Quantitative modeling and data analysis of SELEX experiments
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SELEX (Systematic Evolution of Ligands by Exponential Enrichment) is an ex-
perimental procedure that allows extracting, from an initially random pool of DNA,
those oligomers with high affinity for a given DNA-binding protein. We address what
is a suitable experimental and computational procedure to infer parameters of tran-
scription factor-DNA interaction from SELEX experiments. To answer this, we use a
biophysical model of transcription factor-DNA interactions to quantitatively model
SELEX. We show that a standard procedure is unsuitable for obtaining accurate in-
teraction parameters. However, we theoretically show that a modified experiment in
which chemical potential is fixed through different rounds of the experiment allows
robust generation of an appropriate data set. Based on our quantitative model, we
propose a novel bioinformatic method of data analysis for such modified experiment
and apply it to extract the interaction parameters for a mammalian transcription
factor CTF/NFI. From a practical point of view, our method results in a significantly
improved false positive/false negative trade-off, as compared to both the standard
information theory based method and a widely used empirically formulated proce-
dure. This work will appear in Physical Biology. This work was supported by NIH
grant GM67794. Final parts of this work were supported by NSF under Agreement
No. 0112050 and NSF grant MCB-0418891.

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