Lund:

* Focus on application of CV
* **Assessing evolvability in a fossil lineage using a CV pipeline to produce phenomic data set**
* Inherent in understanding the tempo and mode of evolution is understanding the variation being acted upon and the constraints limiting change. If genetic constraints are important, it is hypothesized that phenotypic change should occur along axes of above-average evolvability (i.e., variance). To test this hypothesis, modern evolutionary quantitative geneticists estimate the G matrix to evaluate evolutionary potential and genetic constraints on the evolution of populations and species over micro-evolutionary time scales. Paleontologists are restricted to estimating the P (phenotypic variance-covariance) matrix when assessing the effects of evolvability and constraints on phenotypic change within and across lineages in the fossil record. While there have been studies showing the P matrix is a good substitute for the G matrix in some groups, this has not been evaluated using fossil data. Estimating G requires adequate sampling of traits and individuals. To expedite this process, we apply a CV pipeline to a lineage of bryozoans, *Steginoporella magnifica*, which currently resides outside of New Zealand and has a fossil record dating back over 2 million years. Each individual (zooid) in a colony acts as a replicate measurement within a colony. The pipeline successfully identifies and landmarks over 15.000 zooids from 446 colonies. We use this extracted phenomic data to examine the extent to which the properties of the G matrices can predict the observed phenotypic evolution within this lineage. Specifically, we quantify the extent to which phenotypic change occurs in directions of higher than expected variation (evolvability).
* Keywords: object detection, landmarking, trait extraction, bryozoan, evolvability
* Background on G for P
* Reasons for using Bryozoa
  + What previous studies have said about heritability
  + What previous studies have said about G and P
* How we approach it, which traits
* CV and pipeline to use
* Results

GSA:

* Focus on what it means for paleo studies
* **Clonal colonial organisms as a model system for applying evolutionary quantitative genetics to the fossil record**
* Inherent in understanding the tempo and mode of evolution is understanding the variation being acted upon and the constraints limiting change. If genetic constraints are important, it is hypothesized that phenotypic change should occur along axes of above-average evolvability (i.e., variance). To test this hypothesis, modern evolutionary quantitative geneticists estimate the G matrix to evaluate evolutionary potential and genetic constraints on the evolution of populations and species over micro-evolutionary time scales. Paleontologists are restricted to estimating the P (phenotypic variance-covariance) matrix when assessing the effects of evolvability and constraints on phenotypic change within and across lineages in the fossil record. Given the potential for the G matrix to evolve rapidly under micro-evolutionary time scales, it remains unclear if the G matrix is stable enough over macro-evolutionary time scales to provide insights into multivariate evolution. Further, while there have been studies showing the P matrix is a good substitute for the G matrix in some groups, this has not been evaluated using fossil data. Clonal organisms with a fossil record, such as bryozoans, provide a unique opportunity to branch micro- to macro-evolutionary studies by disentangling the P from the G and examine changes in the G matrix over longer time scales. Our focus is on a single lineage of bryozoans, *Steginoporella magnifica*, which currently resides outside of New Zealand and has a fossil record dating back over 2 million years. We measured eight morphological traits of thousands of zooids from over 600 colonies across seven geologic formations. We disentangled the G matrices to assess the similarity between the P and G matrices in each formation. We also examined the extent to which the properties of the G matrices can predict the observed phenotypic evolution within this lineage. Specifically, we quantify the extent to which phenotypic change occurs in directions of higher than expected variation (evolvability). Our approach attempts to apply evolutionary quantitative genetics to fossil data to investigate how the G matrix changes within a single lineage over millions of years.
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* Results
* What this means for paleo
  + What would it mean for other traits (i.e., more varying groups?)