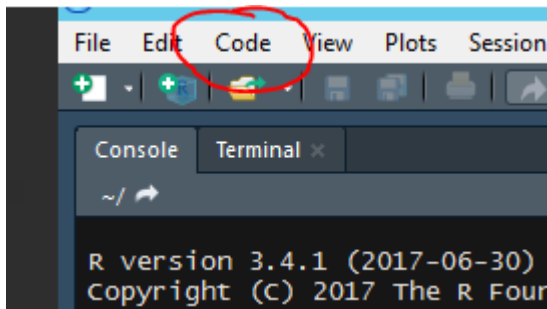
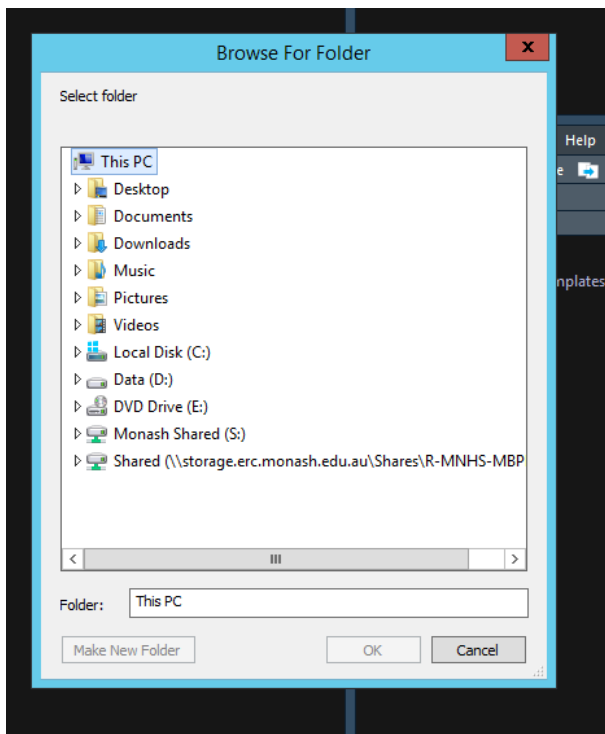


Merge different Byonic output excel files to create result summary file

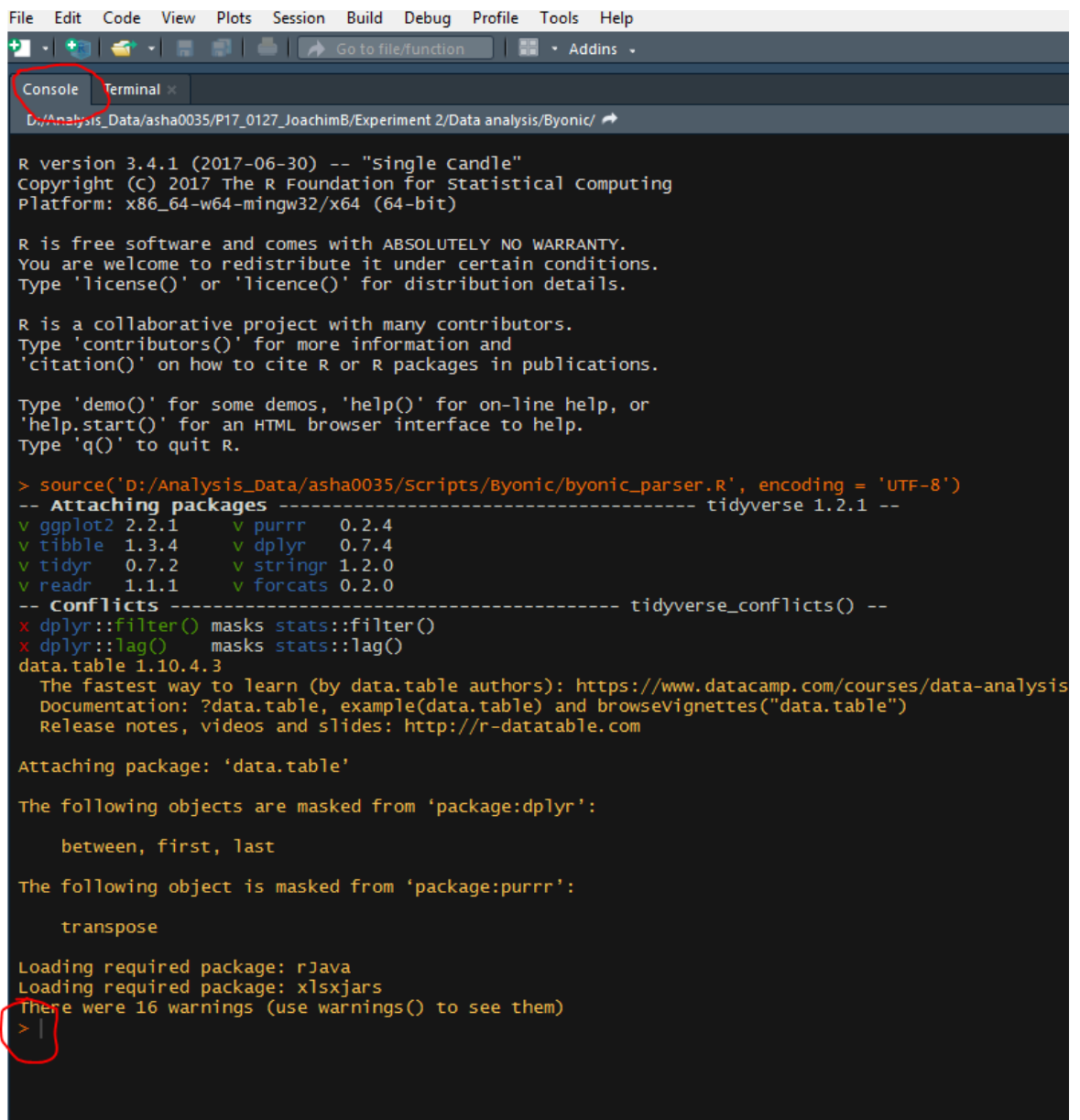
1. Open **RStudio_1.1.383**, (**VERSION IS IMPORTANT**)
2. Click on tab called **"Code"**



