Quantitative modeling and data analysis of SELEX experiments

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Abstract
SELEX (systematic evolution of ligands by exponential enrichment) is an experimental procedure that allows the extraction, from an initially random pool of DNA, of 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 transcription 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 interaction 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 dataset. Based on our quantitative model, we propose a novel bioinformatic method of data analysis for such a 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 procedure.

1. Introduction
One of the most important issues in molecular biology is to understand regulatory mechanisms that control gene expression. Gene expression is often regulated by proteins, called transcription factors (TFs), which bind to short (6 to 20 base pairs) segments of DNA [1]. To understand a regulatory system one needs a detailed knowledge of both TFs and their binding sites in a genome. Binding sites of a given TF share a common sequence pattern [2], which is often represented by a consensus sequence. However, TF binding sites are often highly degenerate, so it is not possible to reliably detect TF binding sites in a genome by using just the consensus sequence [3]. As an alternative, position-weight matrices (PWMs) [2, 4, 5] have been used to search for TF binding sites, with demonstrable advantage over consensus sequence based methods [3].

The most widely used method to construct a PWM originates from information-theoretic considerations [5, 6]. To distinguish such weight matrices from those constructed by other methods, we will further call them information-theoretic weight matrices (see also [7]). To build these weight matrices, one usually starts from a known collection of aligned binding sites and calculates the corresponding matrix elements as the logarithm of the ratio of probability to observe a given base at a given position in a collection of binding sites, compared to the probability of observing the base in the genome as a whole [3]. However, despite the obvious advantages of using such PWMs over the consensus sequence, the majority of PWMs provide a low level of both sensitivity and specificity [8]. In particular, there tend to be a large number of false positives in searches using most PWMs [3, 8, 9].

In general, two problems may lead to the low sensitivity and specificity of PWMs. First, the information-theoretic method may not be the most appropriate one. It does not properly incorporate saturation in binding probability, as shown by [7], and an alternative method of weight matrix...
construction, based on the biophysical model of TF–DNA interaction, was developed. This method reduced the number of false positives and resulted in the explicit appearance—and determination—of the binding threshold. Additionally, there are probably problems with the collection of binding sites used to construct the weight (energy) matrix [8] because, first, the collection of binding sites is most often obtained from a database, and is likely to be assembled under diverse and ill-characterized conditions [7]. Second, for most TFs, only a few binding sites are available [10, 11], making the amount of data insufficient for determining parameters of TF–DNA interaction (i.e., weight matrix).

As an alternative to using binding sites assembled in biological databases, SELEX (systematic evolution of ligands by exponential enrichment) experiments [12, 13] can be suitable for generating an appropriate dataset under controlled (uniform) conditions. Additionally, a recent experimental advance [14] which combines SELEX with SAGE (serial analysis of gene expression) [15], allows an efficient generation of a large number of binding sites for a given TF. In this paper, we ask the following question: What is an appropriate experimental and computational procedure for inferring parameters of TF–DNA interaction from SELEX experiments? In particular, we will address the following two issues: (1) How should SELEX experiments be designed in order to generate a dataset suitable for determining parameters of TF–DNA interactions? (2) How should a correct analysis of data from a suitable experiment be done? To address these questions, we will use a biophysical model of TF–DNA interactions to quantitatively model SELEX experiments. We will incorporate this model in the novel bioinformatic method of data analysis that we will subsequently develop.

The outline of this paper is as follows. In section 2, we will review SELEX experiments and point to the potential problems in the experimental procedure from the viewpoint of constructing the appropriate weight matrix. In section 3 we will quantitatively model the SELEX experiments. Based on this model, we will show that there is a range of experimental parameters for which the energy matrix cannot be inferred by using the standard SELEX procedure. However, we will show that a modified experiment allows a robust generation of the appropriate dataset. In section 4 we will propose a novel bioinformatic method of data analysis for modified SELEX experiments, and apply it to the data obtained in the experiment by Roulet et al [14]. In section 4.2 we will show that our method leads to a significant improvement in the false positive/false negative trade-off compared to the standard methods of data analysis. Quantitative analysis that supports sections 3 and 4 is presented in appendices B–F. Finally, in section 5 we will summarize our results, compare them with some widely held views and put our work in the context of future research.

4 Weight matrices constructed by the method given in [7] were denoted as energy matrices. This emphasizes that weights in the matrix correspond to the estimates of contribution to the binding (free) energy due to the presence of a certain base at a certain position in the binding site.
Cui et al [21] comment that “the poor correlation for the data described here seems surprising . . .”. Further, in [9] a comprehensive comparison between the weight matrices obtained from the eight available SELEX experiments with E. coli TFs and the corresponding weight matrices constructed from natural binding sites was performed. In seven out of these eight cases, large discrepancies between the matrices derived from natural sites and those derived from SELEX were reported. Therefore, obtaining good weight matrices from the standard SELEX procedure appears to be more an exception than a rule.

Why does the procedure described above appear to fail in many cases? The first possibility is that the assumption of additivity in TF–DNA interactions [22], on which the weight matrix representation is based, may not be suitable. This is, however, not likely, since this approximation has proved to be very good in many cases [20, 22–24]. Alternatively, the reason for the failure might be that the analysis was done using the information theory based method. As discussed in the introduction, the information theory based procedure does not properly incorporate saturation in binding probability. Therefore, it is not surprising that this is not the most appropriate method for correctly inferring the energy matrix. In this paper, we will develop a method of data analysis based on the biophysical model of protein–DNA interactions.

However, it seems rather surprising that the information theory based method is the only reason for the apparent problems with the weight matrices inferred from SELEX discussed above. There may be a systematic problem with the high stringency SELEX procedure when it comes to generating a dataset suitable for inferring weight/energy matrices. With regard to this, it is apparent that two possible problems may arise. First, it may be that the noise in the dataset is too large, i.e., many of the extracted sequences are too weak or are non-specific binders (for a discussion on non-specific binding, see appendix B). Second, if the extracted sequences consist of only the strongest binding sites, the inferred weight matrix elements will come with large errors. To observe this, it is useful to take the limit in which only the sequence corresponding to the consensus binding site is extracted, where it is obvious that the energy matrix cannot be obtained from such information. For a more detailed statistical analysis of this issue, refer to [14]. Therefore, our first goal is to address possible systematic problems with the experimental procedure by quantitatively modeling the SELEX experiments. We also incorporate this model in the bioinformatic method of data analysis that we develop in section 4.

3. A quantitative model of SELEX

Our model of SELEX is based on the biophysical view of TF–DNA interactions, which has been used in a few recent papers (see, e.g., [7, 25, 26]). For completeness and to introduce the notation, we briefly review a biophysical model of TF–DNA interaction in appendix A. We start this section by extending this model in several ways, so as to make it suitable for the modeling of SELEX.

First, we take into account non-specific binding of a TF to DNA. As we show in appendix B, the binding probability (equation (A.1)) is (approximately) modified in the following way due to the non-specific binding (see equations (B.5) and (B.9)).

\[
p(S) \approx \frac{1}{\exp(E(S) - \mu) + 1} \cdot c_{ns} = f(E(S) - \mu) + c_{ns},
\]

where \(E(S)\) is binding (free) energy\(^5\) of TF to a DNA sequence \(S\), \(\mu\) is chemical potential (see appendix A), while \(c_{ns}\) depends on the threshold of non-specific binding \(E_{ns}\) (see equation (B.8)). Note that we scale all energies with \(k_BT\). From equation (1) it follows that non-specific binding cannot be distinguished from the so-called background partitioning. Background partitioning [12] is an effect that, during the selection step (section 2), it is not possible to perfectly separate sequences that are bound by protein from those that are not bound. Due to that, in each round of SELEX, some DNA sequences not bound by TF are also selected with probability \(c_0\). A combined effect of non-specific binding and background partitioning can be described by equation (1), where \(c_{ns} \rightarrow c_{ns} + c_0\) (further in the text, we denote \(c = c_{ns} + c_0\)). Although \(c\) itself is likely to be small (e.g., \(c_0 \sim 0.1%\) in [12]), the effect of non-specific binding/background partitioning can be considerable, since in SELEX experiments there is typically a large excess of DNA over protein, so only a small fraction of all DNA sequences are typically (specifically) bound by TFs.

Second, we take into account that the length of DNA sequences in SELEX experiments is usually larger than the length of the TF binding site. For example, in the experiment by Roulet et al [14], which will be the subject of our analysis in section 4, the sequence length is \(l = 25\) bp long, while the length of the binding site for CTF/NFI TF, studied in the experiment, is \(L = 15\) bp. In appendix C we discuss the modification of the binding probability due to the fact that \(l\) is greater than \(L\). We show that this effect can be approximately accounted for by modifying the distribution of binding energies from \(\rho(E)\) (see equation (A.4)) to \(\mu_{bg}(E)\) given by equation (C.4). Additionally, we note that the model has to take into account that the support \(E_S\) of the energy distribution is finite (see equation (C.7)), with ‘bottom of the band’ determined by the energy of the strongest binder in the pool of random DNA sequences.

