

## 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

RBN\_Replicates is a function used to perform the RBN correction algorithm on two datasets, using replicates. 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.

## 4 Usage

```
RBN_Replicates(theInvariantMatrix, theVariantMatrix, theInvariantGroupId = "",  
               theVariantGroupId = "", theMatchedReplicatesFlag = TRUE,  
               theCombineOnlyFlag = FALSE, thePath = NULL, theWriteToFile = FALSE)
```

## 5 Arguments

**theInvariantMatrix** Matrix with sample names in colnames and features (like genes) in rownames. This matrix is invariant.

**theVariantMatrix** Matrix with sample names in colnames and features (like genes) in rownames. This matrix is variant.

**theInvariantGroupId** Group name used for labelling invariant features when combining matrixes. This defaults to "", but the user should generally provide a value.

**theVariantGroupId** Group name used for labelling variant features when combining matrixes. This defaults to "", but the user should generally provide a value.

**theMatchedReplicatesFlag** If TRUE, indicates that NAs should be added for missing replicates. Defaults to TRUE.

**theCombineOnlyFlag** If TRUE, only combined the matrixes, do not correct. Defaults to FALSE.

**thePath** Location for output. Defaults to NULL. If NULL, no output file is created.

**theWriteToFile** TRUE means write corrected data to thePath. Only works if thePath is given. Defaults to FALSE.

## 6 Example Call

The following code is taken from the tests/RBN\_Replicates.R file. Data used is from the testing data as per the MBatch\_01\_InstallLinux.docx document.

```
library(MBatch)

# set the paths
invariantFile="/bea_testing/MATRIX_DATA/rbn-test6-iset.tsv"
variantFile="/bea_testing/MATRIX_DATA/rbn-test6-vset.tsv"
theOutputDir="/bea_testing/output/RBN_Replicates"
theRandomSeed=314

resolveDuplicates <- function(theNames)
{
  # keep first instance of a name
  # number subsequent ones starting with .1
  make.unique(theNames)
}

readRPPAdataAsMatrix_WithTab <- function(theFile)
{
  # read RPPA data as a dataframe
```

```

# column rppaDF[,1] contains row names that may contain duplicates
rppaDF <- readAsGenericDataframe(theFile)
# resolve duplicates in row names here
myRownames <- rppaDF[,1]
myRownames <- resolveDuplicates(myRownames)
# convert to matrix
myMatrix <- data.matrix(rppaDF[,-1])
rownames(myMatrix) <- myRownames
t(myMatrix)
}

readRPPAdataAsMatrix_NoInitialTab <- function(theFile)
{
  # read RPPA data as a dataframe
  # column rppaDF[,1] contains row names that may contain duplicates
  rppaDF <- read.table(theFile, header=TRUE, sep="\t", as.is=TRUE,
    check.names=FALSE, stringsAsFactors=FALSE,
    colClasses="character", na.strings="NA",
    row.names=NULL)
  # resolve duplicates in row names here
  myRownames <- rppaDF[,1]
  myRownames <- resolveDuplicates(myRownames)
  # convert to matrix
  myMatrix <- data.matrix(rppaDF[,-1])
  rownames(myMatrix) <- myRownames
  t(myMatrix)
}

# make sure the output dir exists and is empty
unlink(theOutputDir, recursive=TRUE)
dir.create(theOutputDir, showWarnings=FALSE, recursive=TRUE)

message("Reading invariant file")
invMatrix = readRPPAdataAsMatrix_WithTab(invariantFile)
message("Reading variant file")
varMatrix = readRPPAdataAsMatrix_WithTab(variantFile)
filename <- RBN_Replicates(theInvariantMatrix=invMatrix,
  theVariantMatrix=varMatrix,
  theInvariantGroupId="Grp1",
  theVariantGroupId="Grp2",
  theMatchedReplicatesFlag=TRUE,
  theCombineOnlyFlag=FALSE,
  thePath=theOutputDir,
  theWriteToFile=TRUE)

