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# **R Markdown to PDF**

The addition of citation management

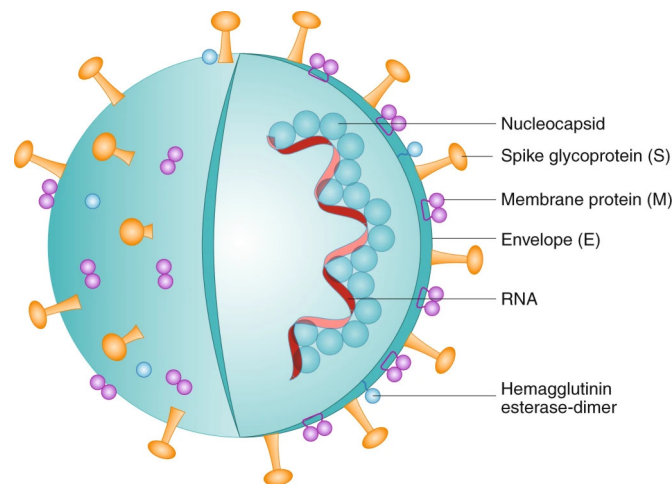
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## 1 Including Images and References



**Figure 1:** Schematic representation of SARS-CoV-2 structure. This is an enveloped, positive-sense RNA virus with four main structural proteins, including spike (S) and membrane (M) glycoproteins, as well as envelope (E) and nucleocapsid (N) proteins. Figure and caption from Florindo et al. (2020).

The figure [1](#) cross-referencing is enabled by `\label{}` and `\ref{}` commands. It refers to a bibtex reference `@Florindo2020` which is rendered as “Florindo et al. (2020),” along with an entry added to the reference list at the end of the document. The handling of reference is very convenient and still readable in plain text. For instance if I want to refer to reproducible science and Docker images (Nüst et al., 2020) the bracketed reference is added by `[@Nuest2020]`. Several references can be used so I can refer to several items of my PhD in a single reference (Collin et al., 2018; Collin, 2018) with `[@Collin2018;@Collin2018b]`. This citation system is flexible enough to allow free text within the citation call (Kapica-Topczewska, 2019, see the Kaplan-Meir step curves); this last reference is as: `[@Kapica-Topczewska2019a, see the Kaplan-Meir step curves]`.

## 2 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>.

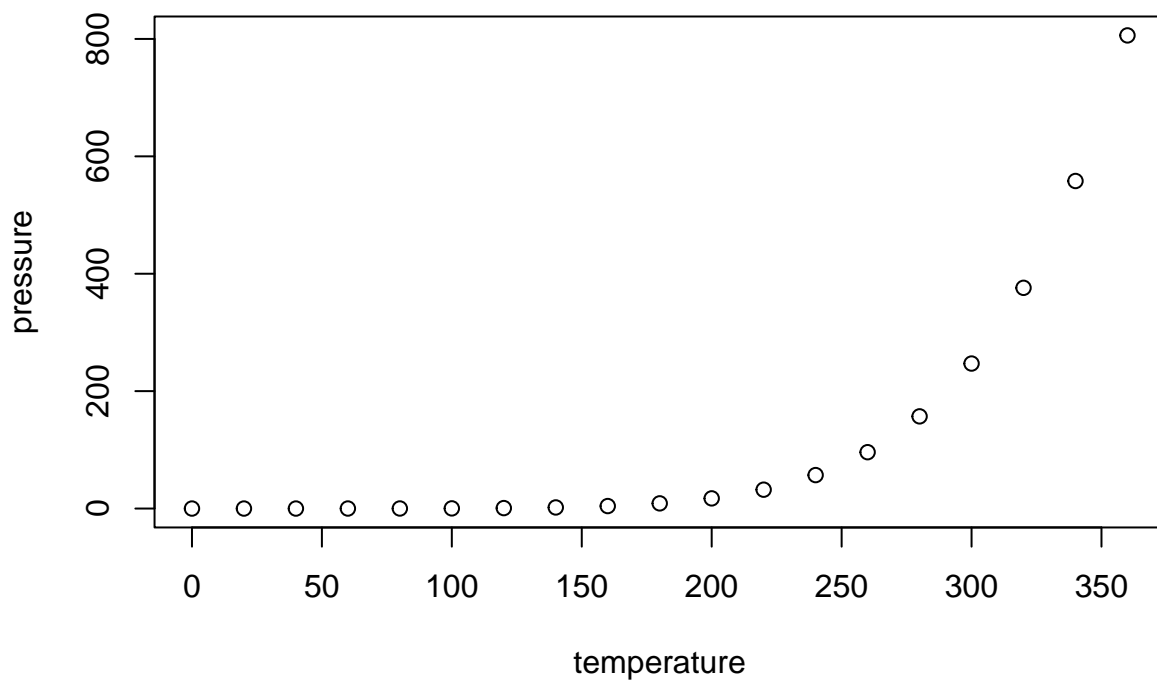
When you click the **Knit** button a document will be generated that includes both content as well as the output of any embedded R code chunks within the document. You can embed an R code chunk like this:

```
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
```

### 3 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.

## References

- Collin, F., Bancal, P., Spink, J., Kock Appelgren, P., Smith, J., Paveley, N.D., Bancal, M.-O., Foulkes, M.J., 2018. Wheat lines exhibiting variation in tolerance of Septoria tritici blotch differentiated by grain source limitation. *Field Crops Research* 217, 1–10. <https://doi.org/10.1016/j.fcr.2017.11.022>
- Collin, F.C., 2018. The tolerance of wheat (*triticum aestivum* L.) To septoria tritici blotch (PhD thesis). The University of Nottingham; L’Institut des sciences et industries du vivant et de l’environnement (AgroParisTech).
- Florindo, H.F., Kleiner, R., Vaskovich-Koubi, D., Acúrcio, R.C., Carreira, B., Yeini, E., Tiram, G., Liubomirski, Y., Satchi-Fainaro, R., 2020. Immune-mediated approaches against COVID-19. *Nature nanotechnology* 15, 630–645. <https://doi.org/10.1038/s41565-020-0732-3>
- Kapica-Topczewska, J.A.C., Katarzyna AND Tarasiuk, 2019. The effectiveness of interferon beta versus glatiramer acetate and natalizumab versus fingolimod in a polish real-world population. *PLOS ONE* 14, 1–12. <https://doi.org/10.1371/journal.pone.0223863>
- Nüst, D., Sochat, V., Marwick, B., Eglén, S.J., Head, T., Hirst, T., Evans, B.D., 2020. Ten simple rules for writing dockerfiles for reproducible data science. <https://doi.org/10.1371/journal.pcbi.1008316>