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R/ qtl: high-throughput multiple qtl mapping

R/qtl is an extensible, interactive environment for the mapping of quantitative trait loci (QTL) in experimental crosses. It is implemented as an add-on package for

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A quantitative trait locus (QTL) is a section of DNA (the locus) that correlates with variation in a phenotype (the quantitative trait). The QTL typically is linked

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CiteSeerX - Document Details (Isaac Councill, Lee Giles, Pradeep Teregowda): Historically QTL mapping studies have employed a variety of crossing schemes including

Influence of outliers on qtl mapping for complex

Feb 10, 2008 We investigated the impact of outliers on QTL mapping for complex traits in a mouse BXD SAS STAT User s Guide. Cary, NC, USA: SAS Institute Inc

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