

Heteroskedastičnost

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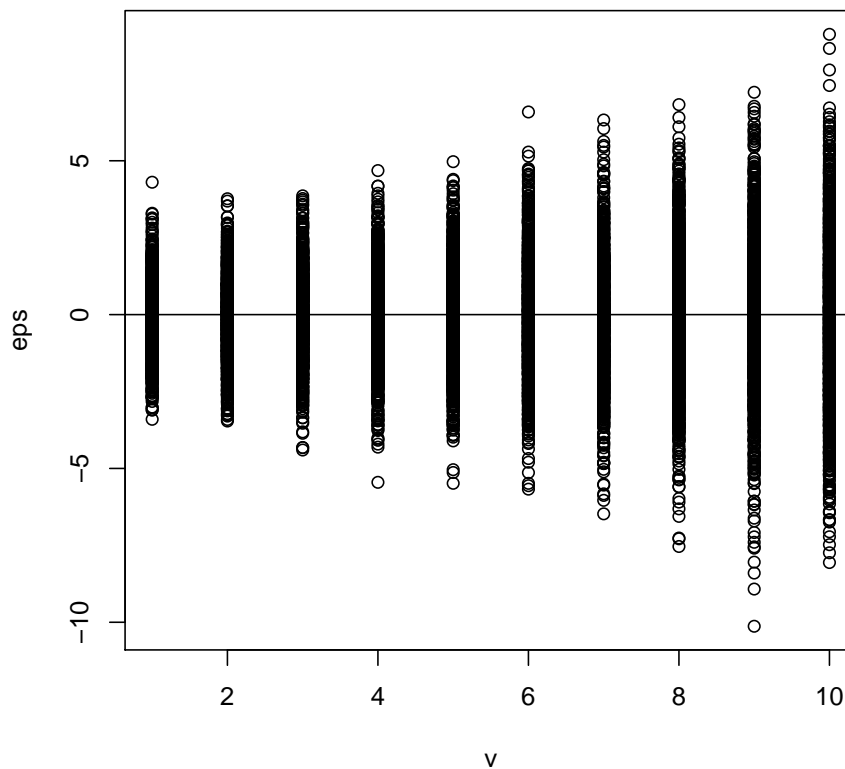
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```
> M <- 10  
> i <- 1:M  
> n <- 1000  
> v <- rep(i, each=n)  
> g <- rep(exp(0.1*i), each=n)  
> eps <- rnorm(n*M, 0, g)  
> plot(v, eps)  
> abline(h=0)
```



SessionInfo

Windows 7 x64 (build 7601) Service Pack 1

- R version 2.15.1 (2012-06-22), x86_64-pc-mingw32
- Locale: LC_COLLATE=Slovenian_Slovenia.1250, LC_CTYPE=Slovenian_Slovenia.1250, LC_MONETARY=Slovenian_Slovenia.1250, LC_NUMERIC=C, LC_TIME=Slovenian_Slovenia.1250
- Base packages: base, datasets, graphics, grDevices, methods, splines, stats, utils
- Other packages: Hmisc 3.9-3, patchDVI 1.8.1584, survival 2.36-14
- Loaded via a namespace (and not attached): cluster 1.14.2, grid 2.15.1, lattice 0.20-6, tools 2.15.1

Project path: D:/_Y/R/Bioinformatika

View as vignette

Project files can be viewed by pasting this code to R console:

```
> projectName <-"Bioinformatika"; mainFile <-"varianceCorrect"  
  
> commandArgs()  
> library(tkWidgets)  
> # getrootpath <- function() {  
> # fp <- (strsplit(getwd(), "/"))[[1]]  
> # file <- file.path(paste(fp[-length(fp)], collapse = "/"))  
> # return(file)  
> # }  
> # fileName <- function(name="bla", ext="PDF") paste(name, ext, sep=".")  
> openPDF(file.path(dirname(getwd()), "doc", paste(mainFile, "PDF", sep=".")))  
> viewVignette("viewVignette", projectName, file.path("../doc", paste(mainFile  
>
```