Ab Initio Identification of Novel Regulatory Elements in the Genome of *Trypanosoma brucei* by Bayesian Inference on Sequence Segmentation

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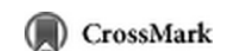| Article	About the Authors	Metrics	Comments	Related Content

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Abstract

Background

The rapid increase in the availability of genome information has created considerable demand for both comparative and ab initio predictive bioinformatic analyses. The biology laid bare in the genomes of many organisms is often novel, presenting new challenges for bioinformatic interrogation. A paradigm for this is the collected genomes of the kinetoplastid parasites, a group which includes Trypanosoma brucei the causative agent of human African trypanosomiasis. These genomes, though outwardly simple in organisation and gene content, have historically challenged many theories for gene expression regulation in eukaryotes.

Methodology/Principle Findings

Here we utilise a Bayesian approach to identify local changes in nucleotide composition in the genome of T. brucei. We show that there are several elements which are found at the starts and ends of multicopy gene arrays and that there are compositional elements that are common to all intergenic regions. We also show that there is a composition-inversion element that occurs at the position of the trans-splice site.