

### Non-Parametric Tests

One	Goodness of Fit	<code>chisq.test(x, y = NULL, p)</code>
	Independence Test	<code>chisq.test(table)</code> <code>cramer.v(table)</code>
	Binomial Test	<code>binom.test(x, n, p = 0.5)</code>
	Runs Test	<code>RunsTest(vector)</code>
	KS Test	<code>ks.test(x, dist)</code>
Two Dep	Kendall's Tau	<code>cor.test(x, y, method = 'kendall')</code>
	Kendall's W	<code>kendall(df)</code>
	Wilcoxon Signed Ranks	<code>wilcox.test(x, y, paired=T)</code>
	McNemar Test	<code>mcnemar.test(matrix)</code>
	Sign Test	<code>binom.test(condition, n, p)</code>
Two Indep	Mann-Whitney U	<code>wilcox.test(x, y, paired=F)</code>
	KS Z Test	<code>ks.test(x, y)</code>
	Moses Extreme Reaction	<code>MosesTest(x, y)</code>
K Dep	Wald-Wolfowitz Runs	<code>RunsTest(x, y)</code>
	Friedman Test	<code>kendall(df)</code>
	Cochran's Q Test	<code>cochran.qtest(data, DV~Group Subj)</code>
K Indep	Kruskal-Wallis	<code>kruskal.test(x, g)</code>
	Jonckheere-Terpstra	<code>JonckheereTerpstraTest(x, g)</code>
	Trend Test	
	Median Test	<code>Median.test(x, g)</code>

Non-parametric tests: distribution-free, less powerful  
 Data: skewness, outliers, tiny samples, nominal & ordinal  
 Chi-square:  $df = \text{category} - 1$ , cell sample  $> 5$   
 Kendall's W: concordance-W, difference- $\chi^2$   
 Wilcoxon: **less** than critical, **swap** and **smaller**

### ANCOVA

Equal Variance	<code>levene.test(y~g)</code>
Independence	<code>anova(aov(Cov~IV, data))</code>
Equal Slope	<code>anova(aov(DV~Cov*IV, data))</code>
ANCOVA	<code>aov(DV~Cov+IV, data);</code> <code>Anova(model, type = '3')</code>
Effect Size	<code>partial_eta_squared(model)</code>
Post-Hoc	<code>summary(glht(cfit, linct=mcp(time='Tukey')))</code>

If more grouping variable, say a & b

- equal variance: `levene.test(y~a*b)`
- independence: `anova(aov(cov~a*b))`
- equal slope: `anova(aov(y~c*a*b))`
- ANCOVA: `anova(aov(y~c+a+b+a*b))`

Covariate: continuous, not manipulated

Latin Square: less error; more power; major & minor with same level & one-time cross; no need for interaction check

### Nested ANOVA

Fit Model	<code>aov(DV~group/subgroup, data)</code> <code>aov(DV~group+Error(group:subg), data)</code>
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Subgroup's effect isn't care-worthy.

### MANOVA

Normality	<code>select(DV)  &gt; mshapiro.test()</code>
Var & Cov	<code>select(DV)  &gt;</code> <code>box.m(group)+leveneTests(group)</code>
Correlation	<code>Corr(DV)</code>
MANOVA	<code>manova(DV~group), summary(model)</code>
Effect Size	<code>rstatix::eta_squared(model)</code>

### Univariate ANOVA

summary.aov(model)	<code>gather(key='var', value='value', DVs)  &gt;</code> <code>group_by(var)  &gt;</code> <code>games_howell_test(value~group)</code>
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Report:

- ANOVA table: F, p, eta-squared
- Post-Hoc test: MD, p
- Wilk's Lambda: residuals' proportion in variance
- MANOVA: less powerful, contain inflation of  $\alpha$

### Logistic Regression

Fit Model	<code>lm(DV~IV+IV, data, family = binomial('logit'))</code>
Effect Size	<code>exp(cbind(coef(fit), confint(fit)))</code>
Predictor Test	<code>wald.test(Sigma = vcov(fit), b = coef(fit), Terms = i:j)</code>
Forward Test	<code>anova(fit, test='Chisq')</code>
Null Test	<code>anova(fit, null, test='Chisq'), null-DV=1</code>
Model Fitting	<code>hoslem.test(x = actual, y=fitted, g)</code>
R Square	<code>pscl::pR2(fit), `r2CU`~Nagelkerke R2</code>
Model Comparison	<code>anova(fit1, fit2, test='Chisq')</code>
Classification Table	<code>confusionMatrix(round(fitted), actual)</code>

