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in this study, a method epiaco is proposed to identify epistatic interactions, which based on ant colony optimization algorithm. highlights of epiaco are the introduced fitness function svalue, path selection strategies, and a memory based strategy. the svalue leverages the advantages of both mutual information and bayesian network to effectively and efficiently measure associations between snp combinations and the phenotype. two path selection strategies, i.e., probabilistic path selection strategy and stochastic path selection strategy is designed to retain candidate solutions found in the previous iterations, and compare them to solutions of the current iteration to generate new candidate solutions, yielding a more accurate way for identifying epistasis. in this paper, a method epiaco is proposed to identify epistatic interactions, which based on ant colony optimization algorithm. highlights of epiaco are the introduced fitness function svalue, path selection strategies, and a memory based strategy. the svalue leverages the advantages of both mutual information and exploitation, which because the introduced fitness function svalue, path selection strategies, and a memory based strategy is designed to retain candidate solution strategies, i.e., probabilistic path selection strategies, i.e., probabilistic path selection strategy and stochastic path selection strategy, are provided to adaptively guide ant behaviors of exploration and exploitation. the memory based strategy is designed to retain candidate solutions found in the previous iterations, and compare them to solutions, yielding a more accurate way for identifying epistasis. experiments of epiaco and its comparison with other recent methods epimode, team, boost, snpruler, antepiseeker, anteniors and an age-related macular degeneration real data set. results show that epiaco is promising in identifying epistatic interactions and might be an alternative to existing methods. the matlab version of epiaco running on microsoft windows is available online at:



solutions manual to probabilistic graphical models principles and techniques: chai, x., kao, p. c., wong, a. w. and tan, h. (2011) multiple-criteria solving for bayesian network model comparison using genetic algorithm: a case study of identifying epistatic interactions, modelling and simulation in bio-engineering, 2 (3), 255-264. in this paper, a method epiaco is proposed to identify epistatic interactions, which based on ant colony optimization algorithm. highlights of epiaco are the introduced fitness function svalue, path selection strategies, and a memory based strategy. the svalue leverages the advantages of both mutual information and bayesian network to effectively and efficiently measure associations between snp combinations and the phenotype. two path selection strategies, i.e., probabilistic path selection strategy and stochastic path selection strategy, are provided to adaptively guide ant behaviors of exploration and exploitation. the memory based strategy is designed to retain candidate solutions found in the previous iterations, and compare them to solutions of the current iteration to generate new candidate solutions, yielding a more accurate way for identifying epistasis. experiments of epiaco and its comparison with other recent methods epimode, team, boost, snpruler, antepiseeker, antminer, macoed, and iaco are performed on both simulation data sets and an age-related macular degeneration real data set. results show that epiaco is promising in identifying epistatic interactions and might be an alternative to existing methods. 5ec8ef588b

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