General From Build Report

- Please evaluate code in the vignette (see comments on vignette) DONE
- Please add unit tests. While you may not be able to test the main functionality, you can add tests for internal and helper functions for expected output. DONE. UNIT TESTS CAN BE FOUND IN TESTS FOLDER
- Please add Add non-empty \value sections to the following man pages: man/ChangePointEstimator.Rd, man/CUSUMChart.Rd, man/CUSUMRadarPlot.Rd, man/CUSUMRiverPlot.Rd, man/DataProcess.Rd, man/DecisionMap.Rd, man/RunShiny.Rd, man/XmRChart.Rd, man/XmRRadarPlot.Rd, man/XmRRiverPlot.Rd
  There should be some indication of what output is expected. DONE. \VALUE SECTIONS ARE UPDATED FOR EACH FUNCTION.
- Add an example of a runnable code for RunShiny.Rd. RUNSHINY FUNCTION IS REMOVED.

General

- You currently do not utilize any Bioconductor objects. We really like to foster interconnectivity with other packages and functions. Please consider also making your application work with the MSnbase (MSnSet) object as well as the data.frame that is currently implemented. A NEW FUNCTION CALLED "MSnbaseToMSstatsQC.R" IS INCLUDED TO CONVERT MSnbase OBJECTS TO MSstatsQC FORMAT.
- Add Bioconductor installation instructions to the README and the vignette. DONE

```
source("https://bioconductor.org/biocLite.R")
biocLite("MSstatsQC")
```

DESCRIPTION

- You might want to consider these additional BiocViews: Proteomics, MassSpectrometry, ReproducibleResearch. ADDITIONAL BiocViews ARE ADDED.

Vignette

- Recommend just calling it MSstatsQC so the call would be vignette("MSstatsQC") rather than vignette("MSstatsQC_v.1.0.0_vignette") as that isn't very intuitive to the user. REPLACED
- Delete MSstatsQC_v1.0.0_vignette.html (note the v1 vs v.1) DELETED
- Some of the code chunks should be run or if for good reason not to eval=TRUE than interactively the calls should work. DONE. ALL THE FUNCTIONS ARE RUNNING EXCEPT FOR MSnbaseToMSstatsQC.R BECAUSE THE RESULT OF THIS FUNCTION IS A DATA TABLE. ADDITIONALLY OPTIONS FOR SAVING RESULTS IS NOT EVALUATED BUT FUNCTIONAL. Ex.

```
S9Site54 <- read.csv('Sampledata_CPTAC_Study_9_1_Site54.csv', header=TRUE)
```

Is not correct based on what you provide. You did not provide the .csv file in your data/ you provided a .Rdata object that is loaded with

```
S9Site54 <-load("S9Site54.RData")
```

Also you should get the path to the file with `system.file()`

- Your argument description should be updated. You are not providing a .csv file as the data argument, you are providing a data.frame that was created with the .csv file. ==S9SITE54 DATASET IN THE PACKAGE IS USED AND OTHER DEFINITIONS ARE REMOVED.==
- It is very confusing that the code you show is not runnable and that you generic your functions. If all your function arguments are the same with minor differences in code than their should be one function available APlotFunction with an argument of which one you want to run. ==APLOTFUNCTION IS REMOVED.==
- I currently cannot run your application because I can't figure out what I should run to actually use it. Most people will look to the vigentte to figure out how to use your application. The examples should work. Perhaps if you want to keep this generalized vignette, you add a second vignette with a concrete example. ==NOW VIGNETTE PROVIDES EXAMPLES.==
- I get that this is a generic function that can't be run and isn't found ==GENERIC FUNCTIONS ARE REMOVED.==

```
> APlotFunction( S9Site54, peptide, L = 1, U = 5, metric, normalization =
FALSE,ytitle = "A Plot", type = "mean", selectMean = NULL,selectSD = NULL )
Error in APlotFunction(S9Site54, peptide, L = 1, U = 5, metric, normalization
=
FALSE,  : could not find function "APlotFunction"
```

