Searching DNA by Brownian Motion of Transcription Factors
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factor proteins are able to locate their DNA operator binding site by slide-skip mo-
tion along DNA without getting trapped by the large binding energy fluctuations
associated with partial recognition. Mirny and Slutsky proposed that this can be
avoided by assuming that partial recognition involves increased strain energy of the
protein. We present an analytical model for such a search in the form of a 2D random
walk with DNA arc-length and an internal configurational parameter as coordinates.
This leads to a relation between the nature of the DNA randomness and the optimal
choice for the internal energy spectrum.

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