How far are we from personalized gene expression prediction using sequence-to-expression deep neural networks?

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Abstract

Deep learning (DL) methods accurately predict gene expression levels from genomic DNA, promising to serve as an important tool in interpreting the full spectrum of genetic variations in personal genomes. However, systematic benchmarking is needed to assess the gap in their utility as personal DNA interpreters. Using paired Whole Genome Sequencing and gene expression data we evaluate DL sequence-to-expression models, identifying their failure to make correct predictions on a substantial number of genomic loci due to their inability to correctly determine the direction of variant effects, highlighting the limits of the current model training paradigm.

Main

Deep learning (DL) methods have recently become the state-of-the-art in a variety of regulatory genomic prediction tasks[1–6]. By adapting convolutional neural networks (CNNs), these models take as input sub-sequences of genomic DNA and predict as outputs functional properties such as epigenomic modifications[2,7], 3D interactions[5,8], and gene expression values[1,9,10]. A key insight has been to formulate model training and evaluation such that genomic regions are treated as data points, resulting in millions of training sequences in a single Reference genome to optimize model parameters[11,12]. This training approach allows models to identify DNA subsequences (motifs) that are shared across the genome and exploits variations in motif combinations across genomic regions to enable their predictions. Indeed, this strategy has enabled accurate prediction of context specific functional profiles from the Reference genome sub-sequences. However, an extraordinary promise of these sequence-based models is to make predictions for sequence alternatives across individuals at a particular locus, each presenting a unique combination of genetic variants – a combinatorial space that is simply not feasible to evaluate with current experimental assays[4,6]. Selective evaluation using natural genetic variation in expression quantitative trait loci (eQTL) studies has shown some promise in the ability of these models to make such predictions[1,13]. Moreover, evaluations using massively parallel reporter assay (MPRA) experiments on select genomic locations[1,14] has shown that these models can predict the effects of single nucleotide changes, despite experimental noise and context differences between in-vivo training datasets and MPRA in-vitro experiments. Here, to assess how far we are from deploying existing sequence-to-expression DL models as personalized DNA interpreters genome-wid, we use paired Whole Genome Sequencing (WGS) and RNA-sequencing from a cohort of 839 individuals to systematically benchmark the utility of existing sequence-to-expression DL models trained on the Reference genome in *in-vivo* prediction of gene expression across individuals.

First, we focus our evaluation on Enformer[1], the top-performing sequence-to-expression CNN-based model that follows the standard training approach, utilizing genomic regions across a single Reference genome to learn the relevant sequence patterns for predicting gene expression, TF binding, and histone modifications across hundreds of cell types in a multitask framework (**Fig. 1A**). We initially evaluated Enformer's prediction of population-average gene expression in the cerebral cortex from the Reference Genome (Methods). We observe a Pearson correlation R=0.58 (**Fig. 1B, S1**, R=0.51 for Enformer's test set; Methods) between observed and predicted gene expression across genes which is consistent with previous reports[1,15].

Next, we evaluated Enformer's performance in predicting individual-specific expression levels based on personalized sequences. As an example, we first present here results for a highly heritable gene (heritability r^2=0.8) related to DNA replication: *DDX11*. *DDX11*'s variance in expression across individuals can be attributed to a single causal single-nucleotide variant (SNV) using statistical fine-mapping[13]. Using WGS data, we created 839 input sequences of length 196,608bp centered at the transcription start site (TSS), one per individual for the gene (**Fig. 1C**). Each individual's input sequence contains all their observed SNVs (**Fig. S2**). Applying Enformer to these input sequences we observed a Pearson correlation of 0.85 between predicted and observed gene expression levels (**Fig. 1D**). Further, *in-silico* mutagenesis (ISM) at this locus showed that Enformer utilized a single SNV with high correlation to gene expression (eQTLs) in making its predictions (**Fig. 1E**). This SNV is the same causal SNV that was identified through statistical fine-mapping with Susie[13]. Thus, at this locus, Enformer is able to identify the causal SNV amongst all those in LD, and in addition provides hypotheses about the underlying functional cause, in this case the extension of a repressive motif (**Fig. S3**).

