Basics of ReportingTools

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1 Introduction

Frequently, when performing an analysis, it is helpful to be able to share these results in several formats at once: as HTML tables, csv files or even as R data packages. ReportingTools attempts to make this as painless as possible. At its heart, ReportingTools is based on a number of pieces of interlocking machinery that transform popular Bioconductor objects into reports.

In this vignette we will highlight the fundamentals of ReportingTools. ReportingTools has several methods for displaying microarray and RNA-seq results and can also be incorporated into shiny applications and knitr reports; for more details, please refer to the corresponding vignettes (knitr.Rmd and shiny.Rnw, respectively) or the ReportingTools site.

For more information on ReportingTools, please see Huntley, Larson, et al. (2013).

2 Basics of Reporting

The easiest type of report to generate is a csv file. This is done using the CSVFile class and the publish method. To start we’ll create a data.frame that we’ll use throughout the vignette.

```r
> my.df <- data.frame(EGID = c("103", "104", "105", "106", "107"),
+ RPKM = c(4, 5, 3, 100, 75),
+ DE = c("Yes", "Yes", "No", "No", "No"))
> my.df

                 EGID RPKM DE
   1         103     4 Yes
   2         104     5 Yes
   3         105     3 No
   4         106    100 No
   5         107     75 No
```

Next, we’ll create the CSVFile object to which we’ll publish our results. We output the results to a new directory called reports. Note that ReportingTools will create this directory for you if it does not exist already.

```r
> library(ReportingTools)
> csvFile <- CSVFile(shortName = "my_csv_file",
+ reportDirectory = "./reports")
> publish(my.df, csvFile)
```

Obviously, this isn’t much less work than just calling write.csv on the data.frame itself, but this is really just a toy example. We can also publish the data.frame as an HTML report.

```r
> htmlRep <- HTMLReport(shortName = "my_html_file",
+ reportDirectory = "./reports")
> publish(my.df, htmlRep)
> finish(htmlRep)
```

It’s necessary to call finish on the HTMLReport, to allow the contents to be written to the file.

It’s also possible to publish the same object in two separate formats at once.

```r
> csvFile2 <- CSVFile(shortName = "my_csv_file2",
+ reportDirectory = "./reports")
```
my_html_file

![Figure 1: Resulting page created by `publish` for `my_df`.](image)

```r
> htmlRep2 <- HTMLReport(shortName = 'my_html_file2',
+   title="Publishing a data frame and csv file together",
+   reportDirectory = "./reports")
> publish(my.df, list(csvFile2, htmlRep2))
> finish(htmlRep2)
```

The same few lines of code could be used to publish, for example, the results of a limma differential expression analysis, or the results of a Gene Ontology analysis, all without worrying about coercing the objects to a tabular format ourselves. For more information, see the microarray and RNA-seq vignettes.

### 3 Adding plots or text to a report

To add links, additional text or plots to a report, simply open the report with HTMLReport, write to it via the publish function and then call publish on the original data frame and finish the report. Below we make a simple plot and then add it and some descriptive text to our report.

```r
> plot(my.df$EGID, my.df$RPKM, xlab="EGID",
+     ylab="RPKM", main="Scatter plot of RPKMs", col="blue")
> scatterPlot <- recordPlot()
> library(lattice)
> barPlot <- barchart(my.df$RPKM ~ my.df$EGID)  # lattice plots behave slightly differently
> htmlRep3 <- HTMLReport(shortName = "my_html_file3", title="Adding a plot directly to the page",
+     reportDirectory = "./reports")
> publish(scatterPlot, htmlRep3, name = "scatterPlot")
> publish("This is a bar plot", htmlRep3)
> publish(barPlot, htmlRep3, name = "barPlot")
> publish(my.df, htmlRep3, name="Table")
> finish(htmlRep3)
```

We can also publish existing images and text directly to sites with hwriter.

```r
> png(filename="reports/barplot.png")
> barplot(my.df$RPKM, names.arg=my.df$EGID, xlab="EGID",
+     ylab="RPKM", main="Bar plot of RPKMs", col="blue")
> dev.off()
```
Figure 2: Resulting page created after adding additional figures and text with publish.
> library(hwriter)
> htmlRep4 <- HTMLReport(shortName = "my_html_file4", title="Adding a link, text and image",
+ reportDirectory = "./reports")
> publish(hwrite("This is a link to Bioconductor", link = "http://www.bioconductor.org"), htmlRep4)
> publish(hwrite("Bar chart of results", heading=2), htmlRep4)
> himg <- hwriteImage("barplot.png", link="barplot.png")
> publish(hwrite(himg, br=TRUE), htmlRep4)
> publish(hwrite("Results Table", heading=2), htmlRep4)
> publish(my.df, htmlRep4)
> finish(htmlRep4)

4 Adding plots or links to a report table

To add additional plots or links to a report table, we can create a new data frame with the path to the plots and our links of interest. We then publish this data frame.

