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Seven myths of how transcription factors read the cis-regulatory code

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Abstract

Genomics data are now being generated at large quantities, of exquisite high resolution and from single cells. They offer a unique opportunity to develop powerful machine learning algorithms, including neural networks, to uncover the rules of the cis-regulatory code. However, current modeling assumptions are often not based on state-of-the-art knowledge of the cis-regulatory code from transcription, developmental genetics, imaging, and structural studies. Here I aim to fill this gap by giving a brief historical overview of the field, describing common misconceptions and providing knowledge that might help to guide computational approaches. I will describe the principles and mechanisms involved in the combinatorial requirement of transcription factor binding motifs for enhancer activity, including the role of chromatin accessibility, repressors, and low-affinity motifs in the cis-regulatory code. Deciphering the cis-regulatory code would unlock an enormous amount of regulatory information in the genome and would allow us to locate cis-regulatory genetic variants involved in development and disease.

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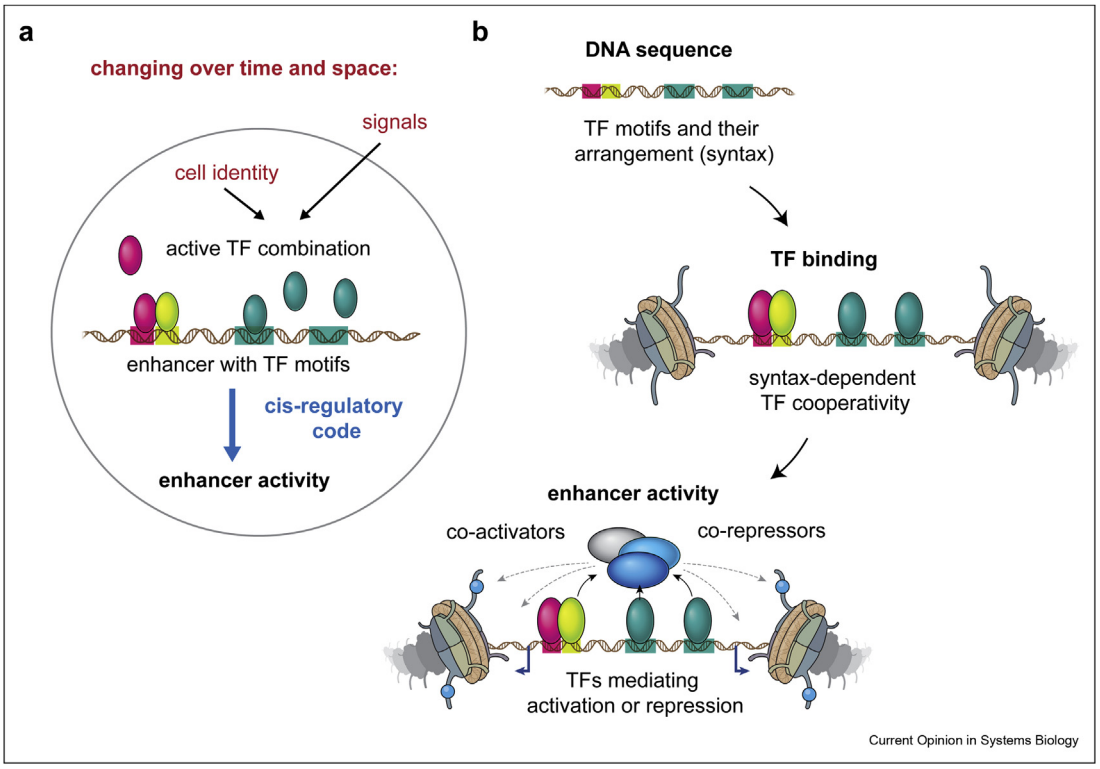
Introduction

A fundamentally unresolved problem in biology is the cis-regulatory code, also known as the genome's 'second code', which provides the means to read regulatory information in the genome. The most abundant cis-regulatory sequences are enhancers, which become active under very specific conditions and "enhance" the transcription of nearby genes. Because the activity of enhancers is determined by their sequence and can be reproduced outside their genomic context (e.g. in reporter assays), deciphering the cis-regulatory code of their activation should be a tractable problem. It is also a problem of great significance as over 80% of genetic variants associated with complex traits and diseases in humans are estimated to be found in cis-regulatory regions [1]. If we could decipher the cis-regulatory code, it would unlock an enormous amount of regulatory information and would allow us to locate cis-regulatory mutations and predict their effect on the organism.