We note that we neglect stochastic effects in our model. This is generally justified by the fact that the typical length \(L\) of a TF binding site is 20 bp or less, while the total number of sequences used in SELEX is typically \(N \sim 10^{15}\) [13], so each possible DNA sequence of length \(L\) is present in about \(N/4^L \sim 10^5\) copies. Additionally, we note that high fidelity DNA polymerase is used in SELEX experiments, so mutations of sequences during the PCR amplification can generally be neglected. In that respect, SELEX is different from the so-called in vitro evolution experiments [27, 28], where reduced fidelity DNA polymerase and a larger number of PCR rounds are used (purposely) to introduce mutations and generate strong binding sequences that do not exist in the initial, small (\(N \sim 10^5\)), random DNA pool.

\(^5\) For brevity, from now on we will refer to the free energy of binding simply as ‘binding energy’. In chemical literature, the commonly used notation for this quantity would be \(\Delta G(S)\) rather than \(E(S)\).
3.1. High stringency SELEX

In this subsection, we model the high stringency SELEX procedure, based on the (extended) model of TF–DNA interactions described above. We introduce equations that allow us to determine the position of chemical potential $\mu(n)$ and energy distribution of selected oligos $\rho_M(E)$, as a function of the number of performed SELEX rounds $n$,

$$\rho_M(E) \sim [f(E - \mu(n)) + c]\rho_M^{(n-1)}(E)$$

and

$$p_i = p_{i}^{(n)} + p_{b}^{(n)} = K \exp(\mu(n)) + \int \rho_M^{(n-1)}(E) \times f(E - \mu(n)) \, dE + d_i \exp(\mu(n) - E_{\text{ns}}).$$

In the equations above, $p_i$, $p_f^{(n)}$ and $p_b^{(n)}$ are respectively total, free and bound concentrations of protein and $d_i$ is the total amount of DNA. $K$ is a multiplicative constant introduced by equation (A,2). Equation (2) connects energy distributions of selected sequences from $n$th and $(n-1)$th round. Equation (3) is the mass conservation law, and it determines the position of $\mu(n)$, $\rho_M^{(n-1)}(E)$ in equation (3) is normalized to $d_i$. Note that all energies are rescaled by $kT$. The equations above are solved recursively, i.e., we first solve them for $n = 1$, then increase $n$ by 1 etc. Note that $\rho_M^{(0)}(E)$ is $\rho_M(E)$ given by equation (C,4) (appendix C). We also note that, since in SELEX experiments there is typically a (large) excess of DNA over protein ($d_i \gg p_i$), most of the protein is bound to DNA and $p_f^{(n)}$ (i.e., $K \exp(\mu(n))$ term in equation (3)) can be neglected compared to $p_b^{(n)}$.

In general, equations (2) and (3) have to be solved numerically; however, the main features can be understood qualitatively. Let us assume that the total amount of DNA and the total amount of DNA (after each amplification step) are kept constant in each round of the experiment (as, e.g., in [12]). It is evident that as $n$ increases, the (average) affinity of selected oligos will also increase, which leads to the increase in the amount of $p_f^{(n)}$ and decrease of $p_b^{(n)}$. Therefore, both $\mu(n)$ (note that $\mu(n) = \log(p_f^{(n)}/K)$) and the maximum $E(n)$ of energy distribution $\rho_M^{(n)}(E)$ move to stronger binding energies with the increase in the number of performed SELEX rounds. (Many experiments are performed in a way that the total amount of protein $p_i \equiv p_i^{(0)}$ is decreased from one SELEX round to the next (e.g., see [29]). It is evident that the previous conclusion about the decrease of $\mu(n)$ holds in this case as well.) A limit in which equations (2) and (3) can be solved analytically is analyzed in appendix D. In particular, equations (D,2) and (D,6) quantitatively support the conclusion above.

In further analysis, we take the following values of parameters: $\chi_1 = 4k_B T$ (see appendix C), $p_i = 10 \text{ nM}$, $d_i = 10 \mu\text{M}$ and $E_S = -4.3\chi_1$, while $E_{\text{ns}} = -2.0\chi_1$ (see appendix B). The assumed values of $p_i$ and $d_i$ are typical for SELEX experiments [12], while (typical) $L \in [6, \ldots, 20]$ bp (base pairs) leads to $E_S$ in the interval from $-3.5\chi_1$ to $-\chi_1$ (see equation (C,7)). Values of $\chi_1$ and $E_{\text{ns}}$ are expected to differ from one TF to the other, but the assumed values are likely inside the realistic range [25]. Figure 2 shows $\rho_M^{(n)}(E)$ numerically obtained from equations (2) and (3), with the parameter values stated above. It is useful to observe how the signal-to-noise ratio changes with $n$, where the noise is the number of selected random binders (corresponding to peaks centered around zero), while the signal is the number of selected specific binders (for signal-to-noise ratio in the limit of unsaturated binding, see appendix D and equation (D,4)). For $n = 1$, we see that there is a small number of specific binders (note the small peak centered at $E/k_BT \approx -3.5$) compared to the number of selected random sequences, so that the signal-to-noise ratio is low. Because of the high noise-to-signal ratio, it is not possible to infer (correct) energy matrix from such a dataset. For $n = 2$, random binders are completely eliminated, so the problem with noise does not exist anymore. However, another problem emerges, i.e., since energy distribution of selected oligos has reached support $E_S$, (only) the strongest binding sites are selected. As discussed in section 2, a correct energy matrix cannot be obtained from such a sequence set. For $n = 3$, we select the sequence set with even stronger binding affinities, etc. We note that the sharp cuts in distributions $\rho_M^{(n)}(E)$ at $E_S$ (see figure 2) are the consequence of the approximation that we use for $\rho_M^{(0)}(E)$ (see equation (C,8)). In reality, $\rho_M^{(n)}(E)$ becomes discrete when one approaches $E_S$, which obviously does not change the conclusions inferred from figure 2.

We solved equations (2) and (3) for different parameter values. As shown by the example above, for a range of realistic parameter values the appropriate choice for the total number of performed rounds $n$ does not exist.$^6$ On the other hand, for some (other) parameters, for which selected DNA sequences have an acceptable signal-to-noise ratio and $E_{\text{ns}}^{(n)}$ does not reach the highest affinity binders, the optimal choice of $n$ does exist. However, we note that, in practice, it is very

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$^6$ In the analysis presented here, we used that $p_i$ is constant in each round of SELEX. If $p_i$ is decreased from one round to the next, as it is, in practice, done in many experiments (e.g., [29]), it is evident that this problem is even more pronounced.
hard to reliably predict such \( n \), i.e., to decide when to stop the experiment, because a studied TF has \textit{a priori} unknown binding parameters (i.e., \( \mu \) and \( E_{\text{m}} \)). Therefore, even in the case when the appropriate choice of \( n \) exists, it cannot, in practice, be simply calculated from equations (2) and (3). From this, it follows that the high stringency SELEX procedure is, in practice, unsuitable for inferring the parameters of TF–DNA interaction. In the next section, we discuss modification of the SELEX procedure that allows a robust generation of the appropriate set of binding sequences.

3.2. SELEX with fixed selection stringency

Let us now assume that instead of moving toward the stronger binding energies, the chemical potential \( \mu^{(n)} = \mu \) is constant in each round of the experiment. In such a case, from equation (2) it follows that the energy distribution is given by the following (simple) expression:

\[
\rho_{\text{M}}^{(n)}(E) \sim f^n(E - \mu) \rho_{\text{M}}^{(0)}(E).
\]  

As we show in appendix E, from equation (4) it follows that \( E_{\text{m}}^{(n)} = E_{\text{m}}^{(0)} - n \chi_{\text{le}}^2 \) in the first rounds of experiment, when \( n < \left( \frac{E_{\text{m}}^{(0)} - \mu}{\chi_{\text{le}}^2} \right)^{2} \). Thus, in the first few rounds, the maximum of energy distribution \( E_{\text{m}}^{(n)} \) rapidly moves to the higher affinities. However, once \( E_{\text{m}}^{(n)} \) reaches \( \mu \), it further drifts very slowly toward stronger binding energies (equation (E.3)). Figure 3 is equivalent to figure 2 with the difference that \( \mu^{(n)} = \mu \) is fixed throughout the experiment. We see that for \( n = 1 \), we have the same situation as in the high stringency experiment, i.e., the signal-to-noise ratio is too low. For \( n = 2 \), non-specific binders are eliminated, similarly as in the high stringency experiment. However, the important difference is that instead of reaching the strongest binders (i.e., \( E_{\text{S}} \)), \( E_{\text{m}}^{(2)} \) is close to \( \mu \). For \( n > 2 \), \( E_{\text{m}}^{(n)} \) drifts very slowly toward the higher binding energies, remaining in the proximity of \( \mu \), and consequently does not reach \( E_{\text{S}} \). More precisely, in appendix E we show that \( E_{\text{m}}^{(n)} \) asymptotically approaches \( \mu - 2kBT \).

