1. Abstract

RBPs, complementarity hypothesis, fuzzy binding

1. Introduction

What are RBPs

**what’s the complementarity hypothesis**

Arthur and Thomas’ work

what is my thought behind using ppms

what datasets did I use

Approach I used (FIMO, matrices)

1. Materials and Methods  
   1. Datasets used
      1. SELEX, ATtRACT, CLIP – CDS, 5UTR, 3UTR
      2. MANE as background, Markov-model with nt-distribution

Why use MANE instead of shuffled version of autologous sequence?

* 1. Thomas‘ and Arthur’s work

In the framework of Thomas’ study on autologous interactions between proteins and mRNAs, Arthur’s work grew

Using exact matching, in-silico translation, matrices, results

* 1. My own project

Matrices

* + 1. Creating PFMs, converting to PPMs, PWMs
       1. what are these matrices, where do they come from  
          where are they used; technical stuff
       2. PSSM: PSSM & binding energy
    2. Threshold
       1. P-Value approach
       2. dynamic programming
       3. Q-value
       4. E-value
    3. Background
       1. background models matter;
       2. Markov-models higher order

How can higher order influence match-finding

* 1. Motif searching via MEME Suite
     1. What is MEME Suite  
        implemented in C

Include MEME-suite graphic with all tools

who made it, how did it come to be, what has it been used for

* + 1. What is FIMO

very fast motif searching

Why are there so many options in FIMO?

input for FIMO

Motifs

Sequences

Background file

P-value cutoff

* + - 1. Statistical approach
         1. Why is the background chosen as it is
         2. Calculating p-values, scores; approximation

plot: score distribution

1. Autologous Binding/Results?
   1. Analysis of FIMO results + nice plots
   2. 1e-4 RNAcompete: amount of len-6 motifs vs matches
   3. 1e-3
   4. 1e-2
   5. 5e-2
   6. 5e-2 with autologous-length background
2. Discussion
3. Discussion
4. Appendix
   1. code
   2. fimo commands