

Evolution of genome-wide methylation profiling technologies

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In this mini-review, we explore the advancements in genome-wide DNA methylation profiling, tracing the evolution from traditional methods such as methylation arrays and whole-genome bisulfite sequencing to the cutting-edge single-molecule profiling enabled by long-read sequencing (LRS) technologies. We highlight how LRS is transforming clinical and translational research, particularly by its ability to simultaneously measure genetic and epigenetic information, providing a more comprehensive understanding of complex disease mechanisms. We discuss current challenges and future directions in the field, emphasizing the need for innovative computational tools and robust, reproducible approaches to fully harness the capabilities of LRS in molecular diagnostics.

What is methylation?

Cytosine DNA methylation (5mC) involves the covalent modification of the fifth carbon atom of cytosine, typically in mammals in a CG dinucleotide context. This dinucleotide is depleted largely across the genome and found predominantly in clusters known as “CpG islands” (Bird 1986). Cytosine methylation is catalyzed by methyltransferases (e.g., DNMT1, DNMT3A) that transfer a methyl group from S-adenosyl-L-methionine to cytosine. Importantly, due to the palindromic nature of the CG dinucleotide, CG methylation can be retained after DNA replication by methylation of hemimethylated (i.e., one-strand methylated) DNA. While most mammalian cells exhibit only CG methylation, neurons, oocytes, and embryonic stem cells have shown DNA methylation (DNAm) in non-CG contexts, such as mCHG and mCHH, where H represents A, C, or T (Kinde et al. 2015). These are notably less mitotically active, presumably because such marks are more difficult to maintain with active replication.

Cytosine methylation plays a critical role in genomic imprinting, gene regulation, X-Chromosome inactivation (XCI), cellular differentiation, aging, and tumorigenesis. Cells have an extensive system of proteins that establish these methylation patterns through de novo methylation or demethylation, copy methylation patterns during DNA replication to sustain methylation levels, and read the DNAm states.

How is methylation measured?

Over the years, genome-wide DNAm profiling has evolved, progressing from methylation arrays to short-read whole-genome sequencing and, most recently, advancing into single-molecule profiling. These profiling methods can be broadly classified into enrichment or conversion methods. Enrichment methods (Fig. 1A) use either immunoprecipitation of methylated DNA (MeDIP) (Weber et al. 2005) or methylation-sensitive restriction enzymes (MSREs) (Khulan et al. 2006; Irizarry et al. 2008), which enrich methylated or unmethylated molecules based on size fraction-

ation (Weber et al. 2005) followed by either quantitative polymerase chain reaction (qPCR), microarrays or sequencing. In contrast, bisulfite treatment of DNA, as developed by Frommer et al. (1992) and later optimized by Clark et al. (1994), enabled quantitative nucleotide resolution of methylation. It converts unmethylated cytosine to uracil by chemical deamination, while methylated DNA remains unconverted (Fig. 1B). After polymerase chain reaction (PCR), the methylated and unmethylated bases are distinguished as cytosine (C) to thymine (T) single nucleotide polymorphisms (SNPs).

The resulting data can be used to identify methylation “epi-signatures”—distinctive patterns of DNAm differences at specific CpG sites that are associated with pathogenic variants in particular genes (Grafodatskaya et al. 2013; Barbosa et al. 2018). Illumina's Infinium MethylationEPIC array, which targets nearly a million methylation sites, is the most widely used platform for this analysis. Microarray methylation data, e.g., The Cancer Genome Atlas (TCGA) Research Network and the International Cancer Research Consortium (ICGC), have facilitated the development of clinical-grade classifiers that leverage machine-learning epigenetic signatures for diagnosing brain tumors (Wu et al. 2022) and certain Mendelian disorders (Sadikovic et al. 2020). While clinical implementation requires careful standardization of analysis pipelines and reporting frameworks, leading laboratories now offer validated testing for over 90 genes and disorders (EpiSign). Despite their diagnostic value in enhancing the genetic testing yield for undiagnosed cases (Louis et al. 2021; LaFlamme et al. 2024), these arrays are not yet routinely used in constitutional molecular diagnostics due to additional costs and labor (Sadikovic et al. 2020).

The additional steps involved in array-based epigenomic profiling have restricted its use compared to larger-scale genomics studies. For instance, the largest population study to date using epigenomic profiling using Illumina Infinium microarrays involved 32,851 participants (Min et al. 2021), compared to the UK Biobank's exome sequencing of 454,787 individuals (Backman et al. 2021) and whole-genome sequencing of 150,119 individuals (Halldorsson et al. 2022).

