Installation Guide

Installing R-Peridot in Windows and GNU/Linux Systems

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Minimum Hardware Requirements:

- 6GB of RAM;
- 600MB of storage;
- 1024x768 display, or larger;
- Using a multi-core processor is very recommended.

1. Windows Installer

System Requirements:
- Microsoft Windows 7, 8 or 10;
- Java JRE/JDK 1.8;

The windows installer is currently our most easy and complete installation option. First, you need to make sure you Java 1.8 installed in your machine. If you don't, download it from here. Along with R-Peridot and it's modules, a R environment (based on the R-Portable project, version 3.4.1) with all the required packages will be installed in your computer. It will be installed under <r-peridot installation dir>/r-portable/.

Just follow the installer and set the options you want. The installation takes 15 to 30 minutes to complete.

2. Universal Installer

System Requirements:
- Internet connection;
- Windows 7/8/10 or GNU\Linux (Ubuntu, Debian or CentOS preferred);

This installer is a .ZIP file, extract it to the desired installation location.

2.1. Installing Dependencies

In case you are using Windows, the only dependencies needed are [Java 1.8](#) and [R 3.4](#) (3.4.1 preferred). Make sure Java is in your system PATH variable. In case you don't know how to do it, here is a [guide](#).

But if you are running a GNU\Linux O.S., there are way more dependencies. To make it easier for the users we created 3 scripts to install the required dependencies in different GNU\Linux distros:

- For Ubuntu >= 17.04: ubuntuDeps.sh
- For Debian >= 9: debianDeps.sh
- For CentOS >= 7.2: centosDeps.sh

They will install Open JRE 8 and R, along with other dependencies.

2.2. Selecting R Environment and Installing Required Packages

The default modules require several R packages from Bioconductor and CRAN repositories. The R Environment Manager takes care of this installation process. It will open at the first time R-Peridot is being used and you can always open it using the "Tools > R Environments" menu option.
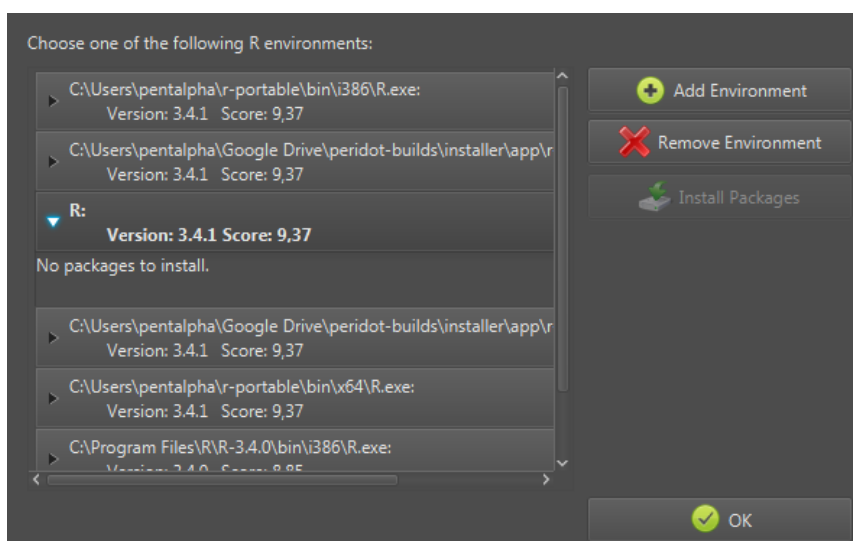
R Environment Manager: Through this interface you can select/add/remove the desired R environment or install missing required packages.

The R Environment Manager scans the system for R environments, but it may not find your R installation if it is in an unusual directory. If no environments are listed, you can click the "Add Environment" button and a file chooser dialog will appear, use it to select the R executable you want to use.

Each listed environment has a score to help you choose the better option. The score ranges from 0.0 to 10.0 and is calculated based on the R version (the recommended version is R 3.4.1) and the currently installed packages. A score above 8.0 is just fine. You can also try to run R-Peridot with environments with low scores, but in this case we cannot assure you the modules will function properly.

After selecting the desired environment, R-Peridot will show which packages are missing. If there are missing packages, click on the "Install Packages" button. It will try to install the packages from R-Peridot's package repository, which contains the more compatible version of each package. If it cannot install from our repository, the installer will try to use CRAN or Bioconductor directly.

2.2.1 Manually installing required packages

In some cases (network connection problems, broken dependencies or old R version) errors may occur in the installation of some packages. If this happens, we recommend you to install the packages directly. Open the desired R environment and use *install.packages("Package Name")* (for CRAN packages) or the [biocLite installer](#) (for Bioconductor packages). The complete list of required packages and their recommended versions are the following:

- **Bioconductor**: **sSeq** 1.14.0, **DESeq2** 1.16.1, **org.Dm.eg.db** 3.4.1, **clusterProfiler** 3.4.2, **org.Hs.eg.db** 3.4.1, **DESeq** 1.28.0, **edgeR** 3.18.1, **limma** 3.32.2, **org.Mm.eg.db** 3.4.1, **EBSeq** 1.16.0;

- **CRAN**: **pvclust** 2.0.0, **ggplot2** 2.2.1, **gplots** 3.0.1;

3. Conclusion

Now that you have the required dependencies and packages installed, just open the shortcut created by the Windows installer of the r-peridot-gui.jar file in the installation directory to run R-Peridot and make your differential expression analysis. For additional information, read the User's Guide and the Guide for Advanced Users.

In case of problems with the installation, please email us with a description of your problem (including the operational system and the output of the "*R.version*" command).

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