

# Package ‘EasyStrata’

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**Type** Package

**Title** Evaluation of stratified genome-wide association meta-analysis results

**Version** 8.6

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**Description** This is a pipelining tool that facilitates evaluation and visualisation of stratified genome-wide association meta-analyses (GWAMAs) results data. It provides (i) statistical methods to test and to account for between-strata difference and to clump genome-wide results into independent loci and (ii) extended graphical features (e.g., Manhattan, Miami and QQ plots) tailored for stratified GWAMA results.

**License** GPL-3

**LazyLoad** yes

**Depends** methods,Cairo,plotrix

**Collate** clsEqcReader4.r clsRCD7.r clsGWADATA45.r clsEASYMERGE.r  
fnEasyPLOT10.r clsREPORT9.r clsMERGE11.r clsSPLOT21.r  
clsADDCOL11.r clsADJUSTALLELES15.r clsANNOTATE8.r  
clsBONFERRONI3.r clsCALCPDIFF6.r clsCALCPHET3.r clsCALCULATE3.r  
clsCLEAN5.r clsCLUMP5.r clsCRITERION6.r clsEDITCOL.r  
clsEVALSTAT7.r clsEXTRACTSNPS3.r clsFDR3.r clsFILTER6.r  
clsGC5.r clsGETCOLS.r clsGETNUM2.r clsINDEP7.r clsJOINTTEST3.r  
clsMERGEEASYIN4.r clsMETAANALYSIS5.r clsMHPlot15.r  
clsMIAMIPlot15.r clsQQPLOT17.r clsREMOVECOL.r clsRENAMECOL2.r  
clsRPlot18.r clsSTRSPLITCOL.r clsWRITE7.r EasyX86.r

**NeedsCompilation** no

**Repository** CRAN

**Date/Publication** 2014-06-24 01:04:13

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EasyStrata	<i>Function to run EasyStrata (v8.6).</i>
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### Description

The Function takes the an EasyStrata config/script (ECF-) file and performs all steps defined in the ECF-file.

### Usage

```
EasyStrata(fileECF)
```

### Arguments

fileECF	fileECF is an EasyStrata config/script (ECF) file. Please see 'EasyStrata_8.6_Commands_140615.pdf' for more information on ECF functions and parameters.
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### Author(s)

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### References

<http://www.genepi-regensburg.de/easystrata>

### Examples

```
extDataDir=system.file("extdata", package="EasyStrata")
## Example Pipeline:
ecfPipe=paste(extDataDir,"example_pipeline.ecf",sep="/")
EasyStrata(ecfPipe)
```

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