Phenotypic selection is a major driver of adaptive evolution, and plays an important role in generating biodiversity. Despite the multitude of studies on selection analyses and the achievement of various milestones in estimating selection, recent attempts to capture the complexity of selection have made it evident that there are a number of challenges that evolutionary biologists still face. In particular, synthetic analyses have determined that many studies may be overlooking the effects of selection on variances and covariances by omitting nonlinear selection analyses and that unmeasured traits can change the strength of selection in measured traits. There can be substantial barriers to conducting nonlinear selection analyses due to mathematical and analytical limitations, and some argue that the solution may compromise biological interpretations. A number of new methods have been developed to address some of these issues, but a consensus is yet to be reached. Also, it is currently unknown how changing different modeling parameters affect measures of phenotypic selection. In this talk, I describe the general framework applied to quantify phenotypic selection, existing challenges, and proposed methods for developing a more systematic approach to measure phenotypic selection.

**Location:** Tom Hallam Auditorium, Room 206 at NIMBioS, Claxton Education Bldg, 1122 Volunteer Blvd.

*Join us for refreshments at 3 p.m. in Room 205.*

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