The procedure described above has a significant practical advantage compared to the high stringency experiment discussed in the previous subsection. Since \( E_{\text{m}}^{(n)} \) remains essentially fixed for larger \( n \), one can perform more rounds (say 4 or 5), thus being sure that random binders are eliminated, without the risk that only the strongest sequences will be selected. Since the procedure tolerates the whole range of \( n \) (in the above example \( n \geq 2 \)), we call it robust.

The next issue is how the constraint of fixed chemical potential can be experimentally implemented. To our knowledge, all but one of the performed experiments correspond to high stringency SELEX. However, in the experiment done by Roulet et al [14], the SELEX experiment was modified by inclusion of the radiolabeled sequence (probe) of moderate binding affinity \( E^* \). The concentration of the DNA, added to the reaction mixture as a competitor to the radiolabeled probe, was in each round adjusted, so that a fixed fraction of the probe is bound by CTF/NFI TF in each SELEX round. From this it follows that \( f(E^* - \mu^{(n)}) = \text{const} \), leading to \( \mu^{(n)} = \text{const} \). Therefore the procedure in [14], provides a practical solution for fixing chemical potential through different rounds of experiment.

We also note that the analysis above gives a practical criterion at what \( n \) the experiment should stop. The procedure can be completed when random binders are eliminated and \( E_{\text{m}}^{(n)} \) has reached \( \mu \), at which point we have a ‘quasi-saturation’ (see figure 3 and equation (E.3)). Since at quasi-saturation the total amount of DNA (adjusted and directly observed by experimentalists) ceases to significantly change from one round to the next, this gives a practical criterion at what \( n \) the experiment should end.

4. SELEX data analysis

In this section, we present a bioinformatic method for the data analysis of fixed stringency (\( \mu = \text{const} \)) SELEX experiments. We will first briefly present the basic idea behind our method. We will then introduce our novel algorithm for constructing an energy matrix in section 4.1. In section 4.2 we will apply the algorithm to the experimental data, and compare the results with both the information theory based method and a widely used empirically formulated procedure, MatInspector [30].

Figure 3 and appendix E show that the maximum of energy distribution for oligos selected in the final rounds of SELEX has to be in the vicinity of the chemical potential. It follows that the majority of sequences extracted from SELEX are in the saturated regime, i.e., bound with the probability close to 1 (see appendix A). In [7] we showed that the information theory method is appropriate to use when sequences are in the unsaturated regime, but that this method does not properly incorporate saturation in the binding probability. In the context of SELEX experiments considered here, the information theory based method would be appropriate to use only if the majority of oligos were in the exponential tail of the binding probability \( f(E - \mu) \). Since this does not happen in the fixed stringency SELEX experiments, we will, in this
section, devise a method which uses the correct binding probability. Additionally, as described in section 3 and appendix C, we have extended a biophysical model of TF–DNA interactions to take into account that the length of a TF binding site is typically shorter than the lengths of DNA sequences in SELEX, which we will also incorporate into our new procedure.

A key point in the implementation of our method will be to obtain TF–DNA interaction parameters through a maximum likelihood procedure. We will infer the initially unknown parameters by maximizing the probability that the extracted set of DNA sequences is observed as the outcome of the experiment. The probability of extracting the given set of DNA sequences will be calculated by taking into account the correct TF–DNA binding probability (which properly describes the saturation effects) and by appropriately modifying affinity distribution of DNA oligos to account for differences in lengths between TF binding sites and SELEX DNA sequences. The set of equations resulting from varying this probability with respect to the unknown parameters will then be numerically solved to compute the elements of the energy matrix.

4.1. Estimating the energy matrix

In this subsection, we introduce a novel algorithm appropriate for data analysis of fixed stringency SELEX experiments. Let us assume that after \( n \) rounds of SELEX, set \( A \), which contains \( nS \) sequences \( S^{(j)} \) (\( j \in 1, \ldots, nS \)), has been extracted and sequenced. As summarized above, we will infer the unknown energy matrix by the maximum likelihood procedure. The probability of observing sequences from set \( A \), but no other sequences from the initial DNA pool, is given by

\[
\exp(A) = \prod_{S \in A} \gamma f^n(E(S) - \mu) \prod_{S' \not\in A} [1 - \gamma f^n(E(S') - \mu)].
\]

Terms \( f^n \) in the equation above account for \( n \) selection processes. The factor \( \gamma \) is a ‘sampling probability’ and it absorbs all extraction and amplification events (there are \( n \) of them), as well as the final sequencing after the \( n \)th round. Probabilities of extraction, amplification and sequencing are all assumed to be independent of sequence \( S \), so \( \gamma \) does not depend on \( S \) either. We also note that we have neglected non-specific binding/background partitioning in equation (5), since we assume that \( n \) in equation (5) is large enough, so that non-specific binders are eliminated by the \( n \)th round (see figure 3). Further, the sum over unbound sequences \( S' \) can be approximated in terms of the binding energy distribution:

\[
\prod_{S' \not\in A} [1 - \gamma f^n(E(S') - \mu)] \approx \exp \left[ -\gamma \sum_{S \not\in A} f^n(E(S') - \mu) \right] \approx \exp \left[ -\gamma \int \rho_M(E) f^n(E - \mu) dE \right].
\]

In the above equation, we use \( \rho_M(E) \) (see equation (C.4)) instead of \( \rho(E) \) (see equation (A.4)) to account for the fact that the length of used DNA sequences is typically larger than the length of the TF binding site (see appendix C). Similarly, we approximate \( f(E(S) - \mu) \) in the first term of equation (5) by \( f(E(s_M) - \mu) \) (see appendix C), where \( s_M \) is the TF binding site of length \( L \), with the maximal binding energy on \( L \) long sequence \( S \). In practice, the set of binding sites \( s_M \) can be identified by an unsupervised search of the set of sequences \( S \) for \( L \) long statistically overrepresented motifs (e.g., by using the Gibbs search algorithm [31]). We also note that in the first (approximate) equality in (6), we used \( \gamma \ll 1 \), which is justified by the fact that the number of DNA sequences with binding energies below \( \mu \) is typically much larger than the number of sequences \( nS \) extracted from the last round of the experiment. For example, if we assume \( \mu = -3\chi \) (as in figure 3), \( nS \sim 10^3 \) [14] and typical \( N \sim 10^{15} \) [13], we have \( \gamma = nS \left( \int f^n(E - \mu) \rho_M(E) dE \right) \sim 10^{-9} \).

Since changing the overall scale of energy corresponds to multiplying energy scores for all binding sites with the (same) constant, for bioinformatic purposes, i.e., for TF binding site identification, it is not necessary to determine the overall scale of energy (see also [7]). The natural quantity to scale all energies is width \( \chi \) (in units of \( k_B T \)) of energy distribution for an ensemble of random oligos of length \( L \) (see [7] as well as equations (A.4)–(A.6) in appendix A). With such scaling, and provided that zero of energy is set to coincide with the mean \( \langle E \rangle \) of energy distribution in the ensemble of random sequences (see equation (A.5) in appendix A), \( E(S)/\chi \) directly gives the estimate of significance of the given energy score. That is, the probability that a random DNA sequence will have a stronger binding energy than \( E(S)/\chi \) is given by

\[
\int_{-\infty}^{E(S)/\chi} \rho(E) dE \approx \frac{1}{2} \left[ 1 - \exp \left( \frac{E(S)/\chi}{\sqrt{2}} \right) \right] \sim \exp(-E(S)^2/(2\chi^2)).
\]

Here \( \rho(E) \) is the energy distribution for the set of random oligos (equation (A.4) in appendix A), \( \text{erf}(x) \) is the error function, and the last approximation is valid for \( |E(S)/\chi| \gg 1 \). Also note that if we consider the energy matrix as a vector in \( 4L \)-dimensional space, \( \chi \) is equal to the norm of this vector (see equation (A.7) in appendix A), so rescaling with \( \chi \) corresponds to normalizing the energy matrix to unit ‘length’. We further use the notation \( \tilde{\xi}_{i,a} = \xi_{i,a} / \chi \).

Additionally, since maximum \( E_M^{(i)} \) (i.e., the mean within the Gaussian approximation of \( \rho_M(E) \)) has to be close to \( \mu \) (see section 3.2 and figure 3), we impose the constraint that

\[
\mu/\chi = \sum_{S \in A} E(S)/\langle nS \rangle = \sum_{i,a} \tilde{\xi}_{i,a} S_{i,a}^* \sim 1
\]

since \( S_{i,a}^* \sim (nS)^\gamma \sim \tilde{\xi}_{i,a} S_{i,a}^* \). In order to obtain \( \tilde{\xi}_{i,a} \), we maximize \( \Lambda \) (defined by equations (5), (6) and (8)) with respect to \( \tilde{\xi}_{i,a} \) and \( \gamma \). Variation of \( \Lambda \) with respect to \( \tilde{\xi}_{i,a} \) and \( \gamma \) then leads to the set of equations which are given in appendix F. Those equations can be numerically solved to obtain \( \tilde{\xi}_{i,a} \).

