

## PSY 8814 Assignment 5

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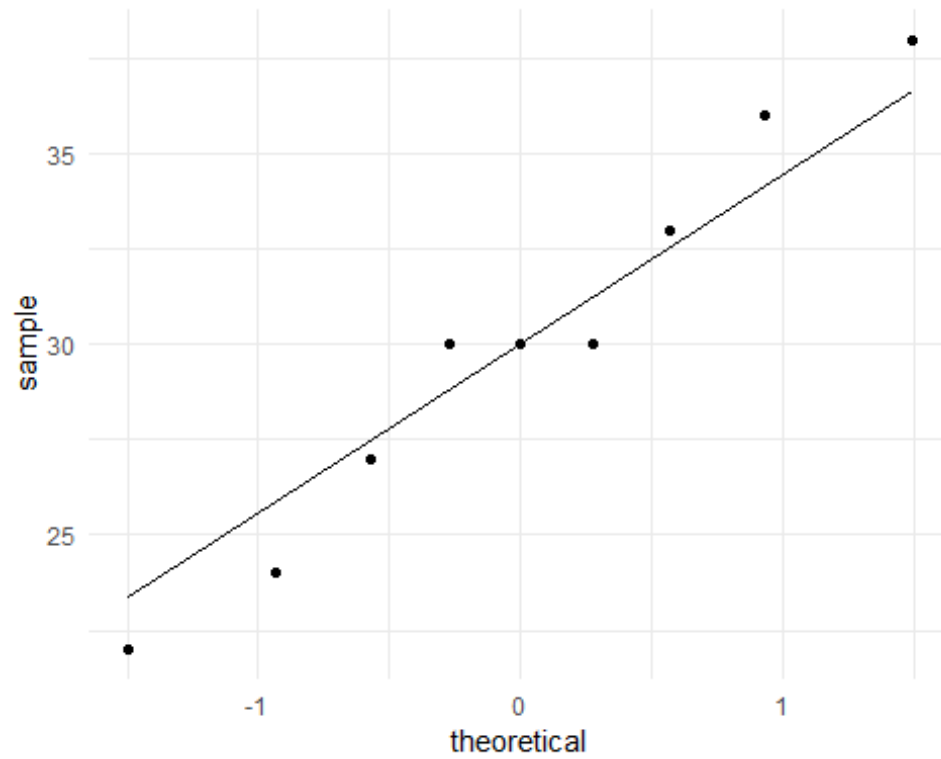
### Exercise 5.1

Jim was interested in testing whether an expensive treatment affected anxiety in a particular population with a mean of  $\mu = 22$  and a standard deviation of  $\sigma = 6$  on a well-known anxiety scale. After collecting  $N = 9$  individuals, he administered the treatment to each of them, and following treatment, gathered their scores on the anxiety scale. The  $N = 9$  individuals had the following scores on the anxiety scale following treatment: 36, 27, 30, 33, 22, 30, 30, 24, 38. Test the research hypothesis that the group who were given the treatment had different scores on the anxiety scale (on average) than the general population. Perform the test using  $\alpha = 0.05$ . Make sure to check for normality and outliers using graphical and/or numerical methods.

