phenoptrReports Instructions for Download and Installation

To use phenoptrReports, please install both phenoptr and phenoptrReports.

- [phenoptr](#) provides functions that consolidate and analyze output tables created by Akoya Bioscience's inForm® software

- [phenoptrReports](#) generates shareable reports and visualizations based on phenoptr output. A simple-to-use front end GUI is provided, removing the need to know R scripting to run phenoptr functions.

Install R

Download the most recent version from [Cloud.r-project](#).

Minimum requirement is Version 3.3.0, *but Version 3.5.0 or higher is recommended. Please do not uninstall version 3.1.0, which was installed along with your inForm activation – it is required for inForm's phenotyping functionality. If you accidentally uninstall version 3.1.0, please* [re-install](#)

Install Working Development Environment

Install one of the following:

- Windows User: Install [Rtools](#)
- Mac User: Install [Xcode](#)
- Linux User: Install a compiler and development library (details vary based on flavor of Linux). If you have any questions, please contact support@akoyabio.com.

Install RStudio

Download the desktop version of [RStudio](#)

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Install *phenoptr* R package

In the RStudio console (see Figure 1),

1. *copy and paste (or manually type in)*
   install.packages("devtools")

   Please note: *You only need to run the install.packages("devtools") command once to install the devtools package.*

