```
> set.seed(1)
> disease <- sample(c(0,1), size=1e6, replace=TRUE, prob=c(0.98,0.02))
> test <- rep(NA, 1e6)</pre>
> test[disease==0] <- sample(c(0,1), size=sum(disease==0), replace=TRUE, prob=c(0.90,0.10))
> test[disease==1] <- sample(c(0,1), size=sum(disease==1), replace=TRUE, prob=c(0.15, 0.85))
> # probability that a test is positive
> mean(test == 1)
[1] 0.114509
> # probability that an individual has the disease if the test is negative
> mean(disease[test == 0] == 1)
[1] 0.003461356
> # probability that an individual has the disease if the test is positive
> mean(disease[test == 1] == 1)
[1] 0.1471762
> # relative risk of having disease when test is positive
> mean(disease[test == 1] == 1) / mean(disease == 1)
[1] 7.389106
```