Bayesian statistics with R

7. Contrast scientific hypotheses with model selection

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Model selection

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- The proportion of explained variance R^2 is problematic, because the more variables you have, the bigger R^2 is.
- Idea: penalize models with too many parameters.

$$AIC = -2\log(L(\hat{\theta}_1,\ldots,\hat{\theta}_K)) + 2K$$

with L the likelihood and K the number of parameters θ_i .

$$\mathsf{AIC} = -2\log(L(\hat{\theta}_1,\ldots,\hat{\theta}_K)) + 2K$$

A measure of goodness-of-fit of the model to the data: the more parameters you have, the smaller the deviance is (or the bigger the likelihood is).

$$\mathsf{AIC} = -2\log(L(\hat{\theta}_1,\ldots,\hat{\theta}_K)) + \frac{2K}{2K}$$

A penalty: twice the number of parameters K

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- \blacksquare Two models are difficult to distinguish if $\Delta \text{AIC} < 2.$

Bayesian version

• Watanabe-Akaike (Widely-Applicable) Information Criteria or WAIC:

WAIC =
$$-2\sum_{i=1}^{n} \log E[\Pr(y_i \mid \theta)] + 2p_{\text{WAIC}}$$

- where $E[p(y_i \mid \theta)]$ is the posterior mean of the likelihood evaluated pointwise at each *i*th observation.
- p_{WAIC} is a penalty computed using the posterior variance of the likelihood.
- More in this video https://www.youtube.com/watch?v=vSjL2Zc-gEQ by McElreath.
- Relatively new and not yet available in Jags in routine.

WAIC in Jags

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```
samples$p_waic <- samples$WAIC
samples$waic <- samples$deviance + samples$p_waic
tmp <- sapply(samples, sum)
waic <- round(c(waic = tmp[["waic"]], p_waic = tmp[["p_waic"]]),1)
waic
#> waic p_waic
#> 216.5 12.1
```

Further reading

- Hooten, M.B. and Hobbs, N.T. (2015), A guide to Bayesian model selection for ecologists. Ecological Monographs, 85: 3-28. https://doi.org/10.1890/14-0661.1
- Conn, P.B., Johnson, D.S., Williams, P.J., Melin, S.R. and Hooten, M.B. (2018), A guide to Bayesian model checking for ecologists. Ecol Monogr, 88: 526-542.
 https://doi.org/10.1002/ecm.1314

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