Predicting transcription factor binding using ensemble random forest models [version 1; referees: 1 approved with reservations]

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Abstract

**Background:** Understanding the location and cell-type specific binding of Transcription Factors (TFs) is important in the study of gene regulation. Computational prediction of TF binding sites is challenging, because TFs often bind only to short DNA motifs and cell-type specific co-factors may work together with the same TF to determine binding. Here, we consider the problem of learning a general model for the prediction of TF binding using DNase1-seq data and TF motif description in form of position specific energy matrices (PSEMs).

**Methods:** We use TF ChIP-seq data as a gold-standard for model training and evaluation. Our contribution is a novel ensemble learning approach using random forest classifiers. In the context of the ENCODE-DREAM in vivo TF binding site prediction challenge we consider different learning setups.

**Results:** Our results indicate that the ensemble learning approach is able to better generalize across tissues and cell-types compared to individual tissue-specific classifiers or a classifier applied to the data aggregated across tissues. Furthermore, we show that incorporating DNase1-seq peaks is essential to reduce the false positive rate of TF binding predictions compared to considering the raw DNase1 signal.

**Conclusions:** Analysis of important features reveals that the models preferentially select motifs of other TFs that are close interaction partners in existing protein-protein-interaction networks. Code generated in the scope of this project is available on GitHub: https://github.com/SchulzLab/TFAnalysis (DOI: 10.5281/zenodo.1409697).

**Keywords**

ENCODE-DREAM in vivo Transcription Factor binding site prediction challenge, Transcription Factors, Chromatin accessibility, Ensemble learning, Indirect-binding, TF-complexes, DNase1-seq
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This article is included in the Max Planck Society collection.

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Introduction

Transcription Factors (TFs) are key players of transcriptional regulation. They are inadmissible to maintain and establish cellular identity and are involved in several diseases. TFs bind to the DNA at distinct positions, mostly in accessible chromatin regions, and regulate transcription by recruiting additional proteins. The TFs can alter chromatin organization or, for example, recruit an RNA polymerase to initiate transcription. Hence, to understand the function of TFs it is vital to identify the genomic location of TF binding sites (TFBS). As TFs regulate distinct genes in distinct tissues, these binding sites are tissue-specific.

Nowadays, the most prevalent and widely used method to experimentally determine TFBS is through ChIPseq experiments, which can be used to generate genome-wide, tissue-specific maps of in-vivo TF binding. However, ChIP-seq experiments are expensive, experimentally challenging, and require an antibody for the target TF. To overcome these limitations, a number of computational methods have been developed to pinpoint TFBS. Most of these methods are based on position weight matrices (PWMs) describing the sequence preference of TFs. PWMs indicate, for each position of a TF binding motif independently, which nucleotide is most likely to occur. Unfortunately, screening the entire genome using a PWM results in too many false positive predictions. Therefore, numerous methods have been proposed to reduce the prediction error by combining PWMs with epigenetics data, such as DNase1-seq, ATAC-seq, or Histone Modifications, reflecting chromatin accessibility. Also, additional features such as nucleotide composition, DNA shape, or sequence conservation can be incorporated into the predictions. Including these additional data sets and information improved the TF binding predictions considerably. A non-exhaustive overview is provided in 12. While PWM based models are still the most common means to assess the likelihood of a TF binding to genomic sequences, more elaborate approaches such as SLIM-models, which capture nucleotide dependencies, have been successfully used as well. Recently, deep learning methods have been used to learn TF binding specificities de novo from large scale data sets comprising not only ChIP-seq but also Selen and protein binding microarray (PBM) data.

The ENCODE-DREAM in vivo Transcription Factor binding site prediction challenge aims to systematically compare various approaches on TFBS prediction in a controlled setup, with the additional complexity of applying the classifiers on the tissues/cell types that were not used for model training. The challenge organizers provide TF-ChIP seq data for 31 TFs, accompanied with RNA-seq and DNase1-seq data in 12 different tissues. Using labels deduced from the TF-ChIP-seq data, predictive models for TF binding should be learned and then applied to a set of hold-out chromosomes on an unseen tissue. Predictions are computed in bins, covering the entire target chromosomes. The main challenge paper will provide a detailed explanation of the challenge setup and a comparison across all competing methods. This article is a companion paper to the main ENCODE-DREAM Challenge paper, in which we describe our contribution to the challenge, delineate the motivation for our work and provide an independent evaluation of our ideas to achieve generalizability across tissues.

We developed an ensemble learning approach using random forest (RF) classifiers, extending the work of Liu et al. Tissue-specific cofactor information was shown to be relevant to accurately model TF binding. Thus, we designed our approach to aggregate tissue-specific cofactor data, via an ensemble step, into a generalizable model. Briefly, we compute TF affinities with TRAP for 557 PWMs in DNase-hypersensitive sites (DHSs) identified with JAMM. TF affinities computed by TRAP are inferred from a biophysical model. In contrast to a simple binary classification, e.g. FIMO, these scores can capture low affinity binding sites, which were shown to be biologically relevant. Here, we show that our ensemble models generalize well between tissues and that they exhibit better classification performance than tissue-specific RF classifiers. Furthermore, we illustrate that only a small subset of TF features is sufficient to predict tissue-specific TFBSs and also show that these TFs are often known co-factors/interaction partners of the target TF.

