Towards Personalized Epigenomics: Learning Shared Chromatin Landscapes and Joint De-Noising of Histone Modification Assays

Tanmayee Narendra[1*], Giovanni Visonà[2], Crhistian de Jesus Cardona[1], James Abbott[1], Gabriele Schweikert[1*]

[1*]Division of Computational Biology, School of Life Sciences, University of Dundee, Dow Street, Dundee, DD15EH, United Kingdom.
[2*]Empirical Inference, Max Planck Institute for Intelligent Systems, Max-Planck-Ring 4, Tübingen, 72076, Germany.

*Corresponding author(s). E-mail(s): tnarendra001@dundee.ac.uk; g.schweikert@dundee.ac.uk;
Contributing authors: giovanni.visona@tuebingen.mpg.de; ccardonavelasquez001@dundee.ac.uk; j.abbott@dundee.ac.uk;

Abstract

Epigenetic mechanisms enable cellular differentiation and the maintenance of distinct cell-types. They enable rapid responses to external signals through changes in gene regulation and their registration over longer time spans. Consequently, chromatin environments exhibit cell-type and individual specificity contributing to phenotypic diversity. Their genomic distributions are measured using ChIP-Seq and related methods. However, the chromatin landscape introduces significant biases into these measurements. Here, we introduce DecoDen to simultaneously learn shared chromatin landscapes while de-biasing individual measurement tracks. We demonstrate DecoDen's effectiveness on an integrative analysis of histone modification patterns across multiple tissues in personal epigenomes.

Keywords: Histone modifications, Chromatin landscapes, Integrative epigenomics

Background

Although the cells of a multicellular organism contains nearly identical copies of DNA, they vary widely in form, shape, and function. One of the many ways cells regulate function is by creating distinct chromatin environments that enable the precise execution of cell-type-specific tasks: A complex array of epigenetic factors dynamically modify the physical properties of DNA, introducing chemical changes to both the DNA molecule itself and to histone proteins, around which DNA is wound. Through these modifications, epigenetic mechanisms either facilitate or restrict access to specific genomic regions, influencing interactions between transcription factors and their corresponding DNA substrates - ultimately enabling the wide range of cellular phenotypes observed across different cell types.

Epigenetic changes play vital roles throughout all stages of life: During development, proliferating cells encode essential information in their chromatin states [1], which is passed down to daughter cells. Cellular differentiation is accompanied by tightly regulated adjustments to the chromatin landscape [2]. Throughout an organism's lifetime, as cells transition into quiescent states, epigenetic changes mediate the integration of environmental signals, molecular cues, and cellular metabolism to maintain homeostasis and preserve cell identity [3]. Eventually, chromatin modifications are involved in regulating aging processes [4], and aberrant chromatin reprogramming is an early hallmark of tumor development [5].

Obtaining cellular snapshots of epigenomic landscapes remains expensive and time-consuming, requiring extensive experimental efforts, with large numbers of individual assays to record histone modifications individually. Over the last decade international efforts have been undertaken to create tissue and cell-type specific epigenomic reference maps, for example, the Roadmap Consortium established epigenomic references for 111 tissue and primary cell types, focusing on a core subset of epigenomic marks [6]. The primary experimental technique used is chromatin immunoprecipitation sequencing (ChIP-Seq) [7–9]. Despite being widely adopted, ChIP-Seq has several limitations. The chromatin fragments used for ChIP-Seq experiments are generated by sonication, which has an inherent bias towards accessible chromatin [10]. Further, ChIP-Seq uses formaldehyde cross-linking which results in biased recovery of accessible chromatin [11]. Together, this may have an unequal impact on different histone marks (see Figure S4 in Supplementary Material) [12, 13], and false positive phantom peaks can be detected in active promoter regions [14].

While reference epigenomes have proven invaluable, they are insufficient for identifying functional important or disease-causing epigenomic variations. Individual-specific epigenomes are now emerging, with the EN-TEx resource providing post mortem data from 15 assays from four individuals across 30 tissues [15]. Additionally, computational methods have been developed to fill remaining experimental gaps through cross-cell type imputation of epigenomic profiles. We have earlier contributed to these efforts by developing a transformer-based method, eDICE [16], which was positively assessed on reference epigenomes in the ENCODE Imputation Challenge [17]. Using eDICE, we have also shown that it is possible to train on data from one individual and use transfer learning to predict histone modification patterns in a target individual, where only limited measurements are available. This proof of concept

illustrates the potential for imputation of tissue specific histone modifications from readily accessible samples.

However, despite these technical advancements and an overall acceleration in data production, the analysis and interpretation of the resulting data sets remains challenging. Notably, individual histone modifications are far from independent of each other, but exhibit non-linear, locally changing combinatorial arrangements. This is not surprising, as epigenetic factors simultaneously interpret and effect upon associated modification patterns. Indeed, the understanding of the dynamic interactions between individual epigenetic components is of particular importance. However, the resulting co-created chromatin landscape strongly impacts the local sensitivity and specificity of the measurements, thus introducing confounding shared biases. To understand the concerted cell-specific interaction between epigenetic factors, as well as to detect subtle changes in individual histone modifications between individuals, it is essential to efficiently and robustly separate the joint effect of the chromatin environment from the interrogated histone modifications itself. To this end, input control experiments are typically conducted that estimate the local effect of the chromatin environment. Typically, these are used computationally to correct for each assay track individually. However, for an effective separation of chromatin bias from the local distribution of histone modification enrichment, the bias has to be correctly estimated genome-wide. This is rarely the case. Typically, only 40-50 million fragments are sequenced in the control experiment, such that large proportions of the human genome remain not represented or undersampled, with sometimes 16% of the genome not covered at all (see Section S1 in Supplementary Material for examples). As a consequence, input control samples alone are not sufficient to correct the measurements and may even introduce additional noise. Without correct debiasing of the measured data, experimental results can be misinterpreted and computational imputation methods which utilize existing data to perform in-silico predictions of missing histone modifications will invariably learn the data inherent biases, and propagate them into the computational predictions.

Despite these challenges, the potential for personalized epigenomics, in which individual-specific chromatin differences are identified in an unbiased manner, presents a compelling case for improving the precision of histone modification profiling and imputation. A deeper understanding of inter-individual chromatin differences is essential for predicting disease progression and developing targeted therapies, underscoring the need for more refined and precise methodologies in chromatin research.

We introduce DecoDen (Deconvolve and Denoise), a new method to remove cell-type-specific bias for samples of different histone modifications derived from the same cell or tissue samples. This method leverages different assays and jointly analyses data to learn a shared chromatin bias common to all assays performed on a given sample. With simulated data we demonstrate that DecoDen accurately reconstructs hidden signals. Applying DecoDen to a number of different experimental data sets, we demonstrate its unique ability to minimize confounding effects. Lastly, we test DecoDen by reanalyzing multi-tissue personal epigenomes from the EN-TEx resource [18] to identify individual-specific differences in histone modification patterns. However, we find severe limitations in the experimental data quality and will therefore

discuss improved experimental guidelines. DecoDen is available as an open-source tool at `https://github.com/ntanmayee/DecoDen`.

