## USING RANDOM EFFECTS SPLINE MODELS FOR SEARCHING FOR QUANTITATIVE TRAIT LOCI AFFECTING CELL COUNTS IN THE DENTATE GYRUS

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Methods for analyzing quantitative trait loci (QTL's) have been extensively developed for organisms which have been genotyped at a large number of loci scattered throughout the genome. However, recombinant inbred mice, for which high-density SNP maps are now available, present special modeling challenges and opportunities due to the hierarchical structure of the recombinant strains. For example, in order to properly model count data, the random effects must be properly accounted for. In addition the availability of multiple covariates, as well as a linear spatial structure for the counts in the dentate gyrus, require the use of spline models with covariates to search for and characterize more complex genetic effects, including interactions and strain-to-strain variance differences. We describe a new QTL mapping procedure that uses random effects Poisson regression to model the profile of counts of proliferating cells along segments of the dentate gyrus and to map QTL's related to components of these profiles in RI strains. In addition we show how to search for genes that affect the variability of the trait.