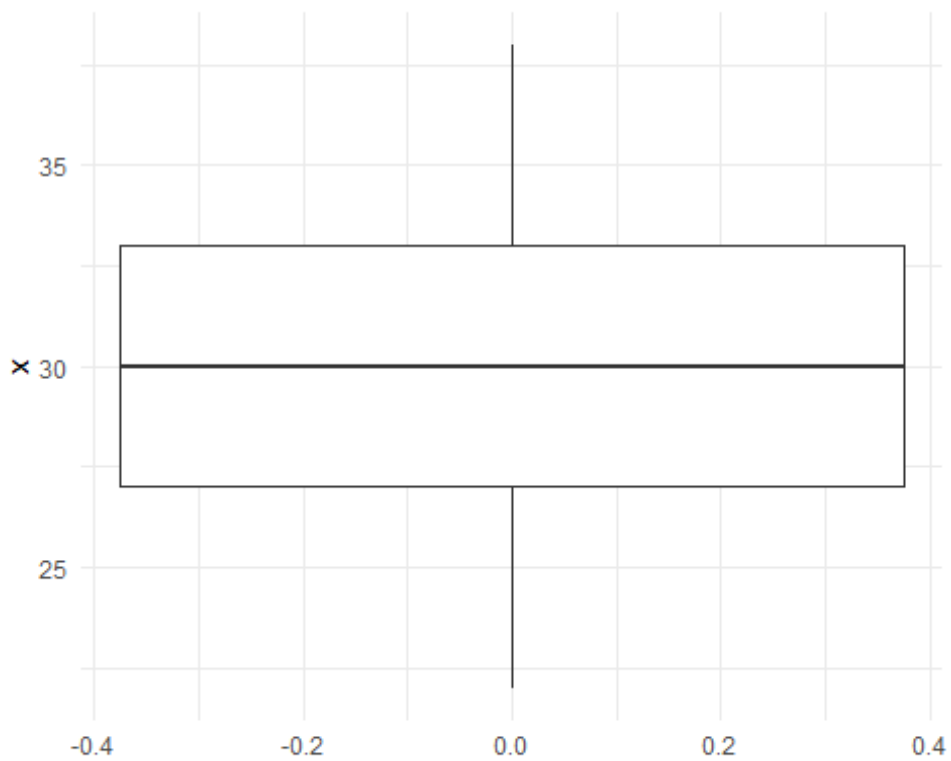
```
# inits
mu = 22;
sd = 6;
N = 9;
x = c(36, 27, 30, 33, 22, 30, 30, 24, 38);
alpha = .05;

# Calculate sample statistics
xhat = mean(x);
sdhat = sd/sqrt(N);

# Look at the Normality
ggplot(data.frame(x), aes(sample=x)) + stat_qq() + stat_qq_line() +
theme_minimal()
```



```
# Look for outliers  
ggplot(data.frame(x), aes(y=x)) + stat_boxplot() + theme_minimal()
```



```

# H0: xhat = mu
# H1: xhat != mu
# We will use a two-tailed hypothesis test.
# Calculate the CI under null distribution
gamma = alpha/2;
H0_low = mu + pnorm(gamma)*sdhat;
H0_high = mu + pnorm(1-gamma)*sdhat;

# One way we could test this is whether the sample mean, xhat, is within the
95% CI
# of the null distribution. If it is, we can accept the null, if not, we
reject the null.
(xhat >= H0_low && xhat <= H0_high)

## [1] FALSE

# Another way is to get the p-value associated with it's z-score
z = (xhat - mu)/sdhat;
pvalue = 1-pnorm(z) # the p-value of sample mean under the null
pvalue

## [1] 3.167124e-05

```

Using NHST, we would reject the null hypothesis,  $\mu_0 = 22$  given the data,  $\alpha = 0.05$ , and the resulting p-value,  $3.167124210^{-5}$ .

## Exercise 5.2

A researcher has developed a test of reading readiness to use as the dependent variable in an experiment. He is certain that the children's scores on the test are independent and normally distributed with a variance of  $\sigma^2 = 4$ , but he does not know the mean of the scores.

(a) Assume that he wants to test the null hypothesis of  $H_0 : \mu \leq 5$ .

i) If he has  $N = 9$  independent observations, what is the cut-off sample mean for a significant result at  $\alpha = 0.05$ ?

```

# init
sd = sqrt(4);
N = 9;
alpha = 0.05;

# calculate sample statistics
mu = 5;
sdhat = sd/sqrt(N);

# H0: mu <= 5
# H1: mu > 5
# For this problem, we will use a one-tailed test, therefore:
gamma = alpha;

