

Molecular Life Sciences



ISMARA: Integrated System for Motif Activity Response Analysis

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POSTER P10



ISMARA



Integrated System for Motif Activity Response Analysis

Web-service for analysis of expression and chromatin dynamics data.

ismara.unibas.ch

- Infers key regulators driving gene expression changes across samples
- Present dynamics of regulator activity in the dataset
- Show genes, pathways and biological processes targeted by each regulator
- Build direct interaction network of regulators
- and more

ISMARA: Automated modeling of genomic signals as a democracy of regulatory motifs Piotr J. Balwierz et al., Genome Research, 2014

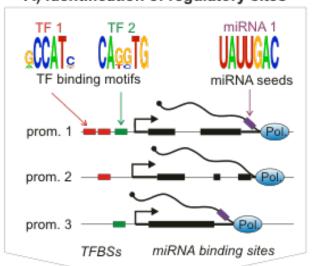


Modelling gene expression in terms of regulatory sites

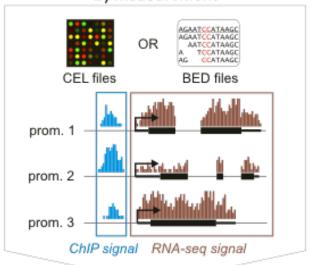
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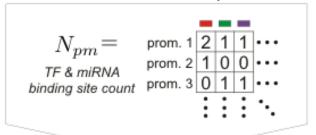
A) identification of regulatory sites

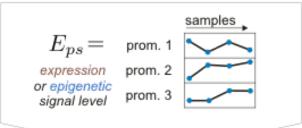


B) measurement



C) normalization and summation





Forrest et al. Nat Genet 2009

D) MARA model

$$E_{ps} = \sum_{m} N_{pm} \cdot A_{ms} + c_p + \tilde{c}_s$$

Balwierz et al. *Genome Res* 2014



ISMARA



features and highlights

- Designed for users without bioinformatics expertize
- Easy to use interface with minimal number of parameters
- Supported species: human, mouse, rat, yeast
- Accepts raw (.CEL, .FASTQ) and mapped data (.BAM, .BED)
- Experiment types: microarray, RNA-Seq, ChIP-Seq
- No size limit for upload
- Free for non-commercial use

RELA



Appetizer



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