4.2. Application of the algorithm

To demonstrate our method, we use it to analyze the data from the experiment by Roulet et al [14]. In addition to the modification discussed in section 3.2, Roulet et al combined SELEX with the SAGE protocol [15], which allowed them to

\[\text{18} \]
sequence a large number of DNA oligos. A large dataset provides an obvious advantage for a precise estimation of energy parameters. In particular, a total of four SELEX rounds were performed, and approximately 880, 960, 1200, 6900 and 230 sequences were obtained from rounds 0, 1, 2, 3 and 4 respectively (note that round 0 refers to the initial, completely random, DNA pool).

We use about 230 sequences obtained after the fourth round of experiment, to estimate $\tilde{\epsilon}_{i,\alpha}$. We first search those 230 sequences $S$, to identify CTF/NFI binding sites $s_M$ that correspond to $L = 15$ bp long statistically overrepresented motifs. The unsupervised search was performed by using a Gibbs search based algorithm [32], and the obtained set of binding sites $s_M$ was used to determine $\tilde{\epsilon}_{i,\alpha}$ by numerically solving equation (F.5). The obtained energy matrix $\tilde{\epsilon}_{i,\alpha}$ is given in appendix F (table F1). We will further call $\tilde{\epsilon}_{i,\alpha}$ the finite $T$ energy matrix, to emphasize that, contrary to the QPMMEME algorithm [7], the optimization of $\Lambda$ (equation (5)) is not done in the $T \to 0$ limit. We shift columns of $\tilde{\epsilon}_{i,\alpha}$, so that the mean of the energy distribution $\rho(E)$ (given by equation (A.5)), for the ensemble of random oligos of length $L$ is zero.

We next compare our method with both the information theory based method and a widely used empirically formulated procedure, MatInspector [30]. For this purpose, we construct both the information theory weight matrix $w_{i,\alpha}$ (see, e.g., [33])

7 Note that a provisional base independent constant can be added to each column of the weight (energy) matrix, which corresponds to the shifting zero of the weight matrix scores.

and the MatInspector weight matrix $w_{i,\alpha}^{MI}$ (see [30]) from the same set of binding sites $s_M$ that we used to compute our finite $T$ energy matrix. The obtained matrices are given and compared in appendix F. We normalize $w_{i,\alpha}$ and $w_{i,\alpha}^{MI}$ and choose the zeros of weight matrix scores (i.e. ‘energies’) for both matrices in the same way as for $\tilde{\epsilon}_{i,\alpha}$. The three matrices are then used to compute the corresponding energy distributions for more than 6000 sequences extracted from the third round of SELEX, and their comparison is shown in figure 4. We see that there is a noticeable difference in the estimates of energies obtained by the three weight matrices.

To compare performance of the methods, we will infer a false positive/false negative trade-off for the three matrices. The fraction of false negatives, for certain threshold $E/\chi$, can be readily estimated by computing cumulatives of the distributions shown in figure 4. Further, the fraction of false positives can be calculated by computing the corresponding cumulative of the energy distribution of random oligos (see equation (A.4) in appendix A). Therefore, with our choice for the zero of energy, it is evident that $\exp(-E^2/(2\chi^2))$ (on the abscissa of figure 5) is proportional to the number of false positives. More precisely, if one searches a random DNA sequence with total length $N_D$, the total number of binding sites with energy scores below $E/\chi$ is approximately $(N_D/\sqrt{2\pi}) \int_{-\infty}^{E/\chi} \exp(-x^2/2) \, dx \sim N_D \exp(-E^2/(2\chi^2))$ (see equations (A.4) and (7)), where the last approximation is valid for $|E/\chi| \gg 1$.

The above estimates of false positives and false negatives can be used to obtain the detection error trade-off (DET) curves (see [7, 34]), which are shown in figure 5.8 We see

Figure 4. Energy distributions obtained by using the finite $T$ energy matrix, the information-theoretic weight matrix and the MatInspector weight matrix are compared. Energy distributions are computed for more than 6000 binding sites extracted from the third round of SELEX [14]. Zero on the horizontal axis corresponds to the mean value of binding energy in a random ensemble. Note that the maximum of energy distribution for non-specific binders is displaced relative to zero (i.e., positioned at around -1.5), caused by the fact that the length of the DNA sequences (25 bp) is larger than the length of the CTF/NFI TF binding site (15 bp). Actually, the energy distribution of non-specific binders matches well with $\rho_M(E)$ calculated in appendix F (equation (C.4)).

Figure 5. Comparison of the DET curves for the finite $T$ energy matrix, the information theory weight matrix and the MatInspector weight matrix. Note that $E/\chi$ is measured relative to the average binding energy in a random ensemble, so that $\exp(-E^2/(2\chi^2))$ on the horizontal axis is proportional to the number of false positives. A false negative fraction is inferred from figure 4, by calculating cumulatives of the corresponding energy distributions.
that over the entire range of fixed false negative values on the vertical axis, fraction of false positives for the finite $T$ energy matrix is few times lower compared to the false positive rate for the information-theory weight matrix. In the case of the MatInspector weight matrix, the finite $T$ energy matrix has about two times smaller false positive rate for false negative fractions smaller than 40\%, while for larger false negative fractions the two DET curves come close to each other. We note that the meaningful range, in which one is likely to operate in practice, is the one with a smaller fraction of false negatives (i.e., 40\% or below), where the finite $T$ energy matrix clearly shows better performance.

Figure 5 shows that, while our method outperforms both MatInspector and the information theory method, it appears that MatInspector shows a better false positive/false negative trade-off compared to the information theory method. We, however, note that MatInspector is an empirically formulated procedure, i.e., it is not founded on either statistical considerations, such as the information theory method, or on a (bio)physical model of TF–DNA interactions, such as the method presented here. We therefore believe that the performance of MatInspector would change from one experiment to the other, and that a better performance of MatInspector compared to the information theory method may not prove to be systematic. On the other hand, since our method is based on a correct physical model of SELEX experiments, we expect that it will systematically produce reliable estimates of the interaction parameters. In any case, fixed stringency SELEX experiments, which will be performed in future, will provide opportunities to more thoroughly test the performance of the algorithms.

Finally, we discuss how the above comparison of the three algorithms may be affected by the possible presence of noise in the input data used to construct the three weight matrices. We obtained the set of (putative) binding sites through a heuristic Gibbs sampling algorithm, which is in principle not guaranteed to find the true binding sites. So if there are misassignments in the input data, the question is whether the better performance of our method could be the result of higher robustness with regard to noise, rather than higher accuracy for error-free data. To assess the amount of noise in the input data we performed a self-consistency check. We scored all DNA sequences selected in the fourth round of the experiment with the finite $T$ energy matrix and classified all binding sites above score $-3.4$ as specific binders and all below $-3.4$ as non-specific binders (note that $-3.4$ corresponds to the saddle of the bimodal distribution shown in figure 4). We find that only one in the 175 large set of input binding sites obtained by the Gibbs algorithm is not contained in the list of 184 specific binders classified with the finite $T$ energy matrix. This indicates that the noise level in the input data is likely quite small. The apparent low number of misassignments in the output of Gibbs alignment is likely a consequence of the low number of random sequences extracted from the fourth round of SELEX\footnote{optional feature at the discretion of the user\[30\], which was not used in the example searches in \[30\]. Additionally, in \[30\] it is not stated how to choose the value of the second threshold, which makes it hard to fairly compare a method with two (arbitrary) thresholds with the methods that use only one threshold.}, and the fact that the length of SELEX sequences is quite short (25 bp).

5. Conclusion and outlook

In this paper, we modeled SELEX experiments and proposed a novel method of data analysis. Our analysis showed that for a certain realistic range of parameters, the suitable solution for the number of rounds that should be performed does not exist at all. We argued that even for the parameters for which the solution exists, it is very hard to find such a solution in practice. However, we showed that the modification of the standard SELEX procedure in which chemical potential is fixed \[14\] robustly selects sequences that allow one to successfully determine the energy matrix. We next proposed a novel method for inferring an energy matrix from the sequences extracted from a SELEX experiment with fixed selection stringency. In contrast to the widely used information theory weight matrix method, our procedure correctly represents saturation in binding probability. As an example of the procedure, we estimated the energy matrix for CTF/NFI TF by analyzing the data from the experiment by Roulet et al \[14\]. We demonstrated that our energy matrix leads to a significantly better false positive/false negative trade-off.

