1, nrow=160, ncol=1),
                       Z=Wheat.M_centered[1:160,AnchorMarkers],
                       K=diag(length(AnchorMarkers)))
markereffects<-mixedmodelout$uhat
```

Using the estimated marker effects we can calculate GEBVs for the 40 prospective parents in the Target set. We also subset the genomic relationship matrix for these 40 genotypes from the whole genomic relationship matrix.

```r
GEBVs40<-Wheat.M_centered[161:200,AnchorMarkers]%*%markereffects
K40<-Wheat.K[161:200,161:200]
```

Since we know the phenotypic values for the Target in our case, we can povide an estimate of the accuracy for the GEBVs in the Target set:

```r
cor(GEBVs40,Wheat.Y[161:200,2])
```

```
##           [,1]
## [1,] 0.5332737
```

Now, we are ready to setup the problem: We want to select 10 genotypes as parents and also obtain the parental proportions for these parents so that the mean GEBVs for the progeny is maximized while the inbreeding in the progeny is minimized.

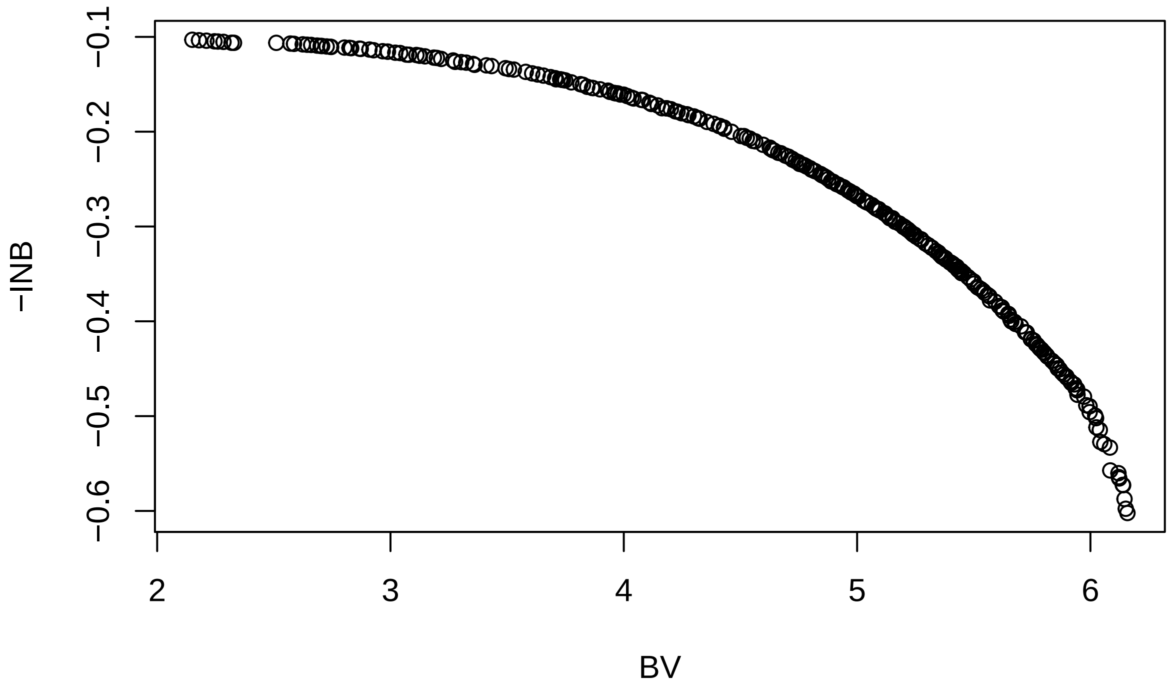
```r
dataOptProp<-list(GEBVs40,K40)
funOptProp<-function(soln_int,soln_dbl,Data){
  props<-soln_dbl/sum(soln_dbl) #to rescale the solution to sum up to 1.
  BV<-crossprod(Data[[1]][soln_int],props)
  Inb<-t(props)%*%Data[[2]][soln_int,soln_int]%*%props
  return(c(BV,-c(Inb)))
}