The cis-regulatory code has been a long-standing problem and the focus of much research. Using genetics and biochemistry, Jacob and Monod discovered in the 1960s that genes in bacteria are regulated by DNA sequences found nearby on the same DNA molecule (in *cis*) [2,3]. With the advent of molecular biology in the 1970s and 1980s, it became possible to cut and paste sequences into different genomic contexts. This showed that an enhancer can function autonomously outside its normal genomic environment, independent of its orientation and exact distance to the gene [4]. Furthermore, it was discovered that enhancers contain short sequence motifs (~6–12 bases) that are recognized by transcription factors (TFs) [5]. Because TFs are often responsive to extracellular signals or are transcriptionally regulated in a spatial and temporal fashion during embryonic development, they provide the means for the cell to regulate when enhancers and the associated genes become active [6] (Figure 1a).

How exactly TFs regulate the activity of specific enhancers remains elusive. Developmental enhancers typically contain motifs for multiple TFs [7,8] and it is the specific combination of motifs that gives them their unique properties [9,10]. Experimental dissections of individual enhancer sequences suggest that enhancer activity may depend on the motif arrangement, also known as motif syntax [11,12]. Syntax includes the overall motif composition, motif order, motif orientation, and the spacing between the motifs. Early studies on the interferon-beta enhancer suggested very strict syntax rules, where multiple TFs assemble as an

Figure 1



The cis-regulatory code defines how DNA sequence regulates enhancer activity. (**a**) TFs are regulated transcriptionally and by extracellular signals such that each cell type contains a unique set of active TFs. Dependent on the specific TF combination, different sets of enhancers become active in each cell type. (**b**) The cis-regulatory DNA sequence contains TF motifs in specific arrangements (syntax). Dependent on syntax, the motifs are bound by TFs cooperatively. TFs then recruit co-activators or co-repressors, which regulate the activity of the enhancer.

'enhanceosome' [13]. However, studies on other enhancers suggested a very flexible syntax ('billboard model') [14]. Thus, individual enhancer studies did not reveal clear rules that could be applied genome-wide. Until today, we cannot predict the regulatory activity of enhancers from sequence alone.

With the advent of genomics technology, finding the rules of the cis-regulatory code seemed to be within reach [9,15]. Co-regulated genes pointed to the existence of enhancers with similar activity [16], chromatin immunoprecipitation (ChIP) technology enabled the identification of genomic regions bound by a TF *in vivo* [17–19], and the eventual development of large-scale reporter assays allowed the identification of large numbers of sequences with similar enhancer activity in a specific cell type [20]. Given large numbers of enhancers, it was reasonable to assume that the rules under which specific combinations and arrangements of motifs leading to enhancer activation could be identified. However, despite extensive experimental and computational efforts in the 2000s, no clear rules of the cis-regulatory code emerged [21,22]. The available data likely lacked the depth and resolution required to map with certainty the exact sequence motifs bound by TFs *in vivo*.

Ironically, with the development of increasingly powerful genomics technologies and computational methods in the last decade, efforts into deciphering the cis-regulatory code have declined rather than increased. Rather than focusing on the relationship between sequence and gene regulation, research efforts have increasingly focused on chromatin states, RNA, and 3D organization of the nucleus. Thus, the scientific questions evolved with the new opportunities that genomics technology offered and diverted from the fundamental problem of the cis-regulatory code, which became to be seen as either solved in principle or intractable.

Now we find ourselves in an era with genomics data of large quantities [23], of exquisite high resolution [24,25] and from single cells [26,27], all of which substantially improve the analysis of cis-regulatory sequences. Furthermore, powerful machine learning algorithms, including neural networks, have been developed for analyzing DNA sequences and predicting many associated genomic measurements [28–32]. This

allowed the discovery of genome-wide syntax for the first time and revealed that syntax is often soft: two motifs may enhance TF binding when found in a preferred distance and do not have to be spaced at an exact base distance [33].

