

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.

Biological questions: How are TFBS affected by WGD? Are they conserved among species, is this linked to expression

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level? Conserved among each species? Is there a bias of TFBS usage in certain species?

Results

Discussion

Conservation among species. Major results is that. Divergent resolution of WGD → divergence in motifs?
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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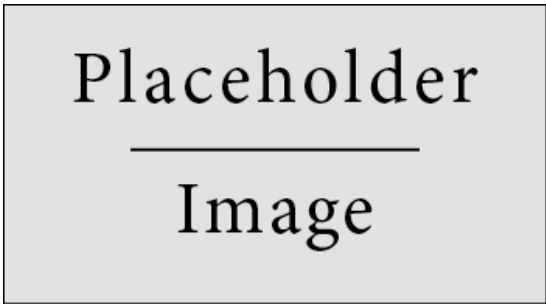


Fig. 1. Figure caption

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