

**Speaker:**

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University of California, Riverside**Date:** Monday, Nov. 30, 2020**Time:** 4:00 pm - 4:50 pm**Zoom:** 952-3324-4564**Passcode:** 835322**Title:**

“Making sense of manzanitas: integrating genetic, morphologic, and environmental data to define species”

Abstract:

In theory, species can be understood as independent evolutionary lineages. In practice, however, identifying and describing such lineages can be exceedingly difficult. Researchers disagree regarding what criteria to use to define species and how to apply them; furthermore, in plants, hybridization, local adaptation, and plasticity lead to variability that makes it difficult to determine where one species ends and another begins. We are interested in exploring methods to define species in manzanitas, iconic California shrubs and trees noted for their red bark, twisting branches, and clusters of small, urn-shaped flowers. There are 60 recognized species of manzanitas, and 109 taxa including subspecies. Many are known from only one or two populations, and are considered rare and/or threatened. Hybridization is thought to be rampant among manzanitas, and most widespread species are highly variable morphologically. As a result, even experts sometimes have difficulty knowing what species they are looking at. We are combining genome-wide SNP data, morphometric analyses, and species distribution modeling to determine if currently recognized species are distinct from each other. Our results to date suggest that some that are highly similar morphologically are nonetheless genetically distinct, but that others cannot be separated from each other.