Despite the breakthrough tools that are now becoming available, the cis-regulatory code is not the primary focus of most current studies. Owing to the diversion of the genomics field into other aspects of gene regulation, there is no longer a clear consensus on what we know about the cis-regulatory code from transcription, developmental genetics, imaging, structural studies, and computational biology. This is problematic because computational analyses of cis-regulatory sequences, for example, as part of transcriptional regulatory networks, often use overly simplified or unrealistic assumptions for how cis-regulatory information is encoded in the DNA. Here, I will outline some of these common misconceptions, point to the evidence that argues against them and describe a path toward more realistic assumptions.

Myth 1: If we understand the cis-regulatory code in one cell type, we can predict enhancer activity in all cell types

A current emphasis in computational genomics is to learn patterns in some cell types and then impute these patterns in other cell types where experimental data are limited or not available [34,35]. Although this can work well, there is often an unquestioned expectation that this is a solvable problem. Similarly, it is sometimes assumed that a complete map of all TF binding motifs and their target genes can be experimentally determined. In both cases, the underlying assumption is that the cis-regulatory code is universally applicable and that by studying a few cell types, other cell types can be inferred. After all, the biochemical and biophysical principles underlying TF binding and gene activation are shared among all cell types. However, unlike the genomic code for proteins, the cis-regulatory code is not a universal code. Cell types use vastly different TF motifs and syntax rules; even a few deviating details can make it impossible to accurately predict which cis-regulatory sequences are read out by a cell type. At the current state of knowledge, it might be more useful to think of each cell type having its own cis-regulatory code. Once we understand the code for a number of cell types in great detail, we might be able to derive general principles and determine the minimal set of experiments required to impute cis-regulatory code for new cell types.

Reality: The cis-regulatory code is highly complex and specific for each cellular state

Cell types read out very different sets of cis-regulatory sequences to have a unique gene expression program and respond appropriately to the environment. Likewise, in the developing embryo, cells use different cis-regulatory sequences across time and space to develop along specified developmental trajectories and acquire specific cell identities [15,22]. To accomplish this, each cellular state has a unique combination of TFs, each with their specific rules of interactions and response to extracellular signals [6,36] (Figure 1a). Mammalian genomes encode over 1000 TFs, and TFs may bind with different sequence specificities and follow different syntax rules depending on their partner TF [37–40]. This large combinatorial complexity allows a vast number of possibilities by which cis-regulatory sequences are accessed in the genome and lead to enhancer activity. Some regions might only be active under very specific conditions, for example, in a particular cell type at a certain time point during development, and their genomic coordinates may overlap with other cis-regulatory regions [41]. Learning this cis-regulatory repertoire will require a large number of high-quality experimental data *in vitro* and *in vivo*, as well as sophisticated computational tools that can learn the interaction rules that underlie the cis-regulatory code.

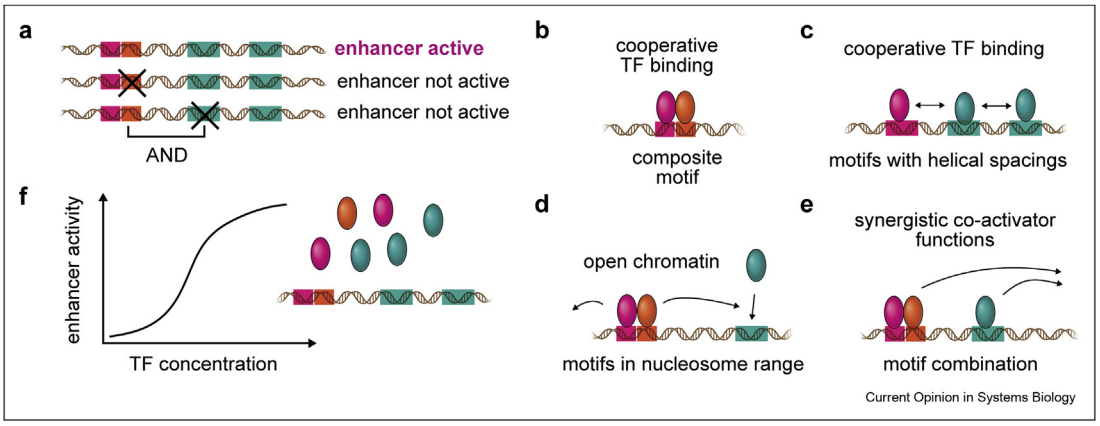
Myth 2: Enhancers are regulated promiscuously by many TFs

Based on ChIP-seq and imaging data, TF binding occurs very promiscuously at hundreds of thousands of regions in the genome [42,43]. Thus, enhancers, especially when active, appear to be bound by a large number of TFs. This can be interpreted as enhancers having a large number of TF inputs, each with small contributions to gene activation [42]. However, ChIP-seq signal can be unspecific or nonfunctional. Furthermore, genetics studies show that deletion of a single TF or mutating an individual DNA binding motif often has very large effects on gene expression (Figure 2a). Thus, enhancers are regulated cooperatively by a small number of TFs, rather than additively by a large number of TFs.

