

# Analysis of Malaria Gene Expression Profiles using the MalariaSync Package

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Each year, the malaria parasite *P. falciparum* infects over 500 million people and kills over 1 million, most of whom are children. Although analyzing *P. falciparum*'s mRNA expression patterns has led to important insights into the disease, the periodicity of the vast majority of patterns presents significant difficulties in analyzing gene expression data from the parasite, particularly from data collected on heterogeneous populations of cells. Increasingly, researchers must use a wide range of malaria-specific statistical techniques in order to perform even the most basic gene expression analysis. Here we present the R package **MalariaSync**, which provides researchers with a suite of maximum likelihood methods for the estimation of important parameters characterizing parasite population development including temporal progression, synchronicity, and lineage commitment. In addition, we present research on new methods for identifying differential gene expression in periodic profiles. The **MalariaSync** package contains several graphical methods for summarizing the estimated parameters. As a demonstration, we show how to use the **MalariaSync** package to analyze published data sets in several common situations.

## References

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