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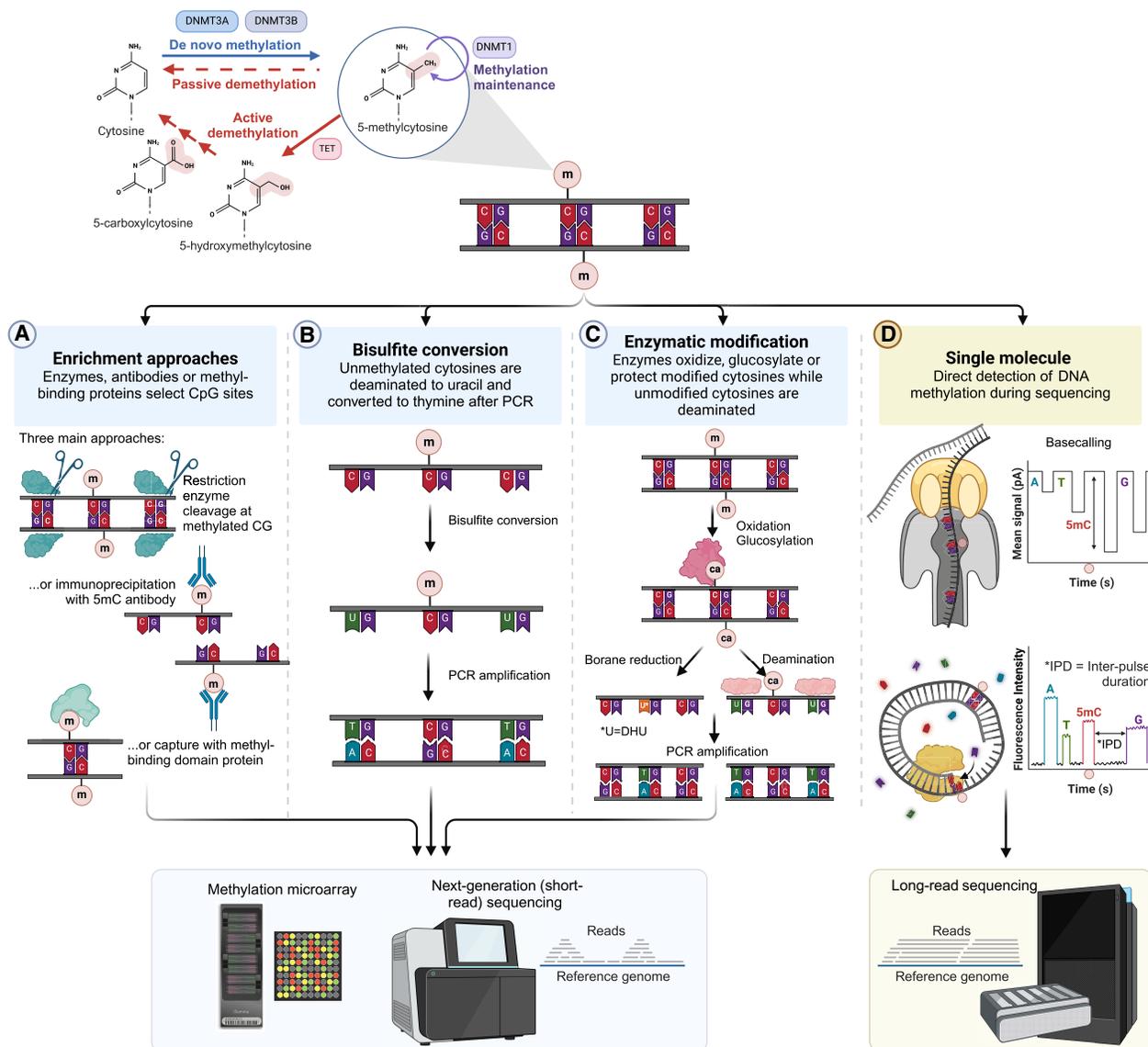


Figure 1. Methods to detect genome-wide 5mC. DNAm can be detected through enrichment, bisulfite conversion, enzymatic modification, or single-molecule approaches. (A) Enrichment methods use restriction enzymes or immunoprecipitation to separate methylated and unmethylated DNA. (B) Bisulfite treatment converts unmethylated cytosine to uracil, allowing differentiation between methylated and unmethylated DNA that can be assayed using microarrays or short-read sequencing. (C) Newer enzymatic methods use a series of proteins that oxidize and glucosylate modified cytosines, followed by deamination that is achieved either through specific enzymes or borane reduction. (D) Single-molecule methods directly measure DNAm as DNA passes through the nanopore (Oxford Nanopore, top panel) or as fluorescent nucleotides are incorporated into the growing strand by a polymerase (PacBio, middle panel). Created in BioRender. Montano, C. (2024). <https://BioRender.com/i42h077>.

Whole-genome bisulfite sequencing

Alternatively, bisulfite-treated DNA can be used directly for sequencing instead of microarrays. This technique, known as whole-genome bisulfite sequencing (WGBS), is now considered the gold standard for detecting 5mC (Cokus et al. 2008; Lister et al. 2009). With the substantial drops in sequencing cost over the past 20 years, this method has come to dominate in smaller cohort sizes. However, WGBS has several limitations: the bisulfite conversion process can degrade DNA, reduce the complexity of the genome, and complicate the alignment process, particularly in repetitive regions (Karimzadeh et al. 2018).

Methods like TET-assisted pyridine borane sequencing (TAPS) (Liu et al. 2019), New England Biolabs Enzymatic Methyl-seq (NEB's EM-seq) (Sun et al. 2021; Vaisvila et al. 2021), and biomodal's duet multiomics evoC (Füllgrabe et al. 2023) offer alternative approaches to WGBS by using enzymatic conversions and avoiding harsh bisulfite treatment which can degrade and fragment DNA (Fig. 1C). These methods use enzymes to oxidize, glucosylate, or protect modified cytosines, followed by deamination of unmodified cytosines. Compared to bisulfite methods, enzymatic methods provide larger library insert sizes, reduced DNA degradation, more uniform and less biased GC coverage, and even the ability to differentiate between 5mC and 5-hydroxymethylcytosine (5hmC) in some cases.

