Statistics for assessing significance of inconsistent discovery trails

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Many areas of study, such as information retrieval, collaborative filtering, and social choice face the preference aggregation problem, in which multiple preferences for objects must be combined into a consensus ranking. We extend these techniques to formal allocation of statistical significance to replicate experiments with inconsistent outcomes. The inconsistency is an endemic feature of biomedical experiments searching for heritable, disease associated DNA mutations, which show weak effects which additionally are population (ethnicity) specific. We focus on techniques for filtering interactions (epistasis) between rare causal mutations using a signature from common markers in high throughput searches evaluating practically multiple trillions ($> 10^{12}$) of candidates at a time.

Lecture co-financed by the European Union in scope of the European Social Fund

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