

Contrastes de hipótesis con R

Test	Sintaxis (parámetros comunes)	Ejemplo
t de Student (1 muestra)	<code>t.test(x, mu = 0, alternative = c("two.sided","less","greater"), conf.level = 0.95)</code>	<code>t.test(x, mu = 5)</code>
t de Welch (2 muestras independientes)	<code>t.test(y ~ g, var.equal = FALSE, alternative = "two.sided", conf.level = 0.95)</code>	<code>t.test(Sepal.Length ~ Species, data = iris[iris\$Species!="setosa",])</code>
t pareada (2 medidas relacionadas)	<code>t.test(x, y, paired = TRUE, alternative = "two.sided", conf.level = 0.95)</code>	<code>t.test(pre, post, paired = TRUE)</code>
ANOVA 1 factor	<code>aov(y ~ g, data = df)</code>	<code>fit <- aov(Sepal.Length ~ Species, data = iris)</code>
ANOVA 2 factores (+ interacción)	<code>aov(y ~ A * B, data = df)</code>	<code>aov(y ~ grupo * tratamiento, data = df)</code>
ANCOVA	<code>lm(y ~ grupo + covar, data = df)</code> (contraste vía <code>anova(fit)</code>)	<code>lm(y ~ grupo + edad, data = df)</code>
Post-hoc (Tukey)	<code>emmeans::emmeans(fit, "g") > emmeans::pairs(adjust = "tukey")</code>	<code>fit <- aov(y ~ g, df); emmeans::emmeans(fit,"g") > emmeans::pairs("tukey")</code>
Correlación de Pearson	<code>cor.test(x, y, method = "pearson", alternative = "two.sided", conf.level = 0.95)</code>	<code>cor.test(iris\$Sepal.Length, iris\$Sepal.Width)</code>
Correlación de Spearman	<code>cor.test(x, y, method = "spearman")</code>	<code>cor.test(x, y, method = "spearman")</code>
Regresión lineal	<code>lm(y ~ x + z, data = df);</code> resumen: <code>summary(fit)</code>	<code>fit <- lm(mpg ~ wt + hp, data = mtcars)</code>
Mann-Whitney (Wilcoxon 2 indep.)	<code>wilcox.test(y ~ g, alternative = "two.sided", conf.level = 0.95, exact = FALSE)</code>	<code>wilcox.test(y ~ g, data = df)</code>
Wilcoxon pareado (signed-rank)	<code>wilcox.test(x, y, paired = TRUE, alternative = "two.sided", exact = FALSE)</code>	<code>wilcox.test(pre, post, paired = TRUE)</code>

Test	Sintaxis (parámetros comunes)	Ejemplo
Kruskal-Wallis (≥3 indep.)	<code>kruskal.test(y ~ g, data = df)</code>	<code>kruskal.test(Sepal.Length ~ Species, data = iris)</code>
Friedman (≥3 relacionados, RM)	<code>friedman.test(y ~ within id, data = df)</code>	<code>friedman.test(valor ~ tiempo sujeto, data = df)</code>
Igualdad de varianzas (Levene)	<code>car::leveneTest(y ~ g, data = df, center = median)</code>	<code>car::leveneTest(mpg ~ cyl, data = mtcars)</code>
F test de varianzas (2 grupos)	<code>var.test(x, y, alternative = "two.sided", conf.level = 0.95)</code>	<code>var.test(x, y)</code>
Normalidad (Shapiro-Wilk)	<code>shapiro.test(x)</code>	<code>shapiro.test(rnorm(50))</code>
Normalidad (Anderson-Darling)	<code>nortest::ad.test(x)</code>	<code>nortest::ad.test(x)</code>
Normalidad (D'Agostino-Pearson)	<code>fBasics::dagoTest(x)</code>	<code>fBasics::dagoTest(x)</code>
χ^2 de independencia (r×c)	<code>chisq.test(tabla)</code> o <code>chisq.test(x = df\$A, y = df\$B)</code>	<code>chisq.test(table(df\$sexo, df\$fuma))</code>
Fisher exacta (2×2 o celdas pequeñas)	<code>fisher.test(tabla, alternative = "two.sided")</code>	<code>fisher.test(matrix(c(5,1,2,6),2))</code>
Proporción 1 muestra (exacta)	<code>binom.test(x = éxitos, n = n, p = p0, alternative = "two.sided", conf.level = 0.95)</code>	<code>binom.test(42, 100, p = 0.5)</code>
Proporciones 1 o 2 muestras (aprox. z)	<code>prop.test(x = c(s1,s2), n = c(n1,n2), correct = TRUE); 1 muestra: <code>prop.test(s, n, p = p0)</code></code>	<code>prop.test(c(30,45), c(100,110))</code>
McNemar (binaria pareada)	<code>mcnemar.test(tabla_2x2)</code>	<code>mcnemar.test(matrix(c(10,3,6,21),2))</code>