

Rapport interro S9

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chargez les packages

```
library(SummarizedExperiment)
library(rWSBIM1207)
library(tidyverse)
```

exercice 1

```
se <- read_rds("data/se.rds")
se

## class: SummarizedExperiment
## dim: 8 24
## metadata(0):
## assays(1): ''
## rownames(8): Gene1 Gene2 ... Gene7 Gene8
## rowData names(2): gene location
## colnames(24): CTRL0_1 CTRL0_2 ... DRUG5_7 DRUG5_8
## colData names(4): samples group rep conc

coldata_se <- colData(se)
```