

# The Integration of Genetic Maps using Bayesian Inference

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## Abstract

In the absence of a comprehensive sequence based map of a species' genome, genetic maps constitute the next best source of genetic information. Information derived from such maps can be used, for example, in identifying the genes that form quantitative trait loci (QTLs) and for performing comparative genomics between species. Integrating information from a collection of maps will provide more accurate inferences on, for example, marker locations. We describe a method for integrating (possibly conflicting) experimentally derived genetic maps. It assumes a fully probabilistic model that describes the relationship between experimentally derived genetic maps and the integrated map. The model views experimentally derived maps for a given species' chromosome as noisy realisations of a single "true" map, where the noise consists of possible linear distortions and measurement error on the marker locations. Bayesian statistical inference methodology is then used to infer the integrated map (the "true" map) and its attendant uncertainties in the marker locations by using data from a number of experimentally determined genetic maps. The method is shown to work on simulated data and is used to integrate linkage radiation hybrid maps of Cow Chromosome 1.