PhenStat: statistical analysis of phenotypic data using Mixed Models and Fisher Exact Test

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PhenStat is a package that provides statistical methods for the identification of abnormal phenotypes. The package contains dataset checks and cleaning in preparation for the analysis. For continuous data, an iterative fitting process is used to fit a regression model that is the most appropriate for the data, whilst for categorical data, a Fisher Exact Test is implemented.

Depending on the user needs, the output can either be interactive where the user can view the graphical output and analysis summary or for a database impelementation the output consists of a vector of output and saved graphical files. PhenStat has been tested and demonstrated with an application of 420 lines of historic mouse phenotyping data.

The full PhenStat User's Guide is available as part of the online documentation. To reach the User's Guide, install the PhenStat package and load it into an R session by `library(PhenStat)`. In R for Windows, the User's Guide will then be available from the drop-down menu called "Vignettes". In other operating systems, type

```
> library(PhenStat)
> PhenStatUsersGuide()
```

at the R prompt to open the User's Guide in a pdf viewer.