Finally, we compared the results of our analysis with some widely held views. It is generally well understood that doing too large a number of SELEX rounds leads to too strong a selection. It is, however, widely believed that the problem can be solved by doing only few selection cycles. For example, in the recent SELEX experiment by Kim et al \[35\], it was noted, “...we used fewer rounds of selection than a conventional SELEX to avoid the enrichment of just a few high affinity winners”. However, as shown by our analysis, this can lead to another problem, i.e., if too few SELEX rounds are performed, too large a number of random sequences are likely to be selected. Moreover, we found that the problems of overselection and too high amount of noise are, in practice, very hard to reconcile within the standard SELEX procedure and that a modified experiment with a fixed chemical potential has to be performed instead. From the aspect of data analysis, we showed that the commonly used information theory based method, widely believed to be well founded in both statistics and thermodynamics \[36\], is not appropriate for analysis of data for SELEX experiments with fixed selection stringency.

In the context of future research, we believe that the analysis presented here, together with the experimental methods introduced in \[14\], opens a perspective to apply high-throughput, fixed stringency, SELEX experiments for a large number of different transcription factors. This would provide a reliable method for detection of transcription factor binding sites, and would facilitate the comprehensive understanding of gene regulation.

\footnote{Note that figure 4 shows that there is a quite small amount of noise even in the third round of experiment. The noise is further reduced in the fourth round.}
**Glossary**

**Weight matrix.** For a binding pattern of length \( L \) it is defined as a matrix of numbers \( w_{i,\alpha} \) where \( i \in [1, 2, \ldots, L] \) and \( \alpha \in \{A, T, C, G\} \). The score of the sequence \( \alpha_1, \ldots, \alpha_L \) is given by \( w_{1,\alpha_1} + w_{2,\alpha_2} + \cdots + w_{L,\alpha_L} \).

**Sensitivity.** It is defined as \( TP/(TP + FN) \), where \( TP \) is the number of true positives and \( FN \) is the number of false negatives. In the context of a TF binding site search, a true positive (TP) arises when an algorithm correctly classifies a true binding site as such, while a false negative (FN) arises when an algorithm classifies a true non-binding site as a non-binding site.

**Specificity.** It is defined as \( TN/(TN + FP) \), where \( TN \) is the number of true negatives and \( FP \) is the number of false positives. In the context of TF binding site search, a true negative arises when an algorithm correctly classifies a true non-binding site as such, while a false positive (FP) arises when a search algorithm classifies a true non-binding site as a binding site.

**Serial analysis of gene expression (SAGE).** It is a method for comprehensive analysis of gene expression patterns. In the context of this paper, a part of the SAGE protocol can be used to link together oligomers extracted from SELEX in order to form longer DNA molecules that can be efficiently sequenced.

**Gel shift.** It is a technique used to separate free DNA molecules from DNA molecules that are in complex with protein, based on the fact that protein–DNA complexes migrate more slowly through gel under the influence of an electric field.

**Polymerase chain reaction (PCR).** It is an experimental technique that allows one to produce a large number of copies of any fragment of DNA. In principle, the number of DNA molecules is doubled in each round of PCR, so there is an exponential increase in the number of molecules with the number of performed PCR rounds.

**Dissociation constant.** For sequence \( S \) it is equal to the concentration of (free) TF for which there is 50\% probability that a DNA molecule \( S \) will be bound by the TF. The relationship between the dissociation constant and the binding energy \( E(S) \) is given by \( K_D(S) = K \exp(E(S)) \), where \( K \) is a proportionality constant.

**Maximum likelihood estimation.** It is a statistical method used to estimate unknown parameters of a (known) probability distribution. The basic principle is to draw a sample from the distribution, calculate the probability that this sample is observed and then determine the unknown parameters such that this probability is maximal.

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**Appendix A. A biophysical model of TF–DNA interaction**

Let us consider an experiment where a certain number of identical DNA oligomers with sequence \( S \) and length \( L \) (equal to the length of the TF binding site) are mixed into a solution with some concentration of TF. It can be shown (see, e.g., [7]) that the equilibrium probability \( p(S) \) that a DNA sequence \( S \) is bound by TF is given by

\[
p(S) = \frac{1}{1 + \exp\left(\frac{E(S) - \mu}{k_B T}\right)} = f(\frac{E(S) - \mu}{k_B T}). \tag{A.1}
\]

In equations (A.1) and (A.2), \( p_f \) is the concentration of free TF, \( \mu \) is the chemical potential, while \( K \) is a multiplicative constant related to the counting number of quantum states in a box (e.g., see [37]).

Chemical potential \( \mu \) is set by the free TF concentration in the solution:

\[
\mu = \log(p_f / K). \tag{A.2}
\]

Note that in the above equations all energies are rescaled by \( k_B T \). The form of the binding probability \( f(\frac{E(S) - \mu}{k_B T}) \) in equation (A.1) corresponds to the Fermi–Dirac distribution (see, e.g., [37]). If the binding energy \( E(S) \) of a sequence \( S \) is well below \( \mu \), then \( f(\frac{E(S) - \mu}{k_B T}) \) is close to 1 and the sequence \( S \) is almost always bound by TF. We will further call sequences with binding energy \( E(S) \) which corresponds to this limit saturated. On the other hand, if \( E(S) \) is well above \( \mu \), the sequence \( S \) is rarely bound, with probability given by the Boltzmann distribution \( f(\frac{E(S) - \mu}{k_B T}) \approx \exp\left(-\frac{E(S) - \mu}{k_B T}\right) \).

As shown in [7], the information theory weight matrix procedure assumes Boltzmann distribution of binding probability, and is, therefore, not appropriate whenever saturation of binding occurs. Further, we need an expression for \( E(S) \). The most simple model of TF–DNA interaction, which we use in this paper, assumes that the interaction of a given base with the factor does not depend on the neighboring bases,

\[
E(S) \approx \epsilon \cdot S = \sum_{i=1}^{L} \sum_{\alpha=1}^{4} \epsilon_\alpha^i S_\alpha^i, \tag{A.3}
\]

where \( S_\alpha^i = 1 \), if base \( \alpha \) is at position \( i \) and \( S_\alpha^i = 0 \) otherwise. \( \epsilon_\alpha^i \) is the interaction energy with the nucleotide \( \alpha \) at the position \( i = 1, \ldots, L \) of the DNA string [20], and \( \epsilon \) is called the energy matrix. The simple parameterization given by equation (A.3) provides a very good approximation in many cases [20, 22–24].
although there are examples where binding at some positions in the binding site shows dependence on dinucleotide pairs [38–40].

We further need to compute the energy distribution $\rho(E)$ for an ensemble of randomly generated oligonucleotides, with length equal to the length $L$ of TF binding site. In [7] it was shown that in the first approximation $\rho(E)$ is given by a Gaussian,

$$
\rho(E) \approx \exp\left(-\left(E - \overline{E}\right)^2/2\chi^2\right)/\sqrt{2\pi}\chi^2
$$

(A.4)

with

$$
\overline{E} = \sum_{i=1}^L \tau_i
$$

(A.5)

and

$$
\chi^2 = \sum_{i=1}^L \sum_{a=1}^4 p_a (\epsilon_{i,a} - \tau_i)^2
$$

(A.6)

where $\tau_i = \sum_{a=1}^4 p_a (\epsilon_{i,a})$.

As noted in footnote 7, each column of an energy matrix can be shifted for a provisional base independent value, and a convenient choice would be to set $\tau_i = 0$, so that $\overline{E} = 0$ and

$$
\chi^2 = \sum_{i=1}^L \sum_{a=1}^4 p_a (\epsilon_{i,a})^2.
$$

(A.7)

From the above equation it follows that $\chi$ is equal to the norm of the energy matrix $\epsilon_{i,a}$, with ‘metric’ given by the background single base frequencies $p_a$.

We further note that $\rho(E)$ is well approximated by equation (A.4) in the proximity of maximum $E = \overline{E}$, however, away from the maximum deviations from Gaussianity appear. In fact, the support of $\rho(E)$ is finite with the ‘bottom of the band’ $E_S = \sum_{\min} \epsilon_{i,a}$ (while the ‘top’ is given by $\sum_{\max} \epsilon_{i,a}$). In this paper, we work with the Gaussian approximation to $\rho(E)$, but we also introduce a cut in the distribution to account for the fact that the support $E_S$ is finite (see appendix C).

Further extensions of the TF–DNA interaction model, necessary for our modeling of SELEX experiments, are given in appendices B and C.

