

Using genomics to conserve and manage wildlife species

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With rapid advances in technology combined with decreasing costs, genomic analyses are no longer restricted to a handful of model organisms. This potential has not yet been fully realized in conservation. During this talk I will use examples from two very different systems to demonstrate what we can learn using traditional population genetics, and where we can go with genomic approaches. First, I will discuss the conservation genetics of a reintroduced canid, and follow with the analysis of lodgepole and jack pine genomics and the contribution made to mountain pine beetle management.

Friday, 6 March, 2015: 3:00 – 4:00 PM

Science 2, room 109

For further information: www.csufresno.edu/biology

