

# RPackUtils: R Package Dependencies Manager and Bioconductor & CRAN Mirroring Tool

Stephane Cano, Sylvain Gubian

PMI R&D, Philip Morris Products S.A., Quai Jeanrenaud 5, CH-2000 Neuchâtel, Switzerland



## Abstract

The installation and maintenance of R packages from public repositories, such as the [Comprehensive R Archive Network \(CRAN\)](#) or [Bioconductor](#), is a process made cumbersome by the need to manage package dependencies. Typically, this forces users to download the versions of the package that are currently available and potentially experience a trial-and-error cycle of installing and updating all dependencies. The reproducibility of an R installation, and therefore of the R code itself, is not guaranteed by the use of standard, out-of-the-box tools.

**RPackUtils** is an R package dependencies manager developed in Python with reproducibility in mind. **RPackUtils** can manage several public and private repositories (e.g., [Artifactory](#)), any existing R environment, or any local file system folder internally as well as install packages from all of them and mirror the main public repositories, [CRAN](#) and [Bioconductor](#), to a specific snapshot in time or release.

## Introduction

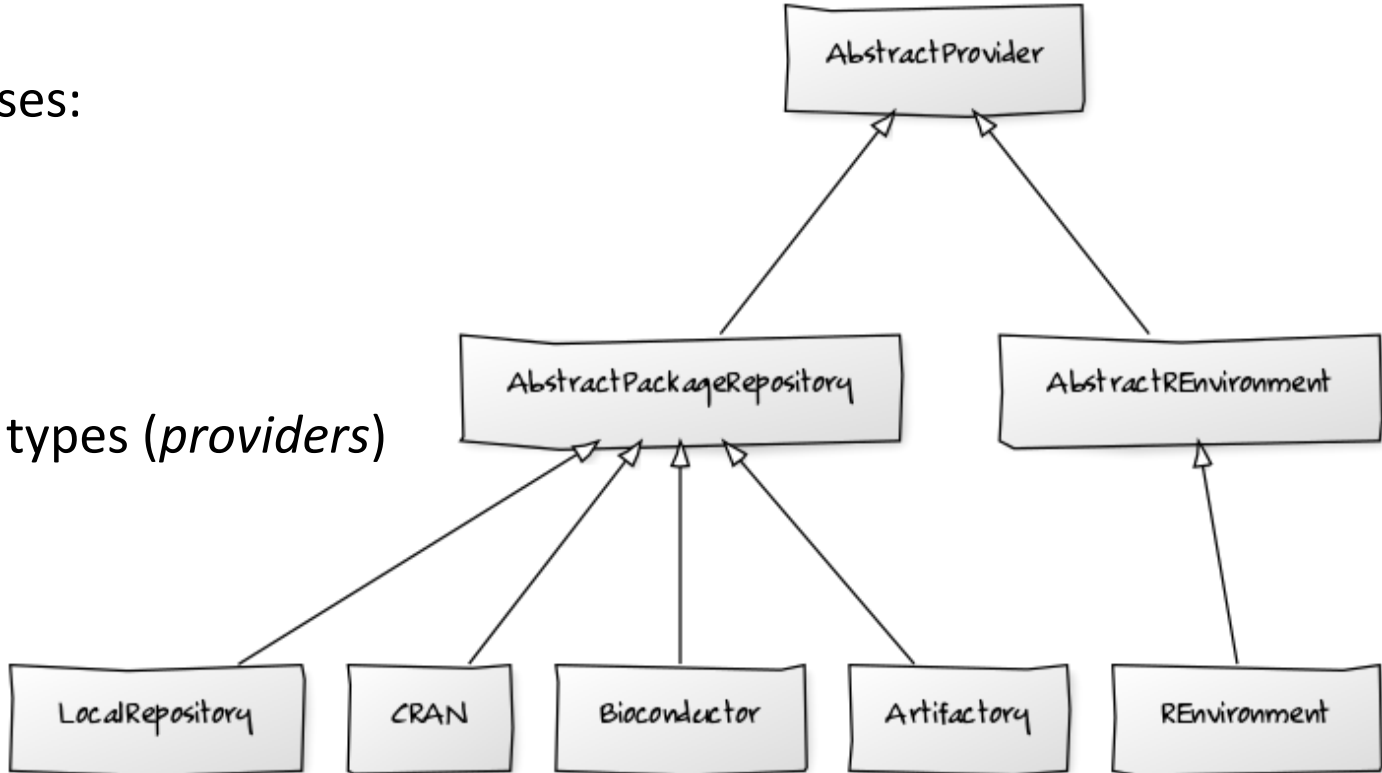
The command line tools of **RPackUtils** enable the following use cases:

- Mirror past and current [CRAN](#) snapshots published on [MRAN](#)
- Mirror past and current [Bioconductor](#) versions
- Clone existing R environments
- Install R packages with dependencies from different repository types (*providers*)
- Create R package dependency graphs

**Table 1** describes the main commands available in the shell.

Command	Purpose
rpacbioc	Query the <a href="#">Bioconductor</a> repository for available releases
rpacmran	Query the <a href="#">MRAN</a> repository for available snapshots
rpacq	Search across repositories for a package or a list of packages
rpaci	Install R packages with resolved dependencies
rpacc	Install R packages based on an existing environments (clone)
rpacd	Download R packages and resolve dependencies
rpacm	Download R packages from a specified repository ( <a href="#">CRAN</a> , <a href="#">Bioconductor</a> ) and upload them to <a href="#">Artifactory</a> (mirror)
rpacg	Generate a dependencies graph

**Table 1:** List of available commands for RPackUtils (CLI).



## Comparison with Packrat

Both tools are meant for different use cases, the typical workflow of **Packrat** occurs inside user workspaces, whereas in **RPackUtils**, it occurs in entire R environments for all users.

**Packrat** is initialized inside an R project in a user's workspace. It maintains a library of packages for each **Packrat**-enabled project. It can install, remove, and snapshot dependencies. For collaboration and sharing, *bundle()* and *unbundle()* functions are provided. The creation of a bundle will actually fetch all necessary sources and make them available along with the project source in an archive.

**RPackUtils** is more administrator-oriented in the sense that it acts on entire R environments. It can mirror the major R repositories ([CRAN](#) and [Bioconductor](#)) even for old snapshots, clone R environments, and install packages.

**Table 2** summarizes the main features of both tools.

	Packrat	RPackUtils
User workspace management	✓	✗
R environment management	✗	✓
<a href="#">Artifactory</a> repository support	✗	✓
Local repository support	✓	✓
Clone an existing R environment	✗	✓
"Isolation" per package (a <b>Packrat</b> project has its own package library)	✓	✗
Reproducibility guaranteed	✓	✓
Resolve dependencies while installing an R package	✗	✓
Repository mirroring	✗	✓
License class filtering	✗	✓

**Table 2:** Packrat and RPackUtils main features.

## Links

RPackUtils on github:

<https://github.com/pmpsa-hpc/RPackUtils>



R package repositories:

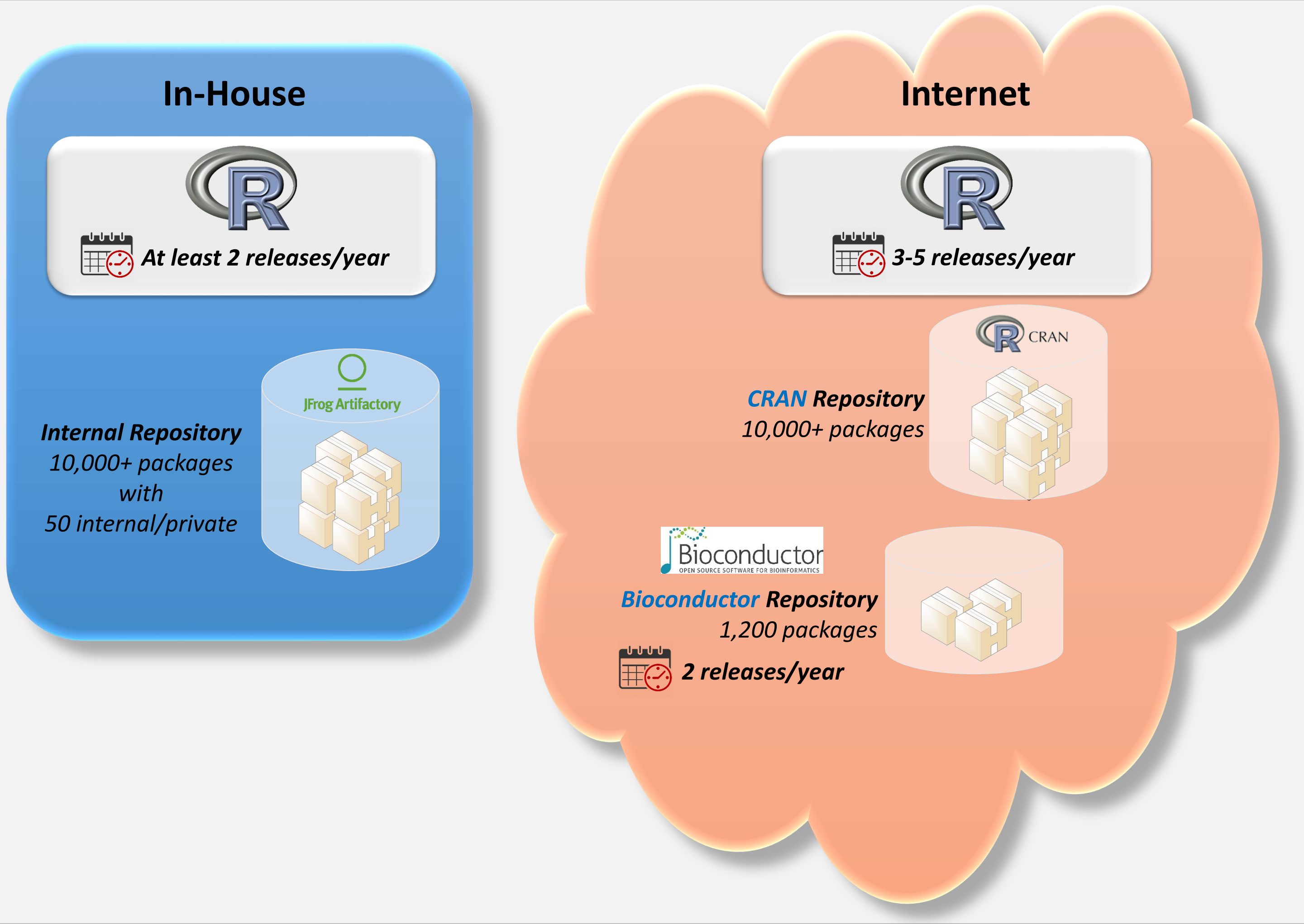


Packrat:

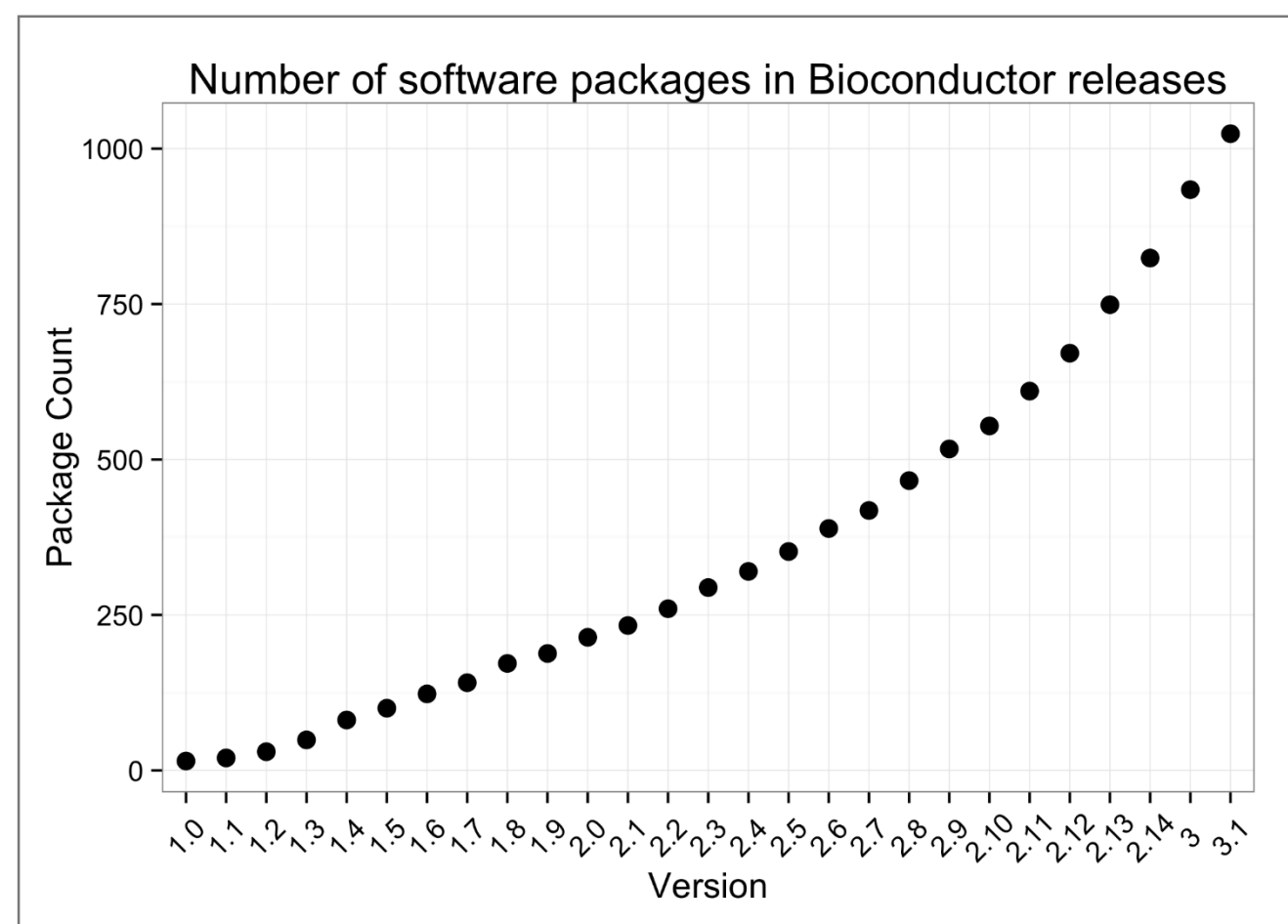
<https://rstudio.github.io/packrat/>