### Appendix B. Non-specific binding of TF to DNA

We here assume that a given TF can bind to DNA in two conformations. The first conformation results in the sequence specific interaction, with the interaction energy $E(S)$. The second conformation results in the sequence independent (non-specific) interaction, with the interaction energy $E_{ns}$ [2]. $E_{ns}$ is called the threshold for non-specific binding. We consider a reversible reaction of binding of the TF to a DNA sequence $S$, where TF can bind with $S$ in two conformations. Sequence specific, and sequence non-specific reactions can, respectively, be represented by

$$
[\text{TF}] + [S] \leftrightarrow [\text{TF} - S]_s \quad \text{(B.1)}
$$

and

$$
[\text{TF}] + [S] \leftrightarrow [\text{TF} - S]_{ns} \quad \text{(B.2)}
$$

Here, $[\text{TF}]$ is the concentration of free TF, $[S]$ is the concentration of sequence $S$ that is not in the complex with protein, while $[\text{TF} - S]$ is the concentration of TF that is bound to the TF in the sequence specific, and in the sequence non-specific conformation respectively. In the equilibrium, the following relations hold:

$$
K \exp(E(S)) = \frac{[\text{TF}] [S]}{[\text{TF} - S]_s}, \quad \text{(B.3)}
$$

$$
K \exp(E_{ns}) = \frac{[\text{TF}] [S]}{[\text{TF} - S]_{ns}}. \quad \text{(B.4)}
$$

From equations (B.3) and (B.4) we have that the probability that a sequence $S$ is bound by the TF is given by

$$
p(S) = \frac{[\text{TF} - S]_s + [\text{TF} - S]_{ns}}{[\text{TF}] + [\text{TF} - S]_s + [\text{TF} - S]_{ns}} = \frac{1}{b \exp(E(S)) + 1 + c_{ns}}. \quad \text{(B.5)}
$$

In the equation above,

$$
a = \frac{1}{1 + \exp(\mu - E_{ns})} \quad \text{and} \quad \exp(-\mu) = \frac{1}{1 + \exp(\mu - E_{ns})} \quad \text{from (B.6) and (B.7) follows that} \quad a \approx 1, b \approx \exp(-\mu) \quad \text{and} \quad c_{ns} \approx \exp(-(E_{ns} - \mu)).
$$

(B.7)

Therefore, the effect of non-specific binding enters through $c_{ns}$, which is determined by the position of $\mu$ relative to $E_{ns}$. We note that values of $E_{ns}$ were not experimentally quantitated [25], so one does not know what range of values $E_{ns}$ can take. Unless $E_{ns}$ is positioned in the strong binding tail of $\rho(E)$, non-specific binding will not have a large effect. As discussed in section 3, non-specific binding is in SELEX experiments essentially indistinguishable from the background partitioning effect.
Appendix C. Binding of TF to a longer DNA sequence

In appendix A, we derived the binding probability under the assumption that the length \( l \) of DNA sequence is equal to the length \( L \) of the TF binding site. However, for DNA sequences used in SELEX, \( l \) is typically larger than \( L \). For example, in the SELEX experiment performed by Roulet et al [14] (see section 3.2) \( l = 25 \) bp, while \( L = 15 \) bp for CTF/NFI TF. It is straightforward to obtain that the probability that sequence with length \( l \) will be bound is given by

\[
p(S) = \frac{\exp(\mu \sum_{i=1}^{l-1} \exp(-E(s_i)))}{1 + \exp(\mu \sum_{i=1}^{l-1} \exp(-E(s_i)))}.
\] (C.1)

In the equation above, the sequences \( s_i \) are \( L \) long binding sites, corresponding to all possible \( l - L \) frame shifts in which the TF can bind to a sequence \( S \), while \( \mu \) is chemical potential (see appendix A). We assume that \( l < 2L \), which is typically the case in SELEX experiments, so that two or more TF molecules cannot simultaneously bind to the sequence \( S \). Note that all quantities in equation (C.1) are rescaled by \( k_BT \). For \( l_r = l - L \) that is not too large, which is typically the case in the experiments, the expression \( \sum_{i=1}^{l-1} \exp(-E(s_i)) \) can be approximated by taking into account only the contribution from the strongest binding site \( s_M \), where \( E_M(S) = E_S(s_M) = \min(E(s_i), i \in (1, l_r)) \). With this approximation, equation (C.1) simplifies to

\[
p(S) \approx f(E_M(S) - \mu) = \frac{1}{1 + \exp(E_M(S) - \mu)}
\] (C.2)

which is the Fermi–Dirac probability encountered before (see appendix A).

From equation (C.2) it follows that binding of a TF to a sequence \( S \) with \( l > L \) is (approximately) equivalent to the binding to the sequence \( s_M \) with length \( L \). Let us now look at the first round of SELEX, where the TF is mixed with a large number of randomly generated sequences of length \( l \). In order to make the problem equivalent to that in which \( l = L \), instead of density of states \( \rho(E) \) (see appendix A), we have to use \( \rho_M(E) \) defined as the number of sequences \( S \), for which \( E_M(S) \) has energy between \( E \) and \( E + dE \).

To calculate \( \rho_M(E) \), we neglect correlations in binding energies \( E(s_i) \) (see equation (C.1)) of \( l_r \) binding sites that belong to the same sequence \( S \). This is in general well justified, unless sequence \( S \) consists of the long repeat. In particular, the validity of this approximation was confirmed by numerically testing equation (C.4) below. Based on this, \( \rho_M(E) \) can be calculated by generating sets of \( l_r \) values of \( E \) from distribution \( \rho(E) \) and retaining only the strongest binding energy from each set. It is straightforward to see that \( \rho_M(E') \) can be obtained from \( \rho(E) \) by

\[
\rho_M(E') = l_r \frac{d\Phi(E')}{dE'} \left(1 - \Phi(E')\right)^{l_r-1},
\] (C.3)

where \( \Phi(E') \) is the cumulative distribution given by \( \Phi(E') = \int_{-\infty}^{E'} \rho(E) \, dE \). The expression on the right-hand side of equation (C.3) is, therefore, equal to the probability that \( l_r - 1 \) values of \( E \) generated from \( \rho(E) \) are above \( E' \), while one of them (the strongest binding energy) is between \( E' \) and \( E' + dE' \).

By plotting \( \rho_M(E) \), given by equation (C.3) we see that \( \rho_M(E) \) can be approximated by a Gaussian,

\[
\rho_M(E) \approx \exp \left(\frac{(E - \overline{E}_M)^2}{2\overline{\chi}^2} \right),
\] (C.4)

with

\[
\overline{E}_M = \overline{E} - a(l_r) \chi,
\] (C.5)

and

\[
\rho_r = b(l_r) \chi,
\] (C.6)

where \( \overline{E} \) and \( \chi \) are respectively mean value and the standard deviation for \( \rho(E) \) (see appendix A), while \( a(l_r) \) and \( b(l_r) \) are respectively monotonically increasing and decreasing functions of \( l_r \). Functions \( a(l_r) \) and \( b(l_r) \) can be calculated numerically (e.g., \( a(10) = 1.4 \) and \( b(10) = 0.3 \)). Numerical analysis shows that approximately, \( a(l_r) \approx 0.6 \log(l_r) \), while \( b(l_r) \approx 1/\sqrt{\overline{E}} \).

Finally, we have to take into account that \( \rho_M(E) \) has the finite support, where ‘bottom of the band’ \( E_S \) is determined by the energy of the strongest binder in the random pool of DNA sequences, and can be approximated by

\[
(4l_r \int_{-\infty}^{E_S} \rho(E) \, dE \sim 1, \quad \text{(C.7)}
\]

where \( \rho(E) \) is normalized to 1.

In equation (C.7), we assumed that the total number of sequences \( N \) (more precisely \( l_rN \) in the DNA pool is larger than \( 4^L \), so that all possible sequences of length \( L \) are present. This is most often the case in practice, since typically \( L < 20 \), while \( N \approx 10^{15} \) [13], so that \( 4^L \ll N \).

To take into account the finite support of \( \rho_M(E) \), we make a simple approximation and introduce a sharp cut in the distribution \( \rho_M(E) \), i.e., we take that

\[
\rho_M(E) \sim \theta(E - E_S) \exp \left(\frac{(E - \overline{E}_M)^2}{2\overline{\chi}^2} \right), \quad \text{(C.8)}
\]

where \( \theta(E - E_S) \) is unit step (Heaviside) function. We note that the top of the band is finite as well, however we do not include it in equation (C.8), since energy distribution of selected oligos moves toward higher binding affinities in SELEX (see section 3.1). In reality, \( \rho_M(E) \) becomes discrete when we approach \( E_S \), however a simple approximation given by equation (C.8) is sufficient for the purpose of our model.