Reality: TFs are required in a combinatorial manner for enhancer activation

Genetics has shown that mutations in TF genes produce specific and striking phenotypes, with drastically altered gene expression patterns [44]. Likewise, mutating individual binding motifs within an enhancer may abolish the enhancer's activity [45–47]. This is often true for multiple motifs within enhancers, suggesting that their function is coupled via AND logic (Figure 2a) [48]. To achieve such coupling, the best understood mechanism is a composite motif, that is, two motifs to which two TFs bind cooperatively through protein–protein interactions (Figure 2b) [21,37,49,50]. This often requires a strict spacing between the two motifs or may involve preferred soft spacing at helical distances (Figure 2c) [33]. TF cooperativity at preferred distances may also occur with weak or no protein–protein interactions

Figure 2



TF motifs often function together in an AND logic. (**a**) Mutating different motifs in an enhancer can each lead to a loss of enhancer activity. Such AND logic between motifs can occur through (**b**) cooperative TF binding to composite motifs, (**c**) cooperative binding to motifs spaced with helical periodicity (~10 bp x N), (**d**) one TF opening chromatin such that another TF can bind (assisted loading), or (**e**) synergistic co-activator function. (**f**) The resulting enhancer activity follows a sigmoidal curve with increasing concentrations of a TF.

between TFs [37,39]. For example, a TF motif may not be able to access a motif in chromatin unless a so-called pioneer TF binds nearby (<~150 bp) and opens chromatin through nucleosome remodeling (Figure 2d) [33,51]. Finally, two TFs may also act synergistically downstream of TF binding, for example, by recruiting different co-factors that synergize in target gene activation (Figure 2e) [52]. Consistent with these mechanisms, the activation of developmental enhancers typically follows a sigmoidal curve and may show ultrasensitivity in response to increasing concentrations of TFs (Figure 2f) [53–55]. This allows genes to be expressed in relatively sharp on–off patterns and makes the cis-regulatory code more specific.

Myth 3: Understanding the cis-regulatory code is a matter of mapping the direct TF binding sites

The recognition of DNA sequence motifs by TFs is the basis for the cis-regulatory code. These interactions have been studied by a variety of experimental techniques *in vitro* and are increasingly performed at high-throughput [37]. From such *in vitro* experiments, simple computational models such as a position weight matrix can be derived and used to predict sequence matches in the genome. Owing to the strong biophysical basis, identifying bona fide TF binding sites is typically the first step when analyzing enhancers. For example, Eric Davidson, who pioneered the study of transcriptional regulatory networks during sea urchin development, saw three steps in the identification of the cis-regulatory code: (1) identify TF binding sites, (2) experimentally determine their individual function (e.g. activation, repression, signal-induced), and (3) identify the rules by which the TF binding sites function together as Boolean input–output devices [56]. However, identifying TF binding sites based on their *in vitro* properties or their statistical significance relies on arbitrary thresholds that do not reflect how TFs bind *in vivo*. To fully understand the cis-regulatory code, binding sites should not be modeled separately from the cooperative interactions or downstream functions they mediate.

Reality: TF binding and function are inherently combinatorial

TF binding *in vivo* depends on other TFs [36,38,57,58]. For example, TFs may cooperate in binding with other TFs through physical interactions, or pioneer TFs may help the binding of other TFs by making the binding site accessible in chromatin [33,51]. Furthermore, TFs may function either as an activator or repressor dependent on nearby motifs [46,59]. Therefore, if we want to systematically decipher the cis-regulatory code from sequence, potential TF binding sites should be modeled directly in their cis-regulatory context and not selected based on a fixed *in vitro* binding threshold before modeling. Convolutional neural networks are ideally suited for this because they model entire cis-regulatory sequences, including their higher-order motif combinations and syntax, without defining any features *a priori* [28–33]. They have therefore emerged as powerful tools for discovering elements of the cis-regulatory code.

