

Typical QIIME Pipeline

- The following pipeline is generated from the Config file: [chinaQiimeClosedPaired.properties](#).
- Only 6 BioModules are listed in the Config file
- The pipeline executes 15 BioModules at runtime after 6 implicit and 3 dependent modules are added by the system.
- [ImportMetadata](#) is a prerequisite implicit module that is always run as the 1st module.
- [RegisterNumReads](#) counts the number of reads per sample and stores the total in the metadata file in a field named Num_Reads.
- [PearMergeReads](#) is a prerequisite module added when *input.dirs* contains paired sequence files since QIIME only accepts forward reads.
- [AwkFastaConverter](#) is a prerequisite module added when *input.dirs* contains fastq sequence files since QIIME only accepts fasta format.
- [BuildQiimeMapping](#) is an implicit module added to all QIIME pipelines to convert the metadata file into a [QIIME mapping file](#).
- Select 1 OTU picking module [[QiimeClosedRefClassifier](#) / [QiimeDeNovoClassifier](#) / [QiimeOpenRefClassifier](#)]
 - Each runs [add_qiime_labels.py](#) to create the required multiplexed input file before calling the OTU picking script.
 - Each outputs 1+ otu_table.biom files.
- [MergeQiimeOtuTables](#) is a post-requisite module after [QiimeClosedRefClassifier](#) (if selected) used to combine batched output into a single otu_table.biom file.
 - Cannot be run after other OTU picking modules.
 - Only necessary if #samples > script.batchSize.
- [QiimeClassifier](#) is an implicit post-requisite module that runs after the OTU-picking module to produce taxonomy-level OTU reports.
- [QiimeParser](#) is a post-requisite module that runs after the classifier to create OTU abundance tables from the taxonomy-level reports.
- [Normalizer](#) log-normalizes the OTU abundance tables.
- [AddMetadataToOtuTables](#) is a pre-requisite module that runs before the 1st R module.
- [CalculateStats](#) is a pre-requisite module that runs before any other R module.
- [BuildMdsPlots](#) generates PCOA analysis and plots the top MDS axis.
- [BuildPvalHistograms](#) plots p-value histograms to identify significant metadata fields.
- [BuildOtuPlots](#) generates box plots and scatterplots to identify significant OTU-metadata correlations.