Prediction of malarial signal peptides using signalHsmm
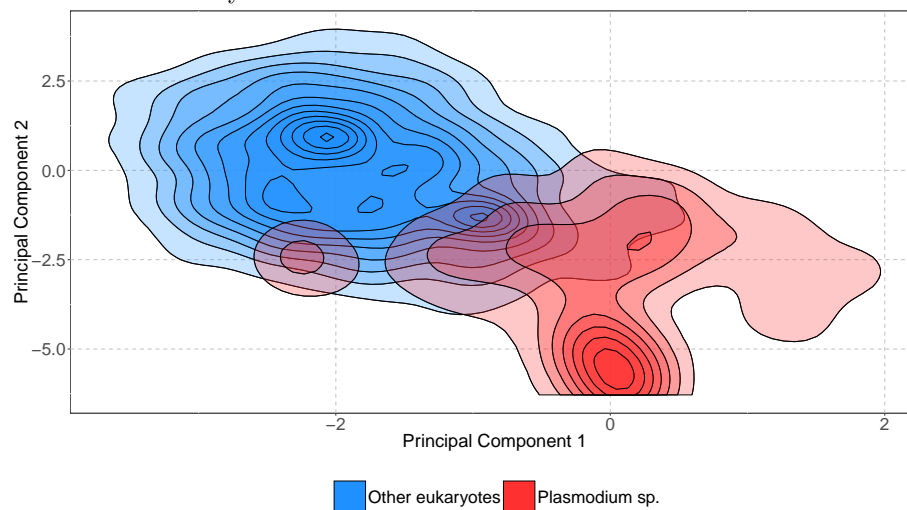
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1 Introduction

Medically significant *Plasmodiidae* have unique composition of signal peptides caused

Heavy adenine-thymine bias of malarial genomes alters amino acid composition of malarial signal peptides making them hard to predict using software trained on other eukaryotes.

2 Reduced alphabet

3 HSMM model