MBatch 05-02
Using MBatch Assessments: EBNPlus_Correction_Structures
Tod Casasent
2017-11-10-1440

Introduction

These instructions are aimed at people familiar with R and familiar with TCGA/GDC platforms and data types. They are intended to introduce the reader to producing the given assessment. These instructions will only rarely, if ever, touch on the appropriateness of the assessment algorithm or interpretation of output. See MBatch_01_InstallLinux.docx for instructions on downloading test data.

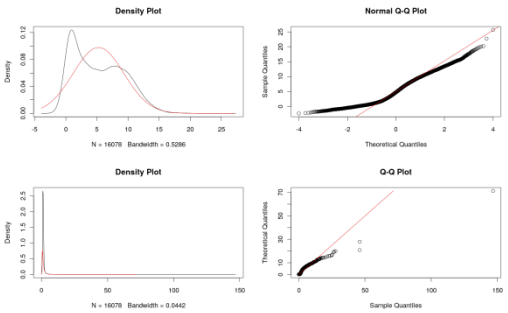
Algorithm

EBNPlus_Correction_Structures is a function used to perform the EBNPlus correction algorithm on two datasets, using all replicates for training. This function takes structures (matrices) and returns a corrected matrix of data.

The function takes the variant data set and corrects it to become part of the invariant data set using replicates shared between the sets. Replicates are determined by finding matching sample ids. It uses a validation ratio value of 0 to use all replicates for training. Any duplicates in genes or barcodes are removed. Genes that start with "?" are also removed. See EBNPlus_CheckData_Structures and EBNPlus_CombineBatches for details on data prep.

Output

The primary output method for MBatch is to view results in the Batch Effects Website. Correction algorithms generally do not create graphical output and instead create TSV output files. EBNPlus optionally creates a prior-plots PNG as shown below.



Usage

EBNPlus_Correction_Structures(theDataMatrix1, theDataMatrix2,

theBatchId1, theBatchId2,

theEBNP_BatchWithZero, theEBNP_FixDataSet, theEBNP_CorrectForZero,

theEBNP_ParametricPriorsFlag,

theSeed = NULL, theEBNP_PriorPlotsFile=NULL, theEBNP_MinSampleNum = 3,

theEBNP_AddData1Rows = FALSE, theEBNP_AddData2Rows = FALSE)

Arguments

theDataMatrix1 A matrix for data set 1 containing numeric values with columns being sample ids and rows being features, such as gene ids.

theDataMatrix2 A matrix for data set 2 containing numeric values with columns being sample ids and rows being features, such as gene ids.

theBatchId1 The group name for data set 1 (for example, RNASeqV2)

theBatchId2 The group name for data set 2 (for example, Agilent4502)

theEBNP_BatchWithZero Batch With Zero indicates which data set contains zero values. This is a string "1", "2", or "both". These values will be changed in a future release.

theEBNP_FixDataSet Fix Data Set indicates which data set should be set as invariate during the corrections. Value are numeric, 1 or 2 for the appropriate data set, or as.numeric(NA) for neither.

theEBNP_CorrectForZero Correct For Zero indicates whether or not data sets marked as "Batch With Zero" should be modified from zero (TRUE or FALSE)

theEBNP_ParametricPriorsFlag Use parametric adjustments for corrections (TRUE or FALSE)

theSeed NULL or a seed to use. Defaults to NULL. This is passed to the standard R set.seed function.

theEBNP_PriorPlotsFile Defaults to NULL and does not create PNG. Non-NULL should be the full path and filename for where to create the prior plots PNG.

theEBNP_MinSampleNum Defaults to 3. Any row (gene) with less than this number of samples is dropped.

theEBNP_AddData1Rows Defaults to FALSE. TRUE indicates rows in data set 2 not in 1 should be added as all NA.

theEBNP_AddData2Rows Defaults to FALSE. TRUE indicates rows in data set 1 not in 2 should be added as all NA.