Methods

Data

Within the scope of the challenge participants were provided with ChIP-seq data for 31 TFs, as well as DNase1-seq and gene expression obtained from RNA-seq data for 13 tissues. From the available 31 TFs, 12 were used to assess the model performance in the final round of the challenge. Hence, we also focus on these 12 TFs in the scope of this article: CTCF, E2F1, EGR1, FOXA1, FOXA2, GABPA, HNF4A, JUND, MAX, NANOG, REST, and TAF1. The number of binding sites per TF and tissue is shown in Table 1. Note that we exclude ambiguous sites from consideration in this study. We refer to the challenge website for a detailed overview on the provided data. The challenge required that the predictions are made in bins of size 200bp, shifted by 50bp each, spanning the whole genome.

Data preprocessing and feature generation

In order to obtain datasets per tissue and per TF that could be handled in terms of memory consumption and processing time, and also to cope with the large imbalance number of bound and unbound sites, we randomly sampled as many negative sites from the provided ChIP-seq tsv files as there were true binding sites per TF. The ChIP-seq labels contained in the balanced and down sampled tsv files are used as the response for training RF models.

Throughout the course of challenge, we have used two distinct ways to generate features for the RF classifiers: (1) with and (2) without considering DHSs. In none of the approaches have we used the provided RNA-seq data nor did we compute DNA shape features. Generally, we computed TF binding affinities with TRAP for 557 distinct TFs using the default parameter settings. The position specific energy matrices (PSEMs) used in our computation are converted from position weight matrices (PWMs) obtained from JASPAR, UniPROBE, and Hocomoco. The code to perform the conversion and to run TRAP is available on GitHub.
We compared two approaches to generate features for the classifier from DNase1-seq data. In the first approach, shown in Figure 1a, we compute tissue-specific DHSs using the peak caller JAMM10 (version 1.0.7.2) and merge the peak calls using the bedtools merge command (bedtools version 2.25.0). Next, TF affinities are calculated in the identified DHS sites using TRAP, and the median DHS signal per peak is computed from the provided bigwig files. The computed data is intersected, using a left outer join with bedtools, with the binned genome structure required for training (using the bins contained in the tsv files mentioned above) and testing (using the provided bed-file containing all test regions).

The second approach for computing the features is depicted in Figure 1b. Here, we do not use the information on DHS sites, instead we compute TF binding affinities and the DNase1-seq signal per bin. To account for variability between both biological and technical replicates, we calculate the median DNase1 coverage across the replicates using the bedtools coverage command. Overall, the features for a single bin are composed of the TF affinities in that bin, the DNase1 signal in the bin itself together with its left and right neighboring bins.

### Ensemble random forest classifier

The Random Forest models, implemented using the randomForest R-package11 (version 4.6-12), are trained on either of the feature setups explained in the previous section. Training the RF models can be seen as a two step approach that is independent from the feature setup. Throughout model training, the balance between the bound and unbound classes is maintained to avoid over-fitting of the RF classifiers and also to ensure an unbiased evaluation of model performance. For fitting the RF classifiers we used 4,500 trees, and also to ensure an unbiased evaluation of model performance. For fitting the RF classifiers we used 4,500 trees, and also to ensure an unbiased evaluation of model performance. For fitting the RF classifiers we used 4,500 trees, and also to ensure an unbiased evaluation of model performance. For fitting the RF classifiers we used 4,500 trees, and also to ensure an unbiased evaluation of model performance. For fitting the RF classifiers we used 4,500 trees, and also to ensure an unbiased evaluation of model performance.

