ESCI 340 Biostatistical Analysis Model Selection with Information Theory

"Far better an approximate answer to the *right* question, which is often vague, than an *exact* answer to the wrong question, which can always be made precise."

− John W. Tukey, (1962), "The future of data analysis." *Annals of Mathematical Statistics* **33,** 1-67.

1 Problems with Statistical Hypothesis Testing

- 1.1 Indirect approach:
	- − effort to reject null hypothesis (*H0*) believed to be false *a priori* (*statistical* hypotheses are not the same as *scientific* hypotheses)
- 1.2 Cannot accommodate multiple hypotheses (e.g., Chamberlin 1890)
- 1.3 Significance level (α) is arbitrary
	- − will obtain "significant" result if *n* large enough
- 1.4 Tendency to focus on *P-*values rather than magnitude of effects

2 Practical Alternative: Direct Evaluation of Multiple Hypotheses

- 2.1 General Approach:
	- 2.1.1 Develop multiple hypotheses to answer research question.
	- 2.1.2 Translate each hypothesis into a model.
	- 2.1.3 Fit each model to the data (using least squares, maximum likelihood, etc.). $(fitting model \cong estimating parameters)$
	- 2.1.4 Evaluate each model using information criterion (e.g., AIC).
	- 2.1.5 Select model that performs best, and determine its likelihood.

2.2 Model Selection Criterion

2.2.1 Akaike Information Criterion (AIC): relates information theory to maximum likelihood $AIC = -2 \log_e[L(\hat{\theta} | data)] + 2K$

 $\hat{\theta}$ = estimated model parameters

 $\log [L(\hat{\theta} | data)] = \log-likelihood$, maximized over all θ

 $K =$ number of parameters in model

Select model that minimizes AIC.

2.2.2 Modification for complex models (*K* large relative to sample size, *n*):

$$
AIC_c = -2\log_e[L(\hat{\theta} | data)] + 2K + \frac{2K(K+1)}{n - K - 1}
$$

use AIC_c when $n/K < 40$.

2.2.3 Application to least squares model fitting:

 $AIC = n \cdot log_{a}(\hat{\sigma}^2) + 2K$

 $\hat{\sigma}^2 = RSS/n$

 RSS = residual sum of squares

Modification for relatively small sample size, *n/K* < 40

$$
AIC_c = n \cdot \log_e(\hat{\sigma}^2) + 2K + \frac{2K(K+1)}{n - K - 1}
$$

- 2.3 Ranking Alternative Models
	- 2.3.1 Re-scale AIC values to give best model value of 0:

 $\Delta_i = AIC_i - min AIC$

2.3.2 Use Δ_i to measure relative plausibility of each model (larger Δ_i means less plausible)

- 2.4 Model likelihood, given the data $L(g_i | data)$
	- 2.4.1 Transform Δ values to likelihood: $exp(-\frac{1}{2}\Delta)$
	- 2.4.2 Normalize transformed values \rightarrow "Akaike weights"

 $=$ probability that model i is best among alternatives considered

$$
w_i = \frac{\exp\left(-\frac{1}{2}\Delta_i\right)}{\sum_{r=1}^R \exp\left(-\frac{1}{2}\Delta_r\right)}
$$

2.4.3 Relative likelihood of model *i* vs. model $j = w_i/w_j$

3 Example: Distribution of Maple seed dispersal distances

- 3.1 Alternative distributions:
	- 3.1.1 Uniform Distribution:

pdf:
$$
f(x) = \frac{1}{B-A}
$$
 for $A \le x \le B$ shape: horizontal line

3.1.2 Binomial Distribution: 2 mutually exclusive outcomes per event

pdf:
$$
P\{x = k\} = \binom{n}{k} p^k (1-p)^{n-k}
$$
, for $k = 0, 1, 2, ..., n$ where $\binom{n}{k} = \frac{n!}{k!(n-k)!}$
mean: *np* var: *np*(1-*np*)

3.1.3 Poisson Distribution: e.g., number of trials until *k* events occur

pdf:
$$
P(x = k) = \frac{e^{-\lambda n} (\lambda n)^k}{k!}
$$
, for $x = 0, 1, 2, ...$
mean: λn var: λn

3.1.4 Normal Distribution:

pdf:
$$
f(x) = \frac{e^{-(x-\mu)^2/(2\sigma^2)}}{\sigma\sqrt{2\pi}}
$$
 mean: μ var: σ^2

- 3.2 Fit each distribution to the data:
	- 3.2.1 Estimate mean, variance.
	- 3.2.2 Calculate expected frequencies, using estimated mean, var.
	- 3.2.3 Calculate residual sum of squares (betw/ data and expected frequencies).
- 3.3 Calculate AIC score for each distribution.
- 3.4 Select model with minimum AIC
- 3.5 Calculate Akaike weight for selected model (and others).

Further Reading:

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