

biolockj.module.implicit modules are added to BioLockJ pipelines automatically if needed. Implicit modules are ignored if included in the Config file unless *project.allowImplicitModules=Y*

This package contains the following sub-packages:

1. [[module.implicit.parser]] contains [ParserModule](#) interface & [ParserModuleImpl](#) superclass.
 2. [[module.implicit.parser.r16s]] contains 16S parser modules.
 3. [[module.implicit.parser.wgs]] contains WGS parser modules.
 4. [[module.implicit.qiime]] contains QIIME Script wrappers.
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Demultiplexer

```
(added by BioLockJ) #BioModule biolockj.module.implicit.ImportMetadata
```

Description: Demultiplex samples into separate files for each sample.

Options:

- *demultiplexer.barcodeCutoff*
 - *demultiplexer.barcodeRevComp*
 - *demultiplexer.strategy*
 - *metadata.filePath*
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ImportMetadata

```
(added by BioLockJ) #BioModule biolockj.module.implicit.ImportMetadata
```

Description: Required 1st module in every pipeline.

If *metadata.filePath* is undefined, a new metadata file will be created with only a single column "SAMPLE_ID".

The imported file is converted to required BioLockJ metadata format: tab-delimited, with unique column headers, and empty cells are now populated with *metadata.nullValue* or "NA" if undefined.

Options:

- *metadata.columnDelim*
- *metadata.commentChar*