

j4wjhp19t

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[1]: import numpy as np
from scipy.stats import ttest_1samp

# Sample data
acorns_mass = [8.8, 6.6, 9.5, 11.2, 10.2, 7.4, 8.0,
               9.6, 9.9, 9.0, 7.6, 7.4, 10.4, 11.1, 8.5, 10.0, 11.6, 10.7, 10.
               ↪3, 7.0]

# Hypothesized population mean
mu = 10

# Perform one-sample t-test
t_stat, p_value = ttest_1samp(acorns_mass, mu)

# Set significance level (alpha)
alpha = 0.05

print("t-statistic:", t_stat)
print("p-value:", p_value)

if p_value < alpha:
    print("Reject the null hypothesis. The average 1 mass of acorns is_
    ↪significantly different from 10 g.")
else:
    print("Fail to reject the null hypothesis. There is not enough evidence to_
    ↪conclude that the average mass of acorns is different from 10 g.")
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t-statistic: -2.2491611580763973

p-value: 0.03655562279112415

Reject the null hypothesis. The average 1 mass of acorns is significantly
different from 10 g.

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[2]: import numpy as np
from scipy.stats import ttest_ind

# Sample data
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upwind_acorns = [10.8, 10.0, 8.2, 9.9, 11.6, 10.1, 11.3, 10.3, 10.7, 9.0, 7.0,
    ↪7.0, 8.0, 9.6, 9.0, 7.0, 11.6, 10.3, 9.0, 12.3, 11.0, 10.4, 10.4]
downwind_acorns = [7.8, 7.5, 9.5, 11.7, 8.1, 8.8, 8.8, 7.7, 9.7, 7.0, 9.0, 9.7,
    ↪11.3, 8.7, 8.8, 10.9, 10.3, 9.6, 8.4, 6.6, 7.2, 7.6, 11.5, 6.6, 8.6, 10.5, 8.
    ↪4, 8.5, 10.2, 9.2]

# Perform independent two-sample t-test, assuming equal variances
t_stat, p_value = ttest_ind(upwind_acorns, downwind_acorns, equal_var=True)

# Set significance level (alpha)
alpha = 0.05

print("t-statistic:", t_stat)
print("p-value:", p_value)

if p_value < alpha:
    print("Reject the null hypothesis. The average mass of acorns from upwind,
    ↪and downwind trees is significantly different.")
else:
    print("Fail to reject the null hypothesis. There is not enough evidence to
    ↪conclude that the average mass of acorns from upwind and downwind trees is
    ↪different.")

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t-statistic: 2.0313163636708316

p-value: 0.04744999450645743

Reject the null hypothesis. The average mass of acorns from upwind and downwind trees is significantly different.

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[3]: import scipy.stats as stats

# Marks of students from three sections
section_A = [51, 45, 33, 45, 67]
section_B = [23, 43, 23, 43, 45]
section_C = [56, 76, 74, 87, 56]

# Perform one-way ANOVA
f_statistic, p_value = stats.f_oneway(section_A, section_B, section_C)

# Set significance level (alpha)
alpha = 0.05

print("F-statistic:", f_statistic)
print("p-value:", p_value)

if p_value < alpha:
    print("Reject the null hypothesis. The mean marks of students in the three,
    ↪sections are significantly different.")

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else:
    print("Fail to reject the null hypothesis. There is not enough evidence to
    ↪conclude that the 1 mean marks of students in the three sections are
    ↪different.")
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F-statistic: 9.747205503009463

p-value: 0.0030597541434430556

Reject the null hypothesis. The mean marks of students in the three sections are significantly different.

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