However, the impressive predictions on *DDX11* proved to be the exception rather than the rule. When we compared the predicted to observed expression levels across individuals for 6,825 cortex-expressed genes that we were able to test, we found a large distribution in the *Pearson's R* (**Fig. 2A, Table S1**). While the model's predicted gene expression values were significantly correlated to observed expression for 598 genes ($FDR_{BH}=0.05$, Methods), the predictions were significantly anti-correlated with the true gene expression values for 195 of these genes (33%). For example, predictions for *GSTM3* gene expression values are anti-correlated with the observed gene expression across individuals (**Fig. 2B**). The results are similar when we select the best output track that matches the cerebral cortex ("CAGE, cortex, adult") instead of fine-tuning the predictions with an elastic net model (**Fig. S4**, Methods). As well, model ensembling, whereby we averaged over model predictions on shifted sub-sequences and reverse and forward strands, did not impact the sign of significant correlations in ~96% of cases (**Fig. S5**). When we focused this analysis on 184 genes with known causal SNVs according to previous eQTL analysis[13], again we observed that while Enformer can make significant predictions, the predicted expression levels are anti-correlated for 80 (43%) of these genes (**Fig. S6A, Table S1**). Overall, these results imply that the model fails to correctly attribute the variants' direction of effect (*i.e.,* whether a given variant decreases or increases gene expression level).

We then compared Enformer against a widely-used linear approach called PrediXcan[16]. PrediXcan constructs an elastic net model per gene from *cis* genotype SNVs across individuals. Unlike Enformer, PrediXcan is explicitly trained to predict gene expression from variants but it does not take into account variants that were not present in its training data and cannot output a prediction for unseen variants. While the models are conceptually different the PrediXcan model gives a lower bound on the fraction of gene expression variance that can be predicted from genotype. For a fair comparison, we used a prediXcan model pretrained on GTEx data[16] and applied it to ROSMAP samples. Hence neither Enformer nor PrediXcan have seen the ROSMAP samples prior to their application. For the 1,570 genes where PrediXcan's elastic net model was available, performance of Enformer is substantially lower than PrediXcan (Mean R Enformer = 0.02, Mean R PrediXcan = 0.26 **Fig. 2C, Table S1**). Further, PrediXcan did not have the same challenge with mis-prediction of the direction of SNV effect. Interestingly, when we compared the absolute Pearson R values across genes between Enformer and PrediXcan, we observed a substantial

correlation (R=0.58, **Fig. S6B**), implying that genes whose expression values from genotype across subjects can be predicted well by PrediXcan overlap the set of genes where Enformer assesses a relationship between SNVs and expression. However, Enformer is not able to determine the sign of SNV effects accurately (hence a very low mean R value between observed and predicted gene expression of 0.02). We note that Enformer predictions were evaluated against eQTLs in the original study using SLDP regression demonstrating improved performance over competing models in terms of z-score. Our results are not in contradiction with these findings. The SLDP approach computes the association of effects genome-wide; taking a conservative estimate for the degrees of freedom to be the number of independent LD blocks (1,361[17]) a z-score of 7 would correspond to an R^2 of 0.034.

To investigate if these observations are specific to Enformer or more broadly apply to sequence-based DL models that follow the same training recipe, we trained a simple CNN that takes as input sub-sequences from the Reference genome centered at genese' TSS (40Kbp) and predicts population-average RNA-seq gene expression from cortex as output (see Supplementary Methods). We observed that while this vanilla method can predict population-average gene expression levels with similar accuracy to Enformer (**Fig. S7A**), it exhibits similar characteristics when applied to predict variation in gene expression across individuals (**Fig. S7B**). Thus, our results on Enformer are likely to generalize to other sequence-based DL models trained in the same way. In parallel work, the results described in the manuscript co-submitted by Huang, Shuai, Baokar *et al.,* 2023 indeed confirm this hypothesis.

To explore the causes for the negative correlation between Enformer predictions and the observed gene expression values we applied two explainable AI (XAI) techniques on all genes with a significant correlation value (abs(R)>0.2, **Fig. 2A**): ISM and gradients (Grad) [18–20]. Both XAI methods decompose the nonlinear neural network into a linear function whose weights approximate the effect and direction of every SNV to the prediction (Methods). While there was a moderate correlation between attributions computed with Grad and ISM (mean *Pearson R* = 0.28, **Fig. S8**), we found that linear decomposition with ISM generated a better approximation of Enformer's predictions (**Fig. S9**), and was able to accurately approximate Enformer's predictions for 95% of the examined genes ($R>0.2$, $p<10^{-8}$).

