

```
library(ggplot2)
data("msleep")
names(msleep)

## [1] "name"          "genus"          "vore"           "order"          "conservation"
## [6] "sleep_total"   "sleep_rem"      "sleep_cycle"    "awake"          "brainwt"
## [11] "bodywt"

ggplot(msleep, aes(sleep_total, sleep_rem)) +
  geom_point(colour = "red")

## Warning: Removed 22 rows containing missing values ('geom_point()').
```