Example Call

The following code is taken from the tests/EBNPlus_Correction_Structures.R file. Data used is from the testing data as per the MBatch_01_InstallLinux.docx document.

```
library(MBatch)

# set the paths

theDataFile1="/bea_testing/MATRIX_DATA/brca_rnaseq2_matrix_data.tsv"

theDataFile2="/bea_testing/MATRIX_DATA/brca_agi4502_matrix_data.tsv"

theOutputDir="/bea_testing/output/ebnplus/EBNPlus_Correction_Structures"

theBatchId1="RNASeqV2"

theBatchId2="Agilent4502"

theRandomSeed=314

# trim genes to get just gene symbols from standardized data

trimGenes <- function(theGenes)

{

foo <- as.vector(unlist(

sapply(theGenes, function(theGene)

{

# keep the same if it starts with ?

if (TRUE==grepl("^[?]+", theGene))

{

return(theGene)

}

else

{

# split on the | and take the first argument

# this makes no change if no pipe
```

```
return(strsplit(theGene, "|", fixed=TRUE)[[1]][1])
}
})
))
foo
}
# remove duplicates from columns (samples)
removeDuplicatesFromColumns <- function(theMatrix)
{
indexOfDuplicates <- which(duplicated(colnames(theMatrix)))
if (length(indexOfDuplicates) > 0)
{
# minus sign uses inverse of indexes
theMatrix <- theMatrix[ ,-indexOfDuplicates]
}
return(theMatrix)
}
# remove duplicates from rows (genes/probes)
removeDuplicatesFromRows <- function(theMatrix)
{
indexOfDuplicates <- which(duplicated(rownames(theMatrix)))
if (length(indexOfDuplicates) > 0)
{
# minus sign uses inverse of indexes
theMatrix <- theMatrix[-indexOfDuplicates, ]
}
return(theMatrix)
}
# make sure the output dir exists and is empty
unlink(theOutputDir, recursive=TRUE)
dir.create(theOutputDir, showWarnings=FALSE, recursive=TRUE)
```

```
# read the files in. This can be done however you want
theDataMatrix1 <- readAsGenericMatrix(theDataFile1)
theDataMatrix2 <- readAsGenericMatrix(theDataFile2)
# this is the reduce genes to just gene symbols, handling those from standardized
data
rownames(theDataMatrix1) <- trimGenes(rownames(theDataMatrix1))
rownames(theDataMatrix2) <- trimGenes(rownames(theDataMatrix2))
# remove any duplicates (this is a requirement for EBNplus)
theDataMatrix1 <- removeDuplicatesFromColumns(removeDuplicatesFromRows(theDataMatrix1))
theDataMatrix2 <- removeDuplicatesFromColumns(removeDuplicatesFromRows(theDataMatrix2))
correctedMatrix <- EBNPlus_Correction_Structures(theDataMatrix1, theData-
Matrix2,
theBatchId1, theBatchId2,
theEBNP_BatchWithZero="1",
theEBNP_FixDataSet=as.numeric(NA),
theEBNP_CorrectForZero=TRUE,
theEBNP_ParametricPriorsFlag=TRUE,
theSeed=theRandomSeed,
theEBNP_PriorPlotsFile=file.path(theOutputDir, "priorplots.PNG"))
writeAsMatrix(file.path(theOutputDir, "CorrectedData.tsv"), correctedMatrix )
```

Example File Output

The above code creates the following output files. Files are named using the following naming convention:

priorplots.PNG

CorrectedData.tsv

The priorplots.PNG file is created by the MBatch package code. The TSV file with the combined/corrected dataset is written by the example code in this case.

