# Data Hypothesis and Testing Statistically

A genotype-phenotype map is a useful tool for conceptualizing relationships between genetic and phenotypic variation. These relationships are often non-linear. (Green et al., 2017) They can be conceptualized where the amount of a particular process(e.g. proliferation and apoptosis) determines the mean phenotype and where the same amount of variation within a process can create different amounts of phenotypic variation. (Green et al., 2017) This change in phenotypic variation is dependent on the robustness of the background examined such that some backgrounds will be able to resist a change in variation differently than others. This is due to the alleles interacting with the gene of interest influencing the specific phenotype. (Yoshiki & Moriwaki, 2006)

From this relationship I believe the magnitude of genetic background effects is predictable given the mean magnitude of phenotypic effects of a given mutant allele and follows a sigmoidal relationship (pictured in the image below). Alleles with weak or severe phenotypic effects will display decreased sensitivity to genetic background effects (GBEs) indicated by reduced phenotypic variation of wing size and semi-quantitative (SQ) measure among and between *Drosophila melanogaster* Genetic Reference Panel (DGRP) strains. Alleles with moderate phenotypic effects will display increased sensitivity to GBEs indicated by increased phenotypic variation of wing size and SQ measure among and between DGRP strains.

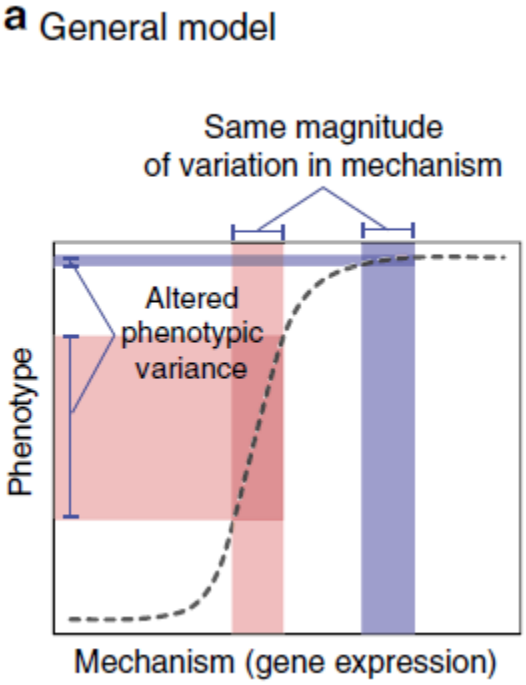


Figure taken from Green et al. displays the sigmoidal relationship of gene expression related to phenotype, whereby the mean phenotype is determined by a developmental process (gene expression). The blue bar represents wild type gene expression, and the red bar represents mutant gene expression. Robustness buffers the change in variation and remains

wild type in phenotypic expression within the blue bar and does fails to buffer the change in variation and appears mutant in phenotypic expression within the red bar. (2017)

The goal of the statistical test will be to measure changes in variability both within and between genetic backgrounds for various mutations from severe to weak. In order to test this change in variability I proposed utilizing either Levene's statistical test or a Brown-Forsythe test within the context of an ANOVA. Both tests can be found in the cars package in R. The reason for this is because I am interested in looking at the relationship between relative variation of mutant phenotypes and if it fits the biological model predictions including alleles of moderate phenotypic effects having increased phenotypic variation of wing size and SQ measure relative to the weak and severe mutant alleles. For these comparisons I am interested in the absolute deviation from the mean or median as a measure of variation and am considering logarithmically transforming my data to account for outliers.

References

Green, R. M., Fish, J. L., Young, N. M., Smith, F. J., Roberts, B., Dolan, K., Choi, I., Leach, C. L., Gordon, P., Cheverud, J. M., Roseman, C. C., Williams, T. J., Marcucio, R. S., & Hallgrímsson, B. (2017). Developmental nonlinearity drives phenotypic robustness. *Nature Communications*, *8*(1). https://doi.org/10.1038/s41467-017-02037-7

Yoshiki, A., & Moriwaki, K. (2006). Mouse phenome research: Implications of genetic background. *ILAR Journal*, *47*(2), 94–102. https://doi.org/10.1093/ilar.47.2.94