
AntEpiSeeker algorithm

Input parameters

D: a dataset of *N* case and control samples genotyped at *L* loci

iEpiModel: number of SNPs in an epistatic interaction

Pvalue: statistical significance threshold

largesetsize: size of the large SNP sets

smallsetsize: size of the small SNP sets

iAntCount: number of ants

iltCountLarge, *iltCountSmall*: number of iterations for large or small SNP sets

τ_0 : initial pheromone level for each locus

ρ : evaporation rate

α : parameter determining the weight given to pheromone deposited by ants

for *setsize* in (*largesetsize*, *smallsetsize*)

 If *setsize*==*largesetsize*, *iltCount*=*iltCountLarge*; else, *iltCount*=*iltCountSmall*

 Initialize the pheromone level of each locus

i=0

 Iteration begins

 Each ant selects a SNP set with *setsize* loci sequentially according to equation (1)

 Calculate the χ^2 test for each SNP set and update the pheromone for each locus in the SNP set

 Record the SNP sets with the highest χ^2 test

 Clear ants

i=*i*+1

 Iteration ends if *i*==*iltCount*

Post-processing: conduct exhaustive search of epistatic interactions of a desired model within the recorded SNP sets with the highest χ^2 test and the loci with top ranking pheromone levels

End for

Optional: minimize false positives

Return epistatic interactions with p-values