For each gene, based on its ISM attributions, we determined the main SNV driver(s) that dominate the differential gene expression predictions across individuals (Methods). Across the 256 examined genes, we found that 32% have a single SNV driver, and the vast majority (85%) have five or fewer drivers (**Fig. S10, Table S2**) which determine the direction and correlation with the observed expression values. To understand how these driver SNVs cause mispredictions, we directly computed the SNV direction of effect by contrasting the gene expression levels across people when stratified by the SNV's genotypes (Methods), referred to as the eQTL effect size. We classified Enformer-identified driver SNVs into "supported" and "unsupported" categories based on the agreement of SNVs ISM attribution sign with the direction of effect according to the eQTL analysis. For example, *GSTM3* has two common driver SNVs and their predicted direction of effect was unsupported by the observed gene expression data (**Fig. 2D**). For all 256 inspected genes, we found that mispredicted genes had almost exclusively unsupported driver SNVs **(Figure 2E**), confirming that this small number of driver SNVs per gene are in fact the cause of Enformer's misprediction for the sign of the effect.

To investigate whether these unsupported attributions are caused by systematically erroneous sequence-based motifs that Enformer learns, we analyzed the genomic sequences around driver SNVs. We did not find any enrichment for specific sequence motifs (**Fig. S11**). When we plotted the location of SNV drivers along the input sequences, we found that most drivers were located close to the TSS (**Fig. 2F, Fig. S12**), supporting a recent report[15] that shows current sequence-based DL models mainly predict gene expression from genomic DNA close to TSS, despite using larger input DNA sequences. Further, we looked at Grad attributions along the entire sequence (**Fig 2G top, S13**) and ISM attributions for large windows around the TSS (**Fig 2G, bottom**) and found that the area around the TSS not only contained distinguishable learned sequence motifs but also both the strongest positive and strongest negative attributions outside of apparent learned motifs. We observe that the majority of the SNVs that drive the significant positive and negative correlations to the observed expression do not fall into one of these distinguishable motifs but instead in regions of increased "spurious attributions" where training data was likely not sufficient to deduce the regulatory logic (**Fig. S14, Table S3**).

In summary, our results suggest that current models trained on the output of a single Reference genome often fail to correctly predict the direction of SNV effects because most predictive SNVs do not fall into the *learned* regulatory motifs. This observation extends evaluation of sequence-based NN models in predicting eQTL effects[1,10,15,19] as summarized across the genome, and instead investigates how accurately differences in gene expression can be predicted across individuals on a per-gene basis with nearly complete genetic information captured in personal genomes. We further show that current NN models perform worse than simple baseline approaches like PrediXcan. Going forward, we recommend that new models are not only assessed on genome-wide statistics of absolute causal eQTL effect sizes but also on a per gene agreement between the sign and the size of the predicted and measured effect of causal variants.

We hypothesize that two complementary strategies will be fruitful for improving the prediction of gene expression across individuals. Firstly, current methods do not accurately model all of the biochemical processes that determine RNA abundance. For example, post-transcription RNA processing (whose dependence on sequence is mediated via RNA-protein or RNA-RNA interactions) is entirely ignored. Similarly, while some models have large receptive fields and are technically capable of modeling long-range interactions, they do so only to a limited extent[15]. Secondly, the mechanisms that explain gene-to-gene variation may be distinct from those that explain interpersonal variation. For example, long-range interaction appears to be much more important for the latter[15]. Thus, training on the input-outputs-pairs of diverse genomes and their corresponding gene expression measurements may be required for accurate personalized predictions.

Figure Legends

Figure 1. Evaluation of Enformer across genomic regions and select loci. (A) Schematic of the training approach implemented by Enformer and other sequence-based CNN models. Different genomic regions from the Reference genome are treated as data points. Genomic DNA underlying a given region is the input to the model, and the model learns to predict various functional properties including gene expression (CAGE-seq), chromatin accessibility (ATAC-Seq), or TF binding (ChIP-Seq). (B) Population-average gene expression levels in cerebral cortex (averaged in ROSMAP samples, n=839) for expressed genes (n=13,397) shown on the x-axis. Enformer's prediction of gene expression levels for cortex based on the Reference genome sequences centered at TSS of each gene (196Kb) is shown on the y-axis. Enformer's output tracks are fine-tuned with an elastic net model (see Methods). (C) Schematic of the per-locus evaluation strategy. Personal genomes are constructed for each individual by inserting their observed SNVs into the Reference genome. The personalized sequences centered at the TSS of gene DDX11 are used as input to Enformer. (D) Prediction of cortex gene expression levels for individuals in the ROSMAP cohort. Each dot represents an individual. Output of Enformer is fine-tuned using an elastic net model. E) In-silico mutagenesis (ISM) values for all SNVs which occur at least once in 839 genomes within 98Kb of DDX11 TSS. SNVs are colored by minor allele frequency (MAF). The border of the "driver" SNV is shown in red and its size is proportional to its impact on the linear approximation (Supplementary Methods).

