

## How to guide: Installing PhenStat

PhenStat is a package of code that was developed for the statistical program R and was developed to analyse phenotyping data [1]. PhenStat is available from Bioconductor [1]. The source code is hosted on Github [2]. We have a wiki page ([https://github.com/mpi2/stats\\_working\\_group/wiki](https://github.com/mpi2/stats_working_group/wiki)) which provides the most up to date code and documentation. This is our recommended route for installation as Bioconductor is limited by a bi-yearly release schedule.

[1] Kurbatova N., *et al.* (2014) PhenStat: A Tool Kit for Standardized Analysis of High Throughput Phenotypic Data. PLOS ONE

[2] <http://www.bioconductor.org/packages/release/bioc/html/PhenStat.html>

[3] [https://github.com/mpi2/stats\\_working\\_group](https://github.com/mpi2/stats_working_group)

### Installation

- Install R from <http://cran.r-project.org/>
- Run R by double clicking on the R icon



- At the prompt (>) type in the following to install dependencies

```
install.packages("methods")
```

```
install.packages("car")
```

```
install.packages("nlme")
```

```
install.packages("nortest")
```

```
install.packages("vcd")
```

```
install.packages("MASS")
```

```
install.packages("logistf")
```

```
install.packages("lme4")
```

- Download the latest version of the package:  
[https://github.com/mpii2/stats\\_working\\_group/blob/master/PhenStat/PhenStatPackage/PhenStat\\_2.2.4.tar.gz?raw=true](https://github.com/mpii2/stats_working_group/blob/master/PhenStat/PhenStatPackage/PhenStat_2.2.4.tar.gz?raw=true)

- Install `install.packages`

```
("path_to_downloaded_file",repos=NULL,type="source")
```

## Load the PhenStat package

- To load the PhenStat library into your workspace:

```
library(PhenStat)
```

This command loads the package and help pages, and returns you to the R prompt ready for the next command. The package is now ready for use.