We are writing to enquire about the suitability of our article entitled “An information-theoretic approach to estimating genetic architectures: moving beyond the joint-scaling test for line cross analysis.” for publication in *Evolution*. The genetic architecture of a trait is important because it fundamentally determines the pace and direction of evolution. Unfortunately, widely implemented methods (i.e. joint-scaling test) for estimating genetic architecture in line cross analysis experiments provide a biased view because there has been no way to quantify the uncertainty in selecting the “right” genetic model from an often vast model space. Genetic parameters estimated with these approaches are thus conditional on the chosen model, which is often biased toward simpler architectures, even when there are many models with similar fits. We develop and demonstrate a full information-theoretic (I-T) approach to line cross analysis implemented in an R package SAGA. We present analyses of simulated data and reanalyze 17 empirical datasets, and find that by quantifying model selection uncertainty and using model weighted averaging, an I-T approach is able to accurately estimate composite genetic effect contributions to complex genetic architectures even when there is substantial uncertainty in which is the best overall model. Future line cross analyses will benefit from the I-T approach implemented in SAGA because it is able to more accurately define the components of complex genetic architectures than previous approaches. Our software package is currently available on GITHUB (https://github.com/coleoguy/SAGA) and will be available on the R package repository CRAN prior to publication.

Sincerely,

Heath Blackmon

Jeff Demuth