Results

The DecoDen Model

The DecoDen model is founded on three specific modeling assumptions, which are addressed in two consecutive steps.

The first assumption is that the observed treatment measurement consists of a target-specific signal and background reads, which originate from *independent* processes. In other words, the final observed measurement is the sum of a target-specific component and a background component. Second, we assume that the process from which background reads are generated is shared across all assays. Further, this process is independent of their specific target, as long as they are performed on the same biological sample. This allows us to share information across multiple assays in order to improve upon a locus-specific background control estimate for the whole genome. The additive bias is addressed using a constrained form of Non-negative Matrix Factorization (NMF), which deconvolves all observed measurements into target-specific signals and a shared background. This step also identifies the coefficients for their linear combinations. These mixing parameters are related to the global specificity of the used antibodies and the observed signal-to-noise ratios of the individual measurements.

The third assumption is that the learned unspecific background purely captures biases such as local chromatin accessibility and sequencing mappability, which equally affect the target specific signals by locally amplifying or reducing the number of sequenced reads. We thus use the unspecific background to further remove confounding biases from the target-specific signals by applying Half-Sibling Regression (HSR) [19], an approach from causal inference that aims to reconstruct a latent quantity of interest. A conceptual overview of the two main steps can be seen in Figure 1.

We can define the previous qualitative description with a suitable formalism (vectors are represented in bold typeface): Let us assume that local biases which depend on the DNA sequence alone, can be described with a vector $\mathbf{m} \in \mathbb{R}^G$, where G is the length of the binned genome. Cell-type-specific biases including chromatin accessibility are represented with $\mathbf{a} \in \mathbb{R}^G$ and $\mathbf{n} \in \mathbb{R}^G$ represents the nonspecific signal that captures any other process not included in the aforementioned biases.

The observed r-th replicate of a control (input) measurement is given by $\mathbf{c}^{(r)} \in \mathbb{R}^G$. The value measured at each genomic bin b can then be written as:

$$c_b^{(r)} = D^{(r)} \cdot a_b \cdot m_b \cdot n_b \tag{1}$$

where $D^{(r)}$ represents the replicate-specific scaling factor accounting for variable sequencing depth.

Further, we can describe the observed data $\mathbf{t}_h^{(r)} \in \mathbb{R}^G$ for an an experimental assay for the h-th histone modification and r-th replicate as:

$$t_{h,b}^{(r)} = D_h^{(r)} \cdot a_b \cdot m_b \cdot \left(k_h^{(r)} \cdot s_{h,b} + n_b\right) \tag{2}$$

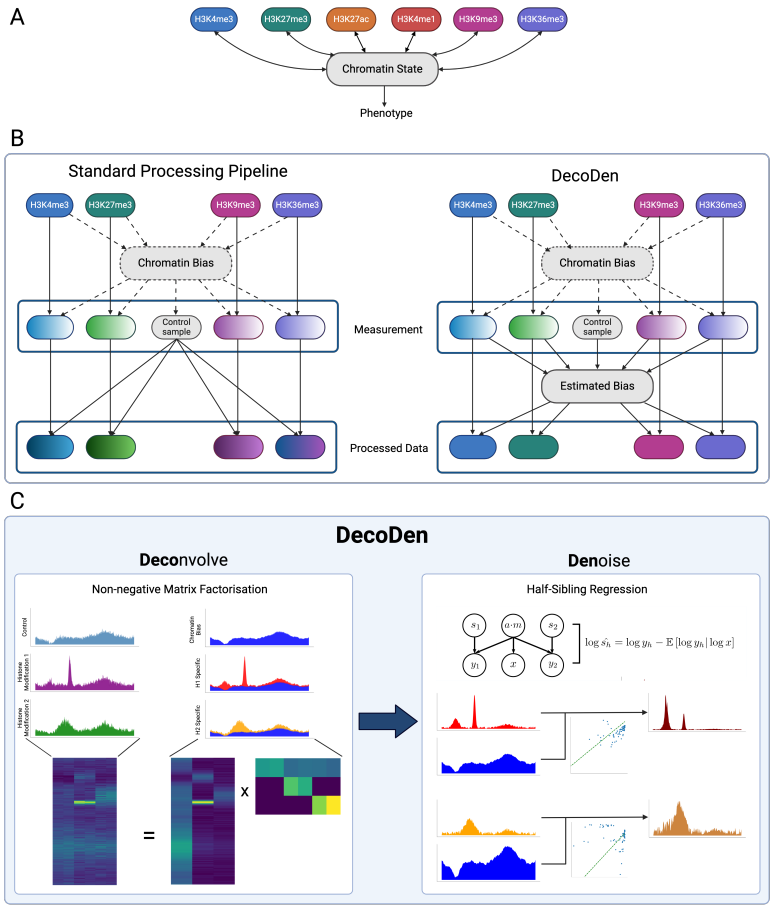

Fig. 1: **Schematic of DecoDen:** (A) Histone modifications interact with each other via chromatin to jointly establish 'chromatin states' that determines the DNA's accessibility to regulatory proteins, thereby influencing transcription and the observed phenotype. Measurement of histone modifications are confounded by this chromatin state. (B) In the standard data processing pipeline, the data for each modification is independently analysed and estimates are implicitly biased by the chromatin state (chromatin bias). With DecoDen, all samples are jointly analysed to estimate a chromatin bias which is consequently minimised from measurement samples. (C) In the first step of DecoDen, Non-negative Matrix Factorization (NMF) is used to separate the cell-type specific chromatin signal from the assay-specific signal of the different histone modification measurements. Next, Half-Sibling Regression (HSR) is used to extract the true (hidden) enrichment pattern by minimizing the bias introduced by accessibility and mappability.

where again $D_h^{(r)}$ represents the scaling factor for the r-th replicate for modification h. $s_{h,b}$ is the true (latent) signal enrichment for the h-th histone modification in genomic bin b, and $k_h^{(r)}$ is a mixing parameter that captures the antibody specificity.

Ultimately, the aim of the experiment is to infer $\mathbf{s}_h$, which is confounded by the previous biases. Intuitively, the NMF step is designed to remove unspecific reads $\mathbf{x} = \mathbf{a} \cdot \mathbf{m} \cdot \mathbf{n}$ from $\mathbf{t}_h^{(r)}$, while the HSR step aims to remove the effect of the confounding biases from $\mathbf{y}_h = \mathbf{a} \cdot \mathbf{m} \cdot \mathbf{s}_h$.