### Table 1. Number of bins labeled as bound per transcription factor (TF) and tissue, deduced from TF ChIPseq data.

<table>
<thead>
<tr>
<th>TF</th>
<th>Number of bound sites per tissue</th>
</tr>
</thead>
<tbody>
<tr>
<td>CTCF</td>
<td>179,672 (A549), 271,097 (H1-hESC), 206,336 (HeLa-S3), 208,868 (HepG2), 170,208 (IMR-90), 215,238 (K562), 305,547 (MCF-7)</td>
</tr>
<tr>
<td>E2F1</td>
<td>93,117 (GM12878), 55,391 (HeLa-S3)</td>
</tr>
<tr>
<td>EGR1</td>
<td>72,595 (GM12878), 52,733 (H1-hESC), 175,994 (HCT116), 58,793 (MCF-7)</td>
</tr>
<tr>
<td>FOXA1</td>
<td>256,632 (HepG2)</td>
</tr>
<tr>
<td>FOXA2</td>
<td>374,750 (HepG2)</td>
</tr>
<tr>
<td>GABPA</td>
<td>26,467 (GM12878), 51,666 (H1-hESC), 31,202 (HeLa-S3), 60,552 (HepG2), 109,423 (MCF-7), 78,403 (SK-N-SH)</td>
</tr>
<tr>
<td>HNF4A</td>
<td>106,308 (HepG2)</td>
</tr>
<tr>
<td>JUND</td>
<td>203,665 (HCT116), 179,999 (HeLa-S3), 183,558 (HepG2), 193,814 (K562), 92,905 (MCF-7), 222,013 (SK-N-SH)</td>
</tr>
<tr>
<td>MAX</td>
<td>301,615 (A549), 98,327 (GM12878), 224,379 (H1-hESC), 321,501 (HCT116), 211,590 (HeLa-S3), 317,579 (HepG2), 318,318 (K562), 250,775 (SK-N-SH)</td>
</tr>
<tr>
<td>NANOG</td>
<td>32,918 (H1-hESC)</td>
</tr>
<tr>
<td>REST</td>
<td>71,251 (H1-hESC), 47,654 (HeLa-S3), 67,453 (HepG2), 59,640 (MCF-7), 48,946 (Panc1), 94,082 (SK-N-SH)</td>
</tr>
<tr>
<td>TAF1</td>
<td>87,109 (GM12878), 185,027 (H1-hESC), 93,824 (HeLa-S3), 110,385 (K562), 83,276 (SK-N-SH)</td>
</tr>
</tbody>
</table>

In the multi-tissue scenario, we retrain tissue-specific RF classifiers using all available features from the input matrix, $T_i \in \mathbb{R}^{n \times m}$; $i \in \{1, ..., m\}$, where $n$ is the number of bins forming the training set, and $m$ denotes the number of training tissues for the target TF:

$$RF_i = \text{RandomForest}(T_i, \text{Binding}(T_i)),$$

here $\text{Binding}(T_i)$ is a vector of length $n$, holding the binding labels for the target TF in tissue $i$, and $\text{RandomForest}(., .)$ generates the RF model trained on the features and labels provided by the first and second arguments respectively. An example of the input matrix $T_i$ and the response vector $\text{Binding}(T_i)$ is shown in Figure 2b. In the second step, to focus only on essential regulators (c.f. Figure 3a), we shrink the feature space to the union of the top 20 regulators taken over all tissue and TF specific RF classifiers, $T'_i$, by ranking the predictors according to their Gini index (Figure 2c):

$$T'_i = \bigcup_{j=1}^{m} \text{TopFeatures}(RF_j),$$

where $\text{TopFeatures}(RF_j)$ denotes the top 20 features of $RF_j$ and $\bigcup_{j=1}^{m}$ generates the reduced feature matrix based on the union of the top TFs. In the following, we refer to a training data set comprised of only one tissue as a single tissue case and to a training data set composed of multiple tissues as a multi tissue case. Considering the single tissue case, we train an RF model, $RF'_i$, on the reduced feature space and use this as the final model for the respective target TF:

$$RF'_i = \text{RandomForest}(T'_i, \text{Binding}(T'_i)).$$

In the multi-tissue scenario, we retrain tissue-specific RF models on the reduced feature space and apply them across all available training tissues:

$$T'_i = \{\text{prediction}(RF'_i, T'_i); i = \{1, \cdots, m\} \in [0, 1]^{n \times m}\}.$$
Figure 1. (a) Data preprocessing workflow using DNase1 Hypersensitive Sites (DHSs). Using JAMM, DHSs are called considering all available replicates for a distinct tissue. Transcription factor (TF) affinities in the identified DHSs are computed using TRAP for 557 TFs, the median signal of DHSs is assessed using bedtools. (b) An alternative data preprocessing workflow without DHSs: TF affinities and median DNase1-seq signal are computed per bin.

Figure 2. (a) An overview of model training for a distinct transcription factor, TF, with multiple training tissues. Using the full feature matrices $T_1$, $T_2$, $T_3$, depicted in (b), TF and tissue-specific random forest (RF) classifiers are trained. From those RF classifiers ($RF_1$, $RF_2$, $RF_3$), we determine the union of the top 20 features from each RF. In this example, the union of top TFs is comprised of 24 TFs. Next, we design reduced tissue-specific feature matrices $T'_1$, $T'_2$, $T'_3$, as shown in (c) based on the union of the top TF features. Subsequently, tissue-specific RF classifiers ($RF'_1$, $RF'_2$, $RF'_3$) are trained on these reduced feature sets. The tissue-specific RF classifiers are applied to all training tissues and their predictions are aggregated to form the feature matrix $T'_U$, visualized in (d), which is used to train an ensemble model ($RF_E$). The ensemble RF is used to make predictions on unseen data $T'_U$ (e). Note that the column "Tissue" in (d) is not included in the model but only shown here for illustration purposes. The feature matrices shown represent feature setup (1) using DNase1 Hypersensitive (DHS) sites.

where Prediction ($RF'_1$, $T'_U$) returns the predictions made by $RF'_1$ when applied on the $T'_U$. Their predictions are combined in a new feature matrix that is used as input to train an ensemble RF, $RF_E$. Note that the input matrix contains predictions of all tissue-specific RF models on all available training tissues (Figure 2d):

$$RF_E = \text{RandomForest}(T'_U, \text{Binding}(T'_U)).$$

By design, the ensemble model incorporates the tissue-specific RF classifiers in a non-linear way to better generalize across all provided training tissues. An example matrix that is used to obtain predictions from an ensemble RF is shown in Figure 2e.

