

DistanceScan: a tool for promoter modeling.

Shelest V, Albrecht D, Shelest E (2010) DistanceScan: a tool for promoter modeling. *Bioinformatics* 26(11), 1460-1462.

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Abstract

The state of the art in promoter modeling for higher eukaryotes is predicting not single transcription factor binding sites (TFBSs), but their combinations. The new tool utilizes a previously developed method of distance distributions of TFBS pairs. We model the random distribution of distances and compare it with the distribution observed in the query sequences. Comparison of the profiles allows filtering out the 'noise' and retaining the potentially functional combinations. This approach has proved its usefulness as a filtering technique for the selection of TFBS pairs for promoter modeling and is now implemented as a tool in R. As an input, it can use the outputs of three different TFBS- and motif-predictive tools (Gibbs Sampler for motifs, Match and MEME/FIMO for PWM-based search). The output is a list of predicted pairs on overrepresented distances with assigned scores, P-values and plots showing the distribution of pairs in the input sequences.

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[Microbiome Dynamics](#) [Gianni Panagiotou](#) [Mehr erfahren](#)

Leibniz-HKI-Autor*innen



Daniela Albrecht-Eckardt

[Details](#)



Ekaterina Shelest

[Details](#)



Vladimir Shelest

[Details](#)

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