The output of DecoDen offers then an approximation of the true hidden signals of histone modification enrichments $\mathbf{s}_h$. Further details on the NMF and HSR implementation in DecoDen are provided in the Methods section.

DecoDen accurately reconstructs the hidden signal

DecoDen is an integrative approach that shares information between multiple assays and samples to reconstruct hidden signals of different histone modifications in the context of a shared chromatin landscape. Since ground truth of histone modification enrichment is unknown for real datasets, DecoDen's ability to infer true enrichment was first assessed with simulated datasets. Further, DecoDen was quantitatively compared to existing peak calling methods. Our results show that DecoDen performs competitively in identifying enriched regions in simulated data sets. Most notably, we find that within enriched regions the reconstructed values by DecoDen preserve true coverage patterns (See Section S2 in Supplementary Material).

Next, we used data from a deeply sequenced experiment from the A549 Lung Carcinoma cell line (equivalent to cell type E114 in the Roadmap Consortium) [20]. This data set will be referred to as E114-Jung in the rest of the manuscript. For this experiment the authors sequenced each sample, including the input background, to generate more than 100M uniquely mapping reads. The authors additionally estimated, that 40M reads would be sufficient to reach saturation. We ran DecoDen run jointly for samples from H3K4me3, H3K27me3 assays and whole cell extract (WCE) as control. Figure 2 demonstrates how the shape of the H3K4me3 enrichment is conserved while eliminating cell-type specific bias at 1.225 Mb. Several other examples highlighting the utility of DecoDen in scenarios where there are a larger number of experimental conditions and replicates available can be seen in Section S4 in Supplementary Material.

DecoDen minimises the effect of confounders

To determine the true enrichment of a genomic position, it is desirable to remove biases that arise from the experimental process itself, which are ideally captured in the control sample. Figure 3A and B are a compilation of 2D histograms showing the distributions of the average coverage of control and treatment replicates for the histone modifications H3K4me3 and H3K27me3 in the E114-Jung dataset. Notably, the dynamic range for control and signal coverage values are comparable, and the histogram of average coverage present pronounced density across the diagonal: In these regions count values for the assay are high, but so are control values, indicating a strong correlation between control and signal. In addition, the H3K4me3 data exhibits genomic bins with high relative enrichment along the y-axis, characterized by low control and high assay coverage. In the H3K27me3 sample, relative signal enrichment above background is less pronounced, suggesting that observed sequencing

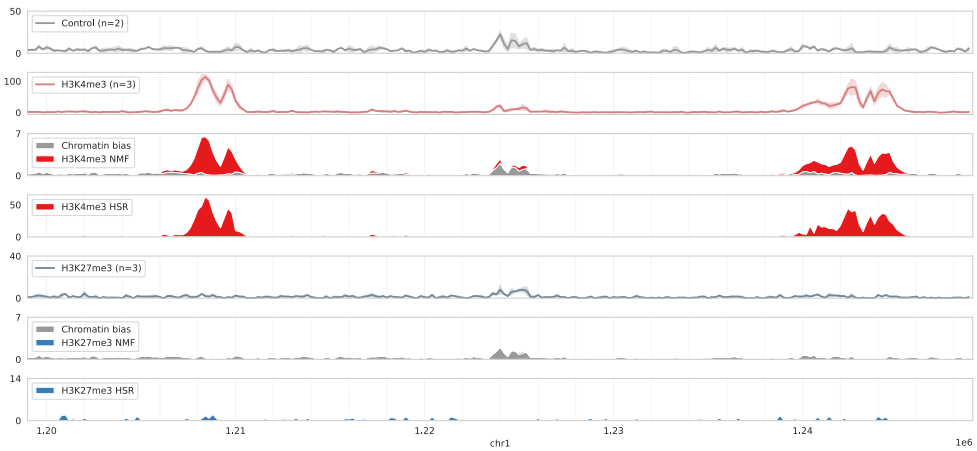

Fig. 2: **Example DecoDen Reconstruction of H3K4me3 and H3K27me3 enrichment from the E114-Jung Dataset:** Measurement data are shown as a solid line with a shaded region around it representing the maximum and minimum read coverage. For each histone modification, the measurement is decomposed into chromatin bias (in grey) and histone modification specific components (in blue and red). While the NMF step reduces noise among replicates, the HSR step eliminates cell-type-specific bias as seen in the region around 1.225 Mb. The shape of the peak is preserved as seen in the H3K4me3 peak on the left side.

depth for the broader and more widespread H3K27me3 signal may not be sufficient to accurately detect H3K27me3 signal enrichment genome-wide. However, after applying DecoDen, the correlation between input and treatment samples can be eliminated. Moreover, the DecoDen signals show stronger correlation with each assay replicate while simultaneously minimizing its correlation with all control samples (Figure 3C) .

When the enrichment signal was independently compared to chromatin accessibility (measured through ATAC-Seq), the correlation was found to be lower than the correlation between assay samples and chromatin accessibility. In addition, the DecoDen signal for H3K4me3, a mark associated with open chromatin, has a higher correlation with chromatin accessibility than the DecoDen signal for H3K27me3, a mark associated with closed chromatin. This finding further demonstrates that DecoDen effectively reduces the influence of confounding factors while preserving true enrichment (Figure 3C).

Comparing histone modification measurements across labs

To compare DecoDen's signal output across experiments, two different datasets were selected that measured the same histone marks in the same cell line. In addition to the E114-Jung dataset, data for the same cell line from the Roadmap Epigenome project was used (henceforth referred to as the E114-Roadmap dataset). Recall that both datasets contain samples for H3K4me3, H3K27me3 and control. Surprisingly, correlation between treatment samples is much higher for H3K27me3 compared to H3K4me3

as seen in Figure 4 A and B. However, this high correlation likely arises through the shared chromatin bias, as we have seen previously that treatment samples are highly