Command Line Output

In the future, we plan to make the output from MBatch more user friendly, but currently, this produces the following output at the command line.

```
> library(MBatch)
```

```
>
> # set the paths
> theDataFile1="/bea_testing/MATRIX_DATA/brca_rnaseq2_matrix_data.tsv"
> theDataFile2="/bea_testing/MATRIX_DATA/brca_agi4502_matrix_data.tsv"
> theOutputDir="/bea_testing/output/ebnplus/EBNPlus_Correction_Structures"
> theBatchId1="RNASeqV2"
> theBatchId2="Agilent4502"
> theRandomSeed=314
>
> # trim genes to get just gene symbols from standardized data
> trimGenes <- function(theGenes)
+ {
+ foo <- as.vector(unlist(
+ sapply(theGenes, function(theGene)
+ {
+ # keep the same if it starts with ?
+ if (TRUE==grepl("^[?]+", theGene))
+ {
+ return(theGene)
+ }
+ else
+ {
+ # split on the | and take the first argument
+ # this makes no change if no pipe
+ return(strsplit(theGene, "|", fixed=TRUE)[[1]][1])
+ }
+ })
+ ))
+ foo
+ }
>
```

```
> # remove duplicates from columns (samples)
> removeDuplicatesFromColumns <- function(theMatrix)
+ {
+ indexOfDuplicates <- which(duplicated(colnames(theMatrix)))
+ if (length(indexOfDuplicates) > 0)
+ {
+ # minus sign uses inverse of indexes
+ theMatrix <- theMatrix[ ,-indexOfDuplicates]
+ }
+ return(theMatrix)
+ }
>
> # remove duplicates from rows (genes/probes)
> removeDuplicatesFromRows <- function(theMatrix)
+ {
+ indexOfDuplicates <- which(duplicated(rownames(theMatrix)))
+ if (length(indexOfDuplicates) > 0)
+ {
+ # minus sign uses inverse of indexes
+ theMatrix <- theMatrix[-indexOfDuplicates, ]
+ }
+ return(theMatrix)
+ }
>
> # make sure the output dir exists and is empty
> unlink(theOutputDir, recursive=TRUE)
> dir.create(theOutputDir, showWarnings=FALSE, recursive=TRUE)
> theDataMatrix1 <- readAsGenericMatrix(theDataFile1)
Read 20531 records
> theDataMatrix2 <- readAsGenericMatrix(theDataFile2)
Read 17814 records
```

> # this is the reduce genes to just gene symbols, handling those from standardized data

> rownames(theDataMatrix1) <- trimGenes(rownames(theDataMatrix1))

> rownames(theDataMatrix2) <- trimGenes(rownames(theDataMatrix2))

> # remove any duplicates (this is a requirement for EBNplus)

> theDataMatrix1 <- removeDuplicatesFromColumns(removeDuplicatesFromRows(theDataMatrix1))

> theDataMatrix2 <- removeDuplicatesFromColumns(removeDuplicatesFromRows(theDataMatrix2))

> correctedMatrix <- EBNPlus_Correction_Structures(theDataMatrix1, theDataMatrix2,

+ theBatchId1, theBatchId2,

+ theEBNP_BatchWithZero="1",

+ theEBNP_FixDataSet=as.numeric(NA),

+ theEBNP_CorrectForZero=TRUE,

+ theEBNP_ParametricPriorsFlag=TRUE,

+ theSeed=theRandomSeed,

+ theEBNP_PriorPlotsFile=file.path(theOutputDir, "priorplots.PNG"))

2017 10 18 09:50:39.331 DEBUG MachineName EBNPlus_Correction_Structures theEBNP_AddData1Rows= FALSE

2017 10 18 09:50:39.331 DEBUG MachineName EBNPlus_Correction_Structures theEBNP_AddData2Rows= FALSE

2017 10 18 09:50:39.331 DEBUG MachineName starting BeaEBNPlus

2017 10 18 09:50:39.332 DEBUG MachineName MBatch Version: 2017-09-19-1530

2017 10 18 09:50:39.332 DEBUG MachineName BeaEBNPlus theEBNP_AddData1Rows= FALSE

2017 10 18 09:50:39.332 DEBUG MachineName BeaEBNPlus theEBNP_AddData2Rows= FALSE

2017 10 18 09:50:39.333 DEBUG MachineName EBNPlus theEBNP_AddData1Rows= FALSE

2017 10 18 09:50:39.333 DEBUG MachineName EBNPlus theEBNP_AddData2Rows= FALSE

2017 10 18 09:50:39.333 DEBUG MachineName EBNPlus theEBNP_PriorPlotsFile= /bea_testing/output/ebnplus/EBNPlus_Correction_Structures/priorplots.PNG

2017 10 18 09:50:39.334 DEBUG MachineName dim(theData1)=20530 1215

2017 10 18 09:50:39.334 DEBUG MachineName dim(theData2)=17814 600

2017 10 18 09:50:39.334 DEBUG MachineName remove unknown genes, that start with ?

