

Consider a hypothesis test about the parameter  $\theta$ :

$$H_0: heta = heta_0 \ H_a: heta > heta_0$$

We let  $\beta = P(\text{fail to reject } H_0|H_0 \text{ is false}) = P(\text{Type II error})$ , then Power =  $P(\text{reject } H_0|H_0 \text{ is false}) = 1 - \beta$ .

Power depends on the distance between the hypothesized value of the parameter  $\theta_0$  and the actual value  $\theta_1$ , so we can write  $1 - \beta(\theta_1)$ .

the effect size.

Why is power important?

- 1. If we have multiple statistical festing methods for the same hypothesis (similar size) choose test that is the most powerful.
- 2. If we are goly to spend time/money to run an experiment, need to check beforehand that the study is powerful enough to detect an effect.

2.3 Power

For a few simple cases, you can derive a closed form expression of power.

Example 2.4 Consider a one-sample z-test. Sample  $X_1, \ldots, X_n \stackrel{iid}{\sim} N(\mu, \sigma^2)$ .

Ho:  $\mu = \mu_0$ Ho:  $\mu = \mu_0$ Using statistic  $Z^* = \frac{\overline{\chi} - \mu_0}{5/\tau_0}$ , where  $\mu_0 = \mu_0$ We reject to if  $Z^* > Z_{1-\alpha}$  control where  $\mu_0 = \mu_0 = \mu_0$ If  $\mu_0 = 5$  (hypothesized value) but time near  $\mu_1 = 6$ What is the probability of creetly rejecting  $\mu_0 = \mu_0 = \mu_0 = \mu_0$ Effect size:  $\mu_1 - \mu_0 = \mu_0 = \mu_0 = \mu_0 = \mu_0 = \mu_0 = \mu_0$ For the  $\mu_0 = \mu_0 = \mu_$ 

the z-test, we can derive point (Chikara & Hesterberg p. 229-230)
$$|-\beta| = P(\text{reject Ho} \mid \text{Ho is felse})$$

$$= P(Z^* > Z_{1-\underline{q}} - \frac{(\mu_1 - \mu_0)}{6/40})$$

So power is a function of

Smillest Z where you will right Ho.

- (1.) Significance level: as &1, power 1 (trade-off between type I and type I error).
- 2. Effect size: M,-Mo as effect size 1, power 1.
- 3.) Sample size: as no, power T
- 4. Variance: as variance to power 1 (no control over this in practice).

Notes: (Das porce = 1-BT, P(type I error) = al. For fixed n, o, & Mi-Mo,
the only way to increase power is to 9 a

2) Only way to simultaneously 1 pour + dod, must 1 n. (fixed effect size).

new

## **2.4** MC Estimator of $1 - \beta$

Assume  $X_1, \ldots, X_n \sim F(\theta_0)$  (i.e., assume  $H_0$  is true).

Then, we have the following hypothesis test -

$$H_0: heta = heta_0 \ H_a: heta heta_0$$

and the statistics  $T^*$ , which is a test statistic computed from data. Then we **reject**  $H_0$  if  $T^* >$  the critical value from the distribution of the test statistic.

This leads to the following algorithm to estimate the power of the test  $(1 - \beta)$ 

$$(x, \alpha)$$
 Sample  $(x, \alpha)$ ,  $(x, \alpha)$  from model under the alternative hypothesis  $(x, \alpha)$   $(x, \alpha)$ 

## Your Turn

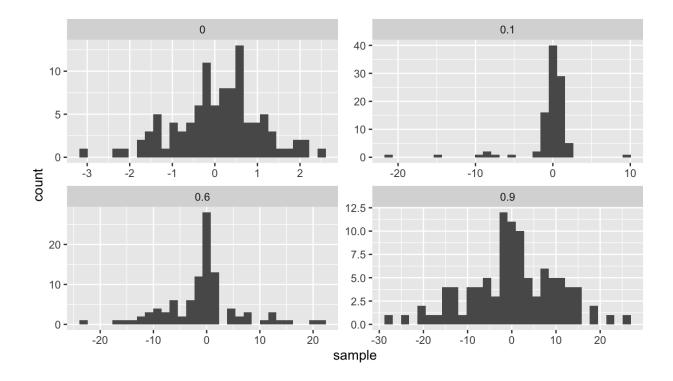
Consider data generated from the following mixture distribution:

$$f(x) = (1 - \epsilon)f_1(x) + \epsilon f_2(x), \quad x \in \mathbb{R}$$

where  $f_1$  is the pdf of a N(0,1) distribution,  $f_2$  is the pdf of a N(0,100) distribution, and  $\epsilon \in [0,1]$ .

```
r_noisy_normal <- function(n, epsilon) {
  z <- rbinom(n, 1, 1 - epsilon)
  z*rnorm(n, 0, 1) + (1 - z)*rnorm(n, 0, 10)
}

n <- 100
data.frame(e = 0, sample = r_noisy_normal(n, 0)) %>%
  rbind(data.frame(e = 0.1, sample = r_noisy_normal(n, 0.1))) %>%
  rbind(data.frame(e = 0.6, sample = r_noisy_normal(n, 0.6))) %>%
  rbind(data.frame(e = 0.9, sample = r_noisy_normal(n, 0.6))) %>%
  rbind(data.frame(e = 0.9, sample = r_noisy_normal(n, 0.9))) %>%
  ggplot() +
  geom_histogram(aes(sample)) +
  facet wrap(.~e, scales = "free")
```



We will compare the power of various tests of normality. Let  $F_X$  be the distribution of a random variable X. We will consider the following hypothesis test,

ill consider the following hypothesis test, i.e. Ho says 
$$\chi$$
 is Normlly  $H_0: F_x \in N$  vs.  $H_a: F_x \notin N$ ,

where N denotes the family of univariate Normal distributions.

Recall Pearson's moment coefficient of skewness (See Example 2.2).

We will compare Monte Carlo estimates of power for different levels of contamination ( $0 \le \epsilon \le 1$ ). We will use  $\alpha = 0.1$ , n = 100, and m = 100.

```
H_0: \sqrt{\beta_1} = 0
                                                             H_a: \int_{B_1} \neq 0.
# skewness statistic function
skew <- function(x) {</pre>
  xbar <- mean(x)
  num \leftarrow mean((x - xbar)^3)
  denom \leftarrow mean((x - xbar)^2)
  num/denom<sup>1.5</sup>
}
# setup for MC
alpha <- .1
n < -100
m < -100
epsilon \leftarrow seq(0, 1, length.out = 200)
var sqrt b1 \leftarrow 6*(n - 2)/((n + 1)*(n + 3)) # adjusted variance for
 skewness test
crit val <- qnorm(1 - alpha/2, 0, sqrt(var sqrt b1)) #crit value for</pre>
  the test
empirical pwr <- rep(NA, length(epsilon)) #storage</pre>
# estimate power for each value of epsilon
for(j in 1:length(epsilon)) {
  # perform MC to estimate empirical power
  ## Your turn
}
                                                  \int \hat{p} (1-\hat{p})/m
## store empirical se
empirical se <- "Your Turn: fill this in"
## plot results --
## x axis = epsilon values
## y axis = empirical power
## use lines + add band of estimate +/- se
```

Compare the power with n=100 to the power with n=10. Make a plot to compare the two for many values of  $\epsilon$ .

for what levels of contamination (E) will be have power ≥ 6,8

Recall pover dyeds on. 1) led of test 2) scrple size