***Materials Required:***

Hardware:

Computers with internet access-- students can work in pairs

Software:

Mega software: Molecular Evolutionary Genetics Analysis (Tamura *et al.* 2011): *this software is freely available for Windows, MacOS, and Linux, http://www.megasoftware.net/*

Raw materials:

Computationally aligned coding sequences of individual genes. Minimum number of sequences needed: 5 strains of a single species and 1 strain of a related species (e.g., Langley *et al.* 2012; Liti *et al.* 2009; McGaugh *et al.* 2012).

EXAMPLES

Included in the supplemental materials is a .zip file of the sequence files (in FASTA format) for four genes in *Drosophila pseudoobscura* and *D. miranda.* Thesefiles can beused as samples so instructors can try this procedure before finding a complete data set. Our results for these genes can be found at these locations:

GA10001: https://geneticsevolution.biology.duke.edu/gene/30/

GA14150: https://geneticsevolution.biology.duke.edu/gene/424/

GA20741: https://geneticsevolution.biology.duke.edu/gene/29/

Ubx: https://geneticsevolution.biology.duke.edu/gene/1337/