

# R Report Modules

Modules in the [biolockj.module.report.r](#) sub-package generate the statistical analysis and visualizations by executing R scripts. The statistical analysis is performed on the taxa abundance tables generated by [AddMetadataToTaxaTables](#).

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## R\_Module

cannot be included in the pipeline run order

**Description:** Abstract implementation of [ScriptModule](#) that other R modules extend to inherit standard R script functionality. Abstract modules cannot be included in the pipeline run order.

### Options:

- [exe.rScript](#)
  - [r.debug](#)
  - [r.nominalFields](#)
  - [r.numericFields](#)
  - [r.rareOtuThreshold](#)
  - [r.reportFields](#)
  - [r.saveRData](#)
  - [r.timeout](#)
  - [report.numHits](#)
  - [report.numReads](#)
  - [report.taxonomyLevel](#)
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## R\_CalculateStats

#BioModule biolockj.module.report.r.R\_CalculateStats

**Description:** Generate a summary statistics table with [adjusted and unadjusted] [parameteric and non-parametric] p-values and  $r^2$  values for each reportable metadata field and each [report.taxonomyLevel](#) configured.

### Options:

- [r\\_CalculateStats.pAdjustMethod](#)
- [r\\_CalculateStats.pAdjustScope](#)