1. **Introduction :** This is the R Package for a web-based tool CGHweb (http://compbio.med.harvard.edu/CGHweb) that applies a number of popular algorithms to a single array CGH profile entered by the user. It generates a heatmap panel of the segmented profiles for each method as well as a consensus profile. The clickable heatmap can be moved along the chromosome and zoomed in or out. It also displays the time that each algorithm took to run and provides numerical values of the segmented profiles.
2. **Installation**: R CMD INSTALL CGHweb_1_0.tar.gz. Windows user should run this on the command prompt. Note that CGHweb requires the following R packages:
    i. waveslim
    ii. quantreg
    iii. snapCGH
    iv. cghFLasso
    v. FASeg
    vi. GLAD
    vii. GDD
    viii. gplots
3. **Loading** : *library (CGHweb)*
4. **Data** : The data should be read as a data frame. The data frame should possess four columns: ProbeID, Chromsome, Position and LogRatio. Please note that the column names are case sensitive. To save disk space, a small portion of a dataset has been included with CGHweb as an example dataset in workspace BacArray.
5. **Example**:
    a. We load the example dataset,
    data(BacArray)
    b. Run the analysis,
    x<- runCGHAnalysis(tab,tempDir=getwd(),resultDir="CGHresults")
    c. tab is the data frame containing the array.
    eg : tab<-read.delim(file="C:/CGH/sample.tab", header=TRUE, sep="\t").
    sample.tab is available at
    http://compbio.med.harvard.edu/CGHweb/HelpFiles/SampleFile_aCGH.txt
    d. tempDir is the directory where resultDir directory will be created.
    resultDir will hold all the temporary files and the file containing results, named "results.html".
6. **Points to consider:**
    a. Chromsome 23 and 24 should be addressed X and Y (in caps)
    b. Detailed help of runCGHAnalysis function can be seen as ?runCGHAnalysis or help("runCGHAnalysis")