TSOUTOptProp<-TrainSel(Data=dataOptProp,
           Candidates = list(1:40, c(.001,.999)),
           setsizes = c(10, 10),
           settypes = c("OS","DBL"),
           Stat = funOptProp, nStat = 2)
```

```
## Maximum number of iterations reached.
```

```r
plot(t(TSOUTOptProp$BestVal), xlab="BV", ylab="-INB")
```



Optimal genomic mating

2 objectives, minimize inbreeding maximize gain We want to select 100 mates so that the mean GEBVs for the progeny is maximized while the inbreeding in the progeny is minimized.

```r
library(rrBLUP)
##All possible mates
```

```r
#males 161:200
#females 161:200
#this gives 1600 possible mates.
DFMates<-expand.grid(rownames(Wheat.M[161:180,]),rownames(Wheat.M[181:200,]))
M1<-Wheat.M[161:180,AnchorMarkers]
M2<-Wheat.M[181:200,AnchorMarkers]
M<-rbind(M1, M2)
K<-A.mat(M)
BVParents<-M%*%markereffects
```

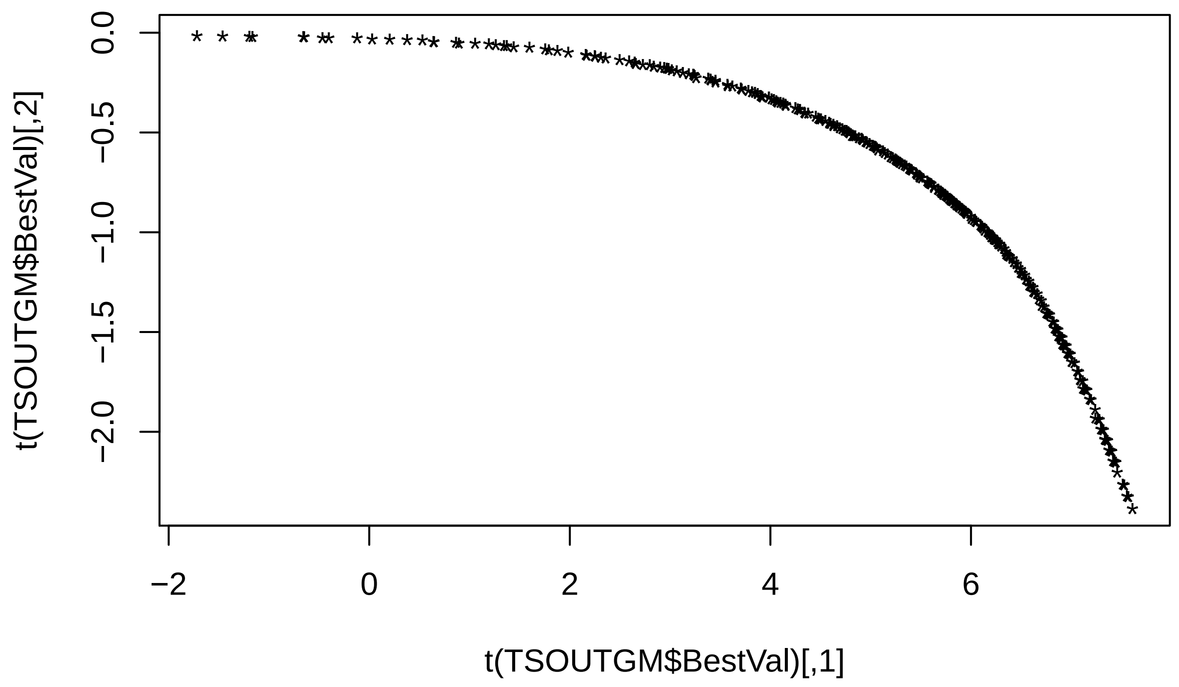
```r
###selecting 50 mates,  setsizes=50
###Note Stat=BV_INB, nStat = 2,
BV_INB<-function(soln){
  DFMatessoln<-DFMates[soln,]
  P1<-factor(DFMatessoln[,1], levels=rownames(M1))
  P2<-factor(DFMatessoln[,2], levels=rownames(M2))
  P1<-model.matrix(~P1-1)
  P2<-model.matrix(~P2-1)
  P<-cbind(P1/2,P2/2)
  PKP<-mean(tcrossprod(P%*%K,P)) #inbreeding
  BVmatessoln<-mean(P%*%BVParents)# gain
  out<-c(BVmatessoln,-as.numeric(PKP))
  names(out)<-c("Gain","-Inb")
  return(out)
}



