Title: One size to fit them all: On calculating dataset size for AICc

Abstract: For those using model selection approaches in phylogenetics, the small-size corrected Akaike Information Criterion (AICc) has become a standard approach. However, the field is unconsciously but deeply split over how to compute the size of a dataset: for tree inference the size is the number of sites, while for trait evolution the size is the number of taxa.

Body:

Choosing the least bad model is key for getting good parameter estimates (\_\_\_\_), whether we want to estimate a tree, rates of evolution, or ancestral states. While likelihood ratio tests were at one point commonly used, criteria based on information theory have largely replaced them due to their ability to compare non-nested models and, to a lesser degree, ease of using multiple models rather than fixing on a single one. Possibly the most commonly used criterion is the Akaike Information Criterion (AIC), which is based on just the number of free parameters and the likelihood. However, for small sample sizes, the Bayesian Information Criterion (also known as the Schwartz Information Criterion) as well as the sample size corrected Akaike Information Criterion (AICc) use the number of free parameters, likelihood and sample size.

However, what *is* the sample size? One of the most frequently used approaches in model selection in phylogenetics is ModelTest and its descendants (\_\_\_cite\_\_\_). {Posada, 2004 #29239}, in describing sample size for both AICc and BIC, mention that while they use sample size of total number of characters, effective sample size remains poorly understood. They explicitly mention that sample size depends on the number of taxa, though this remains unused in their software (which leads to smaller sample sizes being used, which favors simpler models). In contrast, in {Butler, 2004 #20121}’s software OUCH, for AICc and SIC sample size is the number of characters times the number of taxa. In Geiger \_\_\_, the