

# **A Self-adaptive Random Walk Algorithm to Identify Genetic Epistatic Effects**

A new search algorithm for detecting epistasis, or gene interaction, involved in determining quantitative traits. The algorithm is able to simultaneously find several epistatic effects involving any number of genetic loci.

In the search algorithm, a series of random walks in the space of possible groups of epistatic effects is performed. The performance of the algorithm is measured while varying key parameters, including the length of the walk, the number of genetic markers available, and the sample size available. The algorithm was designed to adapt between walks, allowing those loci associated with better models to be guessed more frequently.

The algorithm was compared to several published techniques using simulated data. In addition, in experimental data the algorithm found strong evidence of several epistatic effects for most of the phenotypes that were analyzed. Strong evidence of several epistatic effects involving four loci were found, one with a p-value of less than 0.001 from a permutation test. To the best of our knowledge, this is the first time epistasis involving four loci has been explored for quantitative data.