Single molecule

Direct DNA sequencing using long-read sequencing (LRS) platforms like Oxford Nanopore Technologies (ONT) and Pacific Biosciences (PacBio) offers new opportunities to uncover novel genomic and epigenomic mechanisms implicated in disease. Sequencing reads generated by LRS not only detect single nucleotide variations (SNVs) and structural variations (SVs) but also probe previously uncharacterized repetitive regions and regions with atypical GC content, identify segmentally duplicated genes, and enable the phasing of reads (Logsdon et al. 2020). The phasing specifically allows for the assignment of haplotypes to pathogenic variants, enhancing diagnostic utility. LRS advancements enable the simultaneous measurement of DNAm profiles alongside genetic data, enhancing our understanding of methylation's role in diseases and its potential as a biomarker for Mendelian conditions (Fig. 1D; Flusberg et al. 2010; Simpson et al. 2017). But in contrast to microarray and short-read sequencing methods, DNAm data are inherently generated as a by-product of LRS, requiring no additional processing steps and thus facilitating its integration into existing genomic diagnostic workflows. Ongoing improvements in accuracy, throughput, and cost reduction further broaden LRS's applications across model and nonmodel organisms. With decreasing costs, LRS is now practical for generating comprehensive genomic and epigenomic profiles of patients. Instances of ultra-rapid sequencing in critical care settings have demonstrated the effectiveness of same-day LRS workflows for clinical genetics, as shown by Gorzynski et al. (2022) and Goenka et al. (2022).

LRS technologies have now reached levels of accuracy, scalability, and cost-effectiveness that support their application in detecting variants across populations (De Coster et al. 2021). Major initiatives are demonstrating this capability at scale: deCODE has generated LRS data from 7179 Icelanders (Stefansson et al. 2024), while the Human Pangenome Reference Consortium (HPRC) has released 47 haplotype-resolved human genomes from diverse backgrounds (Liao et al. 2023). Standardizing the workflows, Kolmogorov et al. (2023) have developed a wet laboratory and computational workflow tailored to both cell lines and brain tissue samples. Multiple efforts are now generating crucial control data sets: the 1000 Genomes Project ONT Sequencing Consortium is producing LRS data from 1kGP samples to aid in filtering and prioritizing SNVs and SVs (Gustafson et al. 2024), while the All of Us (AoU) initiative has begun a long-read arm to sequence blood samples from Americans from diverse backgrounds, providing an essential population-level reference for comparing clinical samples. For phase I, they have sequenced 1027 individuals; phase 2 expands sequencing to 14,000 individuals and will incorporate methylation data, generating vast amounts of DNAm data as a “free” by-product of LRS. All of these efforts are generating vast amounts of DNAm data as a “free” by-product of LRS. However, researchers must ensure they conserve base modification information along with the sequencing data, as processing this methylation data requires additional computational tools. Luckily, this is aided and abetted by new standards of encoding methylation information directly into the alignment files (BAMs) as sequence tags.

LRS is changing the landscape of molecular diagnostics

Molecular diagnosis is crucial for managing genetic diseases, offering confirmation, specialized care, risk-based management, in-

formed reproductive choices, and, in some cases, personalized therapies. LRS provides a single assay that can simultaneously measure SNV, SV, copy number variation (CNV), and epigenetic alterations, all with a single sequencing run. With costs continuing to come down and the demonstrated enhanced diagnostic yield (Mastrososa et al. 2023), LRS could provide a clear path forward. Here, we focus on diagnostic applications of haplotype-aware methylation analysis:

Imprinting disorders

Genomic imprinting refers to the parent-of-origin specific expression of genes; the classic example is the *H19/IGF2* locus with paternal expression of *IGF2* while the maternal copy is silenced (Monk et al. 2019). This is often regulated by epigenetic marks, including DNAm and histone posttranslational modifications. In the loss of imprinting disorders, either the active allele is silenced or the normally silent allele is abnormally activated (Eggermann et al. 2015). The underlying molecular defects are diverse, including pathogenic variants in imprinted genes, CNVs, uniparental disomy (UPD), and aberrant methylation over imprinting control regions. Traditionally, diagnosing these disorders required a stepwise combination of methylation (with methylation-specific PCR and MLPA), CNV (with oligo-SNP arrays and MLPA), single gene and microsatellite analysis, and often parental testing for variant phasing. While methylation-sensitive MLPA (MS-MLPA) is now the first-tier test, it is typically limited to single-locus analysis and cannot differentiate between UPD and imprinting defects, requiring additional assays (Grafodatskaya et al. 2017). In contrast, LRS provides a comprehensive solution by simultaneously detecting all types of genetic and epigenetic variation, phasing variants, and distinguishing maternal and paternal haplotypes based on methylation patterns at imprinted loci (Fig. 2A; Paschal et al. 2025). This capability is crucial for identifying multilocus imprinting disturbance (MLID), a condition that single-locus tests would miss (Sanchez-Delgado et al. 2016). Accurate molecular diagnosis using LRS is vital not only for clinical management but also for monitoring tumor risk associated with some imprinting disorders.