Appendix D. High stringency SELEX in the limit of unsaturated binding

In this appendix, we look at the limit in which the binding probability \( f(E - \mu) \) in equations (2) and (3) can be approximated by the Boltzmann factor \( \exp(\mu - E) \). In this limit, those equations can be solved analytically. The above approximation is valid if all selected binding sites are unsaturated in each SELEX round, i.e., if \( \mu^{(k)} < E_S (\forall k \in (1, \ldots, n)) \), where \( n \) is the number of performed SELEX...
rounds. In this limit, equation (2) gives

\[ p_{M}^{(n)}(E) \sim \exp(-E + \exp(-E_{\text{ns}}))^{c_{n}} \rho_{M}(E), \]  

(D.1)

where, for simplicity of notation, we assume that all noise comes from non-specific binding, i.e., \( c \equiv c_{\text{ns}} \) (see equations (1)). If we use the Gaussian approximation for \( \rho_{M}(E) \) (see equation (C.4)), from equation (D.1) it follows that \( p_{M}^{(n)}(E) \) has \( n \) peaks, which are centered at positions \( E_{m,k}^{(n)} = -k\chi^{2}_{m,k} \) (\( k = 1, \ldots, n \)). Here we shifted zero of energy, so that it coincides with \( E_{\text{le}} \) (see equation (C.5)). From equation (D.1) it is obvious that \( n \)th peak \( E_{m,k=n}^{(n)} \equiv E_{m}^{(n)} \) contains only sequence specific binding sites, while \( k = 0 \) peak (centered at zero) corresponds exclusively to non-specific (i.e., random) binders. Therefore, in the limit considered here, the maximum of specifically selected binding sites (the leading maximum) is positioned at

\[ E_{m}^{(n)} = -n\chi^{2}_{m}. \]  

(D.2)

From equation (D.2) it follows that \( E_{m}^{(n)} \) rapidly moves to higher binding energies. For example, for the realistic parameter values of \( \chi_{m} = 2 \) and \( E_{\text{le}} = -5\chi_{m} \) (corresponding to \( L = 12 \), see equation (C.7)), \( E_{m}^{(n)} \) reaches \( E_{\text{le}} \) after (only) three SELEX rounds.

The 'intensity' \( I_{k}^{(n)} \) of \( k \)th peak, i.e., the number of binding sites corresponding to the peak, is

\[ I_{k}^{(n)} \sim \exp(-E_{\text{ns}}(n-k)) \int \exp(-Ek) \rho_{M}(E) \]

\[ \approx \exp(-E_{\text{ns}}(n-k)) \exp(k^{2}\chi^{2}_{m}/2). \]  

(D.3)

From equation (D.3) it is straightforward to obtain that the conditions \( I_{k}^{(n)} > I_{0}^{(n)} \) and \( I_{k}^{(n)} > I_{0}^{(n)} \) cannot be simultaneously satisfied for \( k = 2, \ldots, n-1 \), for any parameter values. Therefore, for any given \( n \), either zeroth or \( n \)th peak has the maximal intensity. Further, it is sensible to define 'signal-to-noise' ratio \( \nu^{(n)} \) as the ratio of the number of specific binders corresponding to the \( n \)th peak and the number of non-specific binders corresponding to the zeroth peak. From equation (D.3) it follows that

\[ \nu^{(n)} = \exp(n^{2}\chi^{2}_{m}/2 + nE_{\text{ns}}), \]  

(D.4)

so the signal-to-noise ratio necessarily increases with increasing \( n \).

We next derive for what parameter values is the 'generated' binding energy compared to the zeroth peak increases with \( n \), if we approximate \( \mu_{(n)}^{(n)} \) by \( \mu^{(n)} \), and consequently in the decrease of \( \chi_{m}^{2}, \nu^{(n)} \) decreases, with increasing \( n \). Further, the following interpretation can be assigned to the terms on the right-hand side of equation (D.6). It is obvious that \( \mu^{(n)} \) increases, with the increase of (total) protein to (total) DNA ratio \( p_{f}/d_{r} \). The term \( \exp[(n-1/2)\chi^{2}_{m}] \) accounts for the fact that the (average) binding energy of sequences corresponding to the \( n \)th peak increases with \( n \) (see equation (D.2)), which results in the decrease of the concentration of free TF and consequently in the decrease of \( \mu^{(n)} \).

We finally discuss how \( \mu^{(n)} \) depends on the parameter values (for further discussion, we let \( j \to n \) in equation (D.6)). From equation (D.6) it is straightforward to show that \( \mu^{(n)} \) necessarily decreases, with increasing \( n \). Further, the following interpretation can be assigned to the terms on the right-hand side of equation (D.6). It is obvious that \( \mu^{(n)} \) increases, with the increase of (total) protein to (total) DNA ratio \( p_{f}/d_{r} \). The term \( \exp[(n-1/2)\chi^{2}_{m}] \) accounts for the fact that the (average) binding energy of sequences corresponding to the \( n \)th peak increases with \( n \) (see equation (D.2)), which results in the decrease of the concentration of free TF and consequently in the decrease of \( \mu^{(n)} \).

We note that the condition (D.5) (with \( \mu^{(n)} \) given by equations (D.6) and (D.7)) is satisfied for the subset of parameter values that are inside the realistic range. For example, the condition (D.5) holds for \( p_{f} = 10 \) nM, \( d_{r} = 10 \) mM (see, e.g., [12]), \( \chi_{m} = 2 \), \( E_{\text{le}} = -2\chi_{m} \), \( E_{\text{le}} = -5\chi_{m} \), and for all \( n \) until \( E_{m}^{(n)} \) reaches \( E_{\text{le}} \) (i.e., for \( n = 1, 2, 3 \)).

We finally discuss how \( \mu^{(n)} \) depends on the parameter values (for further discussion, we let \( j \to n \) in equation (D.6)). From equation (D.6) it is straightforward to show that \( \mu^{(n)} \) necessarily decreases, with increasing \( n \). Further, the following interpretation can be assigned to the terms on the right-hand side of equation (D.6). It is obvious that \( \mu^{(n)} \) increases, with the increase of (total) protein to (total) DNA ratio \( p_{f}/d_{r} \). The term \( \exp[(n-1/2)\chi^{2}_{m}] \) accounts for the fact that the (average) binding energy of sequences corresponding to the \( n \)th peak increases with \( n \) (see equation (D.2)), which results in the decrease of the concentration of free TF and consequently in the decrease of \( \mu^{(n)} \). From equation (D.7) it can be noted that \( \alpha(n, \chi_{m}, E_{\text{le}}) \leq 1 \). This term, therefore, leads to the increase of \( \mu^{(n)} \), which may be explained by the fact that for \( n > 1 \) there are \( n-1 \) peaks of \( \rho_{M}(E) \) 'generated' by non-specific binding. All those peaks have smaller (mean) binding energy compared to the \( n \)th peak, which results in the smaller amount of the specifically bound TF. Finally, the term \( \exp(-E_{\text{ns}}) \) accounts for the fact that some amount of TF is non-specifically bound by DNA sequences, which leads to the decrease of \( \mu^{(n)} \).

The dependence of \( \mu^{(n)} \) from \( E_{\text{le}} \) is, therefore, quite complicated, since increase in non-specific binding decreases \( \mu^{(n)} \) through \( \exp(-E_{\text{ns}}) \), but increases it through \( \alpha(n, \chi_{m}, E_{\text{le}}) \). Similarly, the increase of \( \chi_{m} \) has the opposite effects on \( \mu^{(n)} \) through terms \( \exp[(n-1/2)\chi^{2}_{m}] \) and \( \alpha(n, \chi_{m}, E_{\text{le}}) \).

Appendix E. Maximum of energy distribution in SELEX with fixed selection stringency

We determine how the position of maximum \( E_{m}^{(n)} \) of \( \rho_{M}^{(n)}(E) \) (see equation (4)), changes with the number of performed SELEX rounds \( n \). We first shift zero of energy to coincide with \( E_{\text{le}} \) (see equations (C.4) and (C.5)). Position of maxima of \( \rho_{M}^{(n)}(E) \) is given by

\[ \frac{d\rho_{M}^{(n)}(E)}{dE}\bigg|_{E=E_{m}^{(n)}} = 0. \]  

(E.1)

From equation (4) and the equation above, we obtain

\[ 1 - f(E_{m}^{(n)} - \mu) = -\frac{E_{m}^{(n)}}{\rho_{M}^{(n)}}. \]  

(E.2)

The equation above can be solved graphically, i.e., positions of \( E_{m}^{(n)} \) (for different \( n \)) are determined by the intersections of the family of lines \( \phi_{n}(E) = -E / (n\chi^{2}_{m}) \) and the curve \( 1 - f(E - \mu) \). If we approximate \( f(E - \mu) \) by a step \( \theta(E - \mu) \) (see the dashed line in figure E1), we obtain that \( E_{m}^{(n)} = -n\chi^{2}_{m} \) for \( n < -\mu / \chi^{2}_{m} \) and \( E_{m}^{(n)} = \mu \) otherwise, which is shown in figure E1. Correction, accurate up to the next order
in $1/\chi^2_i$ can be found by linearizing $f(E - \mu)$ around $E = \mu$ (see the dotted line in figure E1). We then obtain

$$E^{(n)}_m = \frac{(\mu - 2)}{1 + 4/(\chi^2_i n)}$$ (E.3)

if $n > (-\mu + 2)/\chi^2_i$, and $E^{(n)}_m = -n\chi^2_i$ otherwise. Note that, for $n$ large enough, i.e., $n \gg 4/\chi^2_i$, $E^{(n)}_m \to (\mu - 2)$. Since in SELEX experiments $\mu$ is typically positioned in the tail of the energy distribution of random binders, we expect $\mu \approx 1$ (see also the comment below equation (E.3)), so $E^{(n)}_m$ for $n > -\mu/\chi^2_i$ is well approximated by $E^{(n)}_m \approx \mu$ (see also figures E1 and 3).

