2016-11-09

# section title

## R Markdown

This is an R Markdown document. Markdown is a simple formatting syntax for authoring HTML, PDF, and MS Word documents. For more details on using R Markdown see <http://rmarkdown.rstudio.com>.

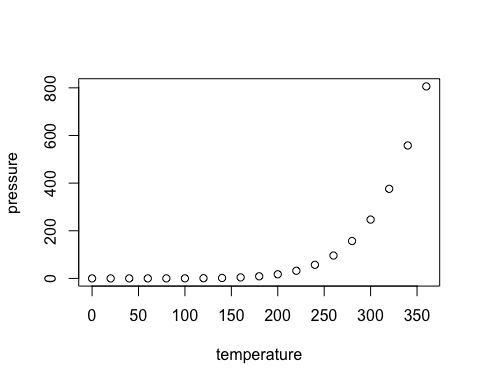
When you click the **Knit** button a document will be generated that includes both content as well as the output of any embedded R code chunks within the document. You can embed an R code chunk like this:

summary(cars)

## speed dist   
## Min. : 4.0 Min. : 2.00   
## 1st Qu.:12.0 1st Qu.: 26.00   
## Median :15.0 Median : 36.00   
## Mean :15.4 Mean : 42.98   
## 3rd Qu.:19.0 3rd Qu.: 56.00   
## Max. :25.0 Max. :120.00

## Including Plots

You can also embed plots, for example:



Note that the echo = FALSE parameter was added to the code chunk to prevent printing of the R code that generated the plot.

# values  
# values$res\_obj

# Session Information

sessionInfo()

## R version 3.3.0 (2016-05-03)  
## Platform: x86\_64-apple-darwin13.4.0 (64-bit)  
## Running under: OS X 10.10.5 (Yosemite)  
##   
## locale:  
## [1] de\_DE.UTF-8/de\_DE.UTF-8/de\_DE.UTF-8/C/de\_DE.UTF-8/de\_DE.UTF-8  
##   
## attached base packages:  
## [1] stats4 parallel stats graphics grDevices utils datasets   
## [8] methods base   
##   
## other attached packages:  
## [1] dplyr\_0.5.0 IHW\_1.2.0   
## [3] FMmisc\_0.2 org.Hs.eg.db\_3.4.0   
## [5] AnnotationDbi\_1.36.0 pheatmap\_1.0.8   
## [7] rmarkdown\_1.1 knitr\_1.14.10   
## [9] DT\_0.2 shinyAce\_0.2.1   
## [11] ggplot2\_2.1.0.9001 DESeq2\_1.14.0   
## [13] airway\_0.107.2 SummarizedExperiment\_1.4.0  
## [15] GenomicRanges\_1.26.0 GenomeInfoDb\_1.10.0   
## [17] IRanges\_2.8.0 S4Vectors\_0.12.0   
## [19] pcaExplorer\_2.0.0 Biobase\_2.34.0   
## [21] BiocGenerics\_0.20.0 d3heatmap\_0.6.1.1   
## [23] shiny\_0.14.1 shinydashboard\_0.5.3   
##   
## loaded via a namespace (and not attached):  
## [1] colorspace\_1.2-7 rsconnect\_0.5 markdown\_0.7.7   
## [4] XVector\_0.14.0 base64enc\_0.1-3 topGO\_2.26.0   
## [7] ggrepel\_0.6.2 codetools\_0.2-15 splines\_3.3.0   
## [10] doParallel\_1.0.10 geneplotter\_1.52.0 Formula\_1.2-1   
## [13] jsonlite\_1.1 gridBase\_0.4-7 annotate\_1.52.0   
## [16] cluster\_2.0.5 GO.db\_3.4.0 png\_0.1-7   
## [19] graph\_1.52.0 GOstats\_2.40.0 assertthat\_0.1   
## [22] Matrix\_1.2-7.1 lazyeval\_0.2.0.9000 limma\_3.30.0   
## [25] acepack\_1.3-3.3 htmltools\_0.3.5 tools\_3.3.0   
## [28] gtable\_0.2.0 Category\_2.40.0 reshape2\_1.4.1   
## [31] Rcpp\_0.12.7 slam\_0.1-37 NMF\_0.20.6   
## [34] gdata\_2.17.0 iterators\_1.0.8 stringr\_1.1.0   
## [37] mime\_0.5 gtools\_3.5.0 rngtools\_1.2.4   
## [40] XML\_3.98-1.4 zlibbioc\_1.20.0 scales\_0.4.0.9003   
## [43] shinyBS\_0.61 RBGL\_1.50.0 SparseM\_1.72   
## [46] RColorBrewer\_1.1-2 yaml\_2.1.13 gridExtra\_2.2.1   
## [49] pkgmaker\_0.22 biomaRt\_2.30.0 ideal\_0.1.0   
## [52] rpart\_4.1-10 latticeExtra\_0.6-28 stringi\_1.1.2   
## [55] RSQLite\_1.0.0 highr\_0.6 genefilter\_1.56.0   
## [58] foreach\_1.4.3 caTools\_1.17.1 BiocParallel\_1.8.0   
## [61] chron\_2.3-47 matrixStats\_0.51.0 bitops\_1.0-6   
## [64] evaluate\_0.10 lattice\_0.20-34 lpsymphony\_1.2.0   
## [67] htmlwidgets\_0.7 labeling\_0.3 GSEABase\_1.36.0   
## [70] AnnotationForge\_1.16.0 plyr\_1.8.4 magrittr\_1.5   
## [73] R6\_2.2.0 gplots\_3.0.1 Hmisc\_3.17-4   
## [76] DBI\_0.5-1 foreign\_0.8-67 survival\_2.39-5   
## [79] RCurl\_1.95-4.8 nnet\_7.3-12 tibble\_1.2   
## [82] KernSmooth\_2.23-15 fdrtool\_1.2.15 locfit\_1.5-9.1   
## [85] grid\_3.3.0 data.table\_1.9.6 threejs\_0.2.2   
## [88] digest\_0.6.10 xtable\_1.8-2 tidyr\_0.6.0   
## [91] httpuv\_1.3.3 munsell\_0.4.3 registry\_0.3

library(shiny)  
footertemplate <- function(){  
 tags$div(  
 class = "footer",  
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 tags$div(  
 class = "foot-inner",  
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 "This report was generated with",  
 tags$a(href="https://github.com/federicomarini/ideal", "ideal"), br(),  
 "ideal is a project developed by Federico Marini in the Bioinformatics division of the ",  
 tags$a(href="http://www.unimedizin-mainz.de/imbei","IMBEI"),br(),  
 "Development of the pcaExplorer package is on ",  
 tags$a(href="https://github.com/federicomarini/ideal", "GitHub")  
 )  
 )  
 )  
}

footertemplate()

This report was generated with ideal ideal is a project developed by Federico Marini in the Bioinformatics division of the IMBEI Development of the pcaExplorer package is on GitHub