2017 10 18 09:50:40.893 DEBUG MachineName check on adding missing rows

2017 10 18 09:50:40.893 DEBUG MachineName dim(theData1)=20501 1215

2017 10 18 09:50:40.893 DEBUG MachineName dim(theData2)=17814 600

2017 10 18 09:50:40.894 DEBUG MachineName make EBNplus

2017 10 18 09:50:40.898 DEBUG MachineName before callNextMethod

2017 10 18 09:50:40.898 DEBUG MachineName dim(mData1)=20501 1215

2017 10 18 09:50:40.898 DEBUG MachineName dim(mData2)=17814 600

2017 10 18 09:50:40.899 DEBUG MachineName removing column duplicates

2017 10 18 09:50:40.899 DEBUG MachineName removeDuplicatesFromColumns

2017 10 18 09:50:40.899 DEBUG MachineName removeDuplicatesFromColumns

2017 10 18 09:50:40.900 DEBUG MachineName dim(mData1)=20501 1215

2017 10 18 09:50:40.900 DEBUG MachineName dim(mData2)=17814 600

2017 10 18 09:50:40.900 DEBUG MachineName removing row duplicates

2017 10 18 09:50:40.901 DEBUG MachineName removeDuplicatesFromRows

2017 10 18 09:50:40.902 DEBUG MachineName removeDuplicatesFromRows

2017 10 18 09:50:40.903 DEBUG MachineName dim(mData1)=20501 1215

2017 10 18 09:50:40.903 DEBUG MachineName dim(mData2)=17814 600

2017 10 18 09:50:40.903 DEBUG MachineName after callNextMethod

2017 10 18 09:50:40.904 DEBUG MachineName dim(mData1)=20501 1215

2017 10 18 09:50:40.904 DEBUG MachineName dim(mData2)=17814 600

2017 10 18 09:50:40.904 DEBUG MachineName after EBNplus

2017 10 18 09:50:40.905 DEBUG MachineName dim(ebObj@mData1)=20501 1215

2017 10 18 09:50:40.905 DEBUG MachineName dim(ebObj@mData2)=17814 600

2017 10 18 09:50:40.929 DEBUG MachineName getBiComOrder

2017 10 18 09:50:40.930 DEBUG MachineName makeCommonRows

2017 10 18 09:50:42.174 DEBUG MachineName dim(mData1)=16146 1215

2017 10 18 09:50:42.174 DEBUG MachineName dim(mData2)=16146 600

2017 10 18 09:50:42.175 DEBUG MachineName makeCommonCols

2017 10 18 09:50:42.767 DEBUG MachineName dim(mData1)=16146 586

2017 10 18 09:50:42.768 DEBUG MachineName dim(mData2)=16146 586

2017 10 18 09:50:42.768 DEBUG MachineName asSameOrder

2017 10 18 09:50:42.791 DEBUG MachineName asSameOrder before

2017 10 18 09:50:42.791 DEBUG MachineName asSameOrder after if 1

2017 10 18 09:50:43.060 DEBUG MachineName asSameOrder after if 2

2017 10 18 09:50:43.061 DEBUG MachineName row.names(mat1)

2017 10 18 09:50:43.061 DEBUG MachineName rownames(mat1)

2017 10 18 09:50:43.061 DEBUG MachineName row.names(mat2)

2017 10 18 09:50:43.062 DEBUG MachineName rownames(mat2)

