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# Example 1: calculate classification measures from Klee et al. (2000)
dat <- as.table(matrix(c(10, 2, 1, 51), nrow = 2, byrow = TRUE))
rval <- epi.tests(dat, conf.level = 0.95)
print(rval) # for point estimates and CIs rounded to 2 DPs
```

```
##           Outcome +   Outcome -   Total
## Test +           10             2      12
## Test -             1          51      52
## Total            11          53      64
##
## Point estimates and 95 % CIs:
## -----
## Apparent prevalence           0.19 (0.10, 0.30)
## True prevalence               0.17 (0.09, 0.29)
## Sensitivity                   0.91 (0.59, 1.00)
## Specificity                   0.96 (0.87, 1.00)
## Positive predictive value     0.83 (0.52, 0.98)
## Negative predictive value     0.98 (0.90, 1.00)
## Positive likelihood ratio     24.09 (6.11, 95.02)
## Negative likelihood ratio     0.09 (0.01, 0.61)
## -----
```