**Fifty years of Neutral Theory: A privileged framework to understand biological evolution and adaptation at the molecular level**  
  
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This presentation addresses the fundamental role that neutral theory has been playing in thefield of population genetics and molecular evolution, since its inception, half a century ago, now and in the foresee able future. In 1968, Motoo Kimura proposed a radically new explanation for the first available descriptions of population variation and substitution rates of proteins. Assuming that most of the existing polymorphisms and the fixed differences between the species are selectively neutral and functionally equivalent, Kimura's neutral theory provides a diaphanous kinetics and dynamics of molecular evolutionary change, encapsulated in one of the most elegant mathematical expressions of science: K = μ. If variants are neutral, then evolutionary rate depends on the mutational rate only. Because of its simplicity, intelligibility, robustness, and feasible theoretical predictions, the (nearly - with Otha's addition) neutral theory of molecular evolution became enthroned as the universal null model against which to test any selective hypothesis. The subsequent advent of polymorphic DNA sequences showing a correlation between recombination rate and amount of polymorphism in most studied species challenged the neutral paradigm, supporting the relevance of recurrent linked selection. If linked selection is common, a neutral framework to analyze genome data would distort the interpretation of variation patterns. In fact, the genomes of some species can be envisaged as mosaics of pieces evolving either under a neutral framework or under recurrent linked selection. Future population genomics should incorporate to the neutral framework integrative models, which allow performing powerful, knowledge-based, population genomics tests.