

What my team can offer

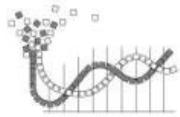
The International HapMap Project was designed to create a genome-wide database of patterns of human genetic variation, with the expectation that these patterns would be useful for genetic association studies of common diseases. This expectation has already been fulfilled with just the initial output of genome-wide association studies, identifying nearly 100 loci for nearly 40 common diseases and traits (Manolio et al 2008). Genetic association studies can therefore be considered central to efforts to identify and characterize genomic variants that underly susceptibility to complex disease (Van Steen et al 2005).

We offer guidance and support to increase the success rate of your genetic association studies, in several areas including:

- Study design (e.g. subject selection: family- or population-based, variant or marker selection)
- Study implementation (e.g. sample-recruitment strategy)
- Power calculations
- Quality control of the data used for association analysis:
 - Detection of genotyping error (e.g. Hardy-Weinberg equilibrium, Mendelian inconsistency checks)
 - Reduction / Minimization of genotyping error
- Relevant data analysis (main effects analysis, interaction analysis, multi-locus analysis or multivariate analysis) using a variety of techniques that appropriately account for multiple testing and confounding factors:
 - Hypothesis testing techniques
 - Effect size estimation techniques
 - Data mining techniques
 - Descriptive data visualization techniques
 - Pattern searching techniques
 - Dimensionality reduction techniques
- Valid interpretation of association findings
- Meta-analysis of effect sizes (e.g. odds ratios), acknowledging any heterogeneity and the potential for bias within included studies (e.g., poor validity, selective reporting) and in the data set as a whole (e.g., publication bias).

Despite the successes of Genome Wide Association studies (GWAs), it has become clear that usually only a small percentage of total genetic heritability can be explained by the identified loci. For instance for inflammatory bowel disease (IBD), 32 loci significantly impact disease but they explain only 10% of disease risk and 20% of genetic risk (Barrett et al 2008). This may be attributed to the fact that reality shows multiple small associations (in contrast to statistical techniques that can only detect moderate to large associations), dominance or over-dominance, and involves non-SNP polymorphisms, as well as epigenetic effects and gene-gene interactions (Dixon et al 2000).

In response to these concerns we develop, evaluate and implement powerful methodologies to detect gene-gene interactions, in small-scale studies, but also at the genome wide level (GWAIs = genome wide association interaction studies). The newly developed strategies aim to have improved power to simultaneously detect multiple genetic loci associated with any clinical endpoint of interest (measured, dichotomous, survival type, longitudinal, etc). Special attention is given to integrating



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information from different –omics data sources, incorporating important confounding information, adequately dealing with missing data (Van Steen et al 2007), adjusting for error sources such as population stratification and substructure in the data, and incorporating multi-staging into the analysis process (cfr multi-stage approaches in family-based association testing: Van Steen et al 2011a). While developing novel approaches, we particularly address the “curse of dimensionality” and the necessity to implement feasible, yet sound, multiple testing strategies. An “in-house” method to detect gene-gene interactions is MB-MDR (Calle et al 2008a,b, 2010; Cattaert et al 2011, Mahachie John et al 2011) and FAM-MDR (Cattaert et al 2010). Its roots lie in Vic (Spain), which initiated a long-term collaboration on the “MB-MDR” project. This multifactor dimensionality reduction method exhibits sufficient power in the presence of genetic heterogeneity (Cattaert et al 2011) and generates low false positive rates when screening at a genome wide scale (unpublished results). Future challenges include combining evidence from different modeling approaches, and visualizing results from epistasis screens (Figure 1: toy example), while adequately adjusting for lower-order effects or possible confounders (Van Steen et al 2011b).

And of course ... genetics is merely one of the playgrounds that we tend to empty our biostatistical tool box on.

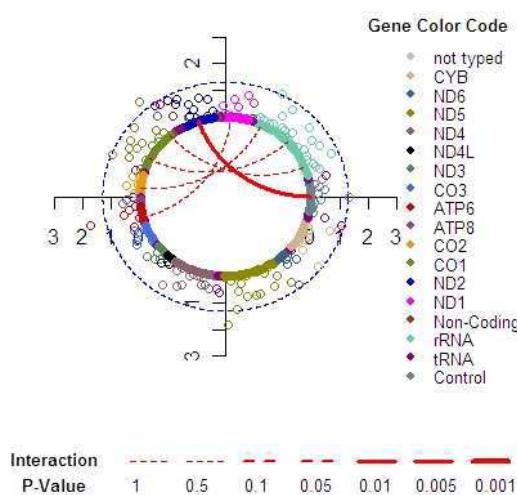
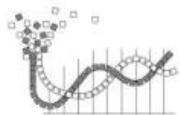


Figure 1: Epistasis results (red lines in the hyperbolic plane) and main effects signals (bullets radiating out in strength from the center of the plot). The dashed blue line demarcates the 0.05 overall significance level for adjusted p-values after an MB-MDR 1D run. The red dashed hyperbolic lines indicate pairs of markers that have a $-\log_{10}$ adjusted p-value above 0.05. As evidence amounts for epistatic pairs, the thickness of the line increases.



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Disclosure

The MB-MDR team consists of two research groups with PI's K Van Steen (Montefiore, Belgium) and M Calle (UVic, Spain).

In general, new methodologies are developed under the umbrella of the University of Liège (Montefiore Institute / Systems and Modelling Research Unit).