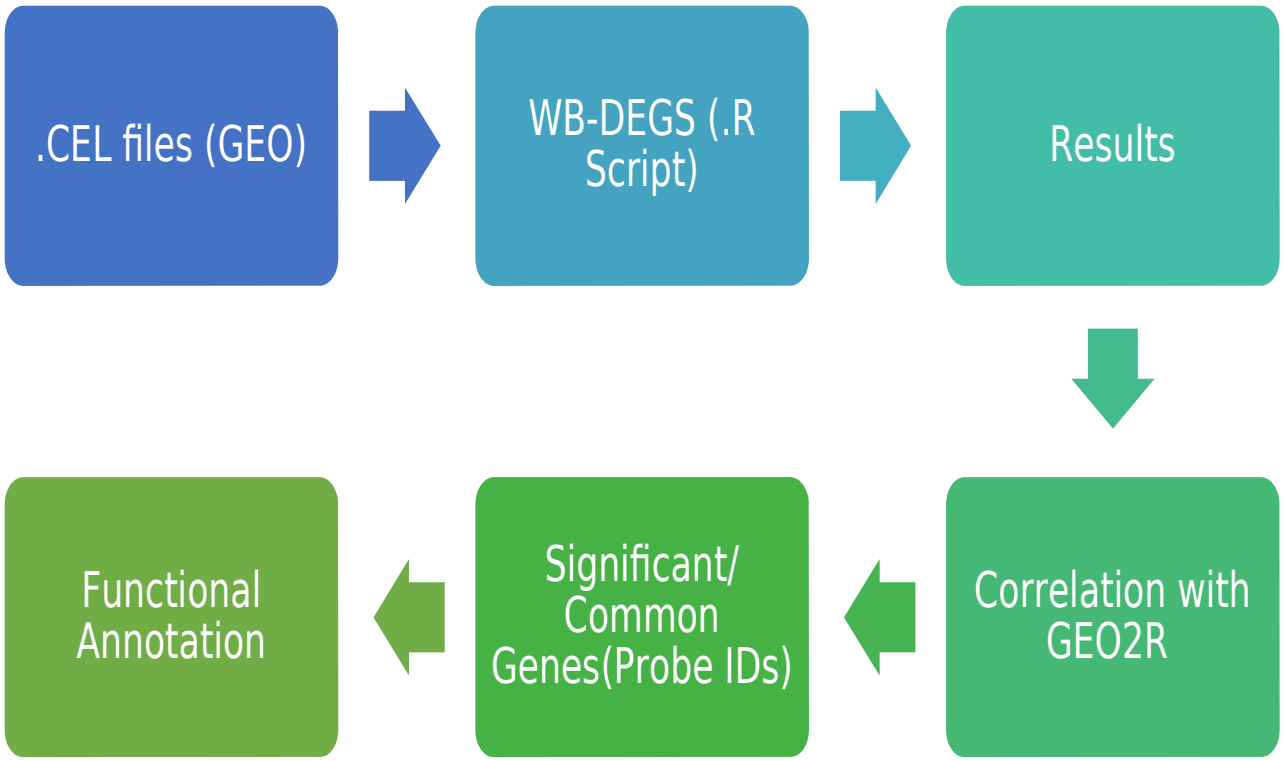

Figure 1. Methodology

We have taken "**Prostate cancer - comparison of androgen-dependent and -independent micro dissected primary tumor**" GSE2443 (20 samples) and processed .CEL files with WB-DEGS.

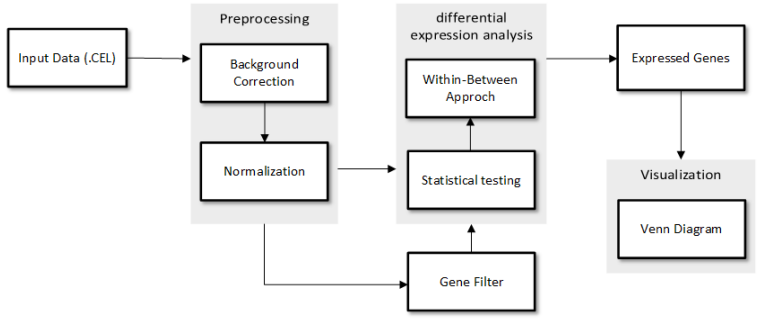

Figure 2. WB-DEGS workflow.