TSOUTGM<-TrainSel(Candidates = list(1:nrow(DFMates)),
                  setsizes=50,
                  settypes = c("UOMS"),
                  Stat=BV_INB,
                  nStat = 2)
```

```
## Maximum number of iterations reached.
```

```r
plot(t(TSOUTGM$BestVal), pch="*")
```



```
##dimension of the problem * number of solutions
dim(TSOUTGM$BestSol_int)
```

```
## [1]  50 294
```

```
########solution 1
head(DFMates[TSOUTGM$BestSol_int[,1],])
```

```
##          Var1    Var2
## 322   Line162 Line197
## 322.1 Line162 Line197
## 322.2 Line162 Line197
## 322.3 Line162 Line197
## 322.4 Line162 Line197
## 322.5 Line162 Line197
```

```
TSOUTGM$BestVal[,1]
```

```
## [1]  6.989923 -1.601578
```

```
########solution 2
head(DFMates[TSOUTGM$BestSol_int[,2],])
```

```
##          Var1    Var2
## 242   Line162 Line193
## 242.1 Line162 Line193
## 242.2 Line162 Line193
## 302   Line162 Line196
## 302.1 Line162 Line196
## 302.2 Line162 Line196
```

```
TSOUTGM$BestVal[,2] ##, etc,...
```

```
## [1]  4.9084792 -0.5199157
```

3 objectives, minimize inbreeding maximize gain and crossvariance When concentrating on mates instead of the parental proportions we can introduce another statistic nto the optimization problem. We want to have high within family variance for the selected mates. We have included two functions to calculate the mean variance of a mating plan, namely, 'calculatecrossvalueM1' and 'calculatecrossvalueM2'.

```
##############################
 BV_VAR_INB<-function(soln){
   DFMatessoln<-DFMates[soln,]
   P1<-factor(DFMatessoln[,1], levels=rownames(M1))
   P2<-factor(DFMatessoln[,2], levels=rownames(M2))
   P1<-model.matrix(~P1-1)
   P2<-model.matrix(~P2-1)
   P<-cbind(P1/2,P2/2)
  BVmatessoln<-mean(P%*%BVParents)# gain


   varI<-mean(sapply(1:nrow(DFMatessoln), function(i){
     p1<-DFMatessoln[i,1]
     p2<-DFMatessoln[i,2]
     m1<-M1[p1,]
     m2<-M2[p2,]
    calculatecrossvalueM1(round(m1),round(m2),markereffects)
    ## calculatecrossvalueM2(round(m1),round(m2),markereffects, markermap)
   }))

  PKP<-mean(tcrossprod(P%*%K,P)) #inbreeding

   out<-c(BVmatessoln, varI,-as.numeric(PKP))
   names(out)<-c("Gain", "Var","-Inb")
   return(out)

 }
```

Note that we increase the 'npop' and 'niterations' parameters to get a good coverage of the frontier surface. Experiment with these parameters!

