

BESack 02B Using Batch Effects Interface Corrections: AN  
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2018-04-30-1045

## Using Batch Effects Interface Corrections: AN

This document focuses on explaining the components of the Batch Effects Interface (BEI) involved with creating a job, loading data, and running assessments. This document will not address statistical issues or "how to spot" batch effects.

The URL for your install should be provided to you, but will likely be something like:

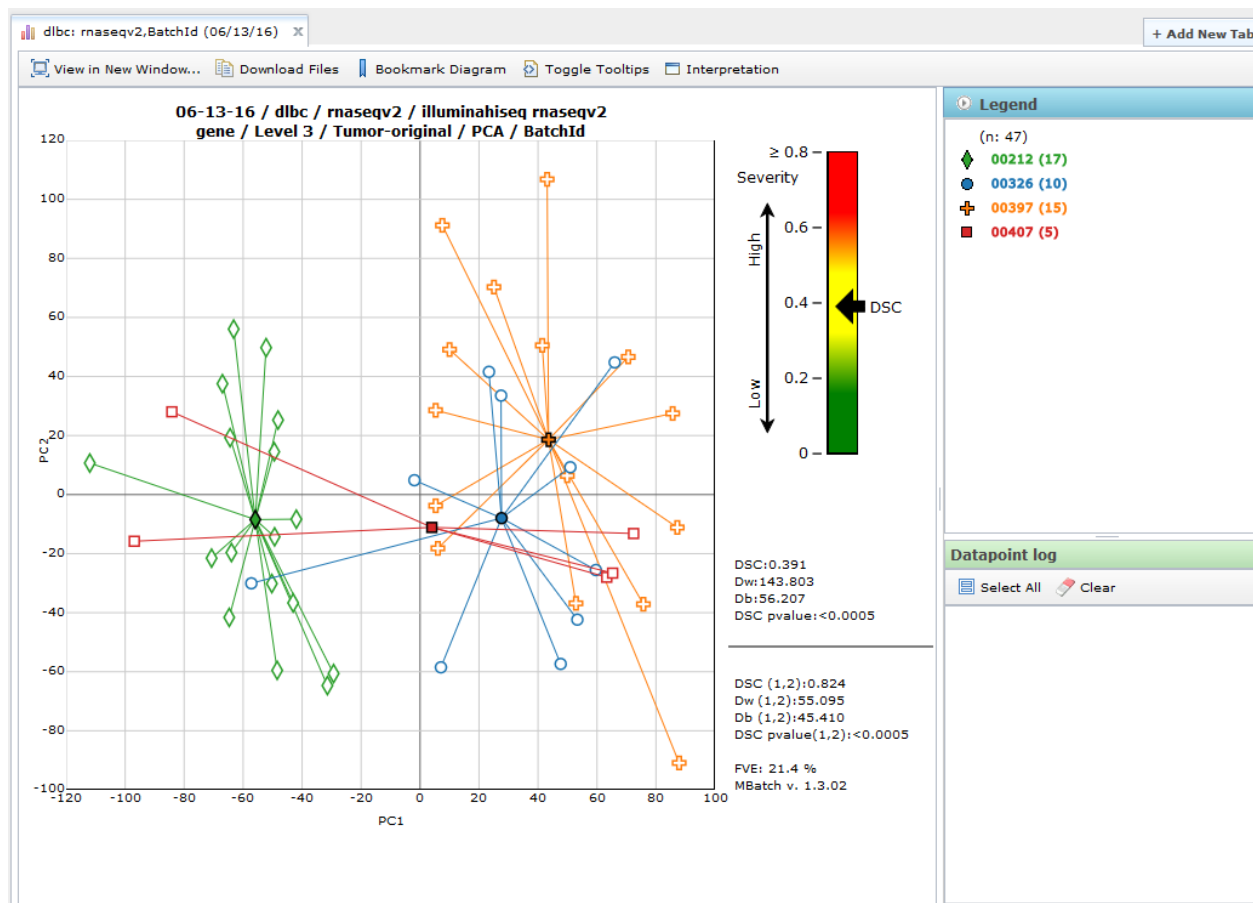
`http://your-server.your-company.com:9999/BatchEffectsInterface/`

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 at <https://github.com/MD-Anderson-Bioinformatics/MBatch/tree/master/pdf> for instructions on downloading test data.