Miller et al. (2022) were among the first to demonstrate the utility of targeted LRS in investigating imprinted loci. They studied a family with autosomal dominant pseudohypoparathyroidism type 1b (PHP-1b) demonstrating the loss of methylation in *GNAS* was due to a maternally inherited retrotransposon insertion, highlighting the ability to detect both structural variants and methylation changes in a single assay. Yamada et al. (2023) further explored the diagnostic potential of targeted LRS in Prader-Willi syndrome (PWS) and Angelman syndrome (AS), two disorders caused by aberrant imprinting in the 15q11.2–q13 region (Yamada et al. 2023). They detected abnormal methylation patterns in the *SNRPN* gene, crucial for differentiating between PWS and AS, while simultaneously identifying the underlying pathogenic mechanisms, including uniparental isodisomy, in a single assay. A larger study by Paschal et al. (2025) extended the application of LRS to whole-genome analysis in a larger cohort of individuals with known PWS or AS. They found 100% concordance with standard clinical testing and could even phase the 15q11–q31.1 region to measure the likely parent of origin of *UBE3A* variants without parental samples. To give an easily interpretable report, Bækgaard et al. (2024) recently developed a tool for analyzing and reporting on 14 imprinted regions. They demonstrated this on samples from Beckwith–Wiedemann, Angelman, and Prader–Willi syndromes. While these studies are promising, further validation of LRS is

