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## Linkage mapping for complex traits : a regression-based approach

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# Stellingen

1. We have yet to see studies adequately powered for detecting loci involved in the architecture of complex traits. High heritability does not guarantee large individual locus effects. *Dit proefschrift.*
2. Genotyping error increases the type II error in ASP designs and the type I error in discordant sib-pair designs. Designs that combine the two types of sib pairs appear to be fairly immune to the effect of genotyping error. *Dit proefschrift.*
3. Classical meta-analytic methods can be easily adapted to linkage studies. In addition to a logistic advantage upon the pooling of raw data, it offers the opportunity to adequately take into account the varying levels of marker information across studies. *Dit proefschrift.*
4. Information on covariate effects at the population level should and can be incorporated into the linkage analysis of common traits. *Dit proefschrift.*
5. Sophisticated statistical methods are not a cure for limited and noisy data. The most straightforward route to mapping a complex trait is to make it simpler. One way to do so is to use extreme ascertainment.
6. Genome-wide association studies are no panacea, their advantage over linkage studies is based upon simplistic assumptions. Linkage studies still have a role in generating candidate regions as well as in confirming results from association studies.
7. Genes implicated in complex diseases are bound to have small effects and their identification will have very limited impact on public health policies.
8. In statistical genetics, the hard part is neither the statistics nor the genetics but the new terms the geneticists dubbed old statistical methods.
9. Ce qui se conçoit bien s'énonce clairement  
Et les mots pour le dire arrivent aisément,  
*Nicolas Boileau*
10. Statistics - A subject which most statisticians find difficult but in which nearly all physicians are expert.  
*Guernsey McPearson*

Jérémie Lebec, 21 february 2007