**Performance assessment**

We used two different ways to assess model performance:

(1) While fitting the RF classifiers, we measure the out-of-bag
Figure 3. a) Classification error for the Bound and Unbound classes for different sets of features: considering all features, the top 10, and the top 20 features. One can see that the difference in model performance between the top 20 and all feature cases is only marginal. b) Comparison of the out of bag (OOB) error between ensemble models and tissue-specific random forest (RF) classifiers. Especially in the Unbound case, the ensemble models show superior performance compared to the tissue-specific RF classifiers. c) Misclassification rate computed on unseen test data for ensemble and tissue-specific RF classifiers. As in b) we see that the ensemble models generally outperform the tissue-specific ones. Note that the scale of the y-axis is different for the Bound and Unbound classes in (a) and (b).
error (OOB), which is defined as the mean prediction error for each training sample \( i \) using trees that were not trained on sample \( i \). The OOB error is computed separately for the Bound and Unbound classes:

\[
\text{Bound} = \frac{\text{FN}}{\text{TP} + \text{FN}}, \quad \text{Unbound} = \frac{\text{FP}}{\text{TN} + \text{FP}},
\]

where \( \text{TP} \) denotes the sites correctly predicted as bound, \( \text{TN} \) denotes the sites correctly predicted as unbound, \( \text{FP} \) and \( \text{FN} \) represent sites incorrectly predicted as bound and unbound, respectively. Note that, because we use balanced data for training the RF classifiers, the OOB is computed on a balanced data set.

Additionally, we compute (2) the misclassification rate for the Bound and Unbound cases on a subset of the test data that was used by the challenge organizers. The test data is composed of three hold-out chromosomes which have not been used for training: chr1, chr8 and chr21. Additionally, TF binding is predicted on an unseen tissue, i.e. a tissue that was not used for training. An overview of the test data is provided in Table 2. Note that, in contrast to the training data, the test data is not balanced, i.e. the Unbound class is larger than the Bound class. Therefore, to avoid misinterpretation of model performance, it is essential to compute the error for both classes separately.

**Protein-protein-interaction score**

We obtained a customized protein-protein-interaction (PPI) probability matrix \( R \) as described previously\(^{29}\), which is derived from a random walk analysis on a protein-protein-association network based on STRING\(^{27} \) (version 9.05). An entry \( R_{ij} \) represents the probability that protein \( i \) interacts with protein \( j \). Note that the probability \( R_{ij} \) is not symmetric by construction, i.e. \( R_{ij} \neq R_{ji} \). To generate a score describing how likely it is that a subset of proteins \( P \) contained in \( R \) interact with a distinct TF \( t \), guided by the feature importances the RF models provide, we define the PPI score \( S_{t,p} \) as

\[
S_{t,p} = -\log(\sum_{p=p_{\text{top1}}}^{p_{\text{topn}}} (R_{ij} + R_{ji}) \times GI(p)) / 2^{|P|},
\]

where \( GI(p) \) denotes the Gini index values of \( p \) obtained from the RF model corresponding to \( t \). Thus, the smaller the value of \( S_{t,p} \), the more likely it is that the regulators in \( P \) interact with TF \( t \).

**Results**

In this section, we first show that shrinking the feature space to those TFs essential for training does not affect model accuracy. Next, we demonstrate the benefits of the ensemble learning and how its accuracy is depending on the number of training tissues. We further investigate the top selected TFs by the RF models and find known interaction partners that possess high PPI scores. Finally, we compare the two feature design schemes, described in the Methods section, and explore their influences on model performance. If not stated otherwise, all figures presented in the following are based on annotation setup (1), including DHSs.

**Reducing the feature space to a small subset does not affect classification performance**

Because having a sparse feature space simplifies model interpretation, we reduce the feature space to contain only a few essential features. As explained above, we determined sets of top features using the Gini index, resulting in TF and tissue-specific sets containing either the top 10 or top 20 features. As shown in Figure 3a the difference in OOB error between the feature set comprised of the top 20 features and the full feature space is only marginal, whereas the difference is increasing when only the top 10 features are considered. Therefore, we decided to use a reduced feature space that consists of the top 20 features per model. The results indicate that the most important feature across all TFs is the DNase1-seq signal within the DHSs for feature setup (1). Similarly, in feature setup (2), the DNase1-seq signal within the bins is found to be more important than the TF features.

