independently usable

Inputs

Bed-file (b) — (n) — chr | start | end | $\overline{activity_1 \ldots activity_n}$

sequence file (g)

TF PSEMs (p) or PSCMs (s)

gtf-gene annotation (a) → 5' TSS

normalized Hi-C contacts (f)

TRAP

Affinities

	TF$_1$ — TF$_n$
region$_1$	$af_{r1,TF1}$
region$_n$	

Gene window   OR   **ABC-Scoring**

window (w)   window (w)

[1]   [2]

Region - TF mapping   **Region - Gene mapping**

$$af_{g,tf} = \sum_{r \in R_g} \frac{af_{r,tf}}{ml_{tf}} \cdot scaler$$

Gene-TF matrices

... activity$_n$

	TF$_1$ — TF$_n$
Gene$_1$	$af_{G1,TF1}$
Gene$_n$	

scaler depends on approach:

Gene window
$$A_r \cdot \frac{e^{-\frac{d_{r,g}}{d_0}}}{(f)}$$

adapted ABC-scoring (q)
$$\begin{cases} A_r \cdot e^{-\frac{d_{r,g}}{d_0}}, & if\ d_{r,g} \leq 2500bp \\ A_{r,g}, & otherwise \end{cases}$$

ABC-scoring
$$\begin{cases} A_r \cdot e^{-\frac{d_{r,g}}{d_0}}, & if\ d_{r,g} \leq 2500bp \\ A_{r,g} \cdot \frac{C_{r,g}}{C_{max}}, & otherwise \end{cases}$$

$af_{g,tf}$: affinity score of TF tf to g
R_g: set of regions mapped to g
$af_{r,tf}$: affinity of tf in r
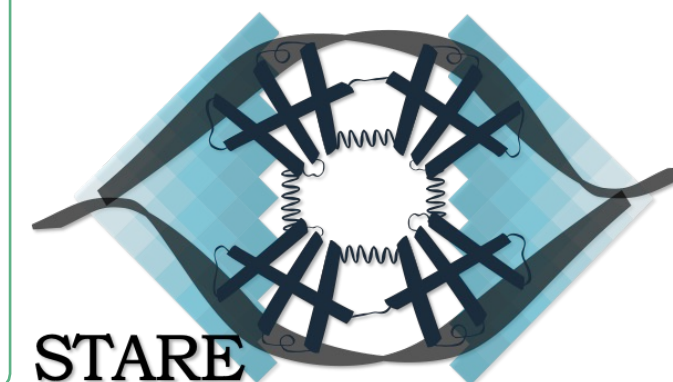ml_{tf}: motif length of
A_r: activity of r
$A_{r,g}$: adapted activity of r to g
$d_{r,g}$: distance of r to g
d_0: distance constant of 5000 bp
$C_{r,g}$: contact of r with g
C_{max}: maximum $C_{r,g}$

STARE

1 principle based on: Florian Schmidt, Fabian Kern, Peter Ebert, Nina Baumgarten, Marcel H Schulz, TEPIC 2—an extended framework for transcription factor binding prediction and integrative epigenomic analysis, *Bioinformatics*, Volume 35, Issue 9, 1 May 2019, Pages 1608–1609, https://doi.org/10.1093/bioinformatics/bty856; https://github.com/SchulzLab/TEPIC

1 principle based on: Fulco CP, Nasser J, Jones TR, Munson G, Bergman DT, Subramanian V, Grossman SR, Anyoha R, Doughty BR, Patwardhan TA, Nguyen TH, Kane M, Perez EM, Durand NC, Lareau CA, Stamenova EK, Aiden EL, Lander ES & Engreitz JM. Activity-by-contact model of enhancer–promoter regulation from thousands of CRISPR perturbations. Nat. Genet. 51, 1664–1669 (2019).
https://www.nature.com/articles/s41588-019-0538-0https://github.com/broadinstitute/ABC-Enhancer-Gene-Prediction