```
####Three objectives, minimize inbreeding maximize gain and cross-variance
###selecting 50 mates, setsizes=50

###Note Stat=BV_INB_VAR, nStat = 3!
tsControl=TrainSelControl()
tsControl$npop=1000
tsControl$niterations=1000
TSOUT<-TrainSel(Candidates = list(1:nrow(DFMates)),
                 setsizes=5,
                 settypes = c("UOMS"),
                 Stat=BV_VAR_INB,
                 nStat = 3,
                 control = tsControl)
```

```
## Maximum number of iterations reached.
```

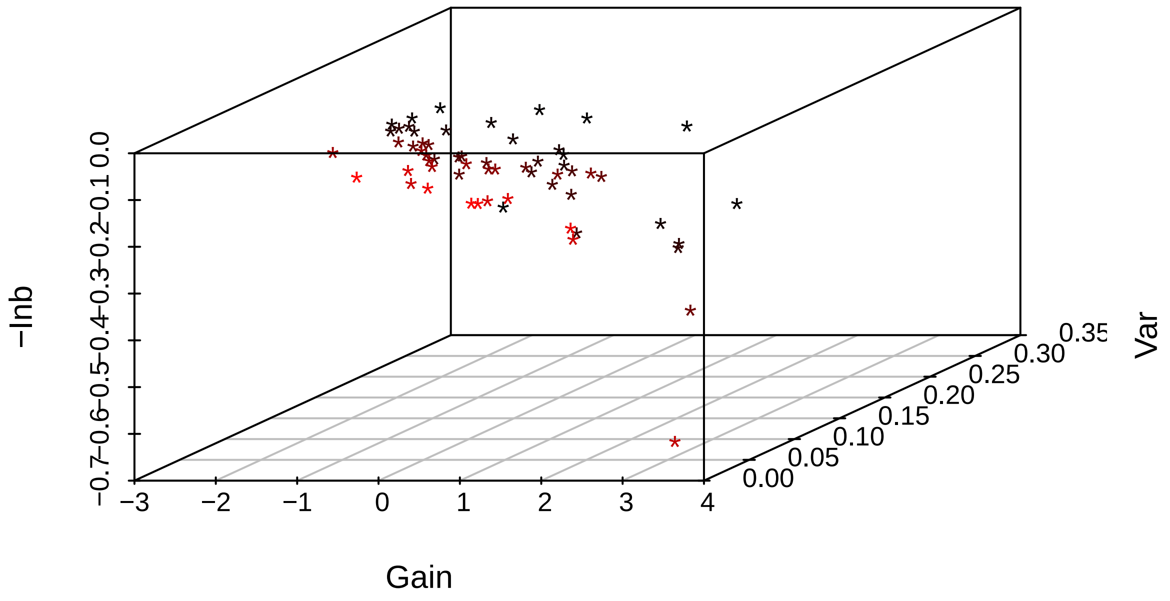
```
TSOUT$BestVal[,1:5] # values for first 5 results
```

```
##             [,1]        [,2]       [,3]       [,4]       [,5]
## [1,] -1.9271911 -0.73224329 -1.8574202 -0.9437055 -0.4385360
## [2,]  0.2105358  0.12131687  0.1805445  0.2629976  0.1313945
## [3,] -0.1076032 -0.08527522 -0.1088586 -0.1364968 -0.1188015
```

```
ncol(TSOUT$BestVal) # Number of solutions found
```

```
## [1] 60
```

```
library(scatterplot3d)
sd3<-scatterplot3d(t(TSOUT$BestVal), pch="*",highlight.3d=TRUE, xlab="Gain",
                   ylab="Var", zlab="-Inb")
```



```
########solution 1
head(DFMates[TSOUT$BestSol_int[,1],])
```

```
##         Var1    Var2
## 16  Line176 Line181
## 113 Line173 Line186
## 130 Line170 Line187
## 186 Line166 Line190
## 232 Line172 Line192
```

```
TSOUT$BestVal[,1]
```

```
## [1] -1.9271911  0.2105358 -0.1076032
```

```r
# ########solution 20
 head(DFMates[TSOUT$BestSol_int[,10],])
```

```
##        Var1    Var2
## 35  Line175 Line182
## 136 Line176 Line187
## 145 Line165 Line188
## 186 Line166 Line190
## 247 Line167 Line193
```