2. press Enter
3. *copy and paste (or manually type in)*
   devtools::install_github("akoyabio/phenoptr")
4. press Enter
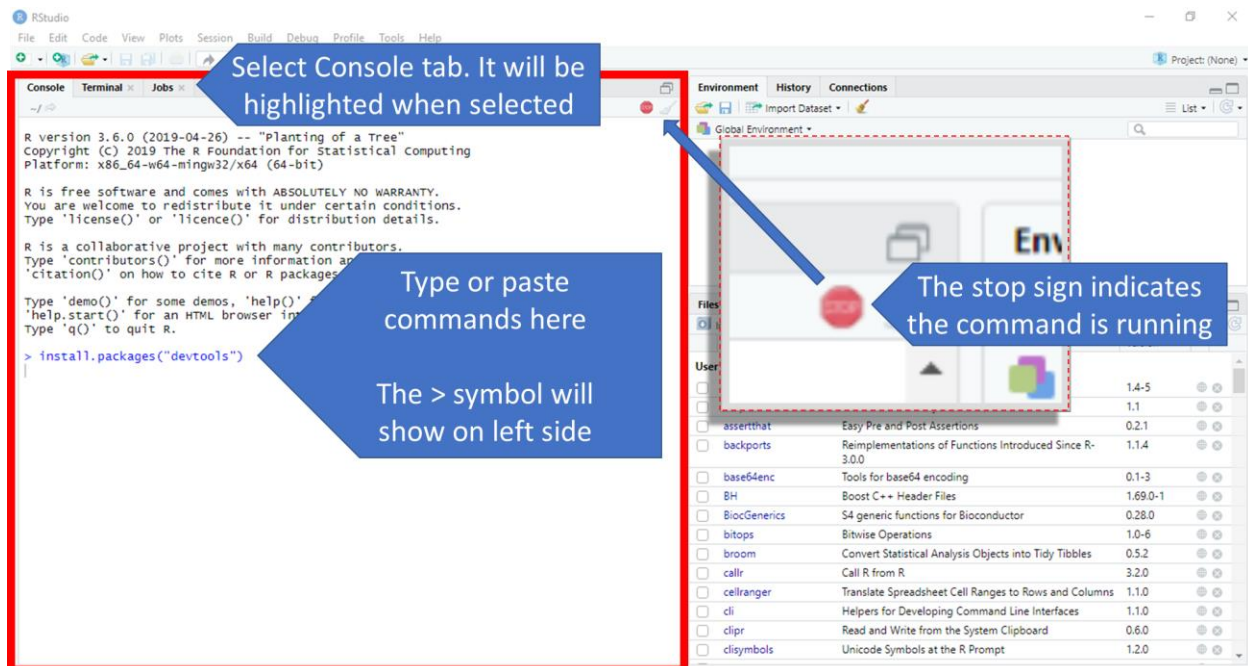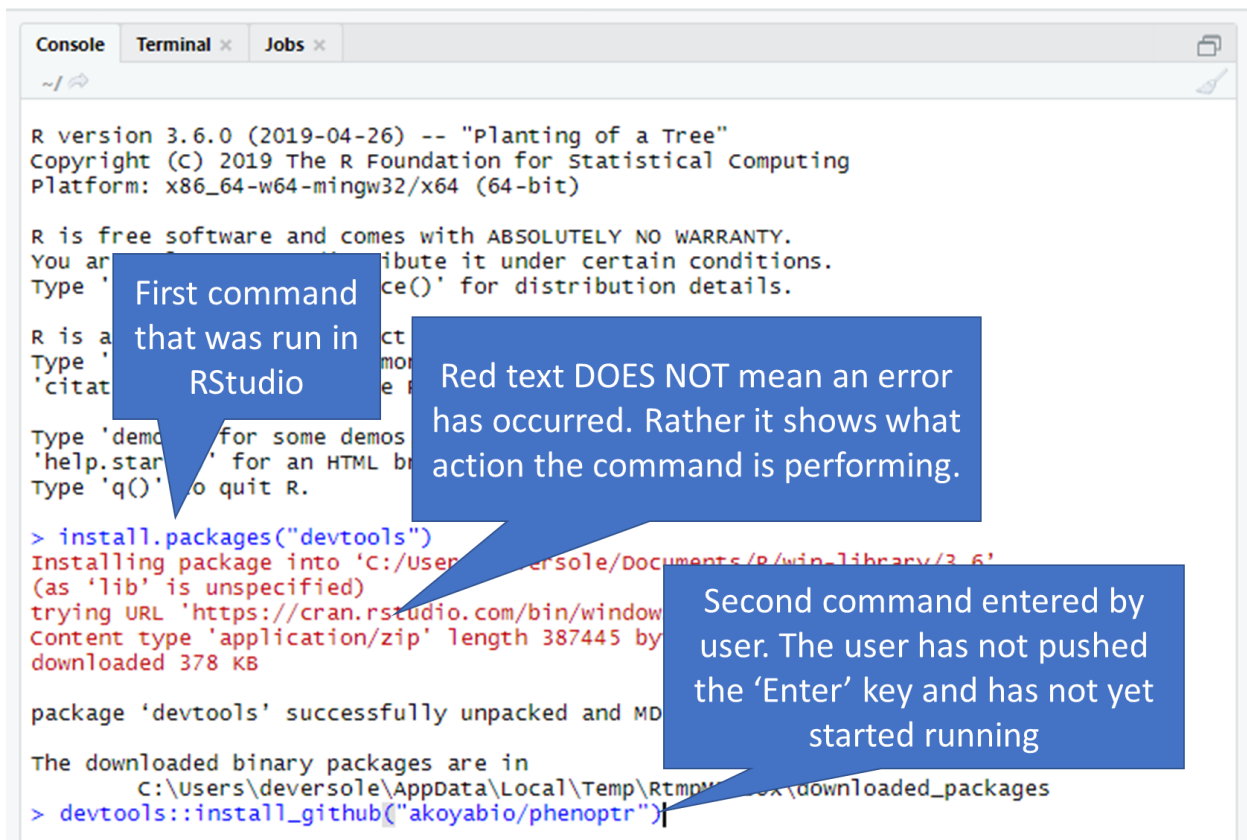5. When requested, enter 1 (Yes) to install BiocInstaller.

