1080-92-162 **Yang Huang*** (huangyan@mail.nih.gov), 8600 Rockville Pike, Building 38A, 8N811I, Bethesda, MD 20894, and **Geoffrey Siwo**, **Stefan Wuchty**, **Michael T Ferdig** and **Teresa M Przytycka**. *Dissecting interaction map of Plasmodium falciparum with symmetric epistasis estimation.*

It is being increasingly recognized that many important phenotypic traits, including various diseases, are governed by a combination of weak genetic effects and their interactions. However, current methods that detect epistatic interactions typically rely on the existence of a strong primary effect, considerably limiting the sensitivity of the search. To fill this gap, we developed a new computational method, SEE (Symmetric Epistasis Estimation), allowing the genome-wide detection of epistatic interactions without the need for a strong primary effect. The core approach is to search for maximal bipartite cliques in a graph representing available biological information. We applied our approach to progeny crosses of the human malaria parasite P. falciparum. We found an abundance of epistatic interactions in the parasite, which gave us a glimpse of its epistatic interaction network. The genome of P. falciparum harboured several epistatic interaction hotspots that putatively play a role in drug resistance mechanisms. The abundance of observed epistatic interactions might suggest a mechanism of compensation for the extremely limited repertoire of transcription factors. (Received January 24, 2012)