3. Click on **"Source File.."**
4. Open file **"byonic_parser.R"** from the folder **"D:\ Applications\Scripts\Byonic\"**
5. Prompt will appear asking for choosing the **MAIN BYONIC** directory where all byonic outputs are located. (**BE CAREFUL WITH CHOOSING THE DIRECTORY!**)
6. Click **OK**



7. Script will run
(Note: check if **>** appears after a while in **"Console"** panel to make sure script finished execution)



```
File Edit Code View Plots Session Build Debug Profile Tools Help
D:/Analysis_Data/asha0035/P17_0127_JoachimB/Experiment 2/Data analysis/Byonic/

Console Terminal x
D:/Analysis_Data/asha0035/P17_0127_JoachimB/Experiment 2/Data analysis/Byonic/

R version 3.4.1 (2017-06-30) -- "Single Candle"
Copyright (c) 2017 The R Foundation for Statistical Computing
Platform: x86_64-w64-mingw32/x64 (64-bit)

R is free software and comes with ABSOLUTELY NO WARRANTY.
You are welcome to redistribute it under certain conditions.
Type 'license()' or 'licence()' for distribution details.

R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

> source('D:/Analysis_Data/asha0035/scripts/Byonic/byonic_parser.R', encoding = 'UTF-8')
-- Attaching packages ----- tidyverse 1.2.1 --
v ggplot2 2.2.1      v purrr  0.2.4
v tibble  1.3.4      v dplyr  0.7.4
v tidyr   0.7.2      v stringr 1.2.0
v readr   1.1.1      v forcats 0.2.0
-- Conflicts ----- tidyverse_conflicts() --
x dplyr::filter() masks stats::filter()
x dplyr::lag()    masks stats::lag()
data.table 1.10.4.3
The fastest way to learn (by data.table authors): https://www.datacamp.com/courses/data-analysis
Documentation: ?data.table, example(data.table) and browseVignettes("data.table")
Release notes, videos and slides: http://r-datatable.com

Attaching package: 'data.table'

The following objects are masked from 'package:dplyr':

  between, first, last

The following object is masked from 'package:purrr':

  transpose

Loading required package: rJava
Loading required package: xlsxjars
There were 16 warnings (use warnings() to see them)
> |
```

8. **Output file** is located in the same **MAIN BYONIC** directory with the name
"Summary_byonic.xlsx"