
Q: If biolockj indicates that my pipeline started successfully, but the pipeline root directory is not created, how do I debug the root cause of the failure?

A: Generally, errors are output to the pipeline log file and documented in the notification email, but invalid configuration settings may cause a fatal error to occur before the pipeline directory is created. In this scenario, look in your \$HOME directory for a file name that starts with "biolockj_FATAL_ERROR_".

- Verify you are running Java 1.8+

```
java -version
```

- Look in the error message found in \$HOME/biolockj_FATAL_ERROR_* for a reference to one of your Config file parameters, the most common culprit is:
 - *pipeline.defaultProps*
 - \$BLJ_PROJ misconfigured in /script/blj_config
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Q: How should I configure *input properties* for a demultiplexed dataset?

A: Name the sequence files using the Sample IDs listed in your metadata file. Sequence file names containing a prefix or suffix (in addition the Sample ID) can be used as long as there is a unique character string that can be used to identify the boundary between the Sample ID and its prefix or suffix. These values can be set via the *input.trimPrefix* & *input.trimSuffix* properties.

1. Set *input.trimPrefix* to a character string that precedes the sample ID **for all samples**
2. Set *input.trimSuffix* to a character string that comes after the sample ID **for all samples**

If a single prefix or suffix identifier cannot be used for all samples, the file names must be updated so that a universal prefix or suffix identifier can be used.

Example

Sample IDs = mbs1, mbs2, mbs3, mbs4