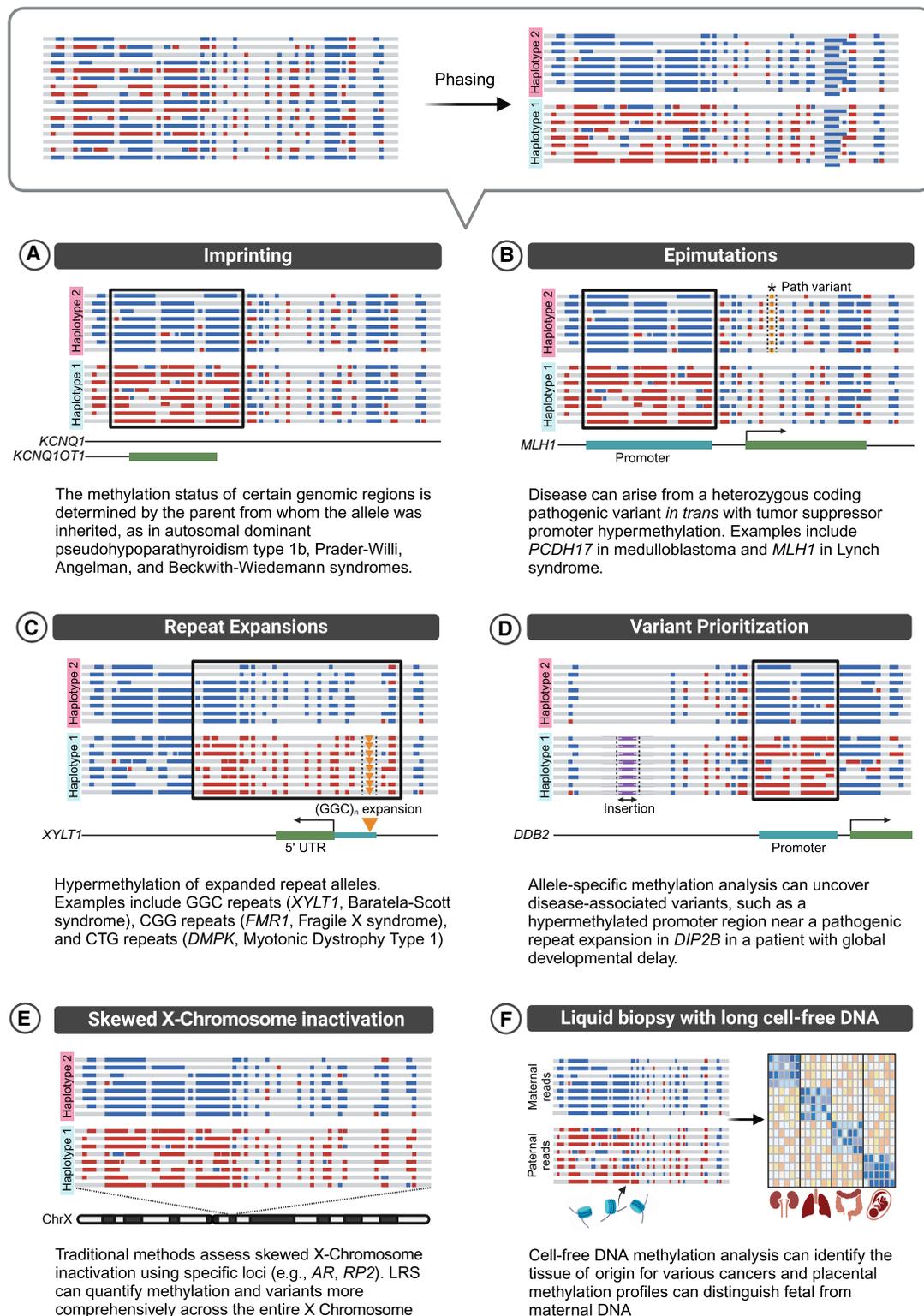


Figure 2. Diagnostic applications of haplotype-aware methylation analysis. Haplotype assignment after phasing significantly enhances the diagnostic utility of LRS. By enabling the simultaneous detection of SNVs, SVs, CNVs, and DNA modifications, it allows disease mechanisms that previously required separate specialized tests to be studied under a single, unified approach, such as imprinting (A), epimutations (B), and repeat expansions (C). It also facilitates variant prioritization (D), enables the investigation of skewed XCI where, instead of mixed inactivation, one haplotype is inactivated consistently (E), and can even be applied to study cell-free DNA (F). Created in BioRender. Montano, C. (2024). <https://BioRender.com/h78t893>.

needed to establish minimum coverage requirements, sensitivity, and specificity in other imprinted regions and for mosaic alterations for clinical applications.

Epimutations

In genomic diagnostics, it is crucial to determine if variants occur in *cis* (same chromosome) or in *trans* (opposite chromosomes). This is particularly valuable for classifying variants according to ACMG guidelines, where detecting variants in *trans* provides stronger evidence of pathogenicity (Richards et al. 2015). In the case of recessive disorders, where two malfunctioning gene copies are required to cause disease, knowing whether two heterozygous variants are in *cis* or *trans* helps determine if both variants are harmful. For example, a variant in *trans* with a pathogenic variant can be considered as evidence of pathogenicity, whereas if this variant is found in *cis*, it is most likely benign. In contrast, for dominant disorders, where a single pathogenic variant is sufficient to cause disease, the presence of a second variant in *trans* with the pathogenic variant typically indicates benign impact. Traditionally, this required testing parental (or offspring) samples to establish variant inheritance and infer phasing, which can be challenging when familial samples are unavailable. LRS simplifies this process by directly covering both variants in a single haplotype-resolved read, allowing immediate *cis/trans* determination (Fig. 2B; Conlin et al. 2022).

The unique combination of phasing and methylation detection offered by LRS enables the identification of epimutations. While the role of epimutations in disease has been recognized for decades, their identification previously required separate, specialized testing (Hitchins et al. 2007). Most epimutations result in epigenetic silencing, frequently through promoter hypermethylation, mimicking the effects of a loss-of-function coding variant in the opposite allele. For example, promoter hypermethylation can serve as the “second hit” in tumors with heterozygous germline variants (Hitchins 2015). Rausch et al. (2023) demonstrated promoter methylation of the tumor suppressor *PCDH17* in medulloblastoma using LRS, underscoring the importance of LRS in elucidating the complex interplay of genetic and epigenetic factors in cancer development. In cancer predisposition disorders like Lynch syndrome, constitutional *MLH1* promoter hypermethylation acts as a “first hit,” requiring only a somatic “second hit” for tumor development. Nakamura et al. (2024) used LRS to evaluate patients with suspected hereditary tumor predisposition syndromes for allele-specific methylation differences, identifying constitutional *MLH1* promoter hypermethylation in a patient with Lynch syndrome after previous uninformative genetic testing. Similarly, O’Neill et al. used LRS to confirm Lynch syndrome in a patient by detecting constitutional *MLH1* promoter methylation in blood. Somatic loss of heterozygosity (LOH) in the patient’s tumor led to the loss of the wild-type *MLH1* allele, leaving only the methylated allele (O’Neill et al. 2024).

Repeat expansion disorders

LRS represents a significant advancement in diagnosing nucleotide repeat expansion disorders, which are notoriously difficult to identify and require multiple tests to characterize fully. Though PCR-based methods, such as genotyping, repeat-primed, and methylation-specific assays, have largely replaced the need for Southern blotting, they still need to be designed specifically for each repeat (Spector et al. 2021). However, these assays are technically challenging due to high GC content, repeat size poly-

morphism, and repeat sequence homology, requiring careful controls and often challenging to measure extreme length values (e.g., >250 CGG for *FMRI* repeats) (Chen et al. 2011). While genotyping software has facilitated the simultaneous detection of multiple tandem repeats using short reads, the repeat lengths require sufficient coverage at the locus and are estimated rather than precisely measured (Dolzhenko et al. 2017; Ibañez et al. 2022). In contrast, LRS provides not just length measurements as capillary electrophoresis does but also methylation and sequencing information (Fig. 2C). LRS data identifies polymorphic repeat counts—even over large and complex expansions that elude standard molecular testing—as well as methylation and even sequence variations within the repeats, all from one assay. This includes detecting repeat interruptions that stabilize alleles and protect against further expansion, allele-specific DNAm, and somatic mosaicism, making LRS a powerful tool for uncovering the epigenetic regulation of such repeats.