```r
 TSOUT$BestVal[,10]# ###,etc,...
```

```
## [1] -0.64378031  0.10535741 -0.08378939
```

```r

fobj <- function(x)  (x^2+x)*cos(x)
lbound <- -10; ubound <- 10
x<-seq(lbound, ubound, length=100)
```

```r

TSout<-TrainSel(Candidates=list(c(lbound,ubound)), setsizes = 1,
                settypes = c("DBL"), Stat=fobj)
```

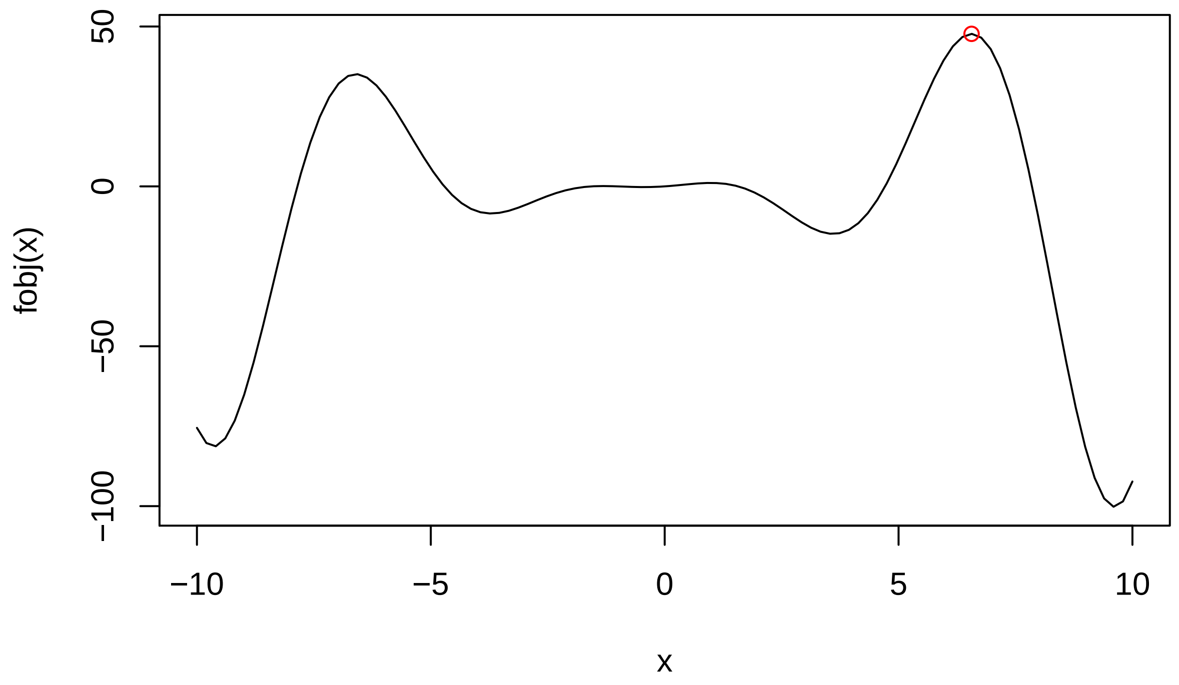
Finding maximum of a function with a single continuous input

```
## Convergence Achieved
##  (no improv in the last 'minitbefstop' iters).
```

```r
TSout$BestSol_DBL
```

```
## [1] 6.56054
```

```r
plot(x, fobj(x), type="l")
points(TSout$BestSol_DBL,TSout$BestVal, col="red")
```