Myth 4: TF binding is secondary to chromatin regulation

It has been known since the first genome-wide ChIP experiments that TF binding *in vivo* does not correlate well with the presence of consensus binding motifs. However, TF binding is vastly improved when taking chromatin accessibility into account [35,60]. This leads

to the impression that chromatin accessibility is regulated before the binding of most TFs. Although this view acknowledges that pioneer TFs are important in creating the chromatin accessibility in a sequence-dependent manner, it prioritizes studying the regulation of chromatin states (histone modifications, 3D organization, etc.) and how they are established and maintained over time. Long-range chromatin repression mechanisms, such as those establishing different types of heterochromatin, indeed play an important role in keeping certain regions in the genome mostly inaccessible. However, the dynamic chromatin accessibility of enhancers during development is, for the most part, determined by TFs binding to cis-regulatory sequences and not the other way around [61–63].

Reality: Chromatin accessibility is determined by cis-regulatory sequences

Although pioneer TFs play an important role in making enhancer regions first accessible, chromatin accessibility is a result of the combined action of TFs (Figure 3) [64]. Pioneer TFs often work together with other TFs to increase chromatin accessibility [39,65,66] and are themselves required for the enhancer's activity [67,68]. When the enhancer is active, the central nucleosome is evicted [69–71] and chromatin accessibility is further increased [72]. Thus, chromatin accessibility appears to be the result of the interplay of multiple TFs and is likely an important mechanism by which these TFs function combinatorially as part of the cis-regulatory code. By using chromatin accessibility as prior probability for TF binding, we miss the opportunity to discover some of the pioneer TFs that mediate this accessibility.

Myth 5: ChIP-seq binding data can be classified as binary events

To simplify models of gene regulation, ChIP-seq data are often classified as binary binding events. However, identifying a set of bound regions based on a chosen threshold has implications. It not only determines the level of unspecific binding or noise that is included in the data set, but also affects the functional contents of these regions. TF binding is higher at functional enhancers [73] and even higher at active enhancers [72] where the chromatin accessibility is highest (Figure 3). Therefore, dependent on the chosen threshold, the cis-regulatory context, including the presence of other TF binding motifs, is likely to be different.

Reality: ChIP-seq binding at enhancers is a quantitative readout

ChIP-seq data show a continuum of binding levels. To understand the various components, ChIP-seq data can be compared with high-resolution ChIP-exo/nexus data, in which the TF binding signal has distinct footprints over motifs. Notably, ChIP-seq data contain higher levels of experimental background noise compared with ChIP-exo/nexus data, suggesting that some signal in ChIP-seq data is not specific for the measured TF [24,25]. Even in ChIP-exo/nexus data, small portions of signal are randomly distributed, most often across regions of highly accessible chromatin. This suggests that TFs may also bind nonspecifically to DNA. This interpretation is consistent with imaging studies showing that TFs may search and bind to many genomic regions very briefly (<1 s) before binding to a region with prolonged dwell time (~10 s), presumably because of a high-affinity binding motif [74]. The TF's dwell time may however not only depend on the motif's binding affinity, but also on the presence/state of the nucleosome or the presence of partner TFs [74,75]. Even with short dwell times, a TF might have a high fractional occupancy in ChIP-seq data if the local TF concentration is high and the TF can quickly rebind without long search times [76]. Such locally high TF concentrations have been observed at enhancers by imaging and described as condensates or hubs [77,78]. Finally, it is important to keep in mind that ChIP-seq data represent cell population averages. For example, if certain TF binding events only occur in a fraction of cells, they will have a reduced ChIP-seq signal overall.