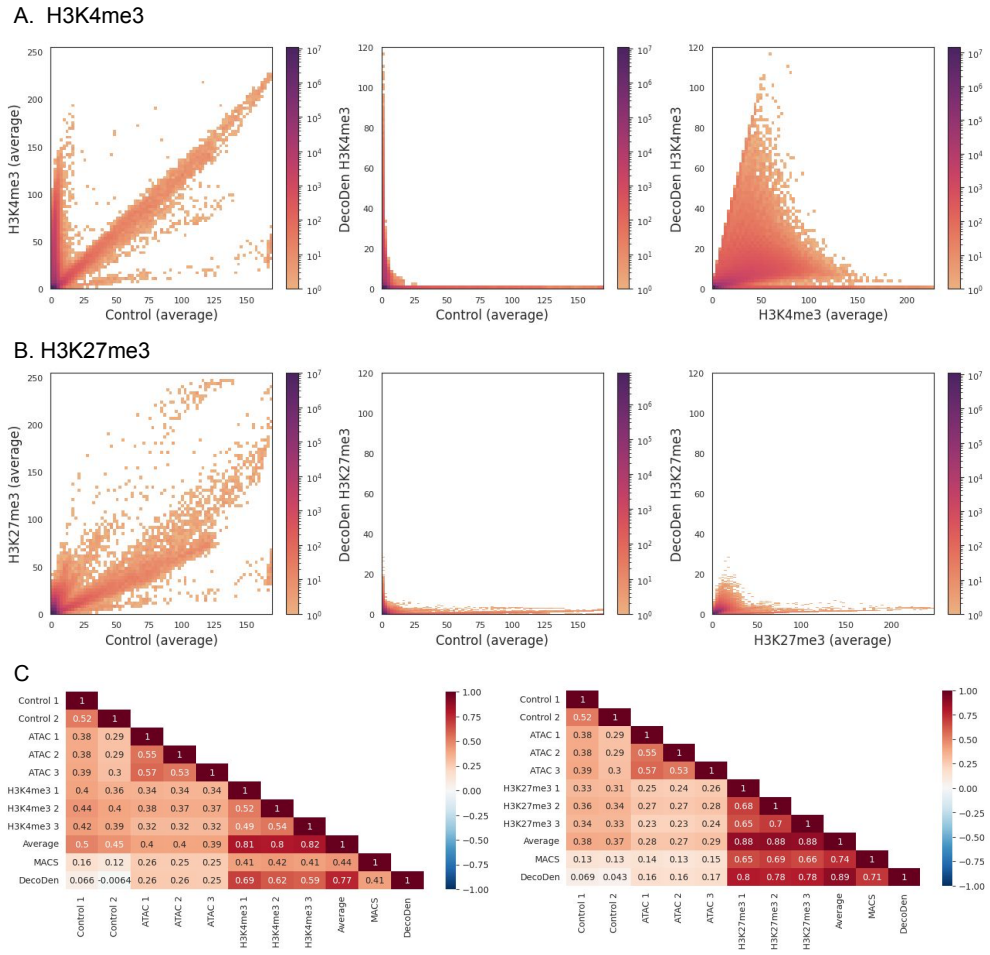

Fig. 3: **Effect of confounders is minimized:** (A) and (B) Histograms comparing the coverage between control and treatment samples are shown for histone marks H3K4me3 and H3K27me27 respectively. As seen in the first columnm, since the local chromatin state influences measurement, treatment and control samples are highly correlated in both histone marks. H3K4me3 has more prominent regions of enrichment than H3K27me3 as seen from the density of genomic bins with high treatment coverage and corresponding low control coverage. DecoDen eliminates this correlation to recover true enrichment as seen in the second and third columns. (C) Heatmaps showing genome-wide correlation demonstrate that while DecoDen signal minimises the correlation with control samples, it enhances the correlation with treatment replicates. Average treatment sample coverage and the p-value signal obtained from MACS are used as a baseline. The E114-Jung dataset has been used here.

correlated with control samples. We also found that the respective control samples from the different labs are highly correlated (See Figure S9 in the Supplementary Material.). Interestingly, correcting for chromatin bias using either MACS or DecoDen reduces genome-wide correlations between experiments, supporting increased plasticity of histone modification patterns observed in different experimental conditions and laboratories (Figure 4 C).

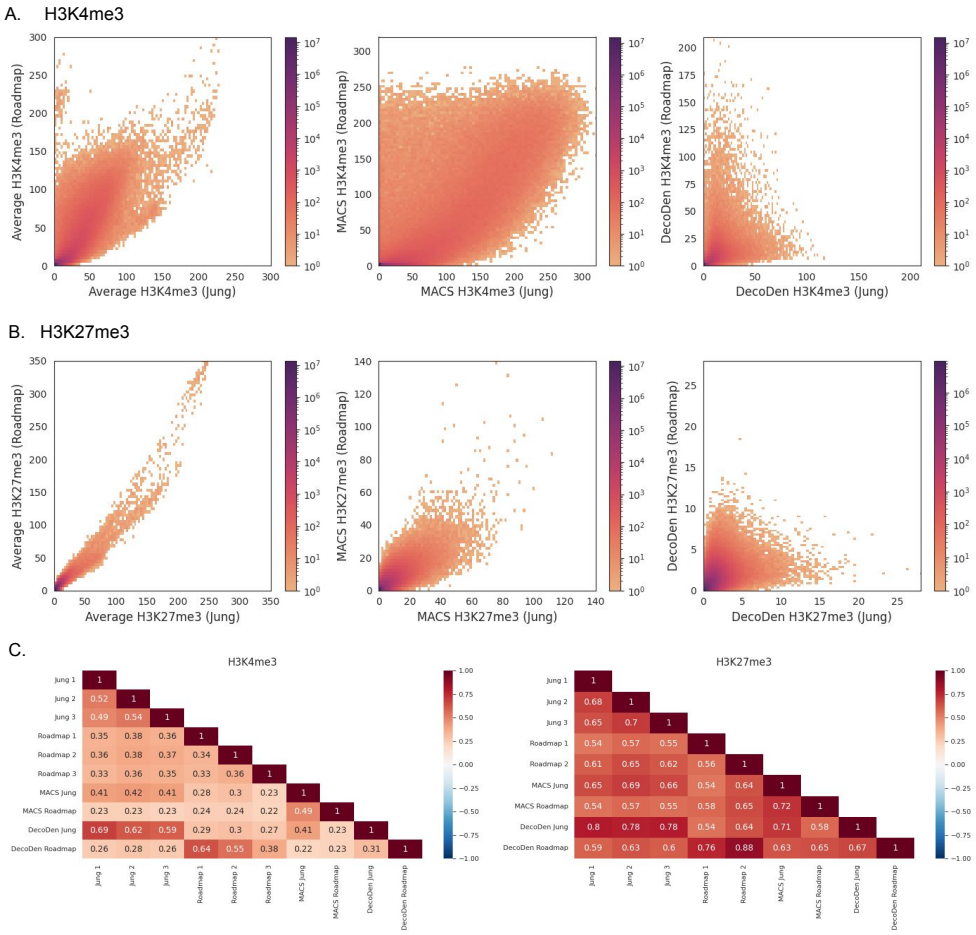

Fig. 4: **Data comparison between labs.** (A) H3K4me3 assays and (B) H3K27me3 assays. (C) Genome-wide correlation between samples from different experiments.

