

GSEApLOT - R package

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a

b

c

```
sleep_for_a_minute <- function() { Sys.sleep(60) }

start_time <- Sys.time()
sleep_for_a_minute()
end_time <- Sys.time()

end_time - start_time
```

```
## Time difference of 1.000092 mins
```

GSEA Analysis

Function and Parameters

In addition to the three data frames, the GSEA analysis requires a number of other parameters.

AnalysisandInputParamaters :

- *input.ds.name* - references differential expression data.
- *input.cls.name* - references phenotype input.
- *gene.set.input* - references geneset database.
- *doc.string* - name of the folder where individual geneset results are saved to. The folder is created if it does not exist.
- *nperm* - determines the number of permutations. Permutations are used to analyze the significance of the association between gene expression and phenotype, and determine whether the associations are more significant than random ones.
- *abs.val* - When set to true (T), genes are ranked according to the absolute value of their signal to noise ratio. This value is set to false (F) by default.