After installation of latest version of R, we installed the necessary packages from CRAN and Bioconductor:

from Cran:

```
install.packages("shiny")
install.packages("VennDiagram")
```

from Bioconductor:

```
source("http://bioconductor.org/biocLite.R")
biocLite("affy")
biocLite("affyPLM")
biocLite("limma")
biocLite("siggenes")
biocLite("twilight")
biocLite("genefilter")
```

Every Shiny app has the same structure: two R scripts saved together in a directory. At a minimum, a Shiny app has `ui.R` and `server.R` files.

We can run WB-DEGS opening `ui.R` or `server.R` or by following code:

```
library(shiny)
runApp("WB_Degs")
```

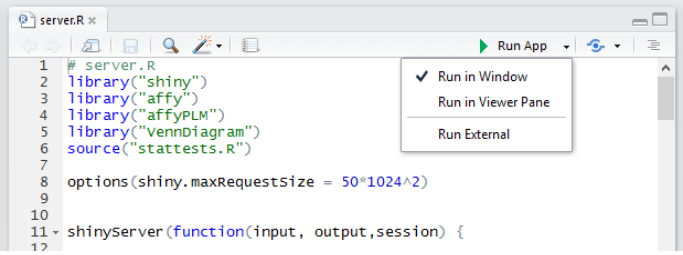

Figure 3. Running WB-DEGS

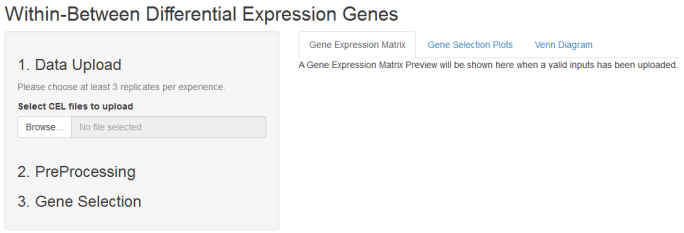

Figure 4. WB-DEGS UI window

We uploaded the selected .CEL files of GSE2443 in Data Upload Option (Figure 5), then, we used RMA as background correction method with Quantiles as normalization method (Figure 6 &7). After the preprocessing of data is done, we divided the samples into two groups: (1) Group 1: test group, (2) Group 2 : control group based on the curated sample data from the cited paper from GEO [Best CJ et. Al.] (Figure 8). In the final step, we applied statistical analysis for estimation of local and global false discovery rate (FDR) and mapping the overexpressed and under expressed genes (Figure 9):

1. Simple Statistical Test (t-test)
2. Linear Models
3. Twilight
4. Significance Analysis of Microarray (SAM)

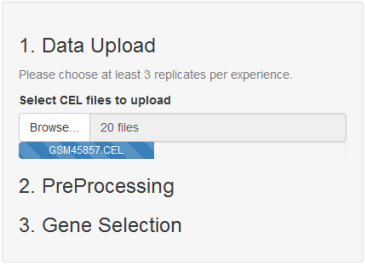

Figure 5. Uploading the. CEL files

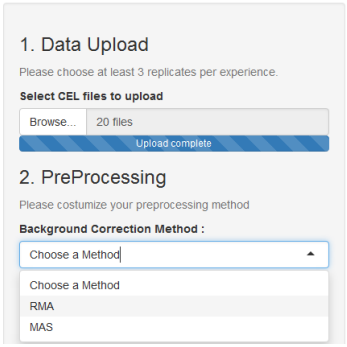

Figure 6. Background Correction Method

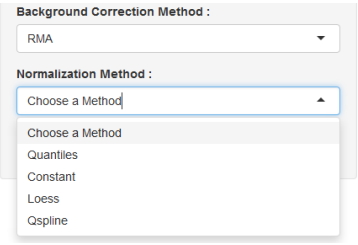

Figure 7. Normalization Methods

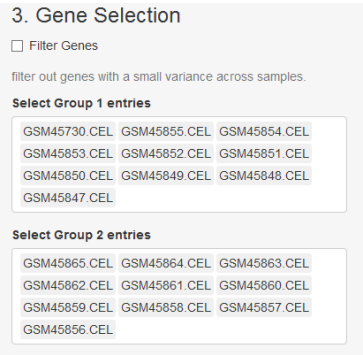

Figure 8. Group 1: control group, Group 2: test group. Gene Selection

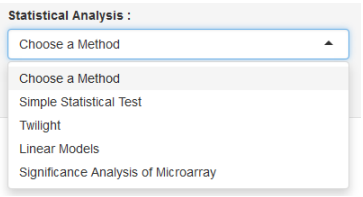

Figure 9. Statistical Analysis (t-test, twilight, linear, SAM).