DecoDen to study multi-tissue personal epigenomes

Tissue-specific histone modification patterns are influenced by aging and external factors such as environmental signals. In addition, aberrant histone modification patterns

have been associated with abnormal chromatin reprogramming and cancer. Thus, it is important to accurately identify histone modification patterns that are specific to an individual in a given tissue, while reducing biases to better characterize subtle enrichment differences. As a case study, we consider histone modifications in spleen and transverse colon tissue from two individuals of the EN-TEx [18, 21, 22] consortium. Figure 5 shows the 2D histograms for the transverse colon of both individuals and highlights the differences between the observed count distributions between different histone modifications; As in the Jung data set (Figure 3) H3K4me3 and H3K27ac have genomic regions with low control coverage and high treatment coverage along the y-axis. However, in contrast to the earlier examined data sets, the density along the diagonal is much lower, suggesting that the input control sample is severely undersequenced. The signal enrichment will therefore likely be overestimated, leading to 'false positive' enrichment calls. In the case of H3K36me3, H3K27me3 and H3K4me1 signal coverage is itself low, and likely not saturated, suggesting that the sensitivity with which significant enrichment can be detected is expected to be low. Applying DecoDen we can share information across the different assays, thus improving the estimation of the background signal. We are thus able to successfully remove correlation with the estimated chromatin bias from the histone modification tracks (Figure 5 A and B bottom rows). However, as the control sample and most assay samples appear to be under-sequenced, the resulting output tracks remain estimates of the true histone modification enrichment.

In Figure 6, we compared two individuals based on the DecoDen output and found that the estimated tissue-specific chromatin bias is more strongly conserved between individuals than the assay tracks, despite the low sequencing depth of the control samples. In contrast, greater inter-individual differences were observed for the corrected histone modifications, particularly for H3K4me3 and H3K27ac—the arguably highest-quality tracks. This suggests that individual histone modifications may be less stable and more dynamic, whereas the chromatin landscape, shaped by the interplay of multiple epigenetic factors, remains highly robust within a given tissue context.As before, it is important to note that a higher correlation between different individuals measured using the same assays (e.g., H3K4me1) does not necessarily indicate high reproducibility or data quality. Instead, it may primarily reflect the strong and overriding influence of chromatin bias in the assay tracks. This underscores the need for careful correction of such biases when interpreting inter-individual variability in chromatin features. Without proper adjustment, these biases could obscure true biological differences and lead to misleading conclusions about the stability or dynamical nature of these histone modifications versus the broader more robust chromatin landscape.

Overall, we observe substantial variability in data quality across histone modifications, likely due to differences in antibody specificity and library sizes, which warrant further investigation. While DecoDen generally enhances enrichment signals, its effectiveness remains constrained by the quality of the input data. Computational methods cannot fully compensate for poor data quality, as seen in histone modifications such as H3K36me3, H3K27me3, and H3K4me1.

Figure 7 examplifies individual-specific H3K4me3 peaks that are more prominent in individual 37M but less pronounced in 51F within the transverse colon. Notably,

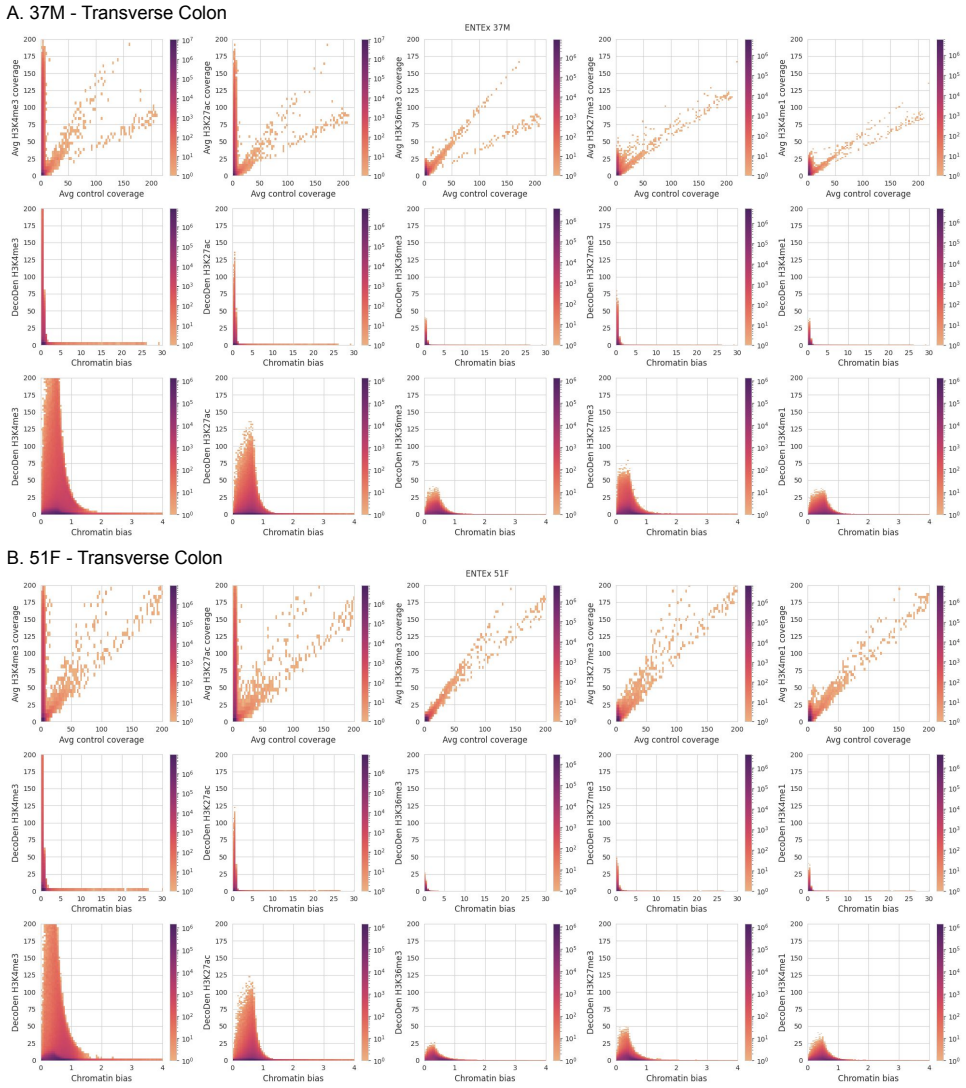

Fig. 5: **DecoDen removes correlation between control and treatment samples in personal epigenomes:** Here, 2D distributions for two individuals from the ENT-Ex dataset are shown. The first row of each sub-figure shows the distributions for binned coverage for input vs assay data. Middle row shows DecoDen estimated histone modification enrichment vs learned chromatin bias. Last row shows enlarged regions of the histograms.

