

# Histopathology Research Template

*true*

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## 0.1 Header Codes

Codes for general settings.<sup>1</sup>

setup global chunk settings

Change echo = FALSE to hide codes after knitting.

```
knitr::opts_chunk$set(  
  eval = TRUE,  
  echo = TRUE,  
  fig.path = here::here("figs/"),  
  message = FALSE,  
  warning = FALSE,  
  error = FALSE,  
  cache = FALSE,  
  comment = NA,  
  tidy = TRUE,  
  fig.width = 12,  
  fig.height = 8  
)
```

load library

see R/loadLibrary.R for the libraries loaded.

```
source(file = here::here("R", "loadLibrary.R"))
```

---

## 0.2 Import Data

Codes for importing data.<sup>2</sup>

Use this code to generate fake clinicopathologic data

```
source(file = here::here("R", "generatingFakeData.R"))
```

Use this code to read the generated fake data

```
library(readxl)  
mydata <- readxl::read_excel(here::here("data", "mydata.xlsx"))  
# View(mydata)
```

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<sup>1</sup>See childRmd/\_header.Rmd file for other general settings

<sup>2</sup>See childRmd/\_importData.Rmd file for other codes