2017 10 18 09:50:43.063 DEBUG MachineName m.i

2017 10 18 09:50:43.331 DEBUG MachineName asSameOrder after if 3

2017 10 18 09:50:43.332 DEBUG MachineName dim(ebObj@mat1Com)=16146 586

2017 10 18 09:50:43.332 DEBUG MachineName dim(ebObj@mat2Com)=16146 586

2017 10 18 09:50:43.332 DEBUG MachineName getValidationSet

2017 10 18 09:50:43.346 INFO MachineName getValidationSet seed= 314

2017 10 18 09:50:43.346 DEBUG MachineName dim(ebObj@mat1Validation)=0 0

2017 10 18 09:50:43.346 DEBUG MachineName dim(ebObj@mat2Validation)=0 0

2017 10 18 09:50:43.347 DEBUG MachineName dim(ebObj@mat1Train)=16146 586

2017 10 18 09:50:43.347 DEBUG MachineName dim(ebObj@mat2Train)=16146 586

2017 10 18 09:50:43.878 DEBUG MachineName train

2017 10 18 09:50:43.878 DEBUG MachineName inside train

2017 10 18 09:50:43.879 DEBUG MachineName train theEBNP_PriorPlotsFile= /bea_testing/output/ebnplus/EBNPlus_Correction_Structures/priorplots.PNG

2017 10 18 09:50:43.996 DEBUG MachineName colnames(Object@mat1Train)=TCGA-A1-A0SD-01A-11R-A115-07.RNASeqV2 TCGA-A1-A0SE-01A-11R-A084-07.RNASeqV2 TCGA-A1-A0SH-01A-11R-A084-07.RNASeqV2

2017 10 18 09:50:43.997 DEBUG MachineName colnames(Object@mat2Train)=TCGA-A1-A0SD-01A-11R-A115-07.Agilent4502 TCGA-A1-A0SE-01A-11R-A084-07.Agilent4502 TCGA-A1-A0SH-01A-11R-A084-07.Agilent4502

2017 10 18 09:50:43.998 DEBUG MachineName inside train, call getData4EB

2017 10 18 09:50:45.329 DEBUG MachineName data4EB <- as.matrix

2017 10 18 09:50:45.329 DEBUG MachineName dim(data4EB)=16146 1172

2017 10 18 09:50:45.329 DEBUG MachineName cbinds and rbinds

2017 10 18 09:50:45.330 DEBUG MachineName Object@DF1batch= RNASeqV2

2017 10 18 09:50:45.330 DEBUG MachineName Object@DF2batch= Agilent4502

2017 10 18 09:50:45.334 DEBUG MachineName row.names(sampBatch)

2017 10 18 09:50:45.334 DEBUG MachineName TCGA-A1-A0SD-01A-11R-A115-07.RNASeqV2 TCGA-A1-A0SE-01A-11R-A084-07.RNASeqV2 TCGA-A1-A0SH-01A-11R-A084-07.RNASeqV2 TCGA-A1-A0SJ-01A-11R-A084-07.RNASeqV2 TCGA-A1-A0SK-01A-12R-A084-07.RNASeqV2 TCGA-A1-A0SM-01A-11R-A084-07.RNASeqV2 TCGA-A1-A0SO-01A-22R-A084-07.RNASeqV2 TCGA-A1-A0SP-01A-11R-A084-07.RNASeqV2 TCGA-A2-A04N-01A-11R-A115-07.RNASeqV2 TCGA-A2-A04P-01A-31R-A034-07.RNASeqV2

2017 10 18 09:50:45.335 DEBUG MachineName colnames(sampBatch)

2017 10 18 09:50:45.335 DEBUG MachineName sample batch

2017 10 18 09:50:45.336 DEBUG MachineName inside train, after getData4EB

2017 10 18 09:50:45.336 DEBUG MachineName call EB MBatch

2017 10 18 09:50:45.336 DEBUG MachineName TDC HERE trainEB mbatch

2017 10 18 09:50:45.337 DEBUG MachineName EBNplus args Obj

2017 10 18 09:50:45.337 DEBUG MachineName EBNplus args par.prior

2017 10 18 09:50:45.337 DEBUG MachineName EBNplus args minSampleNum

2017 10 18 09:50:45.338 DEBUG MachineName EBNplus theEBNP_PriorPlotsFile= /bea_testing/output/ebnplus/EBNPlus_Correction_Structures/priorplots.PNG