This comprehensive approach has not only improved the diagnosis of known repeat expansion disorders but has also contributed to the discovery of novel ones (Gall-Duncan et al. 2022). In Baratela–Scott syndrome, commonly caused by the expansion and methylation of GGC repeats in *XYLT1*, LRS identified methylation of the haplotype containing the permutation allele in some reads from a proband’s mother (Miller et al. 2021). In Fragile X syndrome (FXS), expanded (>200) CGG repeats trigger hypermethylation of the X-linked *FMRI* promoter, resulting in gene silencing (Hunter et al. 1998). Notably, hypermethylation and repeat size do not always correlate perfectly, as some individuals with full mutation alleles lack promoter methylation and exhibit milder phenotypes (Tak et al. 2024). Conversely, we encounter premutation (~55–200) alleles, which pose a risk of increasing in length during reproduction but are not yet at the disease threshold. These alleles often have altered methylation, challenging to measure with methylation-sensitive restriction-based assays, but which has shown an association between repeat length, methylation percentage, and phenotype severity (Pretto et al. 2014). Stevanovski et al. (2022) further validated this approach, demonstrating hypermethylation in both full mutation and premutation carriers. Similarly, Rasmussen et al. (2022) discovered that in patients with Myotonic Dystrophy Type 1 (DM1), hypermethylation of CTG repeats was observed only in the full-penetrance allele of *DMPK* (with the shortest allele detected in the study having 142 repeats). In these cases, hypermethylation of the expanded allele was more evident when allele-specific analysis was performed.

Variant prioritization in rare disease

Allele-specific methylation analysis is also helpful in identifying and prioritizing previously missed SVs associated with methylation changes (Fig. 2D). In a large rare disease cohort, Cheung et al. (2023) discovered a hypermethylated region adjacent to a previously missed pathogenic repeat expansion in the *DIP2B* gene in a proband with global developmental delay. They also identified other genetic variations (insertions, SNVs, SVs, duplications, deletions) occurring in *cis* with proximal regulatory element hypermethylation and predicted to disrupt regulatory element activity.

X-Chromosome inactivation

Allele-specific methylation is a critical mechanism in XCI, a dosage compensation process ensuring a single active X Chromosome in both XY and XX individuals (Lyon 1962). In typical XX

individuals, one X is randomly silenced in each cell during development, with methylation maintaining gene repression on the inactive X (Xi). This random inactivation creates a mosaic of cells with either maternal or paternal X activation, and distinguishing the active X (Xa) and Xi in this mosaic cannot be done using SNPs alone. The gold standard method uses MSREs and PCR to assess methylation at the androgen receptor (*AR*) (Allen et al. 1992) and the *RP2* activator of *ARL3* GTPase (*RP2*) gene (Machado et al. 2014), utilizing their polymorphic repeats for parental allele identification (Caylor 2023). The ratio of inactivation between the two alleles can determine whether XCI is random (balanced) or skewed (nonrandom) (Amos-Landgraf et al. 2006). Skewed XCI can arise from various factors, including cell selection bias in carriers of X-linked pathogenic variants (Migeon 2020), secondary selection in X Chromosome rearrangements, or clonal populations in cancer, and can be informative for genetic counseling and testing (Amos-Landgraf et al. 2006).

We can quantify the entire X Chromosome with long reads measuring the level of methylation and genomic variants to gain allele-specific information (Fig. 2E; Lee et al. 2020). This provides a far more quantitative and comprehensive view than targeting a few genes (Johansson et al. 2023), enabling investigation of severely skewed inactivation cases, potentially uncovering previously missed X-linked pathogenic variants or X Chromosome rearrangements. This can include genes subject to or escaping XCI, satellites (Gershman et al. 2022), or focusing on the most informative CpG islands (Gustafson et al. 2024). LRS allows direct detection of repeat counts combined with methylation over *AR* or *RP2* CpG islands (Johansson et al. 2023) or even using chromatin accessibility (Lee et al. 2020; Vollger et al. 2025).

Long cell-free DNA

Cell-free DNA (cfDNA) fragments circulating in bodily fluids like plasma and urine carry unique methylation patterns, acting as molecular fingerprints that reveal their cellular origins. Scientists have developed highly specific “liquid biopsies,” noninvasive biomarkers that identify the DNA’s tissue or cell-type source by analyzing cfDNA methylation patterns (Yu et al. 2023a). This has led to applications in prenatal screening, where the methylation profile of fetal cfDNA correlates with placental methylation, allowing for the differentiation of maternal from fetal cfDNA without depending on genotypic information (Sun et al. 2015). Methylation patterns in circulating tumor DNA (ctDNA), analyzed through unique methylation signatures, are also emerging as powerful tools for cancer detection, enabling researchers to pinpoint the origin of a tumor, determine tumor burden, and even identify specific cancer types. Historically, this was done by examining differentially methylated loci using microarrays (Moss et al. 2018) or bisulfite sequencing (Guo et al. 2017) within the cfDNA, which offer superior accuracy compared to traditional methods relying on SNV. Multiple studies have revealed the predominance of tumor-derived DNA in the cfDNA pool of various solid cancers and have demonstrated the utility of methylation for estimating tumor load and identifying the tissue of origin across a wide range of cancer types (Guo et al. 2017; Moss et al. 2018; Liu et al. 2020). Enrichment strategies like cfMeDIP have been used to focus methylation profiling on cfDNA to establish cancer-specific patterns for early detection and diagnosis (Shen et al. 2018).

