

## IDENTIFICATION OF TRANS-SPLICING SIGNALS IN TRYPANOSOMES

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Trypanosomes are pathogenic unicellular eukaryotes that are responsible for sleeping sickness in Africa and Chagas' disease in South America. These diseases are not always treatable and often fatal. The trypanosomes diverged from other eukaryotes over 800 million years ago, and their biology is not well understood. It has been shown, for example, that trypanosomes exhibit several molecular processes not consistent with the general eukaryotic gene model. One such process is *trans*-splicing of precursor mRNA to generate the final transcript. The signals that direct this phenomena have only just begun to be understood. We present an *ab initio* algorithm to identify elements of the signals that direct *trans*-splicing. Our algorithm uses several computational methods to determine which patterns are statistically significant, and the method has identified at least four such patterns that may have biological relevance. These patterns have been classified using log odd scores, raw counts, Markov chains, and graphics to view their distribution. The patterns were also characterized as either having a global significance or localized to a specific region. Some of these patterns have been verified by experimental investigation. The results suggest that our analysis can provide rapid and effective analysis to complement on-going experimental investigation.

**Saria would like to be a speaker at the Symposium and will be providing a Power-point presentation by Aug. 9, 2004.**