

Multiple SNP analysis using penalised regression in nonlinear mixed effect pharmacokinetic models

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Pharmacogenetics attempts to explain genetic sources of between-subject variability in drug response, and hence to predict near-optimal treatment regimens without the expensive and often harmful trial-and-error process that currently prevails. Pharmacokinetics (PK) aims at modelling the complex physiological processes underlying the dose–response relationship. Pharmacogenetics in PK is the junction of these two fields, in which genetic variants are examined for association with dose or a clinically relevant outcome.

In this seminar I will present a simulation study where I evaluate

- an adaptation of the SAEM algorithm with a penalized regression step at each iteration
- a Bayesian variable selection method to select and estimate the fixed effects of genetic variants in association with a drug PK.