

BioLockJ requires [Java 1.8+](#) and a [Unix-like](#) operating system such as [Darwin/macOS](#).

- Dependencies are required by modules listed in the **BioModule Function** column.
- Users **DO NOT NEED TO INSTALL** dependencies if not interested in the listed modules.
- For example, if you intend to classify 16S samples with RDP and WGS samples with Kraken, do not install:  
Bowtie2, GNU Awk, GNU Gzip, MetaPhlAn2, Python, QIIME 1, or Vsearch.

#	Program	Version	BioModule Function	Link
1	Bowtie2	2.3.2	<a href="#">Metaphlan2Classifier</a> : Build reference indexes	<a href="#">download</a>
2	GNU Awk	4.0.2	<a href="#">AwkFastaConverter</a> : Convert Fastq to Fasta <a href="#">BuildQiimeMapping</a> : Format metadata as QIIME mapping <a href="#">QiimeClosedRefClassifier</a> : Build batch mapping files	<a href="#">download</a>
3	GNU Gzip	1.5	<a href="#">AwkFastaConverter</a> : Decompress .gz files <a href="#">Gunzipper</a> : Decompress .gz files	<a href="#">download</a>
4	Kraken	0.10.5-beta	<a href="#">KrakenClassifier</a> : Report WGS taxonomic summary	<a href="#">download</a>
5	MetaPhlAn2	2.0	<a href="#">Metaphlan2Classifier</a> : Report WGS taxonomic summary (WGS)	<a href="#">download</a>
6	Python	2.7.12	<a href="#">BuildQiimeMapping</a> : Run validate_mapping_file.py <a href="#">MergeQiimeOtuTables</a> : Run merge_otu_tables.py <a href="#">QiimeClosedRefClassifier</a> : Run pick_closed_reference_otus.py <a href="#">QiimeDeNovoClassifier</a> : Run pick_de_novo_otus.py <a href="#">QiimeOpenRefClassifier</a> : Run pick_open_reference_otus.py <a href="#">QiimeClassifier</a> : Run add_alpha_to_mapping_file.py, add_qiime_labels.py, alpha_diversity.py, filter_otus_from_otu_table.py, print_qiime_config.py, and summarize_taxa.py <a href="#">Metaphlan2Classifier</a> : Run metaphlan2.py	<a href="#">download</a>
7	PEAR	0.9.8	<b>Paired-End reAd merger</b> <a href="#">PearMergeReads</a> Merge paired Fastq files since some classifiers ( <a href="#">RDP</a> & <a href="#">QIIME</a> ) will not accept paired reads.	<a href="#">download</a>
8	QIIME 1	1.9.1	<b>Quantitative Insights Into Microbial Ecology</b> <a href="#">BuildQiimeMapping</a> : Validate QIIME mapping <a href="#">MergeQiimeOtuTables</a> : Merge otu_table.biom files <a href="#">QiimeClosedRefClassifier</a> : Pick OTUs by reference <a href="#">QiimeDeNovoClassifier</a> : Pick OTUs by clustering <a href="#">QiimeOpenRefClassifier</a> : Pick OTUs by reference and clustering <a href="#">QiimeClassifier</a> : Report 16S taxonomic summary	<a href="#">download</a>
9	R	3.5.0	<a href="#">R_CalculateStats</a> : Statistical modeling <a href="#">R_PlotPvalHistograms</a> : Plot p-value histograms for each reportable metadata field <a href="#">R_PlotOtu</a> : Build OTU-metadata boxplots and scatterplots <a href="#">R_PlotMds</a> : Plot by top MDS axis <a href="#">R_PlotEffectSize</a> : Build barplot of effect magnitude by	<a href="#">download</a>