

# hist.dnorm

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Quick and dirty function which draws histogram overlaid with normal distribution curve.

[hist.dnorm.r](#)

```
hist.dnorm <- function (x, lines.col = 'red', lines.lwd = 2, ...)
{
  hist (x, freq = FALSE, ...)
  lines (seq (min (x), max (x), length = 100), dnorm (seq (min (x), max
(x), length = 100), mean = mean (x), sd = sd (x)), col = lines.col, lwd
= lines.lwd)
}
```

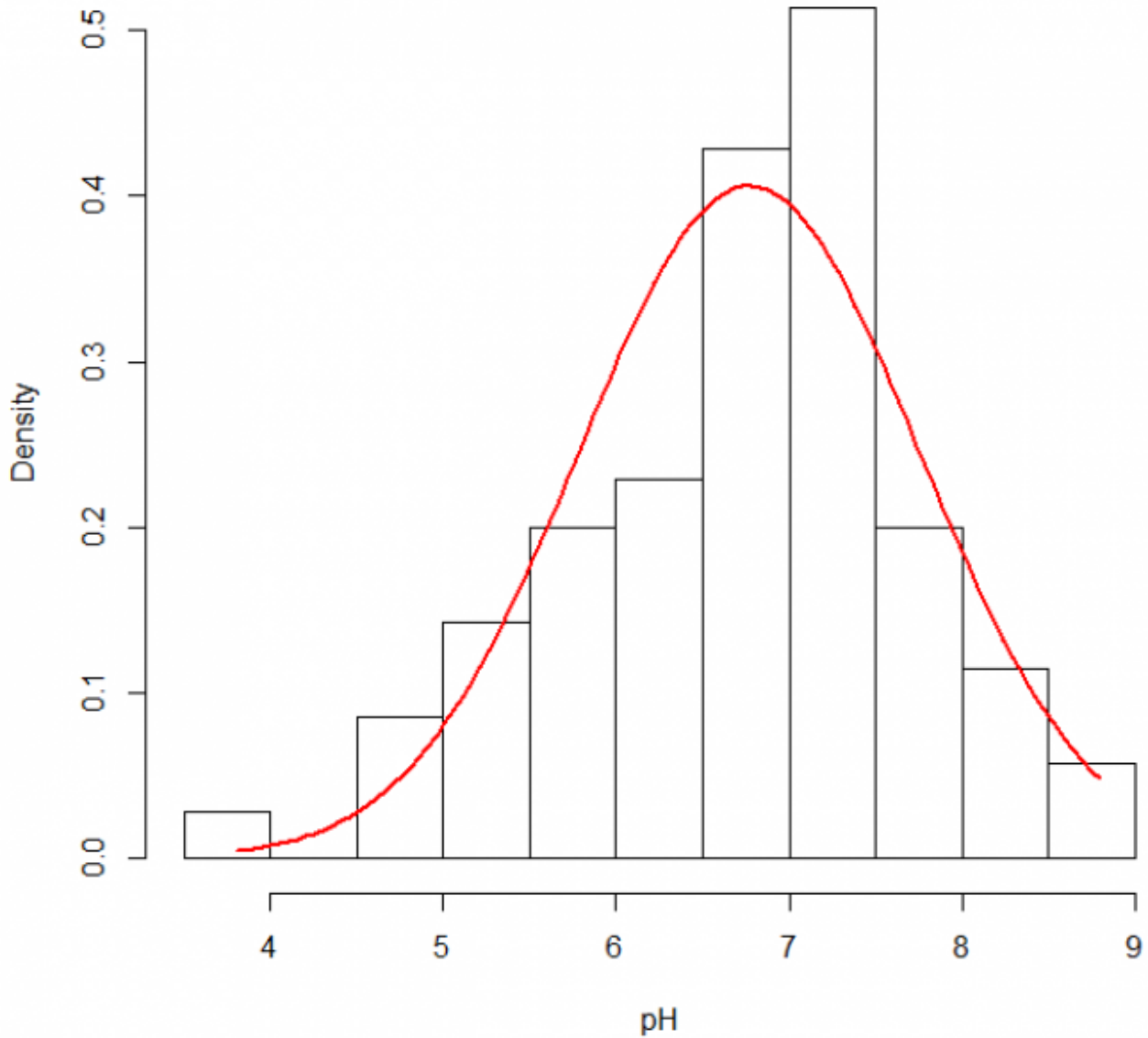
To modify color and thickness of the normal distribution curve, use arguments `lines.col` and `lines.lwd`. The function accepts most other arguments for `hist`, with some limitations.

Example of use (using environmental data from the dataset [Vegetation of Carpathian wetlands](#)):

## source

```
('http://www.davidzeleny.net/anadat-r/doku.php/en:customized_functions:hist.
dnorm?do=export_code&codeblock=0') # reads the function definition from
above
chem <- read.delim
('https://raw.githubusercontent.com/zdealveindy/anadat-r/master/data/chemist
ry.txt', row.names = 1) # reads the 'chem' dataset
hist.dnorm (chem$pH, xlab = 'pH', main = 'Histogram of pH')
```

### Histogram of pH



From: <https://www.davidzeleny.net/anadat-r/> - **Analysis of community ecology data in R**  
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Last update: **2018/03/30 23:04**