Figure 2. Evaluation of Enformer on prediction of gene expression across individuals. (A) Y-axis shows the Pearson R coefficient between observed expression values and Enformer's predicted values per-gene. X-axis shows the negative log10 p-value, computed using a gene-specific null model (Supplementary Method). The color represents the predicted mean expression using the most relevant Enformer output track ("CAGE, adult, brain"). Red dashed line indicates FDRBH=0.05. (B) Prediction of cortex gene expression levels ("CAGE, adult, brain" track) in the ROSMAP cohort (n=839) for the GSTM3 gene, x-axis shows the observed gene expression values. (C) Pearson R coefficient between PrediXcan predicted versus observed expression across 839 individuals (x-axis) versus Enformer's Pearson R values on the same sample (y-axis). Red lines indicate threshold for significance (abs(R)>0.2), darker colored dots are significant genes from panel A. Green cross represents the location of the mean across all x- and y-values. (D) ISM value (x-axis) versus eQTL effect size (y-axis) for all SNVs within the 196Kb input sequence of the GSTM3 gene. Red circles represent SNVs that drive the linear approximation to the predictions. SNVs are defined as supported or unsupported based on the concordance with the sign of the eQTL effect size. (E) Fraction of supported driver SNVs per gene (y-axis) versus Pearson's R values between Enformer's predictions and observed expressions (x-axis). (F) Number of driver SNVs within the 1000bp window to the TSS. Main drivers are the drivers with the strongest impact on linear approximation, shown in different colors. (G) Top: Gradient attributions (grey) across the entire sequence of the GSTM3 gene with location of all SNVs and driver SNVs. Bottom: 300bp window around the TSS with ISM attributions normalized by the estimated standard deviation across the entire sequence. Most significant connected motifs are framed in red. Main driver shown as magenta triangle.

Software and intermediate results

Scripts for running the analyses presented, as well as intermediate results are available from: https://github.com/mostafavilabuw/EnformerAssessment

Accession Codes

Genotype, RNA-seq, and DNAm data for the Religious Orders Study and Rush Memory and Aging Project (ROSMAP) samples are available from the Synapse AMP-AD Data Portal https://www.synapse.org/#!Synapse:syn2580853/discussion/default as well as RADC Research Resource Sharing Hub at www.radc.rush.edu.

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Contributions
Conceived the study: SM, MC. Study design: SM, AS1, MC. Data generation and quality control analyses: BN, AS2, CG, PLD, ST, DAB. Analyses and interpretation: AS1, AS2, BN, SM, MC. Wrote the initial draft: SM, AS1, BN. Read and provided comments on the manuscript: MC, BN, AS2, PLD, CG, ST, DAB.