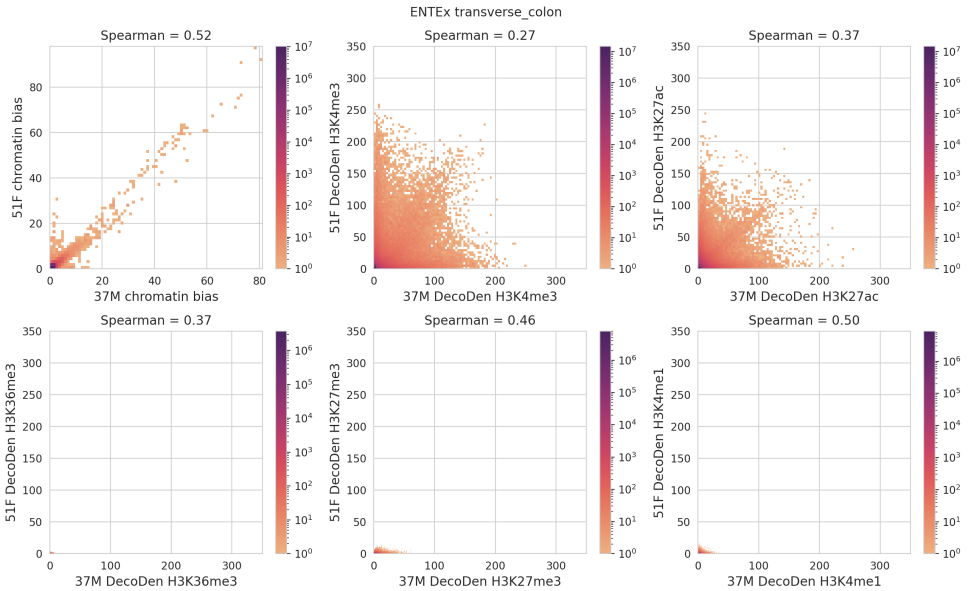

Fig. 6: **Comparison of DecoDen signal across individuals (transverse colon):** 2D histograms for DecoDen computed genome-wide signals of histone modification enrichment and chromatin bias are shown. While chromatin bias is well correlated, histone modifications show a wider range of values. Remarkably, those histone modifications that show a better signal enrichment in average genomic treatment/control coverage (see previous figure) are less correlated across individuals than those histone modifications that have a worse genomic treatment/control coverage.

the replicates for individual 51F exhibit higher variance, leading DecoDen to estimate a lower enrichment value.

Discussion

DecoDen (Deconvolve and Denoise) leverages replicates and different experimental conditions in histone modification ChIP-Seq experiments to reduce systematic noise and cell-type-specific biases. There are two major steps: non-negative matrix factorization (NMF) to deconvolve the histone-specific signal from the background, and half-sibling regression (HSR) to correct the sources of bias shared between different conditions and replicates.

NMF is used with a custom initialization scheme to optimize the estimation of cell-type-specific signals and histone modification-specific signals. The mixing matrix generated during the NMF step is biologically interpretable, quantifying the contribution of histone-modification-specific and cell-type-specific signals in the ChIP sample. This matrix can also be used to qualitatively evaluate the specificity of antibodies under different experimental conditions. By analyzing genome positions collectively rather than independently, the approach operates on a global scale rather than a local

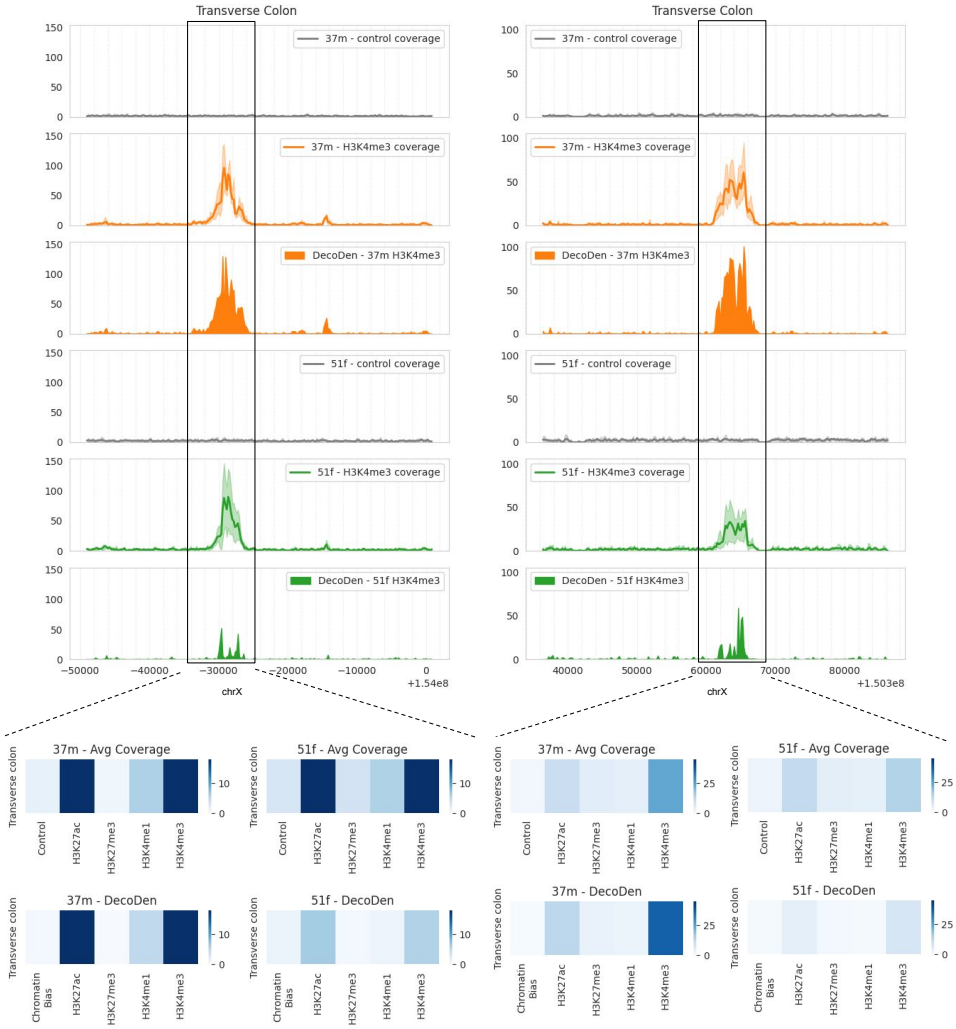

Fig. 7: Two examples of genomic loci in transverse colon where a H3K4me3 peak is more prominent in 37M compared to 51F. The histogram below shows the average coverage over different histone modifications in the highlighted genomic region.

one. Additionally, the joint analysis of all samples allows for information sharing across samples and genomic positions, enhancing the robustness of the results. The HSR step incorporates a causal graph of the data-generating process to remove cell-type-specific confounders, such as chromatin accessibility and mappability. This enables the joint analysis of histone modifications that require varying saturation depths.

