Pathway Modules

Modules in the **biolockj.module.report.humann2** sub-package use ParserModule output to produce and process pathway tables, such as those produced by HumanN2.

Humann2CountModule

```
cannot be included in the pipeline run order
```

Description: Abstract class extends JavaModuleImpl that other humann2 classes extend to inherit shared functionality. Abstract modules cannot be included in the pipeline run order.

Options:

- *humann2.disablePathAbundance*
- *humann2.disablePathCoverage*
- *humann2.disableGeneFamilies*

AddMetadataToPathwayTables

```
#BioModule biolockj.module.report.humann2.AddMetadataToPathwayTables
```

Description: Add metadata columns to the OTU abundance tables.

Options: *none*

RemoveLowPathwayCounts

```
#BioModule biolockj.module.report.humann2.RemoveLowPathwayCounts
```

Description: This BioModule Pathway counts below a configured threshold to zero. These low sample counts are assumed to be miscategorized or genomic contamination.

Options:

- *report.minCount*