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PHD THESIS PRESENTATION

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**Functional Data Methods for Genome Wide
Association Studies**

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ABSTRACT

This thesis is concerned with the development of several statistical tools, based on functional data analysis, for inference on longitudinal data originating from genetic association studies. Functional data analysis, FDA, has become a very active branch of statistics over the last two decades. At the heart of FDA is the idea of viewing certain data structures, not as multivariate objects, but as curves evolving over time. We consider three problems related to analyzing longitudinal data in conjunction with genome wide information. The first problem is the construction of curves from sparsely observed data. We explore a new approach which attempts to pool information across subjects and use various kriging tools to construct the curves. The second problem we consider is carrying out a genome wide association study with a functional phenotype. We provide a new methodology based on reductions of L^2 norms that is very stable and potentially very powerful. The last problem we address is estimating the heritability of a functional phenotype. In the scalar setting, it is possible to use mixed effects models and maximum likelihood/residual maximum likelihood procedures for estimating the variance components that then lead to heritability estimates. In a functional setting, one can define a mixed effects model analogously and we show how they can be used to define heritability. However, fitting such models is complicated as it is difficult to define densities and likelihoods for functional objects. Thus we present a new method we call F-MINQUE for fitting functional mixed effects models and providing heritability estimates.

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