but some that are not generically listed currently are also not found; I think because of the s on the end XmRPlots vs XmRPlot. Please correct appropriately ==CORRECTED==

```
> XmRPlots(S9Site54, "LVNELTEFAK", metric = "RetentionTime", type="mean",
selectMean = 34.5, selectSD = 1)
Error in XmRPlots(S9Site54, "LVNELTEFAK", metric = "RetentionTime", type =
"mean",  : could not find function "XmRPlots"
> CUSUMRiverPlots(S9Site54, L=1, U=20)
Error in CUSUMRiverPlots(S9Site54, L = 1, U = 20) :
  could not find function "CUSUMRiverPlots"
> XmRRiverPlots(S9Site54, L=1, U=20)
Error in XmRRiverPlots(S9Site54, L = 1, U = 20) :
  could not find function "XmRRiverPlots"
```

MAN files

- Have an example in the `RunShiny.Rd`, It should work with your example data. You can incorporate the code in a `dontrun{}` section so that the command is shown but doesn't break in the building/checking of the package. I still can't figure out how to actually run your shiny app. ==RUNSHINY FUNCTION IS REMOVED BUT TIPS FOR SHINY USER IN THE VIGNETTE ARE KEPT FOR PROSPECTIVE USERS.==
- Also it appears you are missing suggest packages in your DESCRIPTION file
```
> RunShiny("S9Site54")
Error in library(shinyBS) : there is no package called 'shinyBS'
>BiocInstaller::BiocLite('shinyBS')
> RunShiny("S9Site54")
Error in library(shinythemes) : there is no package called 'shinythemes'
>BiocInstaller::BiocLite('shinythemes')
> RunShiny("S9Site54")
Error in file(filename, "r", encoding = encoding) :
  cannot open the connection
In addition: Warning message:
In file(filename, "r", encoding = encoding) :
  cannot open file 'QCMetrics.R': No such file or directory
```

```
If shinyBS and shinythemes are required for this portion of the code to run;
they need to be included in appropriate depends/imports/suggest of the
DESCRIPTION.
```

R Code
General:
- You have a lot of repeated code with minor differences based on CUSUM or XmR. It seems like have one general function with an argument to CUSUM or XmR and assign or do difference based on that ex. XmRRiverPlot and CUSUMRiverPlot have essentially the same arguments, and repeat most of the same code. Combined into one function. ==WE PREFER KEEPING THEM SEPARATE AS CUSUM HAS TWO ARGUMENTS THAT ARE NOT AVAILABLE FOR XMR FUNCTION.==
- Why the hard coded values? There are some lingering hard coded values and they may be appropriate but I wanted clarification on reasoning that these are not variable. Examples:
- ==CUSUM.outrange.thld <- 5 and h <- 5== HARD CODED VALUES ARE REMOVED AND ARGUMENTS ARE USED INSTEAD OF THESE VALUES. THE ONLY EXCEPTION IS DECISIONMAP FUNCTION. WE COULDN'T FIND A WAY TO REPLACE THRESHOLD YET. PLEASE LET US KNOW IF YOU HAVE ANY COMMENTS.

DataProcess.R:
- remove commented out code ==REMOVED==

DataValidation.R:
- Avoid use of 1:n and 1:length(n); use seq_len(n) or seq_along(x) instead. this is also true for 1:ncol(). ==REPLACED==

DecisionMap.R
- Have a check for method that it is of correct type (CUSUM or XmR) ==DONE==

getMetricData.R:
- Avoid use of 1:n and 1:length(n); use seq_len(n) or seq_along(x) instead. this is also true for 1:ncol(). ==REPLACED==
- Remove commented out code ==REMOVED==

QCMetric.R:
- remove commented out code ==REMOVED==
- Avoid use of 1:n and 1:length(n); use seq_len(n) or seq_along(x) instead. this is also true for 1:ncol(). ==REPLACED==

Please update based on the above comments. Updating the version number in the DESCRIPTION will kick off new builds. The z of the version number should be incremented only of version x.y.z. When finished with updates, please address all the above comments with how they have been corrected or justification/clarification where appropriate here. Thank you for your submission to Bioconductor.