**Ensemble learning improves model accuracy**

According to the OOB error shown in Figure 3b, the ensemble RF classifiers outperform the tissue-specific models in all cases for both Bound and Unbound classes, thus emphasizing on the improved capability of the ensemble model to generalize across tissues. Additionally, we computed the misclassification rate on all test tissues which are linked to multiple training tissues (Figure 3c). Again, we notice that the ensemble RF classifiers outperform the tissue-specific classifiers by several orders of magnitude in all Unbound instances and in most Bound cases. Overall, these results suggest that ensemble learning is a promising approach to deal with the tissue-specificity of TF binding.

**Increasing the number of training tissues improves prediction accuracy**

Although the results in Figure 3b and 3c suggest that the ensemble methods perform well, it remains unclear what influence the number of training tissues would have on the performance of an RF. To elucidate this, we performed permutation experiments learning multiple RF models using all possible combinations of training tissues that are available for a distinct TF. As this is a computationally demanding task, we performed it for only three, arbitrarily selected, TFs: MAX, TEAD4, and E2F6.

<table>
<thead>
<tr>
<th>TF</th>
<th>Tissues</th>
</tr>
</thead>
<tbody>
<tr>
<td>CTCF</td>
<td>PC-3, Induced pluripotent stem cell</td>
</tr>
<tr>
<td>E2F1</td>
<td>K562</td>
</tr>
<tr>
<td>EGR1</td>
<td>liver</td>
</tr>
<tr>
<td>GABPA</td>
<td>liver</td>
</tr>
<tr>
<td>JUND</td>
<td>liver</td>
</tr>
<tr>
<td>MAX</td>
<td>liver</td>
</tr>
<tr>
<td>REST</td>
<td>liver</td>
</tr>
<tr>
<td>TAF1</td>
<td>liver</td>
</tr>
</tbody>
</table>
Figure 4 illustrates that the OOB error declines when the number of training tissues increases. Hence, we conclude that the ability of an ensemble RF to generalize across tissues improves with larger number of training tissues.

However, it remains to be shown whether the improved accuracy obtained from the ensemble RF classifiers was in fact because of the ensemble learning. To test this, we designed another learning setup in which all tissue-specific data sets were aggregated into one. In other words, we pooled the training data for one TF across all available tissues into one dataset. We then used this pooled dataset to train a new RF model. As depicted in Figure 4b the true ensemble models perform considerably better than the models learned on the pooled training data. This shows that the ensemble technique is better suited to capture tissue-specific information than simple data aggregation.

Predictors selected by the RF classifiers are associated to the target TF

As stated before, we hypothesized that the top predictors selected by the RF classifiers represent regulators that exist either in protein complexes with the target TF via direct or indirect binding, or bind directly to DNA in close proximity to the target TF. To investigate this hypothesis, we computed a PPI score $s_{t,P}$ (see Methods) for the selected predictors $P$ per TF $t$ and compared it against scores computed for randomly sampled sets of TFs (based on 100 randomly drawn TF subsets). The PPI score $s_{t,P}$ for TF $t$ is small, if $t$ is likely to interact with the factors included in the selected predictor set $P$. In contrast, the score is high if $t$ is not likely to be interacting with the factors in $P$. As shown in Figure 5a, except for three TFs (MAX, TAF1, ZNF143), the PPI score of the TFs selected by the RF is better (i.e. smaller) than the scores for the randomly selected set. This indicates that the RF classifiers select features representing regulators that are more likely to be interacting with the target TF, either directly or with indirect contacts.

Interaction partners shown in gray can not be identified by our approach as either these are proteins without regulatory functions or we do not have a PWM available for them.

Feature design influences the FP and FN predictions

In the conference round of the challenge, we were using feature setup (1), which is based on DNase1 Hypersensitive Sites (DHSs), while in the final round, we switched to design (2), which is purely based on bins. This transition had a strong effect on our performance assessed by the challenge organizers. While we improved the recall of our predictions by switching from (1) to (2), the precision decreased. In Figure 6, we show the misclassification rates for the Bound and Unbound classes depending on the feature designs. The performance is assessed and shown on test data. The bin based models (2) outperform the peak based models in the Bound case, whereas the peak based...
Figure 5. a) Log transformed PPI scores computed for a set of TFs. In the Random case, we show the mean PPI score across 100 random draws and its standard deviation. The smaller the PPI score the better. Only for three TFs (MAX, TAF1, ZNF143), the randomly sampled PPI score is better than or equal to the score derived for the TFs selected by the RF classifiers. b) PPI network obtained from STRING centered around the TF MAFF, highlighting proteins that interact with MAFF with high confidence. Proteins colored in green were identified as important features in the RF classifiers, proteins shown in gray could not be retrieved by our model, because they are DNA-binding proteins, or we do not have a PWM for them in our set. Regulators shown in red could have been detected by the RF, but were not included in the top set of regulators.

Figure 6. Comparison of misclassification rate depending on the feature design computed on test data. The bin based model outperforms the peak based model in predicting bound labels, while in the unbound case the model based on DHSs is better than the bin based model.
models show superior performance in the Unbound case. At the same time, bin based models perform poorly in the Unbound case, which is probably driven by the strong dependence of the RF classifiers on the DNase1-seq signal. In contrast to that, models based on DHSs perform well in the Unbound case, because the search space for TFBSs is limited to only DHSs. This increases the precision of the predictions, but at the same time lowers the recall, which is reflected by the high misclassification rate in the Bound case.

