# caRpools Installation Guide

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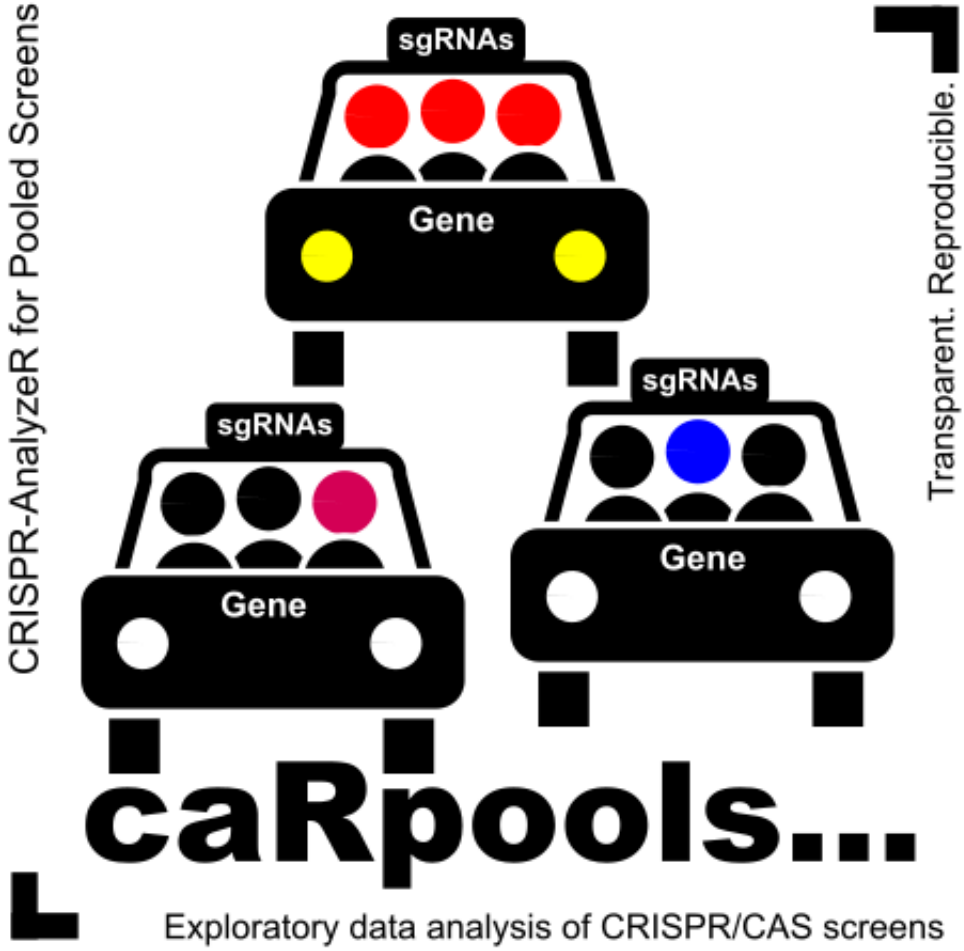
CRISPR-AnalyzeR for Pooled Screens
sgRNAs
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Transparent. Reproducible.
caRpools...
Exploratory data analysis of CRISPR/CAS screens

# 1 Requirements and Installation

## 1.1 Download caRpools

CaRpools is avaible 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) and our website crispr-analyzer.org.

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

We also included a VirtualBox Image that already includes all necessary software and package files. **In this case no additional software to Virtual Box 5 needs to be installed.**
You just need to install VirtualBox 5 from the Website.

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

### 1.2.1 How to use the Virtual Box caRpools

Download and start the caRpools virtual box image file XXXX.

HERE WE NEED A DETAILED EXPLANATION + SCREENSHOTS!

## 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 requirments.

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 >= 1.18.3
  - BiocGenerics >= 0.14.0

- **biomaRt >=2.24.0**
- seqinr >= 3.1-3
- xlsx >= 0.5.7
- rJava >= 0.9.6
- xlsxjars >= 0.6.1
- stringi >= 0.5
- scatterplot3d >= 0.3
- MESS >= 0.3
- DESeq2 >= 1.8.1
- rmarkdown >= 0.7
- knitr >= 1.10.5
- VennDiagram >= 1.6.9
- sm >= 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 neccesarry R packages can be installed automatically by `load.packages()` within R or R-Studio.

See Install R packages or Install R packages with RStudio.