

# Statistical Method HW5

RE6124019

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Given the sepal width of "iris" data, use the following steps to show if the mean of sepal width is 3. Assume the sepal widths are random samples from a normal distribution.

```
data("iris")
sepal_width = iris$Sepal.Width
```

(a) Use the maximum likelihood estimation method to estimate the model parameters of the normal distribution.

```
maxlikelihood.normal <- function(parameters, data) {
  mu <- parameters[1]
  sigma <- parameters[2]
  joint <- dnorm(data, mean = mu, sd = sigma)
  return(-sum(log(joint)))
}

opt <- optim(c(3, 0.1), maxlikelihood.normal, data = sepal_width)

mu_hat_mle <- opt$par[1]
sigma_hat_mle <- opt$par[2]
```

```
cat("Maximum Likelihood Estimates:\n")
```

```
## Maximum Likelihood Estimates:
```

```
cat("  Estimated Mean (mu): ", mu_hat_mle, "\n")
```

```
##   Estimated Mean (mu):  3.057459
```

```
cat("  Estimated Standard Deviation (sigma): ", sigma_hat_mle, "\n")
```

```
##   Estimated Standard Deviation (sigma):  0.4344073
```

(b) According to the question "if the mean of sepal width is 3", what is the estimate for the quantity of interest?

If the mean of sepal width is 3, the estimate for the quantity of interest is the estimated mean ( $\mu_{\text{hat\_mle}}$ ).

```
cat("Estimate for the Quantity of Interest:\n")
```

```
## Estimate for the Quantity of Interest:
```

```
cat("  Estimated Mean (mu): ", mu_hat_mle, "\n")
```

```
##    Estimated Mean (mu):  3.057459
```

(c) Construct the 95% confidence interval for the the true quantity of interest by bootstrapping.

```
set.seed(123) # Set seed for reproducibility
bootstrap_means <- replicate(1000, mean(sample(sepal_width, length(sepal_width), replace = TRUE)))

# Calculate confidence interval
conf_interval <- quantile(bootstrap_means, c(0.025, 0.975))
```

```
cat("\n95% Confidence Interval (Bootstrapping):\n")
```

```
##
```

```
## 95% Confidence Interval (Bootstrapping):
```

```
cat("  Lower bound: ", conf_interval[1], "\n")
```

```
##    Lower bound:  2.9893
```

```
cat("  Upper bound: ", conf_interval[2], "\n")
```

```
##    Upper bound:  3.12535
```

the 95% confidence interval for the the true quantity of interest by bootstrapping is [2.9893, 3.1253]

(d) Based on the 95% confidence interval in (c), how would you conclude the question "if the mean of sepal width is 3"?

```
if (conf_interval[1] <= 3 && conf_interval[2] >= 3) {
  cat("\nConclusion: The true mean of sepal width is likely to be around 3.\n")
} else {
  cat("\nConclusion: The true mean of sepal width is unlikely to be exactly 3.\n")
}
```

```
##  
## Conclusion: The true mean of sepal width is likely to be around 3.
```

We can say that “The true mean of sepal width is likely to be around 3” because 3 is in the interval [2.9893, 3.1253]

(e) If I use a one-sample t-test to test if  $H_0 : \mu = 3$ , is the conclusion as the same as the result in (d)?

```
t_test_result <- t.test(sepal_width, alternative = 'two.sided', mu = 3)  
  
cat("\nOne-Sample t-test Result:\n")
```

```
##  
## One-Sample t-test Result:
```

```
cat("  Test Statistic: ", t_test_result$statistic, "\n")
```

```
##  Test Statistic:  1.611015
```

```
cat("  P-value: ", t_test_result$p.value, "\n")
```

```
##  P-value:  0.1092929
```

```
# Draw a conclusion based on the significance level (e.g., 0.05)  
alpha <- 0.05  
if (t_test_result$p.value < alpha) {  
  cat("\nConclusion: Reject the null hypothesis ( $\mu = 3$ ).\n")  
} else {  
  cat("\nConclusion: Fail to reject the null hypothesis ( $\mu = 3$ ).\n")  
}
```

```
##  
## Conclusion: Fail to reject the null hypothesis ( $\mu = 3$ ).
```

The P-value  $> 0.05$  do not reject the  $H_0$

Compare this conclusion with the conclusion in Part (d) where you constructed a confidence interval using bootstrapping. If the confidence interval includes 3, it suggests that the mean may not be significantly different from 3. If the p-value from the one-sample t-test is greater than your significance level, it aligns with the conclusion from Part (d).

In summary, the conclusions should be consistent between the one-sample t-test and the analysis in Part (d).