Discussion and conclusion
Here, we introduced an RF based ensemble learning approach to predict TFBS in vivo. In this article, we did not compare our approach to competitors in the challenge, as this is done in the main challenge paper. Here, we show the benefits of ensemble learning in a multi-tissue setting and that modeling cofactors is beneficial for the classification.

We show on both test and training data that the ensemble strategy is able to generalize better across tissues, than models trained on only a single tissue (Figure 3). Also the accuracy of the ensemble classifiers increases with an increasing number of available training tissues (Figure 4a). We also illustrate that just using all available training data to learn one RF does not provide as accurate results as an ensemble model (Figure 4b). In this study, we decided to use RF classifiers, because they lead to accurate classification results using non-linear predictions in a reasonable time. Alternative classification approaches, such as logistic regression, or support-vector-machines could have been used too.

RF classifiers have also been proposed recently, independent from the challenge, as an adequate method to predict TF binding. Although the authors of perform cross cell-type predictions, i.e. they predict TF binding in a tissue where the RF was not trained on, they do not use ensemble models as proposed here. However, they did show that it is beneficial for the predictions of a distinct target TF to consider further TFs as predictors, in addition to the target TF itself. This is in agreement with our findings. As shown in Figure 3a, a small subset of features is sufficient to reach similar classification performance as the full feature space. We found that most of these selected TFs are known interaction partners of the target TF, see Figure 5. This is also supported by a recent study illustrating that most TFs bind in dense clusters around genes suggesting a widespread interaction among them.

Only for three TFs, we could not find that the predicted TFs lead to a better PPI score than a randomly chosen set. We note that for two of those three, TAF1 and MAX, the performance of the ensemble RF classifiers improved only marginally, or not at all, compared to the tissue-specific classifiers. This suggests that our model does not account for the true interaction partners of those TFs. Indeed, an inspection of the STRING database for TAF1 revealed that only TAF1 itself and TBP are among the top 20 regulators, which are included in our PWM collection. For the remaining interaction partners, mostly TFs of the TAF family, no binding motif is available in the public repositories, thus they are not included in our PWM collection and can therefore not be used by the RF classifiers. Similarly, for MAX, only 5 out of 20 high confidence interaction partners are included in our PWM collection. Specifically, no PWM is available for 6 TFs interacting with MAX, while the remaining interacting proteins are not categorized as TFs. Overall, our approach benefits from data availability (Figure 4a). If there are only a few TFs available in our PWM collection, it will be harder to model the co-factor binding behavior of a TF across tissues adequately. Also, the more diverse the co-factor landscape of a TF is between the tissues, the harder it will be to learn a general model. Another crucial aspect with respect to that is the quality of the PWM. During the challenge, we realized that the selection of PWMs is crucial for model performance and it is required to compare PWMs obtained from different sources to make sure that one uses the one with highest information content. Nevertheless, instead of using a more recent method to model TF-motifs, we stick to the use of PWMs because they are (1) the most common way to describe the sequence specificity of TFs (2) they are available for a large number of TFs, and (3) they can be interpreted easily.

Switching the feature design for the RF classifiers from (1) DHS-based to (2) bin-based showed that DHS sites are inadmissible to reduce the false positive rate (Figure 6) of TFBS predictions. Using only bins, without DHS information, we could improve the recall of TFBS predictions, but only at the cost of poor precision at the same time. The explanation for this behavior is a difference in size of the genomic search space between both feature setups. The bin based models have a low misclassification rate in the Bound case, because they do consider the whole genome without neglecting any sites beforehand, thus improving recall. However, our observations suggest that considering only the raw signal does not sufficiently correct for false positive sites, as opposed to use DHSs, which yield an improved misclassification rate in the Unbound case compared to the raw signal.

In general, both training and evaluating TFBS prediction methods is challenging due to the class imbalance, i.e. there are many more Unbound (negative) than Bound (positive) binding sites in the genome. This requires both (a) training approaches that avoid over-fitting for one of the two classes and (b) evaluation strategies accounting for this issue. Here, we show misclassification rates separately for both positive and negative classes to avoid a bias caused by the dominant Unbound case.

We note that our current investigation is not meant to construct a genome-wide classifier in which the unbound case is the most abundant. To achieve that, the highly unbalanced training data situation would need to be taken into account, for instance in the loss function of the classifier. Aside from the technical aspects, we show that modeling cofactors is helpful to predict TFBS and that ensemble learning is a promising technique to generalize information across tissues.
Data availability
The raw data used in this study is available online at Synapse: https://www.synapse.org/#!Synapse:syn6112317.