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Figure 1

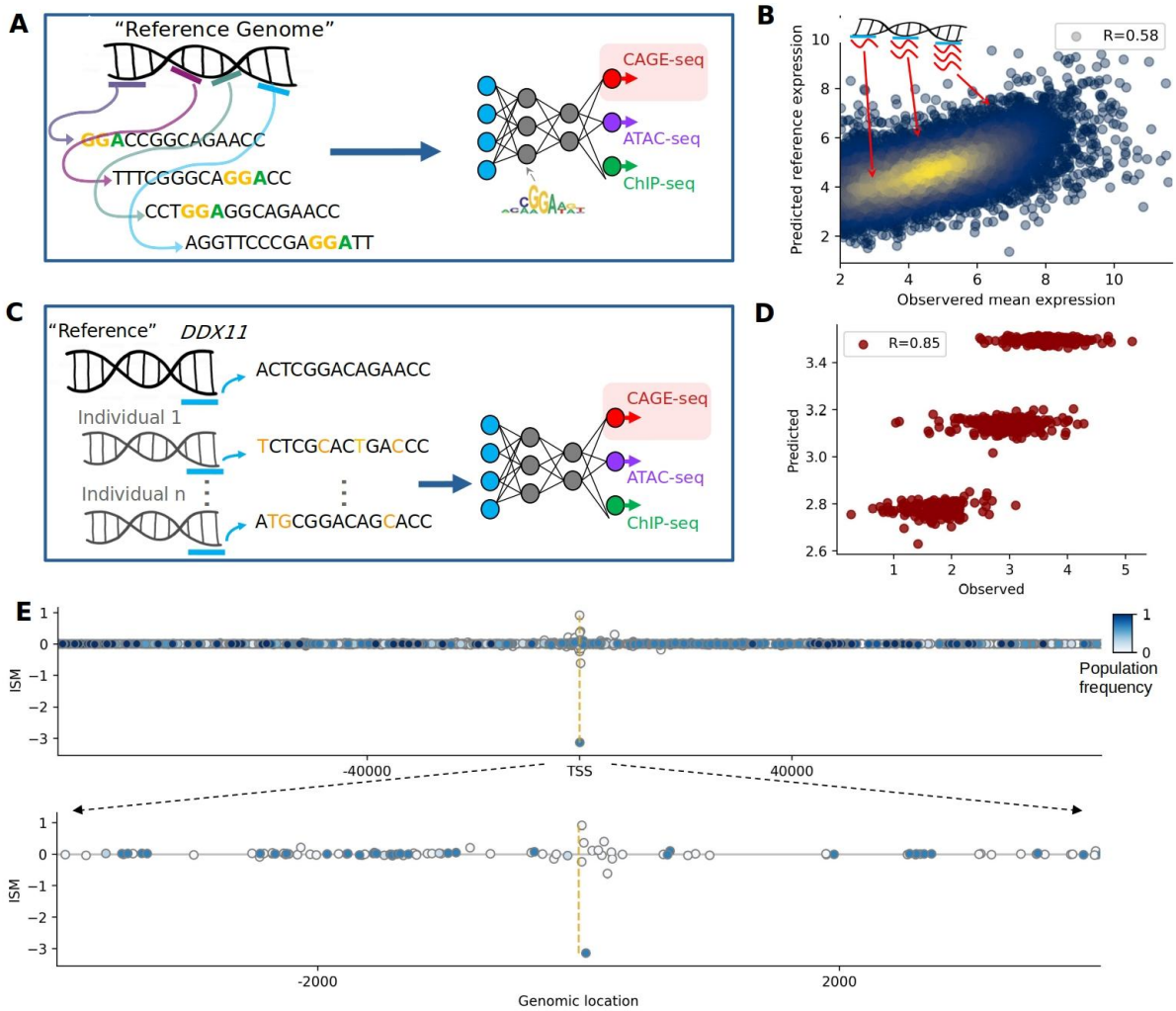

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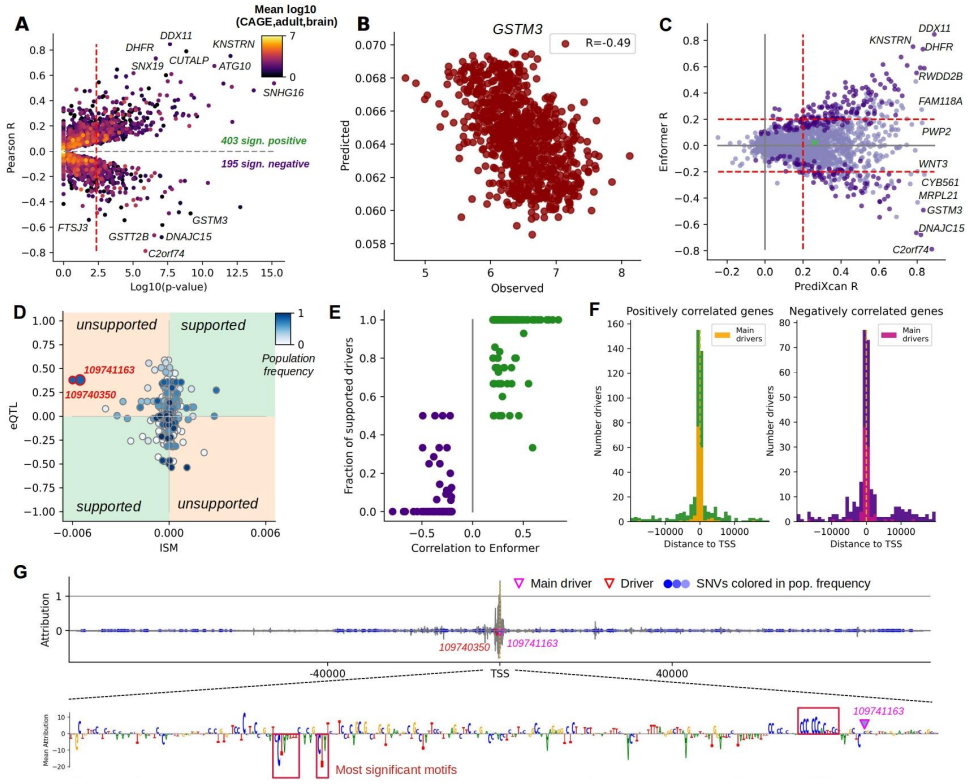
Figure 2



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