

## **"Estimation of Variance Components of Lymphocytes and Cortisol in Inbred Populations"**

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### **ABSTRACT**

The approach of using variance-component estimation for mapping of quantitative-trait loci in humans has attracted a lot interests in the current bioinformatics community. In this paper, a multivariate normal model for the genetic effects is applied to a measure of lymphocytes (as a percentage) and to total serum cortisol on 442 individuals in a 13-generation, 1,623 member pedigree of Hutterites. Both univariate and bivariate analyses are used to detect how the aggregation and co-aggregation of these two traits could be affected by additive and dominance genetic effects and environmental effects. We use maximum likelihood to estimate effect sizes in a variety of models. The univariate analysis shows that the amount of lymphocytes is due to the additive and environmental effects while total serum cortisol, in addition to these two factors, dominance effects seems make a significant contribution to our model. The results of bivariate analysis suggest that the levels of lymphocytes and total serum cortisol in the pedigree are affected by both shared additive polygenes and environmental factors. Also, we note that the covariance of additive effect is very significant.

