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Jesse W Drendel, Michael F Antolin and **Daniel J Bates*** (bates@math.colostate.edu),
CSU Department of Mathematics, 101 Weber, Fort Collins, CO 80523-1874, and **Patrick D
Shipman** and **Simon J. Tavener**. *Linkage disequilibrium between independently assorting loci,
via numerical algebraic geometry.*

In population genetics, linkage disequilibrium is the occurrence of clusters of genes in a population more often (or less often) than expected, based on allele frequencies in the population. Linkage disequilibrium has been observed in reality, but the standard models in population genetics (particularly that of Lewontin and Kojima) do not allow for linkage disequilibrium in the case of independent assortment. However, in order to make calculations feasible, such models make the assumption that homozygotes are equally fit, which is not necessarily the case. By generalizing the model of Lewontin and Kojima to allow homozygotes to have different fitnesses, we arrive at a model for which linkage disequilibrium is feasible under independent assortment.

In this talk, I will define much of what is said in the previous paragraph, provide a short (new) proof that there are no more than 15 equilibria with 2 alleles at each of 2 loci, and show how numerical algebraic geometry led us to the discovery of this generalized model with linkage disequilibrium under independent assortment. (Received September 11, 2013)