

Install BioMedR (version: 1.1.1) form CRAN

Step 1:

Open your RStudio (using current R version: 3.5.3), and type in:

```
> install.packages("BioMedR")
```

You will get:

```
Warning in install.packages :  
dependencies 'Biostrings', 'GOsemSim', 'ChemmineR', 'fmcsR', 'org.Hs.eg.db' are not  
available
```

The *bitops*, *rcdklibs*, *fingerprint*, *rJava*, *png*, *iterators*, *itertools*, *RCurl*, *rjson*, *rcdk*, *pls*, *randomForest* and **BioMedR** will be automatically installed. That means the warning packages should be install via Bioconductor resource.

Step 2:

Type in:

```
> if (!requireNamespace("BiocManager"))  
  install.packages("BiocManager")  
> BiocManager::install(c("Biostrings", "GOsemSim", "ChemmineR", "fmcsR",  
  "org.Hs.eg.db"))
```

Then, these packages will be correctly installed.

Step 3:

Type in:

```
> require(BioMedR);
```

You may get:

```
> rror: package or namespace load failed for 'BioMedR':  
loadNamespace() 'rJava'.onLoad failed, detailed information:  
Call: fun(libname, pkgname)  
Error: JAVA_HOME cannot be determined from the Registry
```

This means the rJava is not correctly configured. Please refer the <https://CRAN.R-project.org/package=rJava>. We also provided a documentation that described how to configure the rJava. After the configuration of java environment, you can go to step 4.

Step 4:

Type in:

```
> require(BioMedR);
```

Successful!