

SIMPLE LINEAR REGRESSION ANALYSIS IN R

```
height <- c(150, 160, 170, 180, 190)
weight <- c(50, 60, 65, 75, 85)
data <- data.frame(height, weight)
model <- lm(weight ~ height, data = data)
summary(model)
plot(data$height, data$weight,
     main = "Height vs Weight",
     xlab = "Height (cm)",
     ylab = "Weight (kg)",
     pch = 19,
     col = "blue")
abline(model, col = "red")
new_height <- data.frame(height = 172.5)
predicted_weight <- predict(model, newdata = new_height)
predicted_weight
```

CHI SQUARE TEST FOR INDEPENDENCE IN R

```
cuisine_table <- matrix(c(25, 30, 20, 35), nrow = 2, byrow = TRUE)
rownames(cuisine_table) <- c("Young", "Middle-aged")
colnames(cuisine_table) <- c("Italian", "Chinese")
cuisine_table
chi_square_result <- chisq.test(cuisine_table)
chi_square_result
if (chi_square_result$p.value < 0.05) {
  print("There is a significant association between age group and cuisine preference.")
} else {
  print("There is no significant association between age group and cuisine preference. The variables are independent.")
}
```

ONE –WAY ANOVA IN R

```
weights <- c(68, 72, 65, 70, 74, 60, 63, 67, 69, 64, 76, 78, 71, 73, 75)
diets <- factor(c(rep("Diet A", 5), rep("Diet B", 5), rep("Diet C", 5)))
data <- data.frame(weights, diets)
data
anova_result <- aov(weights ~ diets, data = data)
summary(anova_result)
if (summary(anova_result)[[1]][["Pr(>F)"]][1] < 0.05) {
  print("There is a significant difference in the mean weights of individuals on different diets.")
} else {
  print("There is no significant difference in the mean weights of individuals on different diets.")
}
```

TWO-SAMPLE t-TEST IN R

```
group_A <- c(85, 88, 90, 78, 95, 80, 85)
group_B <- c(78, 82, 84, 75, 89, 83, 81)
data <- data.frame(group_A, group_B)
t_test_result <- t.test(group_A, group_B, var.equal = FALSE)
t_test_result
if (t_test_result$p.value < 0.05) {
  print("There is a significant difference between the means of the two groups.")
} else {
  print("There is no significant difference between the means of the two groups.")
}
```

PLOTTING GAMMA DISTRIBUTION IN R

```
x <- seq(0, 20, length.out = 100)
gamma_shape1 <- dgamma(x, shape = 2, scale = 1) # Shape = 2, Scale = 1
gamma_shape2 <- dgamma(x, shape = 5, scale = 1) # Shape = 5, Scale = 1
gamma_shape3 <- dgamma(x, shape = 9, scale = 1) # Shape = 9, Scale = 1
plot(x, gamma_shape1, type = "l", col = "blue", lwd = 2,
     main = "Gamma Distribution with Different Shape Parameters",
     xlab = "Time",
     ylab = "Density")
lines(x, gamma_shape2, col = "red", lwd = 2)
lines(x, gamma_shape3, col = "green", lwd = 2)
legend("topright", legend = c("Shape = 2", "Shape = 5", "Shape = 9"),
     col = c("blue", "red", "green"), lwd = 2)
```

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