Software availability
Code generated as part of this analysis is available on GitHub: https://github.com/SchulzLab/TFAnalysis

Archived code as time of publication: http://doi.org/10.5281/zenodo.1409697

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References

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We thank everyone involved in organizing the ENCODE-DREAM in vivo Transcription Factor binding site prediction challenge and are grateful for the opportunity to share this article. The PPI scoring matrix used in this study was kindly provided by Sebastian Köhler.
Transcriptional regulation by transcription factors (TFs) is one of the fundamental steps of gene regulation. Hence, knowing the genome-wide binding regions of a TF is of great interest. Experimentally, those could be determined by ChIP-seq, which, however, is time-consuming and labor-intensive. Hence, computational prediction of cell type-specific, in-vivo transcription factor binding is highly demanded.

In their manuscript "Predicting transcription factor binding using ensemble random forest models", Ardakani, Schmidt and Schulz present a novel method for this purpose, which is based on PWMs describing TF sequence preference, and DNase-seq data capturing chromatin accessibility. This method combines i) learning random forest (RF) classifiers on feature matrices for individual cell types, ii) shrinking feature sets, and iii) learning ensemble classifiers across cell types. The authors illustrate that within their method, peak-based DNase features seem to be favorable compared with bin-based aggregation of DNase-seq coverage. Furthermore, they demonstrate that the ensemble classifier indeed yields an overall improved performance compared with cell type-specific RFs.

As this is a companion paper to the main publication describing the results of the ENCODE-DREAM challenge, I consider a direct comparison to other approaches dispensable in this case.

In general, most of the methods are well described and conclusions are supported by the data. However, I have a few major and several minor comments regarding choices made by the authors (especially with regard to performance assessment) and the presentation of specific details of methods and results, as detailed in the following.

Major comments:

1. In sub-section "Data" of the Methods section, the authors state that they "focus on these 12 TFs in the scope of this article". However, this is contradicted by the list provided in Table 2 listing only 8 TFs. Results for the same 8 TFs are also shown in Fig. 6, whereas several of the remaining figures (Fig 3a/b, Fig 5) present results for a larger set of TFs, i.e., for TFs not listed in sub-section "Data".

2. The third paragraph of sub-section "Data preprocessing and feature generation" of the Methods section is lacking details. How exactly are "tissue-specific DHSs" called using JAMM? What have been the inputs and input formats? Which peaks are merged and why?

3. Results with regard to feature shrinkage (Fig. 3a) are only shown for OOB Misclassification. As I could imagine over-fitting effects to specifics of the training cell types, I considered an evaluation on the test
data highly informative. For instance, I would imagine that we see a decrease in OOB performance when shrinking features to the top 20, whereas on the test data this model achieves a better generalization and, hence, misclassification rate.

4. The authors chose to use misclassification separated by classes, which could also be described as false negative rate and false positive rate, as performance measure for the whole manuscript. For several reasons, I would consider curve-based measures, especially the (area under the) precision-recall curve the more appropriate measure for this application but also in the context of the ENCODE-DREAM challenge. First, we face a highly imbalanced classification problem, and the precision-recall curve has been shown to be highly informative in this case. Second, the areas under the ROC curve and precision-recall curve have also been used for performance assessment in the ENCODE-DREAM challenge and choosing the same performance measure in this paper would foster comparison of results to those of the challenge (especially since both use the same test data). Third, in the discussion of Fig. 6, the authors mention that one choice of DNase data works better for bound regions, while the other works better for unbound regions. Here, we face the typical trade-off between sensitivity and specificity (or false negative rate and false positive rate), where we are unable to decide for one option based on specific, contradictory combinations of the two measures. In the ROC curve, basically \( (1 - \frac{FN}{TP+FN}) \) would be plotted against \( \frac{FP}{TN+FP} \), so we would get a broader impression of classifier performance, including the specific points on the curve chosen by the authors. For these reasons, the area under the ROC curve and the area under the precision-recall curve should be included as performance measures into this study. As the authors illustrate in Fig. 2d, RF classifiers already output continuous scores that could be used for computing these curves. Technically, curves and AUC values could be computed, e.g., using the R packages PRROC or precrec.

5. In sub-section "Ensemble learning improves model accuracy" of the Results section, I agree with the authors that the ensemble classifier performs better than the individual RFs. However, currently it remains unclear if this can really be attributed to "ensemble learning" or just to averaging effects. Hence, I would suggest to include a simple averaging over the predictions of individual RFs (those, for which the predictions are also input of RF_E) as a simple baseline model (in addition to the single RF learned on the pooled data). In addition, for MAX, the authors might also include results for the test data in addition to what is shown in Figure 4.

Minor comments:

6. In the Introduction, second paragraph, the authors state "Most of these methods are based on position weight matrices (PWMs) describing the sequence preference of TFs," giving a reference to the publication of the 2016 update of the Jaspar database. While Jaspar indeed provides PWM models, I do not consider this an appropriate reference for the definition of PWMs in general. Specifically, I would suggest to cite the seminal works of Berg & von Hippel and of Stormo instead.