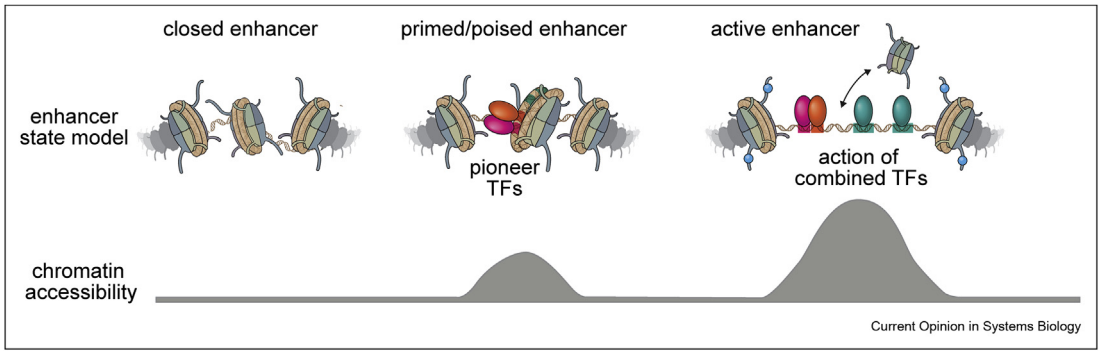
Myth 6: Transcription factors mainly function as activators in mammalian cells

Although the lac and lambda repressors were the first sequence-specific TFs that were identified and extensively characterized [79], the role of repressors in enhancer activation is poorly studied in mammalian systems. This may be because the first mammalian enhancer, derived from SV40 and characterized by Walter Schaffner [4], did not involve relief of repression. Instead, it was proposed that nucleosomes repress enhancers in the absence of activation [79]. However, in model organisms such as Drosophila, sea urchin, or yeast, genetics has shown that repressors are essential for gene regulation [6,44,80]. Mammalian systems have long lacked such extensive genetic characterization, but when in-depth analyses were performed for mouse development the importance of repressors has been clearly documented [81]. Recent genomics analyses have also confirmed that cis-regulatory elements frequently result in repressive activity [82]. This suggests that repressors are common throughout the animal kingdom and should be incorporated into models of gene expression in mammalian systems.

Reality: Transcription factors frequently repress enhancers

The most detailed mechanistic understanding of repressors comes from pioneering work in Drosophila, where precise spatiotemporal gene expression patterns during development require a combination of activating and repressing TFs. A large number of TFs act as

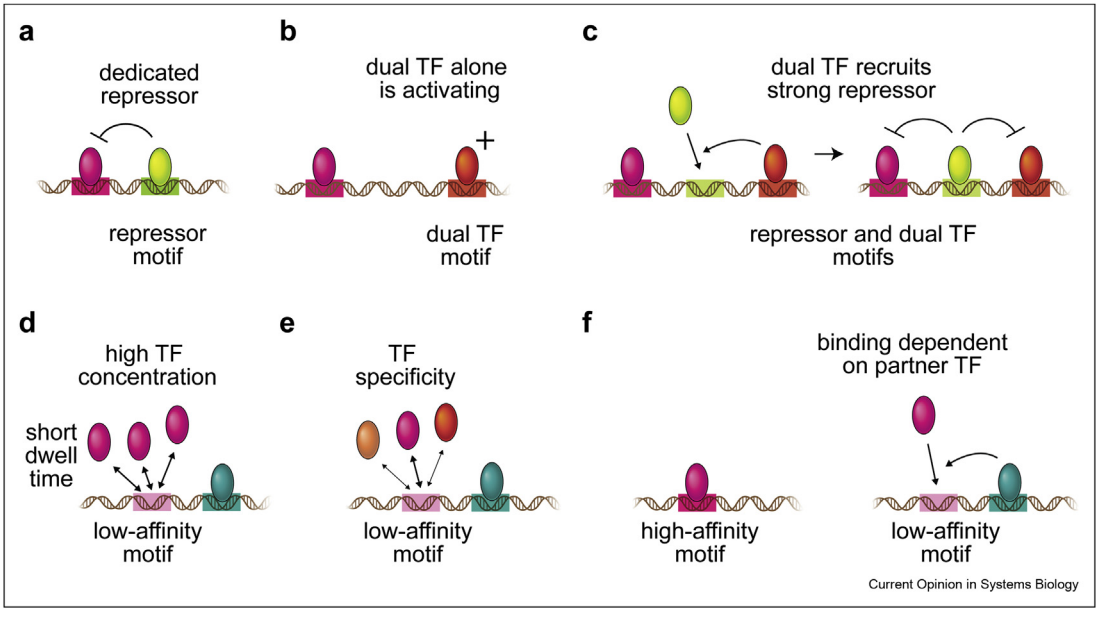
Figure 3



Chromatin accessibility is a readout of multiple TFs. In the absence of appropriate TFs, nucleosomes maintain DNA in an inaccessible state (left). Pioneer TFs can bind their motifs in the presence of chromatin and make the region accessible (primed or poised enhancer, middle). The chromatin accessibility may be further increased by TFs both during the pioneering phase and during enhancer activation.