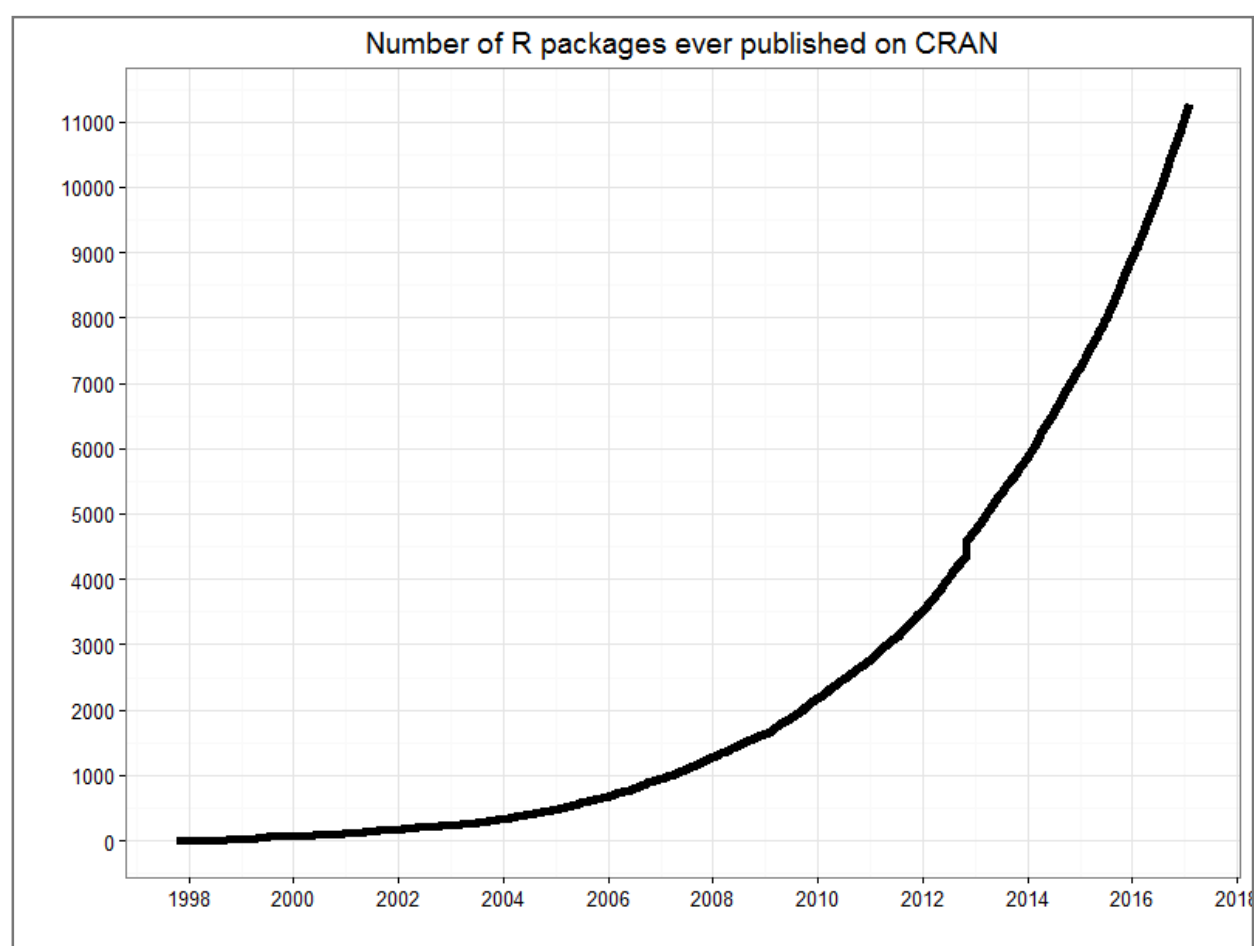
## R releases and main package repositories