7. In the Introduction, second paragraph, the authors state "PWMs indicate [...] which nucleotide is most likely to occur". From my perspective, this description is not fully accurate. The most likely nucleotide is also represented by consensus sequences. PWMs give a specific weight (or log-probability,...) for each of the nucleotides and not only for the most likely one.
8. I appreciate that the authors reference our work regarding dependency models (Slim models) in the second paragraph of the introduction. However, there are several other approaches for modeling dependencies in TF binding sites. I would encourage the authors to broaden the scope of their references by including, e.g. \(^4^5\).

9. In the third paragraph of the introduction, the authors refer to "the main ENCODE-DREAM Challenge paper". I am aware that this paper has not yet been published, but encourage the authors to update their publication including a reference to that paper when available.

10. In the second paragraph of sub-section "Data preprocessing and feature generation" of the Methods section, it is mentioned that TF binding affinities are computed for 557 distinct TFs. After reading the complete paper, I understood (hopefully correctly) that all 557 TFs are used for all RFs (before shrinking the feature space) regardless of the training TF. If my understanding is correct, the authors might consider to include an explicit statement about this fact already at this stage of the manuscript.

11. In the first paragraph of sub-section "Ensemble random forest classifier" of the Methods section, the authors state that "the balance between the bound and unbound classes is maintained to avoid over-fitting". For me, it remains unclear how exactly this helps to avoid over-fitting. For my understanding, over-fitting typically refers to an over-adaption to specifics of the training data, which do not generalize well to other data sets, leading to a poor performance on unseen (test) data. However, the class imbalance is inherent to the problem and should be (roughly) the same for training and test cell types. Please clarify.

12. In the first paragraph of sub-section "Ensemble random forest classifier" of the Methods section, right before the second formula, the shrunken feature space is described to be the union of top 20 regulators. However, later in the Results section, the authors also consider a case where features per RF are restricted to the top 10 ones (Fig 3a). Hence, I would suggest a generic description, here.

13. The third formula of sub-section "Ensemble random forest classifier" of the Methods section refers to an index \(i\), where (for my understanding), according to the previous definition, \(i\) should be in \(\{1\}\), in this case. If that is indeed the case, I would suggest to replace "\(i\)" by "\(1\)" in the formula and explicitly state that this is the only index \(i\) can be.

14. The fourth formula of sub-section "Ensemble random forest classifier" of the Methods section is partly broken. Specifically, the element sign refers to the set of indexes, which does not seem reasonable to me. I rather think this should refer to the matrix resulting from prediction(RF\(_i\),T\(_i\)) Please fix.

15. In Figure 2 (b), (c) and (e), the labels in the table cells are hardly legible in printout. Either increase the thickness of letters or chose a different color.

16. For Figure 2e, it remains unclear from the caption what is shown. It seems to be the input matrix derived from test data, in analogy to the training matrices shown in Figure 2b? Is this the input of each RF? Of RF' (as features might have been shrunken)? Or of RF_E?

17. The fifth formula of sub-section "Ensemble random forest classifier" of the Methods might profit from a bit of additional explanation. Specifically, it took me a while to understand (if I'm right) that for T_E', the outputs of all individual RFs are concatenated row-wise, while "Binding(T_E)" denotes the concatenation of training labels.
18. In the first paragraph of sub-section "Performance assessment" of the Methods section, I wondered what the index "i" refers to. Is this the same index i as before (i.e., an index for the training cell types)? If not, what exactly is "sample i"?

19. In sub-section "Protein-protein-interaction score" of the Methods section, I would have appreciated a bit more motivation before describing the method itself.

20. In sub-section "Reducing the feature space to a small subset [...]" of the Results section, I would not fully agree with the authors that the difference in error between the full model and the model based on top 20 features is "marginal". I would even assume that a statistical test of the difference between the data behind the two boxplots in Fig. 3a would be significant.

21. In sub-section "Reducing the feature space to a small subset [...]" of the Results section, I did not find the last two sentences (regarding importance of DNase-based features) to be supported by the data shown in the manuscript.

22. In section "Data availability", the authors provide a link to the synapse page of the ENCODE-DREAM challenge. However, the data are accessible only after registration and signing a data usage policy.

23. Typos & Grammar:
- first paragraph of "Data preprocessing and feature generation": "down sampled" should be "down-sampled"
- second paragraph of "Data preprocessing and feature generation": "the course of challenge" should be "the course of the challenge"
- third paragraph of "Data preprocessing and feature generation": "data is intersected" should be "data are intersected"
- 7th paragraph of "Discussion and conclusions": "Bound(positive)" should be "Bound (positive)"
- Reference 15: "transcritpion" should be "transcription"

References

Is the work clearly and accurately presented and does it cite the current literature?
Yes

Is the study design appropriate and is the work technically sound?
Partly
Are sufficient details of methods and analysis provided to allow replication by others?
Partly

If applicable, is the statistical analysis and its interpretation appropriate?
Yes

Are all the source data underlying the results available to ensure full reproducibility?
Partly

Are the conclusions drawn adequately supported by the results?
Yes

Competing Interests: We have participated in the same challenge (ENCODE-DREAM) as the authors and the data presented here are closely related to that challenge.

I have read this submission. I believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard, however I have significant reservations, as outlined above.

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