Rate the Model:

- Nagelkerke  $R^2$ : variation accounted for
- HL test: goodness of fit

Report:

- Analysis method + brief model intro.
- Comparison against null; R squared
- Classification table
- Wald test of coefficients
- Effect size (odds ratio)

Predicted	Actual	
	1	0
	1 True positive	False positive
0	False negative	True negative

$$Acc = \frac{TP + TN}{ALL}, Prec = \frac{TP}{pred P}, Sen = \frac{TP}{real P}, Spe = \frac{TN}{actual N}$$

### MLR

Linear Correlation	<code>Corr(), pcor(), spcor(), vif(model)</code>
Fit Model	<code>lm(DV~IV+IV, data)</code>
Standardized	<code>lm(scale(DV)~scale(IV1), data)</code>
Model Comparison	<code>anova(fit1, fit2)</code>
Model's info:	coefficients, confint, residuals, fitted, deviance

Rate the Model:

- $R^2_{adj}$
- $F$  &  $p$ : predicted & actual

Hypothesis Testing:

- Null and Alternative hypothesis
- Statistics (comparison if necessary)
- Conclusion (whether or not to reject)

Part correlation:

- **Unique** contribution, change in  $R^2$  after an IV.
- **Smaller** than partial correlation.
- Read by **ROW**

### Moderation

Center the Data	<code>C_var=var-mean(var)</code>
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### NULL Model

Moderation	<code>lm(y~x+m)</code>
After Significant	<code>model_moderation &lt;- lm(Loyalty ~ Relationship*age_con)</code> <code>emmeans(model_moderation, ~ Relationship*age_con, cov.keep = 3, at = list(age_con = c(m Age-sd Age, m Age, m Age+sd Age), Relationship = c(m Relationship-sd Relationship, m Relationship, m Relationship+sd Relationship)), level = 0.95)</code> <code>emtrends(model_moderation, pairwise ~ age_con, var = "Relationship", cov.keep = 3, at = list(age_con = c(m Age-sd Age, m Age, m Age+sd Age)), level = 0.95)</code> <code>emmip(model_moderation, age_con ~ Relationship, cov.keep = 3, at = list( Relationship = c(m Relationship-sd Relationship, m Relationship, m Relationship+sd Relationship), age_con = c(m Age-sd Age, m Age, m Age+sd Age)), CIs = TRUE, level = 0.95, position = "jitter")</code>
Residual Plot	<code>car::residualPlots(model_moderation)</code>

Moderator influence the direction and strength of the relationship between IV and DV.

Report:

- Moderation: t, p, conclusion
- Main effect: t, p, conclusion
- Multicollinearity
- Model comparison for interaction term

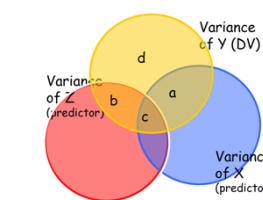
### Mediation

Y on X	<code>Model_0=lm(Y~X)</code>
M on X	<code>Model_M=lm(M~X)</code>
Y on X & M	<code>Model_Y=lm(Y~X+M)</code>
Mediation Effect	<code>mediation::mediate(Model_M, Model_Y, treat=X, mediator=M, boot=T, sims=500)</code>

- \* ACME, average causal mediation effect, indirect effect.
- \* ADE: average direct effect.
- \* Total Effect: sum of direct and indirect effect.
- \* Proportion Mediated: percentage of indirect within total.

Report:

- Mediation; Direct effect
  - Partial/complete mediator, proportion mediated
- Moderation & Mediation is linear relationship essentially.



- Partial: Holding Z from BOTH X and Y; Good for knowing the variance uncounted by other control variables.
- Semi-Partial: Holding Z from X only; Good for knowing the unique contribution of X.

