

Linkage and association mapping: some connections

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Abstract:

Mapping the location of a gene on the chromosomes is a useful first step towards understanding its function. Traditional genetic linkage studies in humans assign a gene to an approximate location by tracking its transmission from parents to offspring in extended families or pedigrees. However, even carefully-executed pedigree studies of simple genetic traits can only localize a gene to a relatively wide interval. Even with current technologies, identifying the gene within a candidate region of such size can be a labour-intensive undertaking. Disequilibrium mapping, which uses population associations to infer the location of a disease mutation, provides one possible strategy for narrowing the candidate region. This talk reviews ideas unifying disequilibrium mapping and traditional genetic linkage mapping, and outlines a statistical approach to fine-scale disequilibrium mapping of a rare mutation.