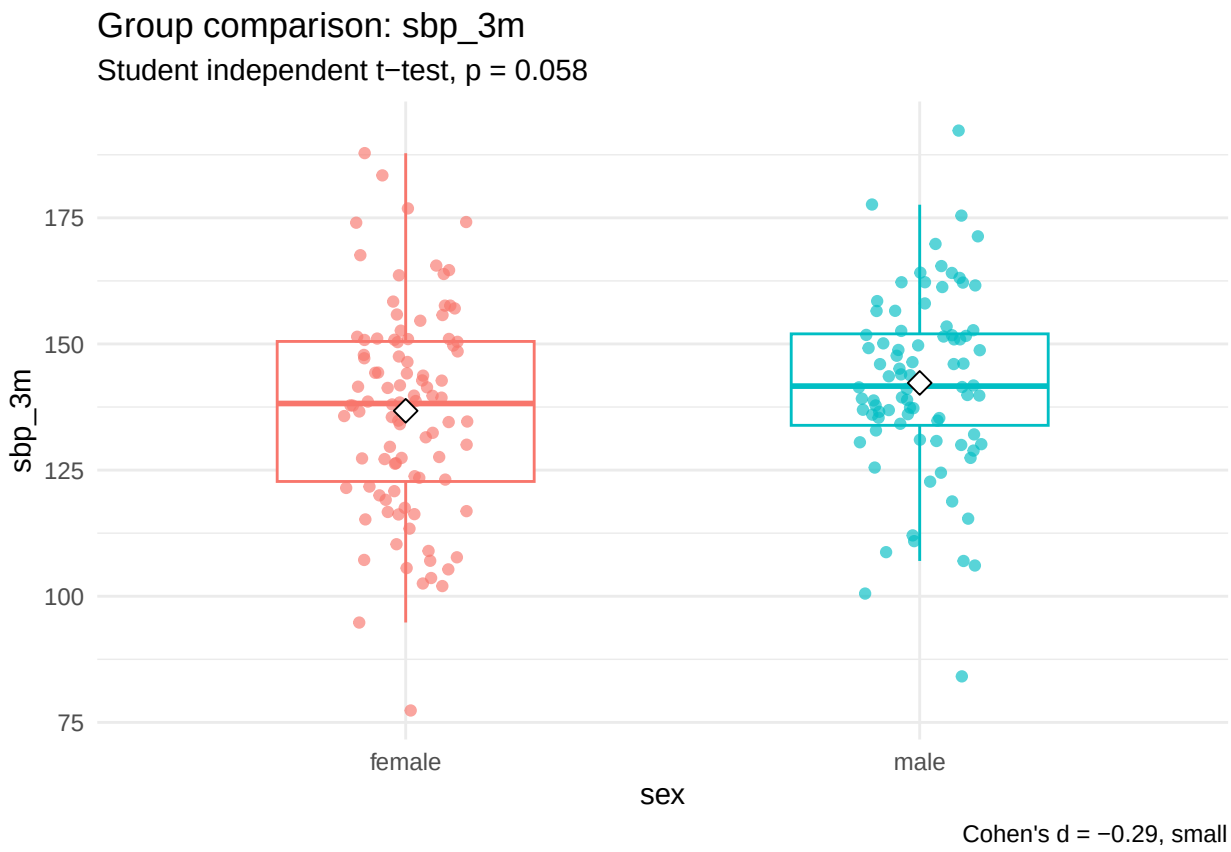
Getting started with testflow

Getting started

`testflow` starts with the study design.

```
library(testflow)
cardio <- make_cardio_data()
x <- test_two_groups(sbp_3m ~ sex, data = cardio)
x
#> Two Independent Groups
#>
#> Outcome: sbp_3m
#> Group: sex
#>
#> Assumptions
#> * Independence of observations: assumed: Assumed from study design.
#> * Normality: sbp_3m (female): acceptable: Approximate normality looks reasonable. (method=Shapiro-Wi
#> * Normality: sbp_3m (male): acceptable: Approximate normality looks reasonable. (method=Shapiro-Wilk
#> * Variance homogeneity: acceptable: Variance homogeneity looks reasonable. (method=Levene test; stat
#> * Extreme outliers: warning: 4 potential outlier(s) flagged by IQR. (IQR rule, n = 4)
#> * Variance ratio check: acceptable: Variance ratio looks reasonable. (statistic=1.27)
#>
#> Recommended test
#> Student independent t-test
#>
#> Result
#> H0: the population mean or location of sbp_3m is equal across levels of sex.
#> statistic = -1.91, df = 178.00, p = 0.058, 95% CI [-11.22, 0.18]
#>
#> Effect size
#> Cohen's d: -0.29, small
#>
#> Report
#> The two independent groups workflow for sbp_3m did not show a statistically significant result using
report(x)
#> [1] "The two independent groups workflow for sbp_3m did not show a statistically significant result
plot(x)
```


Group comparison: sbp_3m
Student independent t−test, p = 0.058
sbp_3m
175
150
125
100
75
female
male
sex
Cohen's d = −0.29, small