Below we make a set of simple plots and then add the images along with new links to the NCBI gene database to our data frame.

> imagename <- c()
> for (i in 1:nrow(my.df)){
+    imagename[i] <- paste0("plot", i, ".png")
+    plot(my.df$RPKM[i], ylab="RPKM", xlab = my.df$EGID[i], main = "RPKM Plot" , col = "blue")
+    dev.off()
>    }
> my.df$Image <- hwriteImage(imagename, link = imagename, table = FALSE, width=100, height=100)
> my.df$Link <- hwrite(as.character(my.df$EGID), link = paste("http://www.ncbi.nlm.nih.gov/gene/",
+ as.character(my.df$EGID), sep = ''), table=FALSE)
> htmlRep5 <- HTMLReport(shortName = "my_html_file5",
+ title = "Adding images and links to data frame directly",
+ reportDirectory = "./reports")
> publish(my.df, htmlRep5)
> finish(htmlRep5)

We can also update our data frame by editing, adding and removing columns with functions. We then include these functions in our publish call as a list with .modifyDF and .toHTML .modifyDF uses the basic data frame as its default object and then modifies it with the corresponding function.

> ##this function adds 5 to each value of my.df$RPKMs
> add5 <- function(object,...){
+    object$plus5 <- object$RPKM+5
+    return(object)
+  }
> ##this function replaces the scatter plot images with new plots
> makeNewImages<-function(object,...){
+    imagename <- c()
+    for (i in 1:nrow(object)){
+        imagename[i] <- paste0("plotNew", i, ".png")
+        plot(object$RPKM[i], ylab ="RPKM", xlab = object$EGID[i],
+        main = "New RPKM Plot",col = "red", pch = 15, cex=3)
Manipulating the data frame directly

Figure 3: Resulting page created after adding figures and links to table with `.modifyDF`.

```r
+ dev.off()
+ }
+ object$Image <- hwriteImage(imagename, link = imagename, table = FALSE, height=150, width=150)
+ return(object)
+ }
> ##This function removes the link column
> removeLink <- function(object, ...){
+ object <- subset(object, select = -Link)
+ return(object)
+ }
> ##This function links the EGID column to the entrez database
> addEGIDLink <- function(object, ...){
+ object$EGID <- hwrite(as.character(object$EGID),
+ as.character(object$EGID)), table = FALSE)
+ return(object)
+ }
> htmlRep6 <- HTMLReport(shortName = "my_html_file6",
+ title = "Manipulating the data frame directly",
+ reportDirectory = "./reports")
> publish(my.df, htmlRep6,
+ .modifyDF = list(add5, makeNewImages, removeLink, addEGIDLink))
> finish(htmlRep6)

5 Multiple Tables to the same page

It is also possible to publish multiple tables to the same html page. We can change the order of the tables via pos.

```r
> df2 <- data.frame(x = 1:5, y = 11:15)
> df3 <- data.frame(x = c("a", "b", "c"), y = 1:3)
> htmlRep7 <- HTMLReport(shortName = "my_html_file7", title = "Many tables, one page",
+ pos = list(df2, df3))
> publish(htmlRep7)
```
Publishing objects that are not data frames

```r
> my.mat <- matrix(rnorm(20), nrow=5)
> makeDF <- function(object, ...){
+   df <- as.data.frame(object[-2,])
+   names(df) <- paste0("New ", 1:4)
+   return(df)
+ }
> htmlRep8 <- HTMLReport(shortName = 'my_html_file8',
+     title="Publishing objects that are not data frames",
+     reportDirectory = ":.//reports")
> publish(my.mat, htmlRep8, .toDF = makeDF)
> finish(htmlRep8)
```

For publishing experimental results, including how to publish a limma-based linear model and a edgeR objects, please see the relevant vignettes. There are built-in ReportingTools methods to publish non-data frame objects typically encountered in microarray and RNA-seq analyses. Example output is shown below.

7 References

## Analysis of BCR/ABL translocation differential expression

<table>
<thead>
<tr>
<th>ProbeId</th>
<th>EntrezId</th>
<th>Symbol</th>
<th>GeneName</th>
<th>$\log_{10}FC$</th>
<th>$p$-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>40202_at</td>
<td>687</td>
<td>KLF9</td>
<td>Knuppen-like factor 9</td>
<td>2.420</td>
<td>1.61e-11</td>
</tr>
<tr>
<td>1635_at</td>
<td>25</td>
<td>ABL1</td>
<td>c-abl oncogene 1, non-receptor tyrosine kinase</td>
<td>1.170</td>
<td>3.48e-10</td>
</tr>
<tr>
<td>40504_at</td>
<td>5445</td>
<td>PON2</td>
<td>paraoxonase 2</td>
<td>1.220</td>
<td>9.77e-10</td>
</tr>
</tbody>
</table>

Figure 5: Resulting page created for analysis of a microarray study with `limma`. 