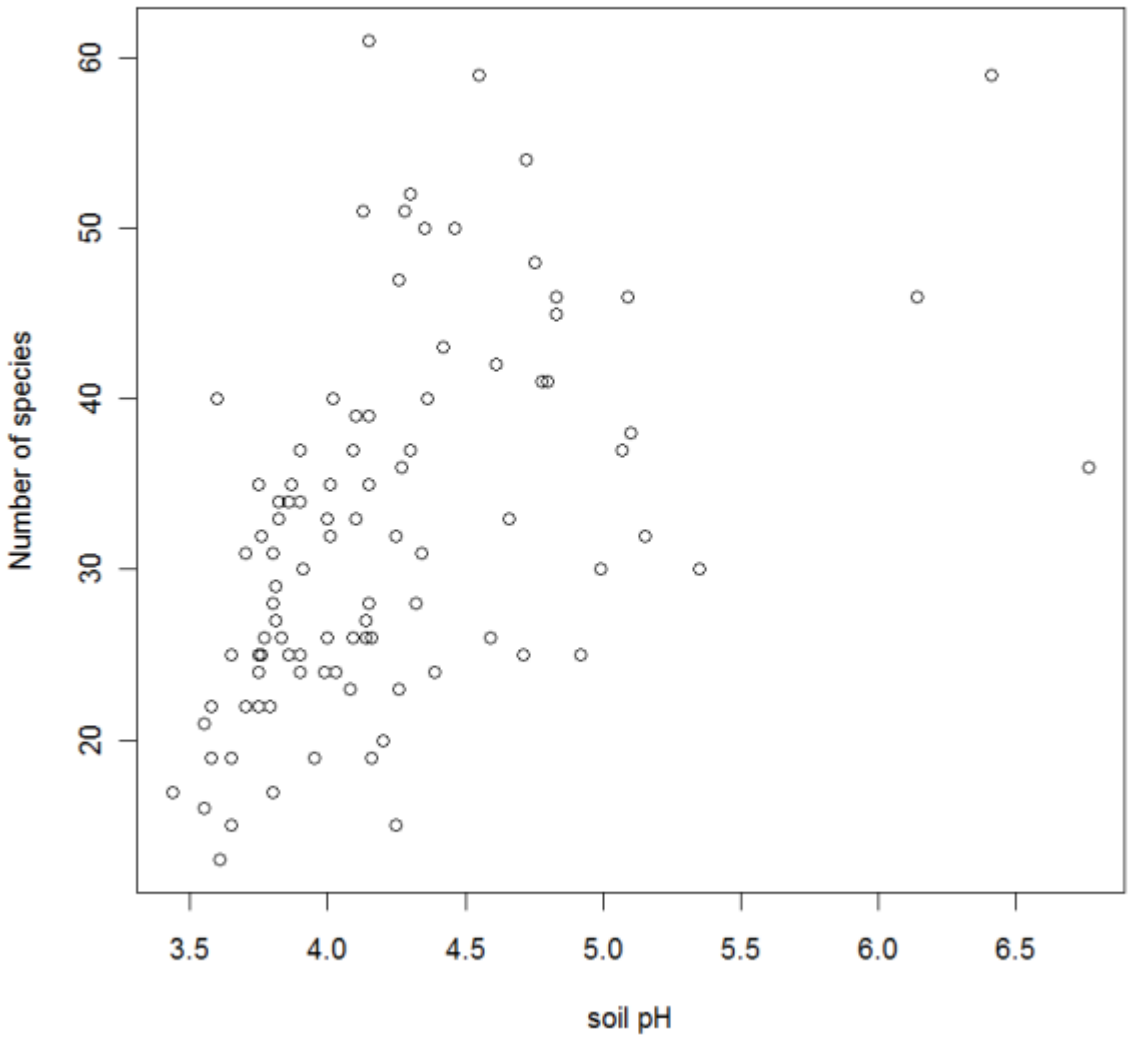
```
vltava.spe <- read.csv2
('http://www.davidzeleny.net/anadat-r/data-download/vltava-spe.csv', row.names = 1)
vltava.env <- read.csv2
('http://www.davidzeleny.net/anadat-r/data-download/vltava-env.csv', dec = '.')
plot (specnumber (vltava.spe) ~ vltava.env$pH.H, xlab = 'soil pH', ylab = 'Number
of species')
```



From:
https://anadat-r.davidzeleny.net/ - **Analysis of community ecology data in R**

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https://anadat-r.davidzeleny.net/doku.php/cs:alpha_beta_diversity:solution_ex1

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