Although most cfDNA studies have focused on shorter sequences, analyzing longer cfDNA fragments with LRS offers distinct advantages due to the increased number of CpG sites,

improving the accuracy of tissue-of-origin determination (Fig. 2F). This enhanced analysis has shown promising results in diverse applications, including identifying the parental origin of fetal cfDNA (Yu et al. 2021), determining the tissue of origin in various cancers (Choy et al. 2022; Lau et al. 2023), and monitoring tumor burden (Katsman et al. 2022). Analysis of tissue origin using single-molecule methylation patterns demonstrated similar performance on ONT and PacBio platforms (Yu et al. 2023b). Finally, even the size of cfDNA can be telling—studies have shown differences in cfDNA length—e.g., from normal to cancer samples (Cristiano et al. 2019).

Biological and technical challenges in methylation analysis using LRS

Though the development and recent price drops in LRS technology provide unique opportunities, they also present unique challenges. With this new potential wealth of genomics data, one has to be careful to consider the epigenetic setting of samples for experimental design and interpretation

Epigenetic experimental design

While genomic studies can reveal identical pathogenic variants in the germline from any sample, epigenomics studies require more attention to the sample source, as the epigenome is highly dynamic with substantial cell-type and tissue specificity (Laird 2010), particularly around noncoding regions of the genome (Kerr et al. 2023). Though large-scale genomic studies will indeed include epigenetic data, this data will likely be confined to easily accessible sample types, e.g., blood and saliva.

Tissue-specific methylation profiles are often the strongest epigenetic signature observed, even above disease or individual-specific epigenetic differences. The most significant methylation differences often occur between distinct tissues within an individual (Rakyan et al. 2008; Lokk et al. 2014; Loyfer et al. 2023). Even within the same tissue, cell heterogeneity and varying cell-type proportions can profoundly influence the observed epigenetic patterns, potentially leading to an underestimation of DNAm (Houseman et al. 2012; Guintivano et al. 2013; Jaffe and Irizarry 2014).

This fundamental tissue and cellular heterogeneity necessitate careful experimental design for epigenomic studies. For instance, LRS analysis of fibroblasts and whole blood from the same individual might identify identical pathogenic variants, yet their respective epigenomic signatures, and even disease-specific differences, will likely differ substantially. Tissue-specific data, as in a recent NIH CARD study (Kolmogorov et al. 2023), can offer valuable insights. But even in this case, the heterogeneity of brain tissue complicates the epigenetic analysis of shifts within specific cell populations, such as neurons. Other studies (Montaño et al. 2013; Rizzardi et al. 2019) have demonstrated that measuring more subtle epigenetic differences requires sorting of specific cell types. Researchers must establish comprehensive baseline epigenetic profiles of relevant tissues from unaffected individuals. Disease studies should then use biological replicates matched as closely as possible for age, sex, and tissue composition to these baseline samples. Tissue samples should either be sorted into specific cell populations or, at minimum, undergo careful profiling to determine their cellular composition, as cellular heterogeneity between samples can mask subtle but important epigenetic changes.

This underscores the importance of validating tissue-specific epigenetic signatures for each condition under investigation. Beyond tissue type, factors such as age, sex chromosome complement, and environmental exposures (e.g., smoking) can also significantly influence the epigenome (Michels et al. 2013). Consequently, robust experimental design for epigenomic studies requires large, age- and sex-matched negative control cohorts (Chater-Diehl et al. 2021), unlike the traditional parent-proband trio analysis typically used in genetic studies.

Technical challenges

Though LRS is maturing as a platform, there are still significant growing pains. Differences in methylation calls between ONT and PacBio, chemistry versions, and methylation calling algorithms require careful consideration when comparing data across platforms (Genner et al. 2024; Sigurpalsdottir et al. 2024). Updates to the software and pore chemistry can also cause shifts—usually small ones, but shifts which may be important when comparing results within large cohorts. This is a significant concern when compared to the relative stability of bisulfite-based sequencing or microarray methods. Batch effect correction between chemistries and methods is necessary to compare technologies, chemistries, and basecallers.

While batch effects are well-studied in methylation arrays with established quality control (QC) pipelines using methods like surrogate variable analysis (SVA) and remove unwanted variation (RUV), standard pipelines for sequencing methylation data, especially LRS methods, still require development and benchmarking. To account for this currently, one needs to use purposeful study design (sample randomization, control samples) and QC metrics like principal component analysis (PCA) on the resulting data. Current work using resources like GIAB and 1000 Genomes data sets as benchmarking standards could result in the establishment of strong methods here, though comprehensive validation across methylation calling methods is still needed. Internal controls such as expected allele-specific methylation patterns or methylation state at housekeeping genes may be useful to normalizing methylation calls across different technologies and runs.

Furthermore, LRS native methylation methods, rather than providing a C or a T call as bisulfite sequencing does, give a probability score that the base is methylated. These scores can be thresholded and generally show high concordance with traditional methylation calling, but there may be biases in methylation calls depending on the local sequence context. To account for technical variability, it is crucial to define sequencing metrics and depth cut-offs for calling modification events or, at the very least, report these details in the methods section. Unfortunately, established tools for correcting batch effects in LRS methylation data are currently lacking (Kong et al. 2023).

