

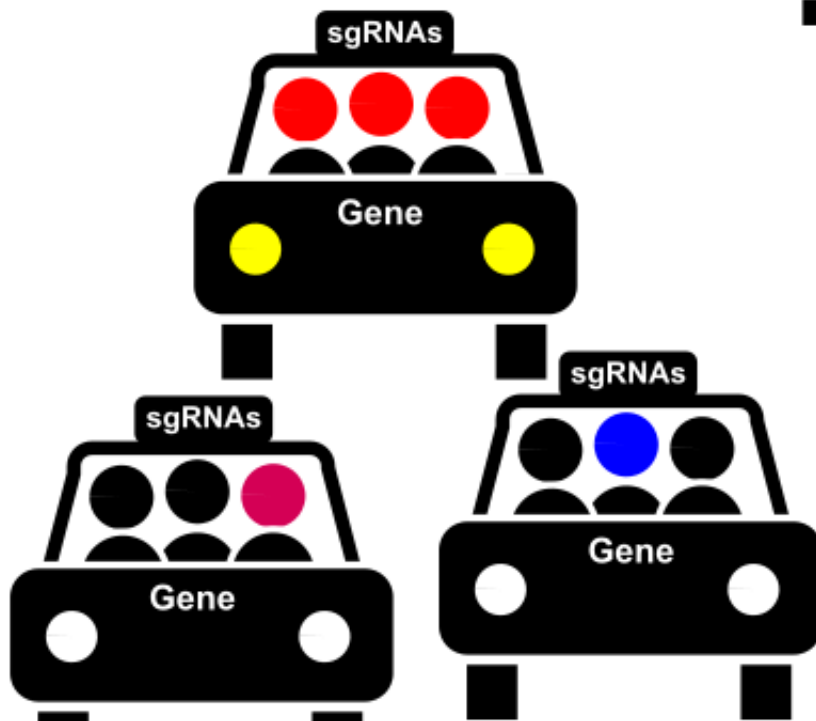
caR pools Installation Guide

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Contents

1	Requirements and Installation	3
1.1	Download caR pools	3
1.2	Virtual Box Image - The FAST-track - RECOMMENDED	3
1.2.1	How to use the Virtual Box caR pools	3
1.3	Hardware Requirements	3
1.4	Software Requirements	3
1.5	BiomaRt and Annotation Requirements	4
1.6	Installation Procedure	4

CRISPR-AnalyzeR for Pooled Screens



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carpools...

Exploratory data analysis of CRISPR/CAS screens

1 Requirements and Installation

1.1 Download caRpools

CaRpools is available as an R package **caRpools** without the scripts and template files.

The complete package with the PERL scripts and all template files can be obtained from [Github](https://github.com/boutroslab/carpools) (<https://github.com/boutroslab/carpools>) and our website crispr-analyzer.de.

We recommend to download the template files and Scripts from Github and install caRpools in R using the package installer ‘install.packages(“caRpools”)’.

1.2 Virtual Box Image - The FAST-track - RECOMMENDED

We also included a VirtualBox Image that already includes all necessary software and package files. **In this case no additional software except for Virtual Box 5 needs to be installed.**

We recommend using the Virtual Box image as it provides a fast, easy and convenient way of using caRpools for the generation of reports for every user.

You just need to install VirtualBox 5 from the [Website](#).

Please follow the manual [here](#)

You can then download the caRpools virtual box image from our website crispr-analyzer.de or [Github](https://github.com/boutroslab/carpools) (<https://github.com/boutroslab/carpools>).

1.2.1 How to use the Virtual Box caRpools

Please follow the manual [here](#)

or the **CaRpools-SHORTGUIDE-VirtualBox.pdf / CaRpools-SHORTGUIDE-VirtualBox.html**

1.3 Hardware Requirements

For CRISPR-Libraries of 12 K size (12K sgRNAs), caRpools will work on any laptop/PC with at least 4GB of RAM and a modern dual-core CPU.

CRISPR-Libraries with a size of more than 100 K (100 K sgRNAs) run best with at least 8 GB of RAM.

1.4 Software Requirements

CaRpools was tested on MacOSX Yosemite and Ubuntu 14.04 LTS.

However, it should work on any operating system that fulfills the software requirements.

The following software needs to be installed:

- PERL 5
- Bowtie2 2.2.0 or higher [Website](#)
- MAGeCK 0.51 (password protected download) [Website](#)
- TexLive [Website](#)
- pdflatex
- xelatex
- R 3.2.0 or higher [Website](#)
- Pandoc 1.15.0.6 [Website](#)
- R-Studio [Website](#) (GUI)

The following **R packages** need be installed (can be done via `load.packages()`):

- Bioconductor Basics
 - BiocInstaller \geq 1.18.3
 - BiocGenerics \geq 0.14.0
- **biomaRt \geq 2.24.0**
- seqinr \geq 3.1-3
- xlsx \geq 0.5.7
- rJava \geq 0.9.6
- xlsxjars \geq 0.6.1
- stringi \geq 0.5
- scatterplot3d \geq 0.3
- MESS \geq 0.3
- DESeq2 \geq 1.8.1
- rmarkdown \geq 0.7
- knitr \geq 1.10.5
- VennDiagram \geq 1.6.9
- sm \geq 2.2

1.5 BiomaRt and Annotation Requirements

Please note that for any annotation, biomaRt needs full access to the internet. In case of incorrect proxy settings, the report generation will fail with a biomaRt error.

This means that if any proxy server is used, this has to be configured before using the CRISPR-Analyzer as described in the following articles:

- [BiomaRt vignette](#)
- [Setting up proxy in R-Studio](#)
- [Setting up proxy in R, Stackoverflow](#)
- [Setting up Proxy for R/R-Studio in Ubuntu](#)
- [Configuration of Proxy for R](#)

1.6 Installation Procedure

Install all software listed above according to the installation information stated on the software website. All necessary R packages can be installed automatically by `load.packages()` within R or R-Studio.

See [Install R packages](#) or [Install R packages with RStudio](#).