```

```
cutoff = mu + qnorm(1-gamma)*sdhat;
cutoff

## [1] 6.096569
```

**The cut-off sample mean in this case is 6.0965691.**

ii) Assume he would like to detect an effect if the true mean is, in fact,  $\mu = 8$ . For i., what is the corresponding “power” of the test to detect a mean of at least  $\mu = 8$ ? In other words, what is the probability of finding a significant result with  $\alpha = 0.05$  when  $\mu = 8$ ?

```
# init
mu2 = 8;

# Calculate power by inverting beta:
beta = pnorm(cutoff,mu2,sdhat); # how much of the true distribution lies
below the cutoff
power = 1 - beta # how much of the true sample distribution lies above the
cutoff
```

**The probability of finding a significant result under these circumstances is 0.9978492.**

iii) What decision about the null hypothesis would the researcher make if he observed a sample mean of  $\bar{x} = 5.5$  or  $\bar{x} = 7.5$ ?

**If the researcher observed  $\bar{x} = 5.5$  they would fail to reject the null, and if the researcher observed  $\bar{x} = 7.5$  they would reject the null.**

(b) Assume that he wishes to test  $H_0 : \mu = 5$  versus a two-sided alternative of  $H_1 : \mu \neq 5$  for the sample of  $N = 9$  observations.

i) What is the relationship of the critical values/rejection region between the two-sided test and the test performed in (a)?

**The test performed in (a) was one-sided; it has the same area under the curve as the two-tailed test of the sample  $\alpha$ , but a larger z-critical value. Therefore, the two-tailed is more critical in any given direction, compared to a one-tailed test of the same alpha.**

ii) When should he prefer to use the critical regions found in (a)? When should he prefer to use the critical regions found in (b)?

**He should prefer the critical regions in (a) if his alternative hypothesis includes a specific direction of an effect. The critical regions found in (b) would be useful if direction is not important, just a difference.**

## Exercise 5.3

When talking about sampling distributions you learned that, if  $X$  is normally distributed,  $X \sim N(\mu, \sigma_{\bar{X}})$ . In hypothesis testing, if  $H_0$  is true, this means that  $X \sim N(\mu_0, \sigma_{\bar{X}})$ . Remember,  $\mu_0$  is the hypothesized population mean under  $H_0$ , i.e.  $H_0 : \mu = \mu_0$ , and  $\sigma_{\bar{X}} = \frac{\sigma}{\sqrt{N}}$ .

Imagine your friend is doing a NHST, testing  $H_0 : \mu = 5$ . They draw a sample from a population of scores which are normally distributed with  $\mu = 5$  and  $\sigma = 12$ . Your friend draws a sample of size 20 and uses  $\alpha = .05$ .

(a) What is the probability that your friend will commit a Type I error?

**The probability of committing a Type I error is  $\alpha$ , or 0.05.**

(b) What is the probability that your friend will commit a Type II error?

**You cannot commit a Type II error, as the null hypothesis is true.**

(c) Use a simulation study in R to demonstrate your answer to (a). You should randomly generate a large number of samples from the appropriate distribution (say, 10,000) and for each sample determine whether your friend would have rejected  $H_0$ . Then calculate in what proportion of the samples your friend would have rejected  $H_0$ .

```
set.seed(8814.4) # set seed for replicability

# Init
mu = 5;
sd = 12;
N = 20;
alpha = 0.05;
sdhat = sd/sqrt(N);

# Generate 95% CI as the boundaries for accept/reject
bounds = c(mu + qnorm(alpha/2)*sdhat, mu + qnorm(1-alpha/2)*sdhat);

# Simulation params
n_reject = 0; # counter
n_sims = 10000; # number of samples generated

# Simulation loop
for (i in 1:n_sims){
  # Generate a sample from the population, and calculate the mean
  sample = rnorm(n=N,mean=mu,sd=sd);
  xhat = mean(sample);
  xhat
  # If xhat is out of the CI boundary, add it to the rejection count
  if (xhat < bounds[1] || xhat > bounds[2]){
    n_reject = n_reject + 1;
  }
}
# Proportion of rejects
P_reject = n_reject/n_sims
P_reject

## [1] 0.0478
```

**The Type I error rate in the simulation is 0.0478, which is approximately  $\alpha = 0.05$ .**