RBN corrections uses replicates between the two datasets to combine the two data sets based on replicates between sets.

For demonstrating ANOVA (AN) corrections, we will use the DLBC RNASeq2 dataset found at: <http://bioinformatics.mdanderson.org/TCGA/databrowser>. You can see the Batch Effects Assessment here: [http://bioinformatics.mdanderson.org/BatchEffects/index.jsp?path=%2F2016\\_06\\_13\\_0834-2016\\_08\\_16\\_1052%2Fdlbc%2Frnaseqv2%2Filluminahiseq\\_rnaseqv2\\_gene%2FLevel\\_3%2FTumor-original%2FFPCA%2FShipDate%252FManyToMany&xaxis=PC1&yaxis=PC2](http://bioinformatics.mdanderson.org/BatchEffects/index.jsp?path=%2F2016_06_13_0834-2016_08_16_1052%2Fdlbc%2Frnaseqv2%2Filluminahiseq_rnaseqv2_gene%2FLevel_3%2FTumor-original%2FFPCA%2FShipDate%252FManyToMany&xaxis=PC1&yaxis=PC2)

For this exercise, we have no idea if this is a real batch effect or biology, we are just using this as an example of removing a batch effects. You can see batch 00212 way to the left in green.



## Starting a Job

See [BESTack\\_02A\\_BEIUsingAssessments](#) for more details about starting a job.

Use the "Start New Job" button and select "User Uploaded Data" for Step 1.a. Use the data matrix and batch file from the Standardized Data Browser website given above.

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Batch Effects Interface External2018-04-25-1433

[Home](#) **Job Id:**1524771804717 **Job State:**NEWJOB\_PRIMARY\_DONE **Job Message:**Primary Data Available. Waiting for Secondary Data. [Edit Details](#)

☒ **Step 1.a.: Specify Primary Dataset Complete**

**Step 1.b.: Specify Secondary Dataset**  
Some correction algorithms use two datasets. Use the Proceed button if you do not need a second dataset.

User Uploaded Data

[Proceed without Secondary Dataset](#)

**Use Data Uploaded**

Matrix File Upload: 

[Browse...](#) No file selected.

[Upload Secondary Matrix](#)

Then for Step 1.b. select Proceed without Secondary Dataset.

## Configuring Assessments

See BEStack\_02A\_BEIUsingAssessmentsExternal for more details about Configuring Assessments.

Below, we have selected Sample as the Sample Identifier, and selected BatchId as well as ShipDate as the assessment batch types. For Step 3, we have kept the defaults.

Note that the batch type you wish to correct must be one of the batch types checked.

[Home](#)

Job Id:1524771804717 Job State:MBATCHCONFIG\_START Job Message:MBatch Configuration in Process

[Edit Details](#)**Step 2: Select Batches**Select Sample Identifier (Select Sample Id Batch Type): 

Selected Types for Batch Analysis: BatchId,ShipDate

[Reset Defaults](#)**Batch Type to Check Batch Type Name Batch Summary (Batch Name and Count)**

<input checked="" type="checkbox"/>	BatchId	00212:17 00248:1 00326:10 00397:15 00407:5
<input type="checkbox"/>	PlateId	2213:17 2404:1 A31O:10 A38C:15 A39D:5
<input checked="" type="checkbox"/>	ShipDate	2012-03-14:17 2012-09-10:1 2013-07-24:10 2014-03-26:15 2014-04-30:5
<input type="checkbox"/>	TSS	FA - Asterand:9 FF - SingHealth:11 FM - International Genomics Consortium:1 G8 - Roswell Park:7 GR - University of Nebraska Medical Center (UNMC):6 GS - Fundacio Clinic per a la Recerca Biomedica:10 RQ - St Josephs Hospital AZ:3 VB - Global BioClinical - Georgia:1
<input type="checkbox"/>	Type	01:48

