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Gene loss plays an important role in plant evolution, polyploidization¹, and adaptation to new environments and lifestyles^{2,3}. Identifying gene loss events requires the quality annotation of shared genes between species, called **orthologs**. While many methods for identifying orthology exist, these tools typically only return “yes/no” ortholog pairs without any quantitative confidence value. Here we evaluate several metrics for estimating orthology uncertainty and their performance on reported gene loss events in *Dendrobium* orchids.

Our goal is to train a classifier for a single orthology confidence score that be used for detecting orthology uncertainty. If an ortholog group O contains g genes, then the confidence score C_O for that group would be

where M_i is a $g \times g$ matrix of pairwise confidence values from a given scoring metric.



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