

Note: the following notes only concern installing R on Linux/Unix Systems for ArrayTrack™. The installation on Windows platforms is completely automated within the application, so the following steps are not necessary on Windows.

R/ BioConductor Installation for Linux/Unix Systems

1) The Linux/Unix administrator should first install R (but not Bioconductor, yet) on the Linux/Unix machine. Any recent version should be fine. The easiest way is to use your distribution's package manager. If no such package is available, R can be installed by visiting <http://www.r-project.org/> and follow the download/CRAN link on the left side to installation archives and instructions.

The standard R installers will install the main parts of the R distribution someplace like /usr/lib/R. It should contain subdirectories like "bin", "lib", and "library" and a few others. We'll call this directory the R home directory.

2) Now the administrator should switch to the user who will be running ArrayTrack™ if not already ("su - <username>"). This is important, because if logged in as root then Bioconductor will default to using a system-wide shared directory for its downloaded modules, which isn't writable by ordinary users, and this will cause failures later when the user does some kinds of processing that attempts to download into and/or modify this area.

3) While logged in as the user who will run ArrayTrack™, start the R interpreter. If the R installer put the "R" command on your path (which it usually would), then you can just run "R":

```
unpriv> R
```

If R is not on your path, you will need to fully qualify the R command instead with the path to the R home (step 1), e.g.:

```
unpriv> /usr/lib/R/bin/R
```

Now within R, install Bioconductor with the following sequence of Commands:

```
> source("http://www.bioconductor.org/biocLite.R");
```

The following command may ask if it's OK to install modules in the user's home directory: say yes. This command may take a while.

```
> biocLite();
```

Support for the Plier algorithm isn't installed by default by the above, so we will install it separately. It may need some compiler components to be installed - if it fails for this reason, try installing these packages and trying this command again until it succeeds. If the Plier

algorithm will not be used then this step may be skipped.

```
> biocLite(c("plier"));
```

ArrayTrack™ Setup

To complete the setup, we need only to tell Local ArrayTrack™ where to find the R/Bioconductor distribution.

1) Non-prompted ArrayTrack™

[http://edkb.fda.gov/webstart/extdb_arraytrack/3.4/]

For the non-prompted ArrayTrack™, start the application as usual, then choose "configure connections..." from the main "database" menu at the top left of the application window. In the dialog, in field "R/BioConductor Location", enter the R home location as discussed in step 1 above, e.g. "/usr/lib/R". After restarting ArrayTrack™, R/Bioconductor functionality should be available to the user.

2) Prompted ArrayTrack™

Please contact us if you need Linux/Unix Bioconductor support with the prompted login version of ArrayTrack™. You will need access to the `jnlp` launch file for this version of ArrayTrack™, which should be on one of your own web servers.

This completes the R/Bioconductor setup for Linux/Unix distributions.