

## 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\_Pseudoreplicates is a function used to perform the RBN correction algorithm on two datasets, using pseudoreplicates. 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_Pseudoreplicates(theInvariantMatrix, theVariantMatrix,  
  theInvariantReplicates, theVariantReplicates, 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.

**theInvariantReplicates** Vector of feature ids indicating replicates for variant data.

**theVariantReplicates** Vector of feature ids indicating replicates for invariant data.

**theInvariantGroupId** Group name used for labelling invariant features when combining matrixes.

**theVariantGroupId** Group name used for labelling variant features when combining matrixes.

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

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

**thePath** Location for output.

**theWriteToFile** TRUE means write corrected data to thePath.

## 6 Example Call

The following code is taken from the tests/RBN\_Pseudoreplicates.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-pseudo-iset.tsv"
variantFile="/bea_testing/MATRIX_DATA/rbn-pseudo-vset.tsv"
theOutputDir="/bea_testing/output/RBN_Pseudoreplicates"
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)
}

# 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)
invPseudo <- c("BN", "BO", "BP", "BQ", "BR", "BS")
varPseudo <- c("AN", "AO", "AP", "AQ", "AR", "AS")
filename <- RBN_Pseudoreplicates(theInvariantMatrix=invMatrix,
                                theVariantMatrix=varMatrix,
                                theInvariantReplicates = invPseudo,
                                theVariantReplicates = varPseudo,
                                theInvariantGroupId="Grp1",
                                theVariantGroupId="Grp2",
                                theMatchedReplicatesFlag=FALSE,
                                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-pseudo-iset.tsv"
> variantFile="/bea_testing/MATRIX_DATA/rbn-pseudo-vset.tsv"
> theOutputDir="/bea_testing/output/RBN_Pseudoreplicates"
> 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)
+ }
>
> # 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)
> invPseudo <- c("BN", "BO", "BP", "BQ", "BR", "BS")
> varPseudo <- c("AN", "AO", "AP", "AQ", "AR", "AS")
> filename <- RBN_Pseudoreplicates(theInvariantMatrix=invMatrix,
+                                   theVariantMatrix=varMatrix,
+                                   theInvariantReplicates = invPseudo,
```

```

+         theVariantReplicates = varPseudo,
+         theInvariantGroupId="Grp1",
+         theVariantGroupId="Grp2",
+         theMatchedReplicatesFlag=FALSE,
+         theCombineOnlyFlag=FALSE,
+         thePath=theOutputDir,
+         theWriteToFile=TRUE)
2017 10 18 12:51:16.693 DEBUG megazone23 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 12:51:16.694 INFO megazone23 RBN_internal - starting
2017 10 18 12:51:16.694 DEBUG megazone23 checkCreateDir:
/bea_testing/output/RBN_Pseudoreplicates
2017 10 18 12:51:16.742 WARN megazone23 Less than 30 replicates provided for Invariant Matrix.
RBN's performance may deteriorate.
2017 10 18 12:51:16.743 WARN megazone23 Less than 30 replicates provided for Variant Matrix.
RBN's performance may deteriorate.
2017 10 18 12:51:16.743 INFO megazone23 Found 213 common features in both matrices.
2017 10 18 12:51:16.763 DEBUG megazone23 Write to file
/bea_testing/output/RBN_Pseudoreplicates/ANY_Corrections-RBN_Pseudoreps.tsv
2017 10 18 12:51:16.772 DEBUG megazone23 Finished write to file
/bea_testing/output/RBN_Pseudoreplicates/ANY_Corrections-RBN_Pseudoreps.tsv
2017 10 18 12:51:16.773 INFO megazone23 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\_Pseudoreps.tsv

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