

# OTU report modules

Modules in the [biolockj.module.report](#) sub-pakcage normalize [ParserModule](#) output, merge the OTU tables with the metadata, or process OTU tables.

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## CompileOtuCounts

```
#BioModule biolockj.module.report.otu.CompileOtuCounts
```

**Description:** Compiles the counts from all OTU count files into a single summary OTU count file containing OTU counts for the entire dataset.

**Options:** *none*

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## RarefyOtuCounts

```
#BioModule biolockj.module.report.otu.RarefyOtuCounts
```

**Description:** Applies a mean iterative post-OTU classification rarefication algorithm so that each output sample will have approximately the same number of OTUs.

**Options:**

- *rarefyOtuCounts.iterations*
  - *rarefyOtuCounts.lowAbundantCutoff*
  - *rarefyOtuCounts.quantile*
  - *rarefyOtuCounts.removeSamplesBelowQuantile*
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## RemoveLowOtuCounts

```
#BioModule biolockj.module.report.otu.RemoveLowOtuCounts
```

**Description:** Removes OTUs with counts below *report.minCount*.

**Options:**

- *report.minCount*
- *report.numHits*