

SEMINARIO

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A MARKOV LATENT SEED MODEL FOR GENOME-WIDE ASSOCIATION STUDIES

Abstract

We propose a Bayesian modelling approach to the analysis of genome-wide association studies based on single nucleotide polymorphism (SNP) data. Our latent seed model combines various aspects of k-means clustering, hidden Markov models (HMMs) and logistic regression into a fully Bayesian model. It is fitted using Markov chain Monte Carlo methods, with Metropolis-Hastings update steps. The approach is flexible, both in allowing different types of genetic models, and because it can be easily extended while remaining computationally feasible due to the use of fast algorithms for HMMs. It allows for inference primarily on the location of the causal locus and also on other parameters of interest. The latent seed model is used here to analyse three data sets, using both synthetic and real disease phenotypes with real SNP data, and shows promising results. Our method is able to correctly identify the causal locus in examples where single SNP analysis is both successful and unsuccessful at identifying the causal SNP. This is joint work with Fay Hosking.

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lunedì 4 ottobre 2010 aula 24 - 3° piano
dalle ore 17:30 alle ore 18:30

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