Differential Methylation Regions within genome of colorectal cancer based on TCGA HumanMethylation450K dataset

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Summary

Sample distribution among different sites of resection or biopsy

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:

Table 1: sample distribution

	site	sampleNumber
1	Cecum	71
2	Sigmoid colon	68
3	Ascending colon	58
4	Rectum, NOS	52
5	Colon, NOS	47
6	Rectosigmoid junction	47
7	Descending colon	14
8	Transverse colon	14
9	Hepatic flexure of colon	13
10	Splenic flexure of colon	5
11	–	3
12	Connective, subcutaneous and other soft tissues of abdomen	2

Including Plots

You can also embed plots, for example:
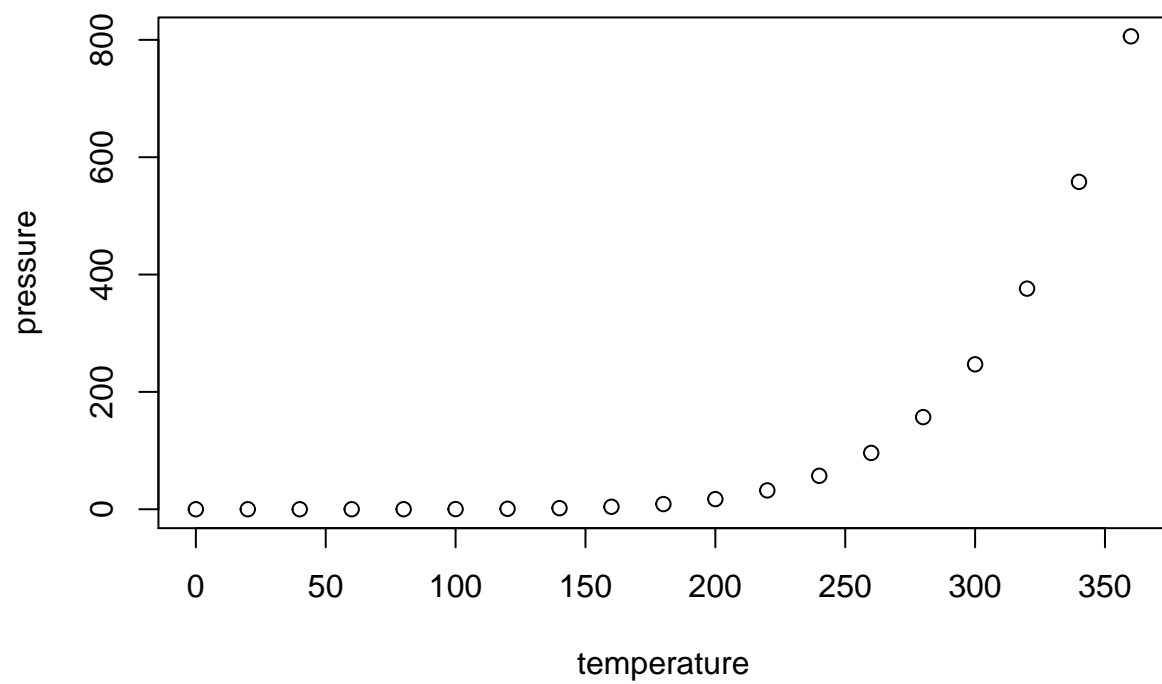
Note that the `echo = FALSE` parameter was added to the code chunk to prevent printing of the R code that generated the plot.