

# Seq Package

Modules from the [biolockj.module.seq](#) package prepare sequence data or metadata prior to classification.

If included, seq modules must be ordered to run before modules from any of the other packages.

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## AwkFastaConverter

```
#BioModule biolockj.module.seq.AwkFastaConverter
```

**Description:** Convert fastq files into fasta format (required by [QIIME](#)).

### Options:

- *exe.awk*
  - *exe.zip*
- 

## Gunzipper

```
#BioModule biolockj.module.seq.Gunzipper
```

**Description:** Decompress gzipped files.

### Options:

- *exe.zip*
- 

## KneadData

```
#BioModule biolockj.module.seq.KneadData
```

**Description:** Runs the Biobakery [KneadData program](#) to remove contaminated DNA.

### Options:

- *kneaddata.dbs*
- *exe.kneaddata*
- *exe kneaddataParams*