### Distance

Correlation	<code>cor() &lt;v&gt;</code>
Euclidean	<code>data %&gt;% scale() %&gt;% dist() &lt;c&gt;</code>
Cosine	<code>data %&gt;% lsa::cosine() &lt;v&gt;</code>

Cox regression:  $n(t) = n_0(t) \cdot \exp(B_0 + B_1 X)$ ;  $B_1$ : hazard ratio

**PCA**

Bartlett Sphericity	<code>bfi_cor=cor(bfi)</code> <code>cortest.bartlett(bfi_cor,nrow(bfi_cor))</code>
KMO MSA	<code>KMO(bfi_cor)</code>
No. of Factors	<code>scee(bfi), fa.parallel(bfi)</code>
Factor Analysis	<code>fa(r,nfactors,rotate,fm)</code>
Factor Diagram	<code>fa.diagram(model)</code>

**Clustering**

Hierarchical	<code>distMat=data %M% scale() %M% dist()</code> <code>hc=hclust(distMat)</code> <code>plot(hc,hang=-1);fviz_dend(hc,k,rect=T)</code> <code>memlab=cutree(hc,k);table(memlab)</code> <code>aggregate(data,list(memlab),mean)</code>
Non-Hierarchical	<code>kmeans(data,centers)</code> <code>fviz_cluster(kmeanmodel,data)</code>
No. of Clusters	<code>fviz_nbclust(data,kmneas,method='wss')</code> <code>fviz_nbclust(data,kmneas,method='silht')</code> <code>nclust=n_clusters(data.frame(data))</code> <code>print(nclust)</code>

KMO: variance explained by common factors  
 Loading: correlation coefficient; Weight: slope coefficient.  
 Commnality: variance explained by selected factors.  
 Item complexity: each item loads on how many factors.  
 SS loadings: eigenvalues, sum of squared loadings.  
 Eigenvalue and communality change after rotation. Total variance explained unchanged.  
 Varimax maximizes variance accounted for by single factor; enhance interpretability. Variable links with min No. of factors. New factors are uncorrelated (Orthogonal).  
 Sample greater than 5 times items. Only continuous data.

FA: Correlation; Cluster: heterogeneity (No prior)  
 No. of clusters depends on measures of distance.  
 Non- and hierarchical clustering rates reliability.  
 Dendrogram: vertical heights imply dissimilarity

Attention:  
`matrix(data, nrow, byrow, dimnames = list(row,column))`  
**Range** for continuous variables

**Factor:** Grouping variables; set as `as.factor(var)` in `lm`  
**Library:** psych, survival, jmv, emmeans, mediation, survminer, ggfortify, parameters, factoextra, cluster, tidyverse, rstatix, DescTools, car, effectsize, irr, bruceR, aod, ggplot2, ResourceSelection, heplots, pscl, ppcor, HH, agricolae, multicomp, caret

**Reliability Analysis**

Reliability	<code>jmv::reliability(data,vars,alphaScale,corPlot,revItems,alphaItems,itemRestCor)</code> <code>athletes %&gt;% Reverse_Coding %&gt;% pivot_longer(cols =everything(),n_ames_prefix = 'x',names_to = 'item',values_to = 'score') %&gt;% mutate(subj = rep(1:nrow(athletes),each = ncol(athletes)))</code>
Nonadditivity Test	<code>nonadd = lm(score ~subj+as.factor(item),athletes_long)</code> <code>MSError = deviance(nonadd)/df.residual(nonadd)</code> <code>res = with(athletes_long, nonadditivity(score,subj,item,df.residual(nonadd), MSError))</code>
ICC	<code>icc=ICC(data,check.keys=T)</code> <code>icc\$results,icc\$stats</code>

More items, higher Cronbach's alpha.  
 Higher ICC, higher consistency within group (subj).  
 Qualitative: consistency; Quantitative: absolute agreement  
 ICC1: random, missing data.

<b>ICC Terms</b>	Only the subject (item) is the random factor. Not every rater measures every subject. Ratings are randomly drawn from a population	
One-way Random Effects	Consistency <u>ICC(1)</u>	
TYPE:	AND the effects of rater and subject (item) are mixed together	
Two-way Random Effects Sample	Consistency <u>ICC(2)</u> difference not matter → consistency; absolute agreement	<u>ICC(2)</u> absolute agreement
Two-way Mixed Model: Raters Fixed, Subjects Random Population	Consistency does not mean agreement	<u>ICC(3)</u> ICC3 greater than ICC2

Single: accuracy of each rater; Mean: overall consistency  
 R code: ICC2-abs agreement; ICC3-consistency

**Survival Analysis**

Survobj	<code>Surv(time,event)</code>
Survival Model	<code>survfit(Survobj~1,data)</code> <code>survfit(Survobj~group,data)</code> <code>coxph(Survobj~as.factor(g),dt,model=T)</code> <code>survdiff(Survobj~group,data)</code>
Survival Plots	<code>ggsurvplot(model,data,fun='pct')</code>

Median is used, since not everyone will have an event.  
 Hazard function: (ds/s)/dt