Transcription factor binding sites detection in

Paramecium

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Keyword1 | Keyword2 | Keyword3

Abbreviations: SAM, self-assembled monolayer ; OTS, octadecyltrichlorosilane

Introduction

Structure of the introduction

— Whole Genome Duplications background
— WGD influences on Transcription Factor Binding Sites ?
— the *Paramecium* project, experimental part, etc. some work is done and random sequences ?
— Here, focusing on the computational part, developing pipeline, showed that etc.

Results

Discussion

Conservation among species. Major results is that.

Motifs detection should take phylogeny into account for comparative analysis. Not the same value.

Materials and Methods

developped a whole pipeline (show simple pipeline graph)
— Families upstream sequences extraction
— CDSs extraction and alignment
— CDSs phylogenetic tree
— BigFoot identification (explanation of phylogenetic score and alignment score)
— MEME research
— Comparison MEME and BigFoot
— Identification of given motif in species genome
— Correlation between motifs and expression levels

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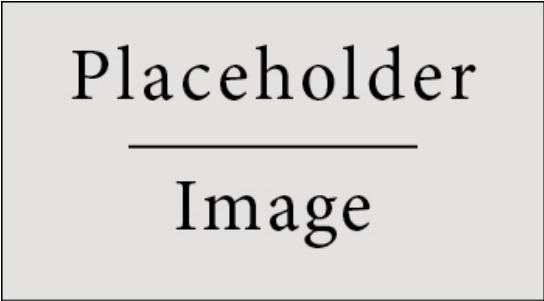
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FIGURE 1. Figure caption

TABLE 1. **Table caption**

Treatments	Response 1	Response 2
Treatment 1	0.0003262	0.562
Treatment 2	0.0015681	0.910
Treatment 3	0.0009271	0.296