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Research Abstract

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Title: <u>Comparative genome-wide analysis of transcription initiation and promoter architecture in</u> <u>eukaryotes</u>

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Abstract Text:

Accurate annotation and prediction of *cis*-regulatory sequences within genomes is a major goal of computational biology. Given the current abundance of transcriptome sequence data, recent studies have considered positions of transcription initiation, namely transcription start sites (TSSs), to annotate and ultimately characterize promoters for a given genome. However, characterizations of promoter architecture with TSS have been heretofore restricted to metazoans. As such, the current sample is inadequate to comprehensively address the evolution of eukaryotic promoter architecture.

Seeking to address this gap in knowledge, we embarked upon a comparative analysis of promoter architecture using a diverse array of 13 species in four kingdoms of eukaryotes (<u>Table 1</u>), utilizing TSS data deriving from either CAGE or EST datasets. This work has three major objectives: 1) To computationally define the position, breadth and shape of promoters for genes within each species (see <u>Figure 1</u>), 2) To directly compare the annotated promoter architectures between species for orthologous genes, and finally 3) To generate a more complete picture of core promoter composition, potentially providing a hypothesis concerning its evolution across eukaryotes.

To accomplish these objectives, we apply a novel computational tool (TSRchitect), developed to identify and annotate <u>Transcription Start Regions</u> (TSRs) from global TSS studies. Using TSRchitect, we report efficient and accurate definition of TSRs using transcriptome data. Once complete, this work aims to provide a comprehensive analysis of core promoter architecture across eukaryotic diversity.

Appendix

Table 1: List of taxa analyzed in this study.

_ Common Name	Scientific Name	Kingdom
Human	Homo sapiens	Animalia
House Mouse	Mus musculus	Animalia
Zebrafish	Danio rerio	Animalia
Fruit Fly	Drosophila melanogaster	Animalia
Budding Yeast	Saccharomyces cerevisiae	Fungi
Gray Shag Mushroom	Coprinopsis cinerea	Fungi
Shittake Mushroom	Lentinula edodes	Fungi
Red Algae	Cyanidioschyzon merolae	Plantae
Thale Cross	Arabidopsis thaliana	Plantae
Soybean	Glycine max	Plantae
Rice	Oryza Sativasativa	Plantae
Toxoplasma	Toxoplasma gondii	Protista
Plasmodium	Plasmodium falciparum	Protista





Figure 1. Output of our TSR identification algorithm on a representative set of human genes. Panels A) and B) show the distributions of the TSR breadth and shape attributes of human TSRs, respectively. The median breadth is 147bp, but a notable subset of these are extremely narrow (<10bp). Future work will determine the biological relationships to these attributes, if any. C) An example of a TSR for a human gene (HSPB8 with a very 'peaked' shape. The peak is highlighed from the intergenic space by a red dashed rectangle, while the inset histogram shows a more detailed view.