**Figure 1:** Our in-house R environment and packages (for a given version of R) versus the outside situation.



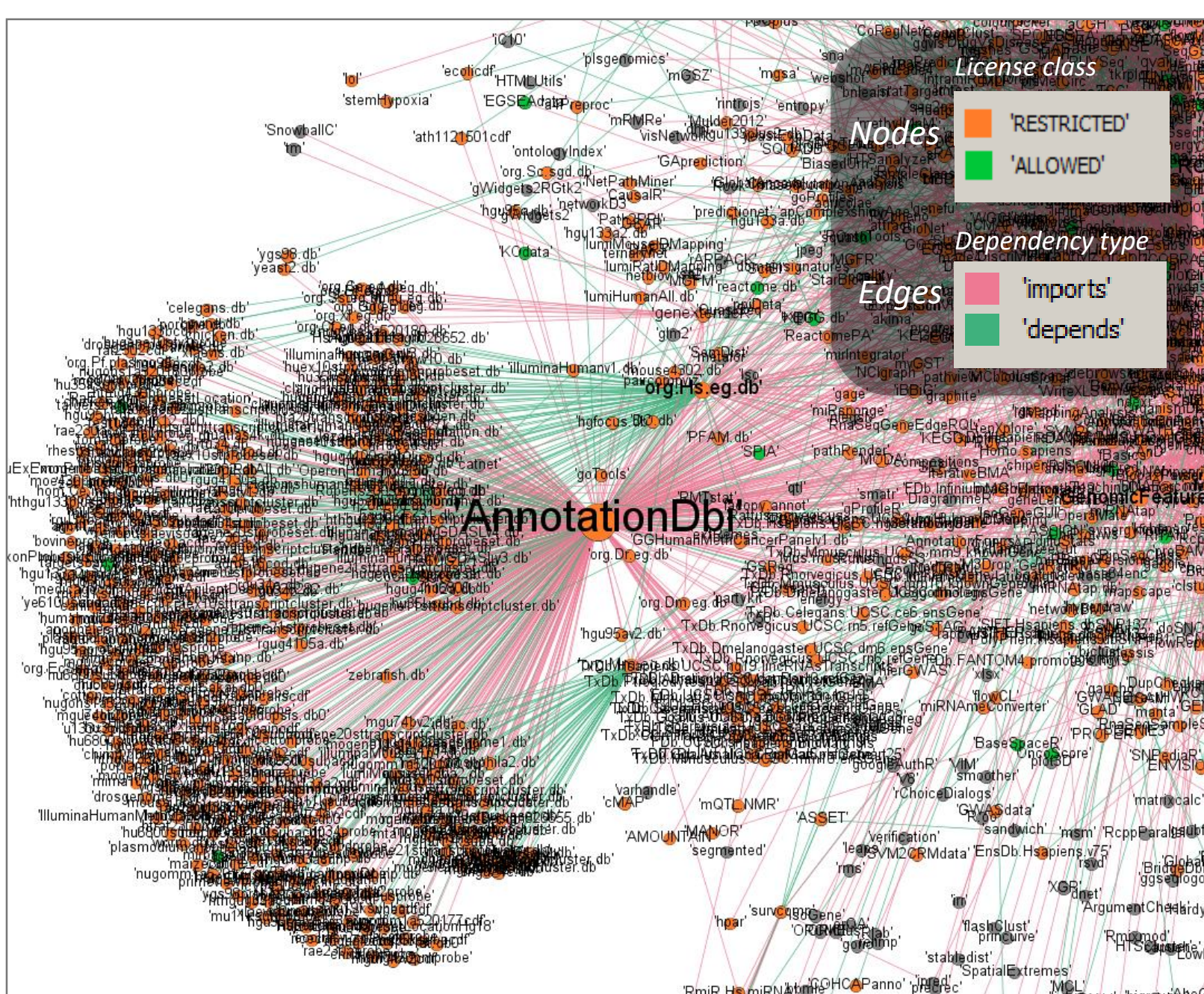
**Figure 2:** Number of packages in [Bioconductor](#).