```

## 6.1 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
> invariantFile="/bea_testing/MATRIX_DATA/rbn-test6-iset.tsv"
> variantFile="/bea_testing/MATRIX_DATA/rbn-test6-vset.tsv"
> theOutputDir="/bea_testing/output/RBN_Replicates"
> theRandomSeed=314
>
> resolveDuplicates <- function(theNames)
+ {
+   # keep first instance of a name

```

```

+ # number subsequent ones starting with .1
+ make.unique(theNames)
+ }
>
> readRPPAdataAsMatrix_WithTab <- function(theFile)
+ {
+ # read RPPA data as a dataframe
+ # column rppaDF[,1] contains row names that may contain duplicates
+ rppaDF <- readAsGenericDataframe(theFile)
+ # resolve duplicates in row names here
+ myRownames <- rppaDF[,1]
+ myRownames <- resolveDuplicates(myRownames)
+ # convert to matrix
+ myMatrix <- data.matrix(rppaDF[,-1])
+ rownames(myMatrix) <- myRownames
+ t(myMatrix)
+ }
>
> readRPPAdataAsMatrix_NoInitialTab <- function(theFile)
+ {
+ # read RPPA data as a dataframe
+ # column rppaDF[,1] contains row names that may contain duplicates
+ rppaDF <- read.table(theFile, header=TRUE, sep="\t", as.is=TRUE,
+ check.names=FALSE, stringsAsFactors=FALSE,
+ colClasses="character", na.strings="NA",
+ row.names=NULL)
+ # resolve duplicates in row names here
+ myRownames <- rppaDF[,1]
+ myRownames <- resolveDuplicates(myRownames)
+ # convert to matrix
+ myMatrix <- data.matrix(rppaDF[,-1])
+ rownames(myMatrix) <- myRownames
+ t(myMatrix)
+ }
>
> # make sure the output dir exists and is empty
> unlink(theOutputDir, recursive=TRUE)
> dir.create(theOutputDir, showWarnings=FALSE, recursive=TRUE)
>
> message("Reading invariant file")
Reading invariant file
> invMatrix = readRPPAdataAsMatrix_WithTab(invariantFile)
> message("Reading variant file")
Reading variant file
> varMatrix = readRPPAdataAsMatrix_WithTab(variantFile)
> filename <- RBN_Replicates(theInvariantMatrix=invMatrix,
+ theVariantMatrix=varMatrix,
+ theInvariantGroupId="Grp1",
+ theVariantGroupId="Grp2",
+ theMatchedReplicatesFlag=TRUE,
+ theCombineOnlyFlag=FALSE,

```

```
+         thePath=theOutputDir,  
+         theWriteToFile=TRUE)  
2017 10 18 12:30:38.107 DEBUG MachineName please note: internally, RBN processes transposed the  
data, output (file and matrix) match the submitted data with samples across columns and features down  
the rows  
2017 10 18 12:30:38.108 INFO MachineName RBN_internal - starting  
2017 10 18 12:30:38.108 DEBUG MachineName checkCreateDir: /bea_testing/output/RBN_Replicates  
2017 10 18 12:30:38.112 INFO MachineName Found 213 common features in both matrices.  
2017 10 18 12:30:38.505 DEBUG MachineName Write to file  
/bea_testing/output/RBN_Replicates/ANY_Corrections-RBN_Replicates.tsv  
2017 10 18 12:30:38.982 DEBUG MachineName Finished write to file  
/bea_testing/output/RBN_Replicates/ANY_Corrections-RBN_Replicates.tsv  
2017 10 18 12:30:38.982 INFO MachineName RBN_internal - completed  
>
```

## 6.2 Example File Output

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

ANY\_Corrections-RBN\_Replicates.tsv

The TSV file with the combined/corrected dataset is written by the MBatch package.