2017 10 18 09:50:45.338 DEBUG MachineName dat

[1] 16146 1172

2017 10 18 09:50:45.339 DEBUG MachineName saminfo

[1] 1172 2

2017 10 18 09:50:45.339 DEBUG MachineName check column and row names

2017 10 18 09:50:45.676 DEBUG MachineName in design.mat_plus

2017 10 18 09:50:45.677 DEBUG MachineName in build.design_plus

2017 10 18 09:50:45.679 DEBUG MachineName after build.design_plus loop

2017 10 18 09:50:45.679 DEBUG MachineName design

2017 10 18 09:50:45.680 DEBUG MachineName list.batch_plus(saminfo)

2017 10 18 09:50:45.680 DEBUG MachineName in list.batch_plus

2017 10 18 09:50:45.681 DEBUG MachineName list.batch_plus tmp1

2017 10 18 09:50:45.682 DEBUG MachineName list.batch_plus uniTmp[i]

2017 10 18 09:50:45.682 DEBUG MachineName list.batch_plus uniTmp[i]

2017 10 18 09:50:45.682 DEBUG MachineName list.batch_plus batches

2017 10 18 09:50:45.683 DEBUG MachineName after list.batch_plus(saminfo)

2017 10 18 09:50:45.683 DEBUG MachineName n.batches

2017 10 18 09:50:45.683 DEBUG MachineName n.array

2017 10 18 09:50:52.613 DEBUG MachineName missbatch matrix

2017 10 18 09:50:53.643 DEBUG MachineName There are 68 genes that were removed because of whole batch missing, no variation or all zero in original data

2017 10 18 09:50:56.283 DEBUG MachineName B.hat

2017 10 18 09:50:56.284 DEBUG MachineName grand.mean

2017 10 18 09:50:57.977 DEBUG MachineName var.pooled

2017 10 18 09:50:58.030 DEBUG MachineName stand.mean 1

2017 10 18 09:50:58.638 DEBUG MachineName stand.mean 2

2017 10 18 09:50:58.845 DEBUG MachineName s.data

2017 10 18 09:51:01.367 DEBUG MachineName gamma.hat

2017 10 18 09:51:03.262 DEBUG MachineName plot priors

2017 10 18 09:51:03.263 DEBUG MachineName plotPrior priorPlotsFile= /bea_testing/output/ebnplus/EBNPlus_Correction_Structures/priorplots.PNG

2017 10 18 09:51:04.132 DEBUG MachineName parametric adjustments

2017 10 18 09:51:06.707 DEBUG MachineName parametric adjustments

2017 10 18 09:51:08.118 DEBUG MachineName in getBayesData

2017 10 18 09:51:08.119 DEBUG MachineName dim(s.data)=16078 1172

2017 10 18 09:51:08.119 DEBUG MachineName dim(stand.mean)=16078 1172

2017 10 18 09:51:09.527 DEBUG MachineName dim(bayesdata)=16078 1172

2017 10 18 09:51:09.673 DEBUG MachineName Second dim(bayesdata)=16078 1172

2017 10 18 09:51:09.673 DEBUG MachineName keep the dim of Original.dat, keep the gene with all NA