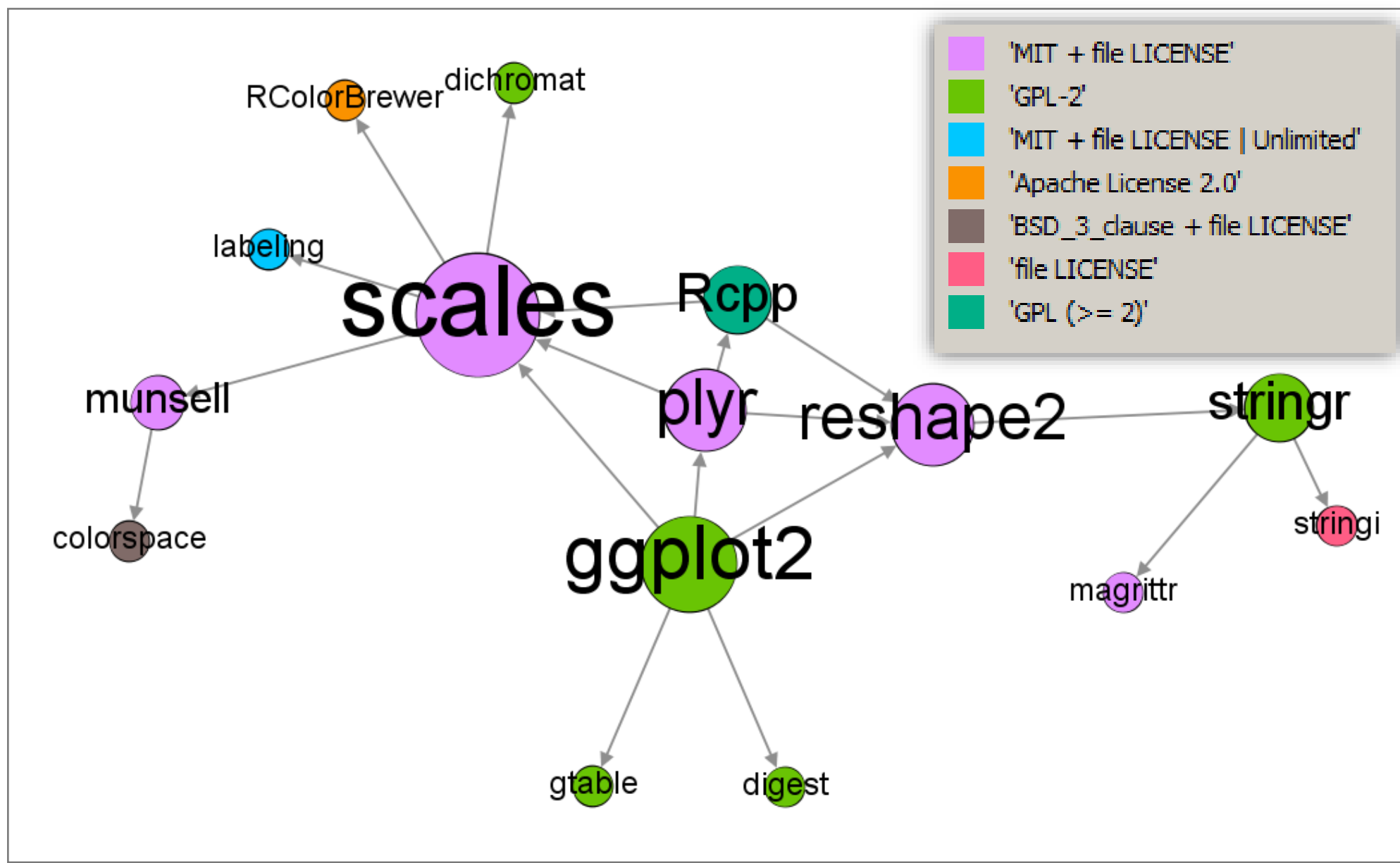
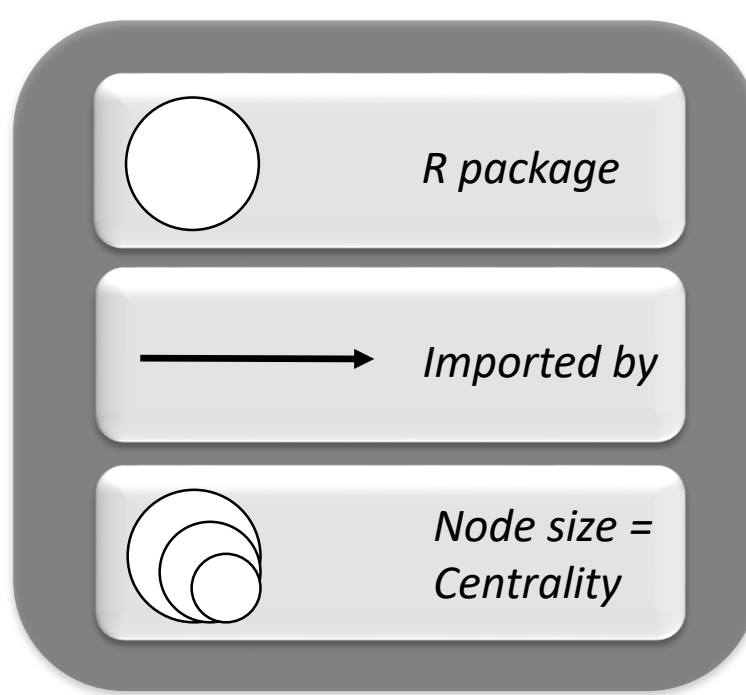
**Figure 3:** Number of packages in [CRAN](#).



## Dependencies graph



**Figure 4:** Dependency graph for [Bioconductor](#) with license classes (detail).



**Figure 5:** ggplot2 dependencies with licenses.



Bastian M., Heymann S., Jacomy M. (2009). Gephi: an open source software for exploring and manipulating networks. International AAAI Conference on Weblogs and Social Media.