Materials Required:

<u>Hardware</u>:
Computers with internet access-- students can work in pairs

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

<u>Raw materials</u>:
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., Lᴀɴɢʟᴇʏ *et al.* 2012; Lɪᴛɪ *et al.* 2009; McGᴀᴜɢʜ *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.* These files can be used 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/