

# Package ‘popprxl’

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**Type** Package

**Title** Read GenAIEx Files Directly from Excel

**Version** 0.1.4

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**Encoding** UTF-8

**Description** GenAIEx is a popular Excel macro for genetic analysis and the 'poppr' R package allows import of GenAIEx formatted CSV data for genetic data analysis in R. This package allows for the import of GenAIEx formatted Excel files, serving as a small 'poppr' add on for those who have trouble or simply do not want to export their data into CSV format.

**Depends** poppr (>= 2.0.2)

**Imports** readxl, utils

**URL** <https://github.com/zkamvar/popprxl>

**BugReports** <https://github.com/zkamvar/popprxl/issues>

**License** GPL-3

**LazyData** TRUE

**Suggests** testthat, knitr, rmarkdown, adegenet

**RoxygenNote** 6.0.1.9000

**VignetteBuilder** knitr

**NeedsCompilation** no

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popprxl                      *popprxl*.

### Description

This package has one function: [read.genalexcel](#).

### Citation

To cite this package, please use the citation for the poppr package. You can find it by typing `citation(package = "poppr")`.

### Author(s)

Zhian N. Kamvar and Niklaus J. Grünwald

read.genalexcel              *Read GenAIEx formatted data from excel*

### Description

The **poppr** function [read.genalex](#) provides a way to read GenAIEx formatted data into R. The only stipulation is that the file must be saved as a CSV text file beforehand. This function provides a wrapper for [read.genalex](#) and [read\\_excel](#) from the **readxl** package.

### Usage

```
read.genalexcel(x, sheet = 1, ...)
```

### Arguments

x	a path to your excel file
sheet	the sheet in which your data is contained.
...	any arguments to be passed on to <a href="#">read.genalex</a>

### Value

a [genclone](#) or [genind](#) object.

### Author(s)

Zhian N. Kamvar

**See Also**[read.genalex](#)**Examples**

```
# Read in the data set nancycats from an example excel file in this
# package.

nancy <- system.file("files/nancycats.xlsx", package = "popprxl")
nancy # This is the address to our excel file.
read.genalexcel(nancy, sheet = 1, genclone = FALSE)

# Note that system.file() is only for examples. You can use
# file.choose() for an interactive way of choosing files.
#
# e.g.
# myfile <- file.choose()
# read.genalexcel(myfile)
## Not run:
nancy_ex_rows <- system.file("files/nancycats_extra_rows.xlsx", package = "popprxl")
# This will give a warning
read.genalexcel(nancy_ex_cols, sheet = 1, genclone = FALSE)

## End(Not run)
```

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