In ChIP-Seq experiments, treatment and control samples are typically highly correlated. However, the genome-wide enrichment signal derived from DecoDen exhibits a lower correlation with control samples compared to other methods, highlighting its

effectiveness in de-biasing ChIP samples. By mitigating confounding effects caused by DNA fragmentation, sonication, and chromatin accessibility, DecoDen recovers previously obscured unbiased enrichment signals.

Interestingly, comparisons across experiments from different laboratories reveal higher concordance for histone modifications associated with lower-quality data. This is likely due to the pronounced similarity in chromatin bias, as lower-quality ChIP-Seq samples tend to show stronger correlations with input controls.

A similar trend emerges in the analysis of individual epigenomes within the EN-TEx dataset, where substantial variability in data quality is observed across histone modifications. To accurately quantify individual-specific epigenomic differences, further investigation using higher-quality data is essential. The effectiveness of downstream computational models, including imputation methods, is heavily dependent on data quality; thus, robust quality assessment is critical for developing reliable machine learning models in personalized epigenomics.

Conclusion

In conclusion, we introduce DecoDen, a computational method designed to share information across measurements, thereby enhancing data quality through computational means. The effectiveness of DecoDen is demonstrated by its ability to improve histone modification enrichment, as evidenced by comparisons across laboratories for the same cell type and its application to individual epigenome data from the ENTEx dataset.

Methods

Data

Simulated Data

Since true unbiased histone modification enrichment for experimental data are unknown, synthetic data using the ChIP-Seq simulation tool ChIPsim [23] was generated. ChIPsim is a flexible framework that enables simulation of a wide variety of ChIP-Seq experiments. Data was simulated for 10 sets of experiments, each with three types of histone modifications (narrow, broad and random peak) and three replicates each. The lengths of background, narrow, broad and random peaks are of 1000 bp, 450 bp, 1200 bp and 750 bp respectively. Details of the simulation procedure are in Section S2 in the Supplementary Material.

Experimental Data

E114-Jung: Deeply sequenced ChIP-Seq data from Jung et al. [20] measured on the A549 Lung Carcinoma cell line, was used for histone modifications H3K4me3 and H3K27me3 (three technical replicates each) and the whole cell extract (WCE) input sample (two replicates). Raw read data was aligned to the Hg19 reference genome.
E114-Roadmap: Raw read data for E114 cell line was obtained from the ENCODE platform and aligned to the Hg19 genome. The two histone modifications H3K4me3

and H3K27me3 had 3 and 2 replicates each, with each treatment sample having a corresponding control sample. Control samples from both assays were used.
EN-TEx: DecoDen was run on data for two individuals (37M and 51F) for two tissues (transverse colon and spleen) and for the following histone modifications - H3K4me3, H3K36me3, H3K4me1, H3K27ac and H3K27me3.

Accession numbers are provided in Section S3.2 in the Supplementary Material.

Data Preprocessing

A detailed summary of all datasets used with assays and number of replicates is provided as an additional file. The following procedure was followed when performing alignment of raw sequencing data. SAMtools [24] was used to align the data to the reference genome. Picard was used for quality control of the aligned reads. In particular, reads failing vendor quality checks, those which are PCR duplicates and unmapped reads were removed.

To generate a genome-wide enrichment signal from MACS2, the `bdgcmp` command was used to compare the lambda and treatment tracks obtained from `callpeak` command. This procedure generates a genome-wide $-\log_{10}$ p-value enrichment signal in bedgraph format. The Chipseq R package [25] was used to bin this signal for equivalent comparison with DecoDen.

DecoDen Preprocessing

DecoDen has been implemented in Python. For preprocessing, it requires a CSV file specifying details about the sequencing data, such as BAM file location, experimental condition and whether it is a treatment or control file. For each treatment condition, a single fragment length is estimated and reads are extended in the 5' to 3' direction. For input control data, the fragment length is estimated as the median of treatment fragment lengths and reads are extended equally in both directions. Next, each BAM file is normalized to have a total library size of 25 million reads. Average coverage is computed for contiguous non-overlapping genomic bins of the specified size (default size is 200). For analyses with real experimental data, the *Low Mappability* regions from the ENCODE blacklist [26] are removed. Deeptools [27] and Samtools are used internally for the manipulation of BAM files. Preprocessed data are written to disk as numpy [28] matrices, with each condition written to a separate file.

DecoDen: Non-negative Matrix Factorisation

Non-negative matrix factorisation (NMF) is a general methodology to decompose a given matrix V with dimensions $G \times N$ into two matrices W and K with dimensions $G \times l$ and $l \times N$ respectively such that:

$$V \approx W \cdot K$$

where $\cdot$ denotes the scalar product. The motivation for using NMF is to distinguish histone-specific signals from unspecific additive noise. To achieve this, all ChIP and

input measurements are analyzed simultaneously. NMF is used to estimate two quantities - First, consolidated genome-wide signal W for each assay h and second, a mixing matrix K, specifying the composition found in each replicate r. Since this step explicitly uses replicates to share information across samples, experimental noise among samples is minimized.

In DecoDen, the matrix $V \in \mathbb{R}^{G \times N}$ consists of a concatenation of treatment and input samples,

$$V_{G \times N} = \left[\mathbf{c}^{(1)} \cdots \mathbf{c}^{(r_c)} \ \mathbf{t}_{h_1}^{(1)} \cdots \mathbf{t}_{h_1}^{(r_{h_1})} \ \cdots \ \mathbf{t}_{h_k}^{(1)} \cdots \mathbf{t}_{h_k}^{(r_{h_k})} \right]$$

where $G = \frac{\texttt{genome length}}{\texttt{bin size}}$, N is the total number of samples, r_c is the number of control replicates and each histone modification h_i has a total of r_{h_i} replicates.

The l parameter is chosen as the sum of total experimental conditions present in the dataset. For example, in the case where there are ChIP-Seq experiments for two histone modifications with a control, $l = 3$. The learned signal matrix

$$\mathbf{W} = \left[\mathbf{y_1} \ \dots \ \mathbf{y_{l-1}} \ \mathbf{x} \right]$$

thus contains specific signals for each histone modification $\mathbf{y}_h = \mathbf{a} \cdot \mathbf{m} \cdot \mathbf{s}_h$, and an additional chromatin bias signal $\mathbf{x} = \mathbf{a} \cdot \mathbf{m} \cdot \mathbf{n}$, containing valuable information about common biases $\mathbf{a} \cdot \mathbf{m}$. The mixing matrix K contains coefficients , such that the the original measurements $\mathbf{t}_h^{(r)}$ can be reconstructed as linear combinations from $\mathbf{y}_h$ and $\mathbf{x}$. The biases captured in the $\mathbf{x}$ and $\mathbf{y}_h$ signals affect both control and ChIP samples, and $\mathbf{x}$ is thus used in subsequent steps to de-bias the assay-specific signals.

