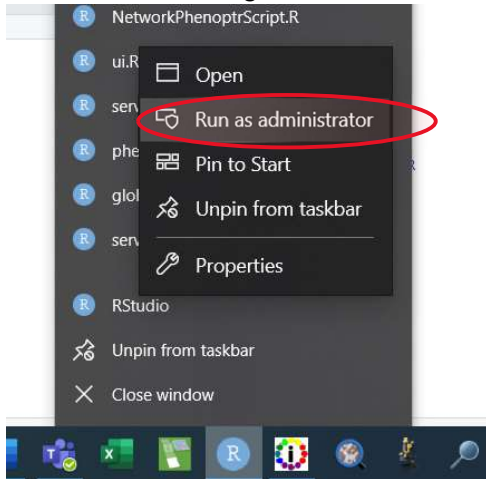


Ryan Deaton-Akoya Biosciences 4-18-2022

1. Install R 4.2.2 to the default location.
2. Install RStudio 2022.07.2-576 to the default location.
3. Install RTools42 in the default location.
4. Start RStudio using “run as administrator”



5. Test RTools install using: `Sys.which("make")` command in RStudio command window. You may need to restart the computer. It should return the following: `## "C:\\rtools42\\usr\\bin\\make.exe"`
6. Run the command `install.packages("jsonlite", type = "source")` to test that RTools is working properly.
7. Run script below. If there is a permissions error, you did not start RStudio as an administrator. If you are asked to update packages, you will want to update all packages (option 1). If asked to compile from source you will say ‘yes’.

```
#Ryan Deaton - Akoya Biosciences 2-28-2022
```

```
#Script for installing Phenoptr Reports for all users
```

```
#Install R 4.2.2
```

```
#Install most recent version of RStudio
```

```
#Install RTools 42
```

```
#R library folder will be different if newer version of R is installed
```

```
#Run RStudio as Administrator-right click on .exe and 'run as administrator'
```

```
#Make the following line the r library location for the installed version of R
myLib <- 'C:/Program Files/R/R-4.2.2/library'
```

```
install.packages("devtools", lib=myLib, force=TRUE, dependencies=TRUE)
```

```
#line below will fail, but install dependencies for archived package
```

```
devtools::install_github("akoyabio/phenoptr", lib=myLib, force=TRUE, dependencies=TRUE)
```

```
#install archived package  
install.packages("https://cran.r-project.org/src/contrib/Archive/spatstat.core/spatstat.core_2.4-4.tar.gz",  
  repos = NULL, type = "source", lib=myLib, force=TRUE, dependencies=TRUE)
```

```
#install phenoptr for real this time  
devtools::install_github("akoyabio/phenoptr", lib=myLib, force=TRUE, dependencies=TRUE)
```

```
#install remaining packages  
devtools::install_github("akoyabio/rtree", lib=myLib, force=TRUE, dependencies=TRUE)  
devtools::install_github("akoyabio/phenoptrReports", lib=myLib, force=TRUE, dependencies=TRUE)  
install.packages("tiff", lib = myLib, force=TRUE, dependencies=TRUE)  
install.packages("ggridges", lib = myLib, force=TRUE, dependencies=TRUE)
```

8. For new user accounts, the phenoptrReports Addins should show up when they launch RStudio.
9. Users will not be able to update the global r package location as it is in the 'Program Files' directory. If necessary you can give **users full control** over this folder if they need to update packages. Updating packages or package dependencies used by phenoptrReports can result in phenoptrReports not working.