Configuration files contain all system properties, program inputs, cutoff values, external dependencies, and format specifications used during pipeline execution.
BioLockJ takes a single configuration file as a runtime parameter. Although all properties can be configured in one file, we recommend chaining default files through the pipeline.defaultProps option. This can often improve the portability, maintainability, and readability of the project-specific configuration files.

Our recommended approach is as follows:

1. Use standard.properties to assign universal default values:

- Set input, mail, report, & R properties
- We recommend using the standard.properties file packaged with BioLockJ under resources/config/default/.

2. Use environment.properties to assign envionment-specific defaults

- Set cluster & script properties
- Set paths to key executables through exe properties
- Set *pipeline.defaultProps* = standard.properties
- Override standard.properties as needed

3. Create a new configuration file for each pipeline to assign project-specific properties:

- Set the BioModule execution order
- Set *pipeline.defaultProps* = environment.properties
- Override environment.properties and standard.properties as needed
- Example project configuration files can be found in templates.

A copy of each configuration file is stored in the pipeline root directory to serve as primary project documentation.

BioModule execution order

To include a BioModule in your pipeline, add a `#BioModule` line to the top your configuration file, as shown in the examples found in templates. Each line has the `#BioModule` keyword followed by the path to the jar file for that module. For example:

```
#BioModule biolockj.module.seq.PearMergeReads
#BioModule biolockj.module.classifier.wgs.Kraken2Classifier
#BioModule biolockj.module.report.r.R_PlotMds
```