

1 Unzip the folder in a known directory, such as your Desktop. Open the unzipped folder

→ > marbel008-R_project-0a48a17
R_project-V.04.zip

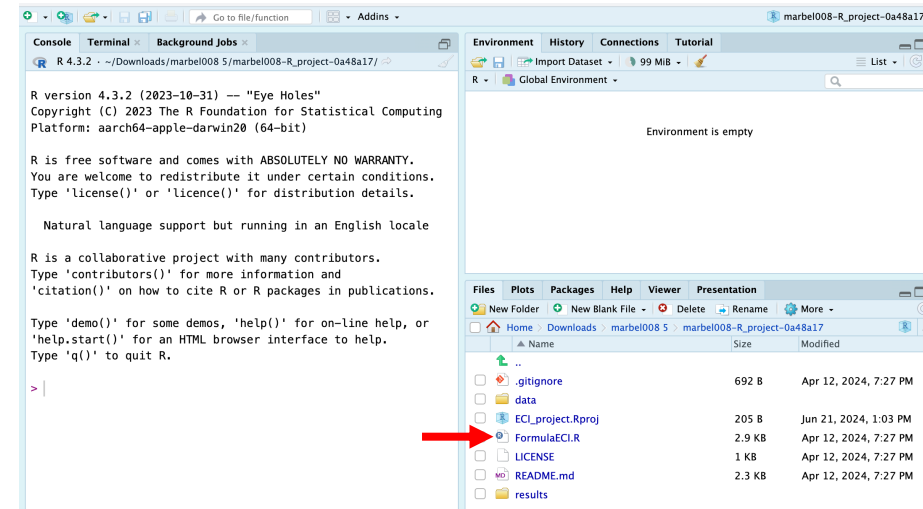
2 Add your own dataset(s) into the 'query_datasets' subfolder in the 'data' folder (arrow)

> data
→ > query_datasets
> required_datasets
ECI_project.Rproj
FormulaECI.R
LICENSE
README.md
> results
Step-by-step.pdf

3 Click on "ECI_project.Rproj" to open RStudio

> data
→ ECI_project.Rproj
FormulaECI.R
LICENSE
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> results
Step-by-step.pdf

4 Click on "FormulaECI.R" to load the script into the environment



5 Replace "GSE130954_BlastoIVT_PR.txt" for the name corresponding to your own dataset and run the full script

```
1 library(bapred)
2
3 embryo_index <- function(df) {
4
5
6
60
61 # required datasets can be found in /data/required_datasets
62 setwd("/data/required_datasets")
63 df_tr <- read.table("Data_BlastoIVT_TRAINING.txt", header = TRUE, sep = "\t", row.names = 1)
64 bio <- read.table("Biomarkers_Bo.txt", header = TRUE, sep = "\t", row.names = 1)
65
66 # example datasets can be found in /data/query_datasets
67 # include the dataset of interest in that folder (/data/query_datasets)
68 # replace "GSE130954_BlastoIVT_PR.txt" for the name corresponding to dataset of interest
69 setwd("../query_datasets")
70 data <- read.table("GSE130954_BlastoIVT_PR.txt", header = TRUE, sep = "\t", row.names = 1)
71
72 # Output ECI
73 ECI <- embryo_index(data); View(ECI)
74
75 setwd("../results")
76 write.table(ECI, "ECI_Values.txt", sep = "\t", col.names = NA)
77
78 }
```

6 Results are exported into the 'results' folder

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