2017 10 18 09:51:09.760 DEBUG MachineName resultsDat

2017 10 18 09:51:09.761 DEBUG MachineName after EB MBatch

2017 10 18 09:51:09.761 DEBUG MachineName after train

2017 10 18 09:51:09.762 DEBUG MachineName EBadj

2017 10 18 09:51:09.762 DEBUG MachineName EBadj whole 1

2017 10 18 09:51:09.762 DEBUG MachineName whole

2017 10 18 09:51:09.959 DEBUG MachineName dim(mat1)=20501 1215

2017 10 18 09:51:09.959 DEBUG MachineName dim(mat1)=

2017 10 18 09:51:09.960 DEBUG MachineName dim(mat2)=17814 600

2017 10 18 09:51:09.960 DEBUG MachineName dim(mat2)=

2017 10 18 09:51:11.859 DEBUG MachineName dim(dat)=16146 1815

2017 10 18 09:51:11.860 DEBUG MachineName dim(dat)=

2017 10 18 09:51:13.628 DEBUG MachineName after parlist

2017 10 18 09:51:13.629 DEBUG MachineName dim(dat)=16146 1815

2017 10 18 09:51:13.629 DEBUG MachineName valid.genes

2017 10 18 09:51:13.631 DEBUG MachineName nonValidGenes

2017 10 18 09:51:15.259 DEBUG MachineName Non-valid genes were removed before adjustment

2017 10 18 09:51:15.260 DEBUG MachineName after Non-valid

2017 10 18 09:51:15.260 DEBUG MachineName dim(dat)=16078 1815

2017 10 18 09:51:16.021 DEBUG MachineName after getStandData

2017 10 18 09:51:16.021 DEBUG MachineName dim(stand.data)=16078 1815

2017 10 18 09:51:16.022 DEBUG MachineName batches

2017 10 18 09:51:16.022 DEBUG MachineName after batch.design

2017 10 18 09:51:16.023 DEBUG MachineName dim(batch.design)=1815 2

2017 10 18 09:51:16.023 DEBUG MachineName n.batches

2017 10 18 09:51:16.045 DEBUG MachineName in getBayesData

2017 10 18 09:51:16.046 DEBUG MachineName dim(s.data)=16078 1815

2017 10 18 09:51:16.046 DEBUG MachineName dim(stand.mean)=16078 1815

2017 10 18 09:51:18.605 DEBUG MachineName dim(bayesdata)=16078 1815

2017 10 18 09:51:18.877 DEBUG MachineName Second dim(bayesdata)=16078 1815

2017 10 18 09:51:18.878 DEBUG MachineName after bayesData

2017 10 18 09:51:18.878 DEBUG MachineName dim(bayesData)=16078 1815

2017 10 18 09:51:18.879 DEBUG MachineName EBadj datNonValid

2017 10 18 09:51:20.702 DEBUG MachineName EBadj EBadj after non valid

2017 10 18 09:51:20.702 DEBUG MachineName objafterEB@wholeEB

2017 10 18 09:51:22.374 DEBUG MachineName finishing BeaEBNPlus

> writeAsMatrix(file.path(theOutputDir, "CorrectedData.tsv"), correctedMatrix)

2017 10 18 09:51:22.393 DEBUG MachineName writeAsMatrix - thePar -Xmx2000m

2017 10 18 09:51:22.393 DEBUG MachineName writeAsMatrix - theFile /bea_testing/output/ebnplus/EBNPlus_Correction_Structures/CorrectedData.tsv

2017 10 18 09:51:23.196 DEBUG MachineName writeAsMatrix - length(myData) 29304990

2017 10 18 09:51:23.197 DEBUG MachineName writeAsMatrix - length(myCols) 1815

2017 10 18 09:51:23.197 DEBUG MachineName writeAsMatrix - length(myRows) 16146

2017 10 18 09:51:23.198 DEBUG MachineName writeAsMatrix - Calling .jinit /home/linux/R/x86_64-pc-linux-gnu-library/3.4/MBatch/ReadRJava/ReadRJava.jar

2017 10 18 09:51:24.758 DEBUG MachineName writeAsMatrix - .jinit complete

2017 10 18 09:51:24.759 DEBUG MachineName writeAsMatrix before java

ReadRJava::writeDoubleData_All 2014-04-20-1523

writeFile - start

writeFile - done

ReadRJava::writeDoubleData_All done

2017 10 18 09:51:36.729 DEBUG MachineName writeAsMatrix after java

2017 10 18 09:51:36.730 DEBUG MachineName writeAsMatrix success= TRUE

[1] TRUE