Non-negative matrix factorization is NP-hard in general, and convergence heuristics are dependent on initialization [29]. As the computational cost of NMF is heavily influenced by the sizes the matrix to factorize [30], a heuristic procedure was devised to perform the factorization efficiently and with interpretable structures. $100,000$ genomic bins are sampled from the data matrix as a training set. This training set is used to calculate a mixing matrix with a specified structure, which is then fixed and used to extract the signal matrix from the genome-wide data.

To ensure that the deconvolution step captures the desired information, the matrix factorization operations used to calculate the mixing matrix are split into three steps. Firstly, only the signals for the control replicates are factorized, which results in learning a cell type-specific background and the mixing matrix parameters for the input control samples. Subsequently, this background signal $\mathbf{x}$ is fixed and the mixing coefficients $k_s^{(r)}$ are extracted for the treatment sample that minimize the loss function, to "explain" as much of the treatment signal as possible using only the control signal. Afterwards, the treatment signal is subtracted from this background component and the remaining mixing coefficients jointly with the histone-specific signals $\mathbf{y}_h$ is estimated, to explain the remaining information. And finally, the hard constraints on the mixing matrix structure are relaxed to share information across experimental conditions, and to capture the imperfect specificity of antibodies. In this step, we perform NMF optimization using the previously extracted matrices as initialization values; the optimization alternates between fixing the mixing matrix to optimize the signal

matrix, and vice versa. This alternated optimization has shown empirically to better preserve the inductive biases encoded in the structure of the factorization procedure. The optimization of all the factorization steps is carried out by minimizing the KL Divergence as loss function.

In summary, the learning scheme is set up in such a way as to explain most of the genomic bins in the ChIP samples with the input sample. This is motivated by the fact that enriched regions constitute about 5-10% of the genome and most of the reads constitute the background signal. Hence, the cell-type specific chromatin background signal x in the W matrix of NMF contains information common to all replicates and conditions.

As an additional post-processing step, the signals in W are normalized so that the 98th percentile is equal to 1, and are multiplied by the corresponding components of H to maintain the reconstruction of the original replicates. This additional design choice is intended to concentrate the replicate-specific scaling factors $D_h^{(r)}$ (e.g. due to varying library sizes) in the mixing matrix coefficients, and to make the signals comparable. The choice of percentile to align to a unit value is made to avoid excessive influence of outlier values.

DecoDen: Half-Sibling Regression

Half-sibling regression [19] is a method inspired by causal inference to remove the effect of confounders. For instance, mappability $\mathbf{m}$ is a sequence-specific bias, which varies over the genome and confounds measurements at different genomic regions. It is a measure of the number of unique genome positions that a k-mer can be aligned against. Another known confounder in estimating the true enrichment of a histone modification is chromatin accessibility $\mathbf{a}$. For instance, the highest values for ChIP tracks are higher for histone marks associated with open chromatin when compared to those associated with closed chromatin (See Figure S4 in the Supplementary Material). For a given cell type, this confounder is fixed, and affects both the control sample and the histone-specific signals. In our approach, we model a cell-type-specific confounder as a combination of accessibility and mappability (Refer to the directed graph in Figure 1 C).

In addition, we make the simplifying assumption that the true underlying histone modification signal is independent of the measurement of the cell-type specific signal from the NMF step, implying $\mathbf{s}_h \perp\!\!\!\perp \mathbf{x}$. This allows us to use half-sibling regression to remove the effect of confounding factors between the ChIP signal and the cell-type specific background signal. The true histone modification signal $\mathbf{s}_h$ is estimated as

$$\log \hat{\mathbf{s}}_h = \log \mathbf{y}_h - \mathbb{E}[\log \mathbf{y}_h \mid \log \mathbf{x}]$$

As a design choice, we estimate $\mathbb{E}[\log \mathbf{y}_h \mid \log \mathbf{x}]$ using a linear regression model.

The application of HSR to logarithm-transformed signals allows us to filter multiplicative noise with better numerical stability. Since subtraction in the log scale translates to division in the linear scale, this is similar to computing fold-change. The estimated signal $\hat{\mathbf{s}}_h$ is recovered by exponentiation of the estimate from half-sibling regression.

Since the HSR step is equivalent to dividing by a confounding factor, certain genomic loci may present extreme values due to a background signal that is essentially 0. To avoid this pitfall, we bounded the divisor to a minimum value of 0.1 (i.e. capping the predictions of the fit in log scale to $\log(0.1)$), essentially ensuring that the signal is at most amplified by a factor of ten.

Non-negative matrix factorization and half-sibling regression are carried out using the Python package *scikit-learn* [31].

Identifying enriched regions

We use the estimated fold-change from the previous Half-Sibling Regression step and a fixed threshold to identify regions of enrichment. Regions that are close together are merged, and extremely small enriched regions are eliminated. Since no significance tests are done, there is no requirement to correct for multiple testing.

Training and Validation

In the case of experimental datasets, to evaluate the components of the mixing matrix that describe the proportions of each signal that compose the measured replicates, we select 400,000 genomic bins (bin-width of 200 bp) as training set from regions with average read coverage more than 1. We employed L2 regularization on both the signal matrix and the mixing matrix; to determine the weights of the regularization term in the loss function, we selected 10,000 additional bins to use as validation set to choose a sufficiently high regularization that would not adversely impact the reconstruction of the signal. The final configuration of the algorithm used a weight of 0.01 for the L2 regularization of the signal matrix and 0.001 for the regularization of the mixing matrix. For simulated data, the same regularization parameters were used. Since the simulated genomic region is much smaller than experimental data, the number of genomic bins for training was 5000.

Declarations

Ethics approval and consent to participate

All datasets used are publicly available. In particular the EN-TEx data used is open-consented and is accessible without registration. According to the EN-TEx publication, an Institutional Review Board-approved consent form was written and given to the next-of-kin of each donor. Details of the consent document can be found here - https://www.genome.gov/Pages/Research/ENCODE/GTEx_Consent_ENCODE_addendum_10-9-14.pdf

Consent for publication

EN-TEx data used is open-consented and is accessible without registration. According to EN-TEx publication an Institutional Review Board-approved consent form was written and given to the next-of-kin of each donor. Details of the consent

document can be found here - https://www.genome.gov/Pages/Research/ENCODE/GTEx_Consent_ENCODE_addendum_10-9-14.pdf

Availability of data and materials

Accession numbers for data used in provided in the supplement. DecoDen is available at https://github.com/ntanmayee/decoden.

Competing interests

The authors declare no competing interests.

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Author contribution

TN, GV and GS were involved in the formulation of DecoDen. TN and GV implemented the software. TN, GV, CC and JA performed experiments. TN, GV and GS contributed to the writing of the manuscript.

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Supplementary information

Supplementary information can be found in a separate document.

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