Figure 1: Screen shot of Rstudio. A red box has been drawn around the console, where installation command codes are entered. Ensure the console tab is selected. All commands are entered on lines starting with the > symbol. When a program is running, a stop sign will show on the upper right-hand corner of the console (see insert for magnified view); please do not try to enter additional commands until the > symbol reappears and the stop sign disappears.

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Install Optional Packages

(Highly Recommended Install) If you are planning on analyzing spatial metrics, such as nearest neighbors and count within, the following package will dramatically increase calculation speeds and reduce memory requirements.

In the RStudio console,

1. *copy and paste (or manually type in)*
   install.packages("devtools")
2. press Enter
3. *copy and paste (or manually type in)*
   devtools::install_github("akoyabio/rtree")
4. press Enter

Figure 2: Visualizing how the console will look as commands are run. Command lines show as blue text. Actions initiated by the command show as red and black text. Please remember, red text DOES NOT indicate an error has occurred. When an error has occurred, it will always start with the text "Error in".

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(Optional Install) If you work with 2x2 component images fields from inForm, please install the following package.

In the RStudio console,

2. *copy and paste (or manually type in)*
   install.packages("devtools")
3. press Enter
4. *copy and paste (or manually type in)*
   devtools::install_github("akoyabio/tiff")
5. press Enter

Install *phenoptrReports* R Package

In the RStudio console,

1. *copy and paste (or manually type in)*
   devtools::install_github("akoyabio/phenoptrReports")
2. press Enter

Restart RStudio and Enjoy!

phenoptrReports functionality can be found in the "Addins" tab (see Figure 3)
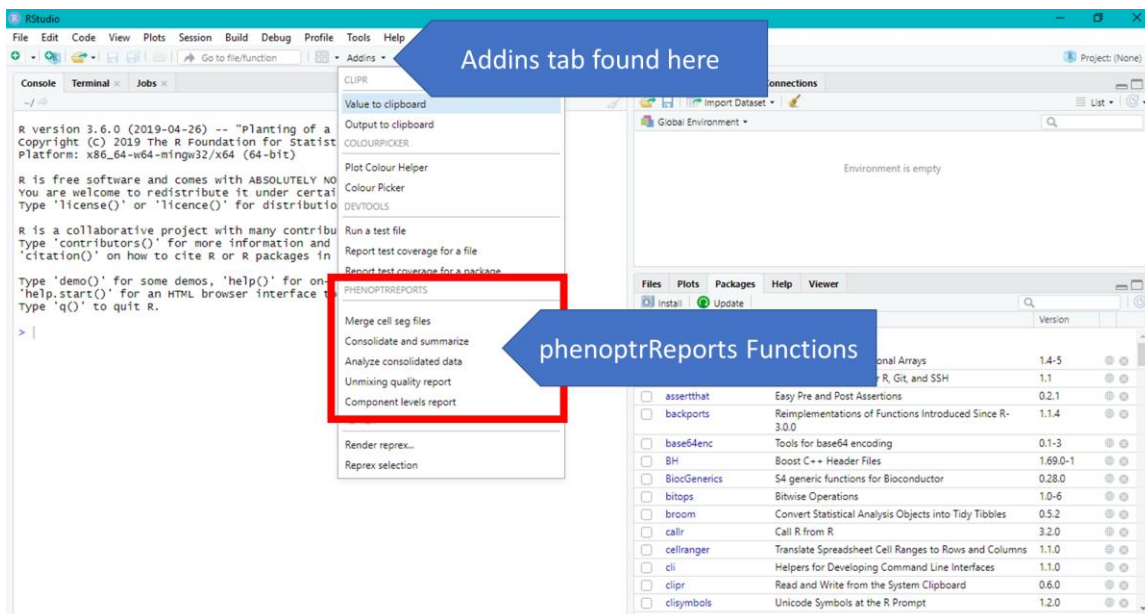

Figure 3: Select Addins tab to access phenoptrReports functions. The Addins tab is found in the taskbar above the console. When selected, phenoptrReports functions can be found near the bottom of the tab's list.

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