

R Markdown Template

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S1 Introduction

For large files, we can cache the file, and use `cache.lazy = T` to reuse the pre-computed results. To avoid overwriting the previously cached file, it is better to set the `cache= F`, when you want to use `cache.lazy` to get the previously saved results. In this case, you do not need to cache the file again. You can also load the cached file, and check the environment to see whether the variables have already been saved.

If `cache = T`, knitr will skip the execution of this code chunk if it has been executed before and nothing in the code chunk has changed since then. This is particularly useful when you want to reuse the figure (time-consuming). **When you modify the code chunk (e.g., revise the code or the chunk options), the previous cache will be automatically invalidated, and knitr will cache the chunk again.**

```
print("Hello R markdown!")
```

```
[1] "Hello R markdown!"
```

S2 Data and Methods

```
#include <Rcpp.h>
using namespace Rcpp;
// [[Rcpp::export]]
NumericVector timesTwo(NumericVector x) {
  return x * 2;
}

timesTwo(10) # test function in R chunk or console
```

S3 Results

We can also save the plot as png files, by setting the `dev = "png"`, and change the quality of the picture by setting `dpi = 300`.

Alternatively, you can convert all the saved pdfs into pngs with `imagemagick` in terminal:

```
convert -density 150 *.pdf -quality 100 -set filename:basename "[%basename]" "[%filename:basename].png"
```

S3.1 Cross-reference of figures, tables and equations

```
hist(rnorm(100))
```

We can also co-refer a plot in Figure S1. Pls avoid using underscore (`_`) or white space in the co-reference labels. Likewise, you can also use `\@ref{tab/eq:}` to refer to the specific table or equation. See Figure S3.

S4 Discussion

S5 Conclusions

We can also add the cross-reference inside the figure caption via `\@ref{fig:}`.

S6 References

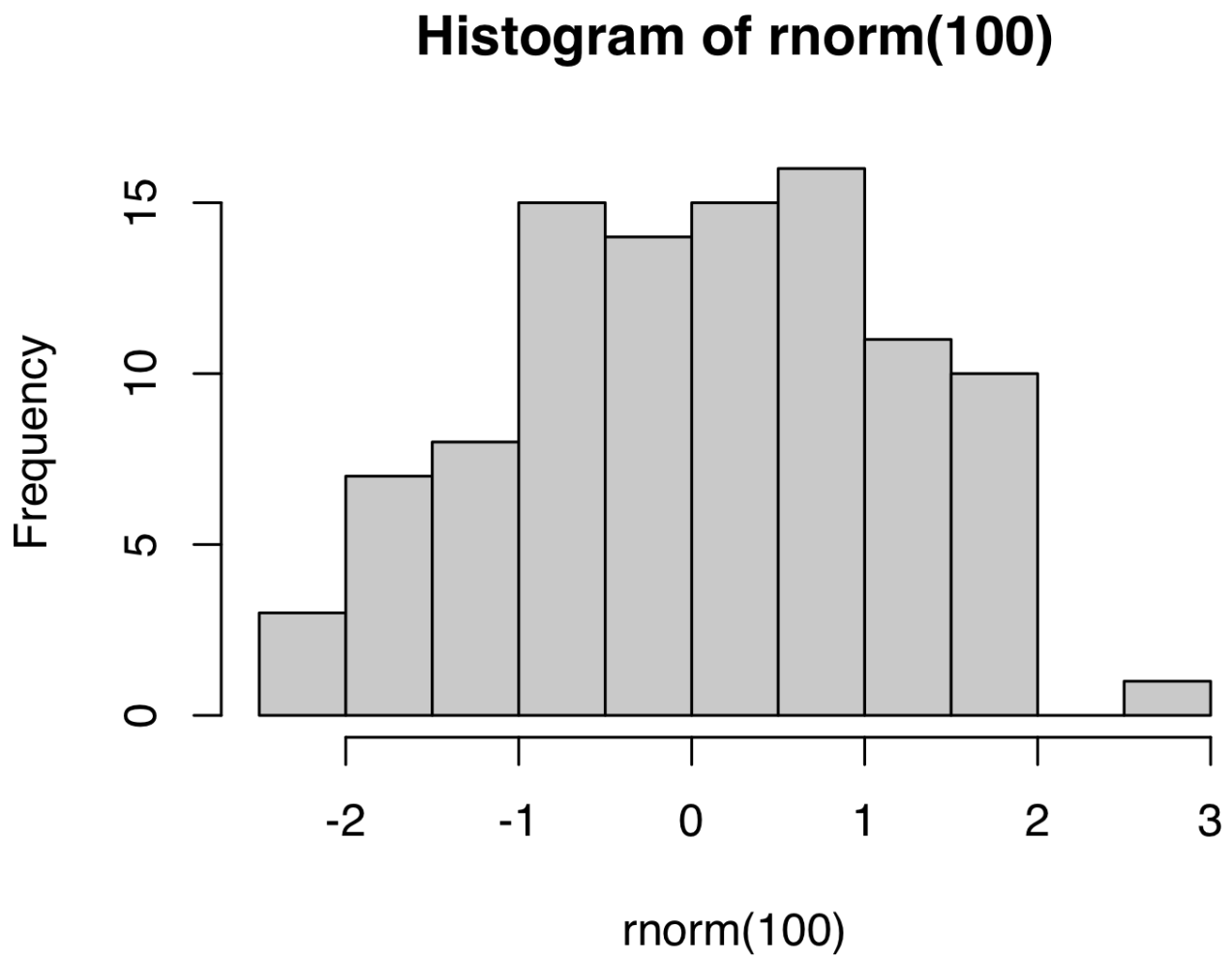


Figure S1: Histogram plot

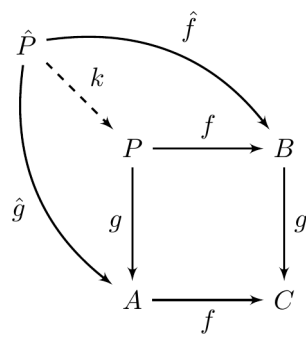
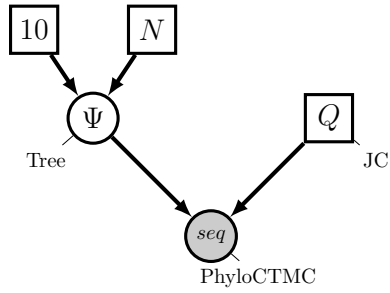


Figure S2: Tikz graph example



```
psi ~ dnUniformTopologyBranchLength(names, dnExponential(10))

Q_morpho <- fnJC(2)

phyMorpho ~ dnPhyloCTMC( tree=phylogeny,
  siteRates=rates_morpho, Q=Q_morpho,
  type="Standard", coding="variable" )
phyMorpho.clamp( data )
```

Figure S3: A example graphs of CTMC model (fig.size cannot be changed via fig.width or fig.height)

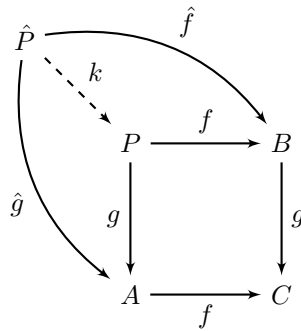


Figure S4: A copy of CTMC model in Figure S1 or Figure S1 (reuse by its labels; doesn't work for read_utf8)