### 1. Download the latest release & unpack the tarball.

```
> tar -zxf BioLockJ-1.2.0-beta
```

Put the folder to wherever you like to keep executables.

If you choose to download the source code, you will need to compile it by running `ant` from the resources folder.

### 2. Run the install script

- The **install** script updates the $USER bash profile to call **blj_config**. See **[[Commands]]** for a full description of **blj_config**

```
> ./install
>     Saved backup:  /users/msioda/.bash_profile~
>     Saved profile:  /users/msioda/.bash_profile
> BioLockJ installation complete!
```

This will add the required variables to your path when you start your next session.
To use BioLockJ in the same session, run `source ~/.bash_profile`.

### 3. Install the software [[Dependencies]] required by the modules you wish to include in your pipeline.

# Notes

## Environments

The main BioLockJ program can be used in these environments: * a local machine with a unix-like system * any machine running docker * * a cluster, running a scheduler such as torque * AWS cloud computing *

(* The launch scripts will still be run from your local machine.)

The launch process requires a unix-like environment. This includes linux, macOS, or an ubuntu environment running on Windows.

If using **docker**, you will need to run the install script to create the variables used by the launch scripts, even though the main BioLockJ program will run within the biolockj_controller