

**Abstract:** Neurocysticercosis (NCC), the infection of the brain with larvae of *Taenia solium*, is the commonest cause of late-onset seizures in countries where the infection is endemic. Subjects reporting to the Department of Neurological Sciences at the Christian Medical College in Vellore, India were recruited for participation in a study to determine relevant gene expression profiles specific to NCC-associated epilepsy in peripheral blood monocytes. While technology to measure and describe gene regulation has become quite sophisticated, statistical methods for analyzing such data have remained somewhat pedestrian. Traditional statistical analyses of microarray data often rely on unwarranted assumptions of normality and a battery of several thousand t-tests to assist in identifying significantly up or down regulated genes between groups. In this work we propose a semi-parametric Bayesian framework as a robust, probability-based alternative to the t-test approach in order to identify differentially regulated genes from a microarray analysis. We compare the top differentially expressed genes identified by the proposed method to several competing alternatives.