Appendix F. Computing energy matrix from extracted SELEX sequences

We determine the energy matrix $\tilde{e}_{i,a}$ and the parameter $\gamma$ by maximizing the likelihood function $\Lambda$ (see equations (5) and (6)), subject to the constraints

$$\sum_{i,a} p_a\tilde{e}_{i,a}^2 = 1$$ (F.1)

and

$$\sum_a p_a \tilde{e}_{i,a} = 0 \quad (\forall i).$$ (F.2)

The constraint (F.1) follows from $\tilde{e}_{i,a} = e_{i,a}/\chi$ and $\chi^2 = \sum_{i,a} p_a e_{i,a}^2$ (see equation (A.6)), while the constraint (F.2) shifts columns of $\tilde{e}_{i,a}$ (see footnote 7) so that $\tilde{e}_i = 0$ and consequently $\tilde{E} = 0$ (see equations A.4 and A.5). As discussed in section 4 and appendix C, we approximate the binding probability $f(E(S) - \mu)$ in $\Lambda$ by using the strongest binding site $s_M$ with length $L$, on each sequence $S(S \in A)$ of length $L$. To simplify notation, we further, in this appendix, use $s_M \equiv s$. If we use $\mu/\chi$ from equation (8), variation of $\Lambda$ with respect to $\tilde{e}_{i,a}$ and $\gamma$ leads to

$$\frac{\partial \Lambda}{\partial \tilde{e}_{i,a}} = -(n\chi) \sum_{s \in \Lambda} [1 - f(E(s) - \mu)](e_{i,a} - s_{i,a}^*)$$

$$- 2\alpha p_a \tilde{e}_{i,a} - \lambda p_a = 0,$$ (F.3)

$$\frac{\partial \Lambda}{\partial \gamma} = nS - \int f^{\alpha} (E - \mu) \rho_M(E) dE = 0,$$ (F.4)

where $\alpha$ and $\lambda$ are the Lagrange multipliers associated with the constraints (F.1) and (F.2) respectively, while $\rho_M(E)$ is given by equation (C.4). Eliminating $\alpha$ and $\lambda$ and $\gamma$, using respectively equations (F.1), (F.2) and (F.4), leads to the equation that implicitly determines $\tilde{e}_{i,a}$,

$$\tilde{e}_{i,a} = \frac{\sum_{s \in \Lambda} (1 - f(E(s) - \mu))(e_{i,a} - s_{i,a}^*) + (\gamma p_a/\rho_M(E))}{\sum_{s \in \Lambda} (1 - f(E(s) - \mu))(E(s) - \mu) + (1 - \gamma)/\rho_M(E)}.$$ (F.5)

From equation (2) it can be observed that $\psi^{(s+1)}$ is equal to the fraction of DNA that is in the complex with protein in the $(n + 1)$th round of SELEX, when non-specific binding is small (i.e., $n$ large enough, as discussed in section 4.1).

In practice, we typically do not know the exact value of $\chi$, so we fix it to some reasonable value and then (numerically) solve equation (F.5) with respect to $\tilde{e}_{i,a}$. We can estimate the reasonable range of $\chi$ values, if we adopt the so-called ‘two state’ model [2], in which (the same) penalty in binding energy $e_0$ is assigned for each nucleotide that does not match the consensus sequence. Since one or two hydrogen bonds are formed per contact of the TF surface with a preferred nucleotide (energy of a hydrogen bond is $\sim k_B T$), $e_0$ can be estimated to be $(1-3) k_B T$ [25]. From equation (A.6) it follows that $\chi \approx \sqrt{\chi_0 E_0}$, and with $L = 12$ for CTF/NFI (we ignore the contribution of the 3 bp spacer to the binding energy), we obtain that $\chi$ is expected to take values from 3 to 12. Numerical solutions of equation (F.5) show that for $\chi$ in this range, the quantity $\tilde{e}_{i,a}$ depends weakly on the imposed value of $\chi$. More precisely, we tested that $\tilde{e}_{i,a}$, which corresponds to solving equation (F.5) with (different) values of $\chi$ in the indicated range, leads to negligible differences in energy distribution and the DET curve for the finite $T$ energy matrix (data now shown), which justifies solving the equation without the knowledge of the exact value of $\chi$. The energy matrix $\tilde{e}_{i,a}$ obtained by our method (corresponding to $\chi = 5$) is given in table F1.

Finally, we use table F1 to discuss the differences between the weight matrix parameters estimated by the three different methods. In figure F1(A) histograms of energy levels corresponding to the finite $T$ energy matrix and to the information-theoretic weight matrix are shown together. Similarly figure F1(B) compares the matrix
Figure F1. Comparison of the finite $T$ matrix elements with (A) the information theory weight matrix and (B) the MatInspector matrix elements. CTF/NFI binds DNA as a homodimer, and recognizes two 6 bp long palindrome symmetric motifs, separated by a 3 bp spacer. Consequently, matrices in table F1 were appropriately symmetrized and only the first six positions are shown. Four bars at each position on the horizontal axis correspond to A, T, C and G respectively, while heights of the bars correspond to the values of the matrix elements.

Table F1. (a) The finite $T$ energy matrix for CTF/NFI transcription factor. (b) The information-theoretic weight matrix. (c) The MatInspector weight matrix.

|   | 1  | 2  | 3  | 4  | 5  | 6  | 7  | 8  | 9  | 10 | 11 | 12 | 13 | 14 | 15 |
|---|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|
| A | 0.13 | 0.23 | 0.24 | 0.13 | −0.07 | −0.16 | 0.03 | 0.02 | 0.00 | 0.05 | 0.18 | 0.19 | 0.24 | −0.54 | −0.31 |
| T | −0.29 | −0.54 | 0.24 | 0.23 | 0.18 | 0.01 | −0.02 | 0.02 | 0.03 | −0.17 | −0.07 | 0.21 | 0.24 | 0.22 | 0.15 |
| C | −0.04 | 0.20 | 0.24 | 0.24 | −0.32 | 0.07 | −0.03 | 0.00 | 0.03 | 0.07 | 0.21 | −0.64 | −0.72 | 0.13 | 0.21 |
| G | 0.20 | 0.11 | −0.72 | −0.61 | 0.21 | 0.09 | 0.02 | −0.04 | −0.06 | 0.04 | −0.33 | 0.24 | 0.24 | 0.19 | −0.05 |
|   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |
| A | 0.07 | 0.28 | 0.26 | −0.15 | −0.15 | −0.11 | 0.04 | 0.04 | 0.01 | 0.01 | 0.18 | −0.02 | 0.26 | −0.39 | −0.23 |
| T | −0.22 | −0.40 | 0.26 | 0.23 | 0.21 | 0.02 | −0.03 | 0.02 | −0.01 | −0.11 | −0.12 | 0.08 | 0.26 | 0.29 | 0.07 |
| C | −0.05 | 0.18 | 0.26 | 0.49 | −0.25 | 0.05 | −0.01 | −0.01 | 0.03 | 0.07 | 0.21 | −0.55 | −0.79 | −0.04 | 0.26 |
| G | 0.20 | −0.05 | −0.79 | −0.56 | 0.19 | 0.04 | 0.00 | −0.04 | −0.03 | 0.03 | −0.27 | 0.50 | 0.26 | 0.15 | −0.10 |

parameters corresponding to the finite $T$ energy matrix and the MatInspector weight matrix. The figure directly indicates which parameters are most different between the two matrices. For example, there is $\sim 150\%$ difference between the information-theoretic and our matrix at position 2G, $\sim 100\%$ difference at positions 4C and 5A, etc. Similarly, comparison with the MatInspector weight matrix in figure F1(B) shows that there are significant differences (from 40% to 100%)
between the two matrices at positions 1, 5 and 6 while the matrices mostly agree with each other at positions 2, 3 and 4. Since positions 2, 3 and 4 contribute more to the binding energy than positions 1, 5 and 6, the smaller difference between the DET curves of the finite T and the MatInspector matrices (as compared to the difference between the finite T and the information theory DET curves) can be attributed to the localization of the matrix differences at the less conserved positions. We note that, while the differences between the individual matrix elements are generally not very large, when binding site scores are calculated the individual differences add up to produce significant differences in, for example, the false positive/false negative trade-off shown in figure 5.

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