**Step 3: Select Filtering Options**

Auto-Filter to Maximum Number of Values:

Max Number of Values: 

Exclude User Specified Batches:

Batch Type for Exclusion: [Reset Defaults](#)

## Step 4 ANOVA-Adjusted

In Step 4, we begin by selecting ANOVA-Adjusted as the optional Correction Type. Since we want the problem within the Batch Id type corrected, we select that.

**Step 4: Select a Correction (optional)**Correction Type: 

Correlation Density Plot (CDP) for Original versus Corrected Data:

☒ Select to generate CDPBatch Type to Correct: Minimum Valid Batch Size for Corrections: [Reset Defaults](#)

We accept the defaults for the rest of the data.

## Step 4 ANOVA Unadjusted

In Step 4, if we want “Unadjusted” instead, we select ANOVA-Unadjusted as the optional Correction Type. Since we want the problem within the Batch Id type corrected, we select that.

**Step 4: Select a Correction (optional)**

Correction Type: ANOVA-Unadjusted

Correlation Density Plot (CDP) for Original versus Corrected Data:  
☒ Select to generate CDP

Batch Type to Correct: BatchId

Minimum Valid Batch Size for Corrections: 1

Reset Defaults

We accept the defaults for the rest of the data.

## Do MBatch Run

See BEstack\_02A\_BEIUsingAssessments for more details about running and monitoring a run. We press Do MBatch Run from the configuration page.

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Home Job Id:1524771804717 Job State:MBATCHRUN\_START\_WAIT Job Message:MBatch Run Queued Edit Details

The MBatch run is queued and waiting for assignment to a processing node.

The DSC Permutations step will take some time, which can take 30+ minutes.

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Home Job Id:1524669586504 Job State:MBATCHRUN\_RUNNING\_WAIT Job Message:MBatch Run in Progress Edit Details

The MBatch run is underway on a processing node.

Log File Tail (last 100 lines):  

```

2018 04 25 15:44:37.058 DEBUG 1549a9e9f75d pvalueDSCwithExcerpt start
2018 04 25 15:44:37.059 DEBUG 1549a9e9f75d nrow(thePcaDataExcerpt)= 1815
2018 04 25 15:44:37.060 DEBUG 1549a9e9f75d ncol(thePcaDataExcerpt)= 1815
2018 04 25 15:44:37.061 DEBUG 1549a9e9f75d length(theBatchIdsForSamples)= 1815
2018 04 25 15:44:37.064 DEBUG 1549a9e9f75d getDSCwithExcerpt before java
2018 04 25 15:44:38.491 DEBUG 1549a9e9f75d getDSCwithExcerpt after java
2018 04 25 15:44:38.494 DEBUG 1549a9e9f75d pvalueDSCwithExcerpt after getDSCwithExcerpt
2018 04 25 15:44:38.496 DEBUG 1549a9e9f75d pvalueDSCwithExcerpt length(unique(theBatchIdsForSamples))= 38
2018 04 25 15:44:38.499 DEBUG 1549a9e9f75d pvalueDSCwithExcerpt call doDscPerms
2018 04 25 15:44:38.502 DEBUG 1549a9e9f75d doDscPerms before java

```

## Finished Job

After the job has finished, use the Download option to get the corrected data.

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Home Job Id:1524775346620 Job State:MBATCHRUN\_END\_SUCCESS Job Message:MBatch Run Finished Successfully Edit Details

✓ **MBatch succeeded.**  
 Download MBatch Results view on the visualization website.

