

# Cheat sheet: fast container builds for R

## docker command line

### Run container interactively

```
docker run -it \
namespace/repo:tag
```

### Run rocker/rstudio container

```
docker run --rm -p 8787:8787 \
-it -e PASSWORD=mypassword \
rocker/rstudio
```

### Build from Dockerfile

```
docker build \
-t namespace/repo:tag .
```

## Convenient R commands

### Dockerfile from DESCRIPTION file

```
dockerfiler::dock_from_desc()
```

### Package system requirements

```
pak::pkg_system_requirements(
  "DT", "ubuntu", "20.04")
```

### Reducing image size

```
- Install2.r: rm -rf /tmp/downloaded_packages
- RSPM: strip /usr/local/lib/R/site-library/*/libs/*.so
- apt-get: rm -rf /var/lib/apt/lists/*
```

### Acknowledgements

[Rocker](#) and [r2u](#) are mainly developed by [Carl Boettiger](#) and [Dirk Eddebuetel](#). This cheat sheet was created by [Geert van Geest](#)

## Dockerfile examples

### apt-get

interacts with the system package manager, that usually includes R packages

```
FROM ubuntu
```

```
RUN apt-get update \
&& apt-get install -y \
--no-install-recommends \
r-cran-rmarkdown \
r-cran-dt \
r-bioc-biostings
```

```
FROM r-base:latest
```

```
RUN apt-get update \
&& apt-get install -y \
--no-install-recommends \
r-cran-rmarkdown \
r-cran-dt \
r-bioc-biostings
```

### install2.r/install.r scripts

Helpers for installing R packages ([littler](#) package). All options [here](#).

```
FROM rocker/rstudio:4
```

```
RUN install2.r \
rmarkdown \
DT
```

```
FROM rocker/r2u:jammy
```

```
RUN install2.r \
rmarkdown \
DT Biostings
```




### Binary or source installation?


For most applications, a *binary installation is recommended*. It's faster and it's easier to handle dependencies.

## Choosing your base image

The base images below have many different characteristics. Refer to their specifications for a full overview.

*fastest!* 

	<a href="#">Versioned</a>	<a href="#">Base</a>	<a href="#">rocker/r2u</a>
apt-get install	No	Yes 	Yes 
repo install2.r or install.packages()	RSPM ( <a href="#">binary</a> )	CRAN ( <a href="#">source</a> )	 r2u ( <a href="#">binary</a> )
base image	ubuntu	debian	ubuntu

 : default bioconductor support

