MBatch 05-02
Using MBatch Assessments: EBNPlus_Correction_Structures
Tod Casasent
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1 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.

2 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.

3 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.
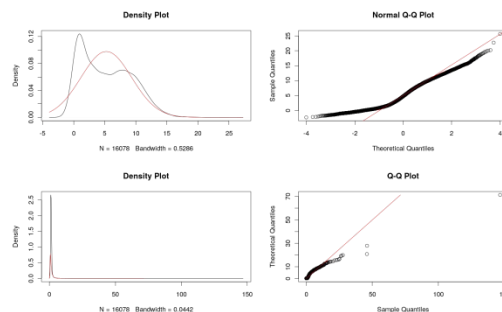
4 Usage

```
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)
```

5 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.

6 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, 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"))
writeAsMatrix(file.path(theOutputDir, "CorrectedData.tsv"), correctedMatrix )
```

6.1 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.

6.2 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)
```

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```
+ {
+     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