**Using R to Access Bioanalyzer Results Quickly**

*This method was developed by Brian, as a way to pull out only the information that we are really interested in without having to type out each individual piece of sample data from the Bioanalyzer using only the .pdf files as a reference. This method uses .csv files that the Bioanalyzer software produces with the combination of the R program. If you need any other variations with the coding or want to know more, contact him.*

**How to Use the Code for Your Data:**

1. Open the Bioanalyzer 2100 expert software with the .XAD file of interest open (whether a saved file or after a run) and set the regions of interest in the smear analysis options. Select Save As, and make a new folder subdirectory in the location you are working in, or want to save to.

**Example Location:**

[*File:\\S:\Genomics\Next\_Gen\_Sequencing\Solexa\_Illumina\HiSEQ\Shilatifard\DHU\MOLNG-737\R\_PippinSel\_Test*](File:\\S:\Genomics\Next_Gen_Sequencing\Solexa_Illumina\HiSEQ\Shilatifard\DHU\MOLNG-737\R_PippinSel_Test)

1. Return to Bioanalyzer software, and go to the File menu, and select Export from the drop down list. Select only the bubbles for “Results Tables” and “Sample Data”. Also set the directory as a custom, and use the file pathway created above as your location. Select Export, and then select Save a few times to the dialog boxes that pop up afterwards.
2. Next, open the text file containing the coding of interest “HS\_DNA\_R\_code\_my\_regions.txt” from the file pathway below, or from the email attachment if you have not saved your own copy.

**Text File Location on S: drive for NGS Group:**

[*File:\\S:\Genomics\Next\_Gen\_Sequencing\Solexa\_Illumina\Molbio\_NGS\NGS\_Experiments\Bioanalyzer\_R\_Coding*](File:\\S:\Genomics\Next_Gen_Sequencing\Solexa_Illumina\Molbio_NGS\NGS_Experiments\Bioanalyzer_R_Coding)

1. Select Save As, and save to the working directory that you are working from, “example location” made in the first Step from above. In the open text file you should see the below information at the start of the file. In the yellow highlighted region you should copy and paste your “example location” working directory and replace any “\” with two “\\” as shown below. Select save to save changes made to text file.

##START##

#The working directory is where your exported results file from the bioanalyzer is.

#Note the double backslashes, you need double backslashes or a single forward slash

#Your working directory must be within double quotes

#example: dir <- "S:\\Genomics\\Molbio\_Users\\BEF\\Bioanalyzer"

#change it and copy and paste into R (Ensure Results file is exported into directory

dir <- "S:\\Genomics\\Next\_Gen\_Sequencing\\Solexa\_Illumina\\HiSEQ\\Shilatifard\\DHU\\MOLNG-737\\R\_PippinSel\_Test"

1. Next open R program, the link below should work for the current version of the download for Windows.

<http://cran.r-project.org/bin/windows/base/>

1. Next go back to your open text file created in Step 4, and select all, followed by copy, then paste this information into the open R program workspace, the code should automatically run, hit enter if necessary.
2. Return to the working folder directory, created in Step 1 and you should see some new files generated by the R program such as “ba lane, region 1, region 2, region 3, and my region”. Select and open the file “my region” from the list and select all of the information in the text file and select copy.
3. Open an Excel workbook and paste this text into a fresh sheet. The relevant information from the regions of interest should now be shown in the columns of the Excel workbook, arranged by region for each sample. This coding works for 3 or less regions in the smear analysis.