```
Rastrigin <- function( x)
{
  x1=x[1]
  x2=x[2]
 -(20 + x1^2 + x2^2 - 10*(cos(2*pi*x1) + cos(2*pi*x2)))
}
```

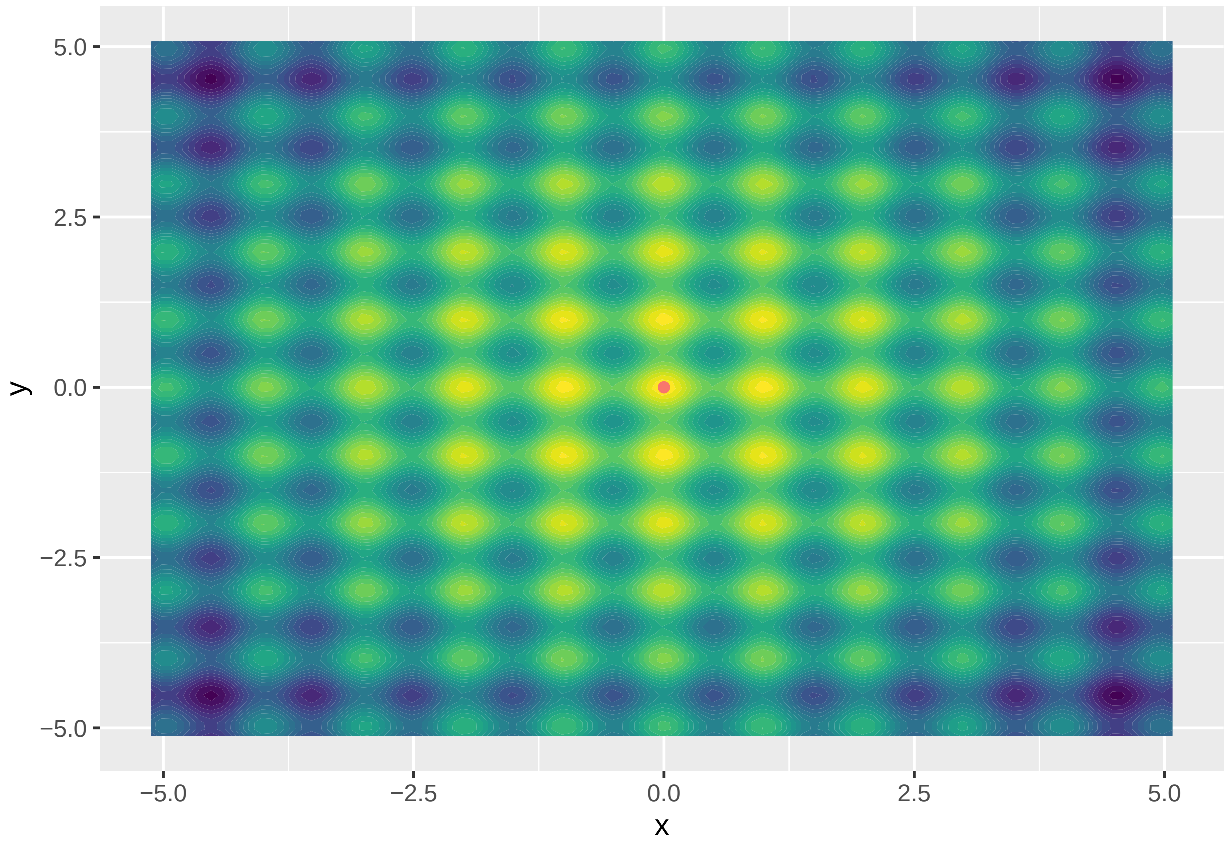
```
TSout2<-TrainSel(Candidates=list(c(-10, 5.12), c(-5.12, 10)),
                 setsizes = 2, settypes = c("DBL", "DBL"), Stat=Rastrigin)
```

Finding maximum of a function with two continuous inputs

```
## Convergence Achieved
##  (no improv in the last 'minitbefstop' iters).
```

```
x1best<-TSout2$BestSol_DBL[1]
x2best<-TSout2$BestSol_DBL[2]
xbest<-data.frame(x=x1best, y=x2best)
x1 <- x2 <- seq(-5.12, 5.12, by = 0.1)
x12<-expand.grid(x1, x2)
f <- apply(x12, 1,function(x){Rastrigin(x)})
plotdata<-cbind(x12,f)
colnames(plotdata)<-c("x","y","z")
```