dedicated repressors (Figure 4a) and thus are generally repressive when bound to an enhancer [6,8,46]. Other TFs are dual TFs that can act as both an activator and repressor (Figure 4b and c). For example, binding sites for Drosophila NFkB are essential for either activating or repressing an enhancer [6]. It does so by acting intrinsically as a weak activator, but strongly promotes repression by helping the binding of a repressor to specific sequences nearby [83]. A repressor typically serves to repress and fine-tune the activity of enhancers by counteracting the effect of activating TFs that are bound nearby, for example, through histone deacetylation [53,59,72]. Repressed enhancers are accessible in chromatin and show a poised/weakly active histone modification signature, a signature that is very common during mammalian development [72,82].

Figure 4



Mechanisms by which repressors (a–c) or low-affinity TF binding motifs (d–f) regulate enhancer activity and specificity. (**a**) When dedicated repressors bind to their motifs, they counteract the activity of TFs bound nearby. (**b**) Dual TFs may be weakly activating by themselves, but (**c**) have a repressing effect when they recruit a repressor to a nearby repressor motif. Low-affinity motifs (**d**) are likely bound with shorter dwell times and require higher TF concentration to mediate enhancer activation, (**e**) may discriminate between closely related TF family members, or (**f**) may be dependent on a partner TF for binding.

Myth 7: Low-affinity binding motifs do not have a strong effect on enhancer function

Binding sequences that deviate from the consensus binding motif and are bound *in vitro* at low affinity are often omitted from analyses. They occur with high frequency by chance in genomic sequences and are therefore hard to identify as functional motifs *in vivo*. However, experimental evidence suggests that we miss crucial cis-regulatory information if we ignore low-affinity motifs [12,83,84]. It is therefore important to increase efforts into identifying and characterizing the effects of low-affinity motifs in cis-regulatory regions, especially with the emergence of neural networks which can detect low-affinity motifs [33]. Similarly, sequence information beyond motifs, such as DNA shape, subtle base preferences in motif flanks, and dinucleotide repeats may contribute to TF binding specificity [21].

Reality: Low-affinity binding motifs are critical for the specificity of enhancers in vivo

Systematic analysis of synthetic enhancer constructs in Ciona has shown that low-affinity motifs are critical for producing *in vivo* expression patterns that are highly tissue-specific [12]. Several mechanisms could explain the requirement of low-affinity motifs for enhancer specificity. First, low-affinity motifs resulting in shorter TF dwell times may nevertheless be bound when the local TF concentration is high (Figure 4d). The shorter dwell times may even be advantageous by making the enhancer more tunable [76]. Second, some TF families, such as homeodomain TFs, bind very similar binding motifs, thus a low-affinity motif can render an enhancer more specific for a particular TF (Figure 4e) [84,85]. Finally, low-affinity motifs may make the binding of a TF dependent on its partner TF if high-affinity motifs are constitutively bound (Figure 4f) [83]. Thus, low-affinity motifs might be a common mechanism by which combinatorial TF requirements are embedded into the cis-regulatory code.

Conclusions

There is still much to be learned about the cis-regulatory code. We are only beginning to understand the mechanisms of how TFs function combinatorially in enhancer activation and how subtle motif syntax and low-affinity motifs influence this process. So far, there are too few examples to derive general principles. However, we likely have sufficient information to make reasonable assumptions when developing computational models. The goal is go beyond the identification of relevant motifs and to learn the rules of syntax and combinatorial interactions that predict enhancer activity from raw sequence. Neural networks are ideally suited for this because they can learn highly complex sequence patterns with unprecedented predictive power, allowing motifs to be directly modeled in their cis-regulatory context. Moreover, interpretation tools have recently been developed to extract the relevant sequence information, including motifs and their rules of syntax [28,29,33]. Combined with cutting-edge genomics technology and large-scale data sets, these approaches promise to revolutionize our ability to predict the function of cis-regulatory sequences in any genome and provide us with unprecedented opportunities to study genetic cis-regulatory variation during development and disease.

Conflict of interest statement

J.Z. owns a patent on ChIP-nexus (patent no. 10287628).

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