Log File Tail (last 100 lines):

```

2018 04 26 20:55:42.304 INFO da7671a17f31 CDP_Plot theData1UnmatchedReplicates= 0
2018 04 26 20:55:42.305 INFO da7671a17f31 CDP_Plot theData2UnmatchedReplicates= 0
2018 04 26 20:55:42.388 INFO da7671a17f31 CDP_Plot pairedCorr= 48
2018 04 26 20:55:42.389 INFO da7671a17f31 CDP_Plot unmatchedCorr= 0
2018 04 26 20:55:42.395 INFO da7671a17f31 CDP_Plot pairedDensity3x= 512
2018 04 26 20:55:42.396 INFO da7671a17f31 CDP_Plot pairedDensity3y= 512
2018 04 26 20:55:42.396 INFO da7671a17f31 CDP_Plot pairedDensity3bw= 0.000268770563211184
2018 04 26 20:55:42.397 INFO da7671a17f31 CDP_Plot unmatchedDensity3x= 0
2018 04 26 20:55:42.398 INFO da7671a17f31 CDP_Plot unmatchedDensity3y= 0
2018 04 26 20:55:42.398 INFO da7671a17f31 CDP_Plot unmatchedDensity3bw=
  
```

Click the Download MBatch Results button. Open or unzip the archive and enter the MBatch directory.

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Home Job Id:1524775346620 Job State:MBATCHRUN\_END\_SUCCESS Job Message:MBatch Run Finished Successfully Edit Details

✓ **MBatch succeeded.**  
 Download MBatch Results view on the visualization website.

Log File Tail (last 100 lines):

```

2018 04 26 20:55:42.304 INFO da7671a17f31 CDP_Plot theData1UnmatchedReplicates= 0
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2018 04 26 20:55:42.388 INFO da7671a17f31 CDP_Plot pairedCorr= 48
2018 04 26 20:55:42.389 INFO da7671a17f31 CDP_Plot unmatchedCorr= 0
2018 04 26 20:55:42.395 INFO da7671a17f31 CDP_Plot pairedDensity3x= 512
2018 04 26 20:55:42.396 INFO da7671a17f31 CDP_Plot pairedDensity3y= 512
2018 04 26 20:55:42.396 INFO da7671a17f31 CDP_Plot pairedDensity3bw= 0.000268770563211184
2018 04 26 20:55:42.397 INFO da7671a17f31 CDP_Plot unmatchedDensity3x= 0
2018 04 26 20:55:42.398 INFO da7671a17f31 CDP_Plot unmatchedDensity3y= 0
2018 04 26 20:55:42.398 INFO da7671a17f31 CDP_Plot unmatchedDensity3bw=
  
```

Opening 1524775346620\_Results.zip

You have chosen to open:  
 1524775346620\_Results.zip  
 which is: Zip archive  
 from: http://localhost:9999

What should Firefox do with this file?

☐ Open with Xarchiver (default)

☒ Save File

☐ Do this automatically for files like this from now on.

Cancel OK

When we examine the PCA plot, we see the correction has been performed. (We will not comment on whether or not this has removed biological effects.)



The BatchData.tsv contains the batch files. Looking at an excerpt from that file below, you see the batch data used.

Sample	BatchId	ShipDate
TCGA-FA-8693-01A-11R-2404-07	00248	2012-09-10
TCGA-FA-A4BB-01A-11R-A31O-07	00326	2013-07-24
TCGA-FA-A4XK-01A-11R-A31O-07	00326	2013-07-24
TCGA-FA-A6HN-01A-11R-A31O-07	00326	2013-07-24
TCGA-FA-A6HO-01A-11R-A31O-07	00326	2013-07-24
TCGA-FA-A7DS-01A-11R-A38C-07	00397	2014-03-26
TCGA-FA-A7Q1-01A-11R-A38C-07	00397	2014-03-26
TCGA-FA-A82F-01A-11R-A38C-07	00397	2014-03-26