```
library(ggplot2)
p<-ggplot(plotdata, aes(x, y)) + stat_contour_filled(aes(z = z), bins=30)
p<-p+ geom_point(data = xbest, aes(color="blue"))+theme(legend.position = "none")
p
```



```
library(TrainSel)
library(devtools)
```

```
## Loading required package: usethis
```

```
library(BBmisc)
```

```
##
## Attaching package: 'BBmisc'

## The following object is masked from 'package:base':
##
##     isFALSE
```

```
library(smoof)
```

```
## Loading required package: ParamHelpers

## Loading required package: checkmate
```

```
fn = function(x){
  return(c(x[1]^2-x[2]^2,sin(x[2]^2-x[1]^2),x[1]^2+x[2]^2))
  }
lower = c(0,0,0)
```

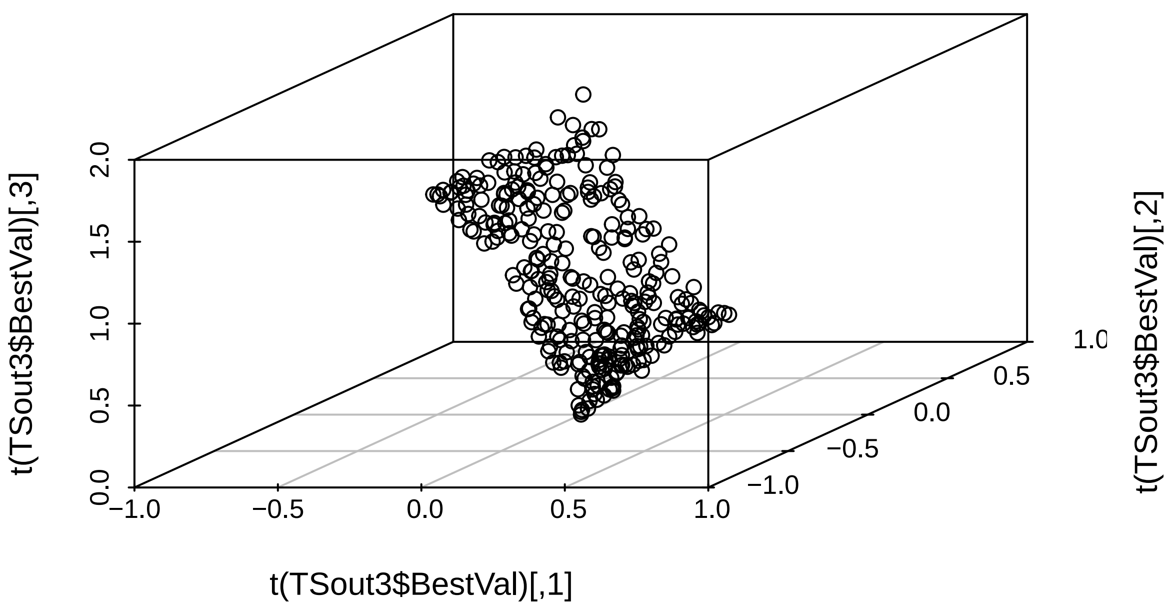
```
upper = c(1,1,1)
fn(c(0,1))
```

```
## [1] -1.000000  0.841471  1.000000
```

```
tsControl=TrainSelControl()
tsControl$npop=300
tsControl$niterations=10
TSout3<-TrainSel(Candidates=list(c(lower[1], upper[1]), c(lower[2], upper[2]),c(lower[3], upper[3])),
                 setsizes = 2, settypes = c("DBL", "DBL"), Stat=fn, nStat=3, control=tsControl)
```

```
## Maximum number of iterations reached.
```

```
scatterplot3d::scatterplot3d(t(TSout3$BestVal))
```


t(TSout3$BestVal)[,3]
t(TSout3$BestVal)[,1]
t(TSout3$BestVal)[,2]