Cancer and disorders with somatic mosaicism present unique challenges, requiring specialized analysis tools to address issues like variant allele frequency thresholds to detect cellular mosaicism, intratumor heterogeneity, normal cell contamination, and variations in tumor methylation levels. To overcome some of these obstacles, targeted sequencing of specific regions using Cas9-targeted sequencing (Tsai et al. 2017; Höijer et al. 2018; Gilpatrick et al. 2020), adaptive sampling (Miller et al. 2021), or hybridization capture (Mahmoud et al. 2024) has been used to isolate and analyze specific genomic regions of interest at higher coverage depth, akin to deep high-throughput sequencing panels. While standard methylation detection resolution is limited to 1/coverage levels

(~5% for an average 30× sequencing run), Ziller et al. (2015) demonstrated that even lower per-sample coverage (5–15×) can be sufficient to detect regional methylation differences between groups, especially when using more replicates.

Data storage challenges

The storage and retention of raw sequencing data presents significant challenges for LRS methylation analysis. While raw signal files contain valuable information that enables rebasecalling with improved algorithms, their size makes long-term storage impractical. For example, ONT POD5 files from a single PromethION flow cell can exceed 1TB. This mirrors the historical practice of retaining Illumina BCL files, which long since have been discarded immediately after runs; the cost-benefit analysis increasingly favors resequencing over maintaining such large data archives. PacBio presents similar considerations. Kinetics and subreads are typically no longer stored directly due to the large file sizes from PacBio.

For methylation analysis specifically, the key decision point comes during basecalling. Advancements in BAM file specifications now allow for efficient storage of modification information directly within a BAM file itself using modification call (MM) and its associated probability (ML) tags for downstream analysis. This approach results in files ~100 GB in size—a significant but manageable footprint. While traditional FASTQ files remain a mainstay of sequencing workflows, they strip out this crucial methylation information, making them unsuitable for methylation analysis despite their smaller size.

Analysis of LRS methylation data presents unique opportunities

Analyzing DNAm data from LRS demands innovative computational and statistical approaches. Though one *can* take the methylation frequency files generated from pileups of methylation calls from LRS data and process them the same way one would a WGBS data set or even look at individual CpG methylation frequency like a microarray, this is throwing away some of the novelty of LRS data.

LRS has two significant virtues that are neglected by conventional analysis pipelines. First, it is a single molecule. Each LRS read represents one molecule from one allele from one cell in a sample. Typically, there is no amplification, so the measurements are a sampling of the molecules present in the DNA mix. The methylation patterns along the molecule can be phased along with the genotype to produce allele-specific methylation information—allowing us to interrogate methylation associated with specific alleles. It can even be phased to group with specific somatic mutations, allowing us to observe genomic and epigenomic interactions.

We lack robust statistical or analytical tools that identify loci with different methylation between germline alleles or between mutated and reference molecular groups. The use of simple Fisher tests to compare methylation levels is problematic, as single CpG analysis is susceptible to noise, which could lead to false conclusions. To address this, smoothing techniques (Hansen et al. 2012) are often used to exploit the natural correlation between adjacent CpGs, which helps reduce noise and improve the detection of differentially methylated regions (DMRs), especially in areas with nonuniform methylation.

These comethylation patterns, known as “methylation haplotype blocks” (Guo et al. 2017), are valuable for identifying tissue-

and cell-specific signatures, facilitating cell-of-origin deconvolution in bulk tissue (Loyfer et al. 2023; Unterman et al. 2024). Although this approach can work with short-read sequencing, longer reads significantly enhance the likelihood of capturing cell-type-specific DMRs, thereby improving the effectiveness of deconvolution. However, identifying allele-specific DMRs requires more sophisticated methods.

However, there remains a need to establish appropriate thresholds for methylation frequency and region size while also developing haplotype-aware tools for novel DMR discovery. The inherent noise in methylation data, combined with reduced coverage due to haplotype splitting, remains a challenge for clinical applications. Moreover, linking haplotypes across multiple samples to define the *same* haplotype group is particularly challenging, and may require graph genome approaches or *k*-mer analyses to effectively connect haplotypes across larger data sets (Liao et al. 2023).

We can also use the single molecules to measure epigenetic and genetic interactions *along* a molecule. Consider that the length of LRS reads will often enable simultaneous measurement on a single molecule of enhancers and promoters, which are typically too distal to directly measure with short-read sequencing. This capability allows researchers to capture the regulatory landscape holistically, linking regulatory elements with their target genes on the same read. For instance, Nanopore sequencing has been used to phase enhancers and promoters, revealing allele-specific regulatory interactions that are crucial for understanding gene expression regulation and epigenetic modifications (Gigante et al. 2019). Additionally, this approach facilitates the study of chromatin interactions and the 3D genome architecture, providing insights into how distant regulatory elements come together to control gene activity (Lee et al. 2020; Zhong et al. 2023). Methods like nanoNOMe (Lee et al. 2020), Fiber-seq (Stergachis et al. 2020), DiMeLo-seq (Altemose et al. 2022), and SAMOSA-tag (Nanda et al. 2024) use methyltransferase enzymes to encode epigenetic information into DNA molecules, enabling LRS to simultaneously map chromatin accessibility, protein binding, and DNA modifications at single-molecule resolution. Such detailed mapping of regulatory landscapes is essential for identifying the mechanisms underlying complex traits and diseases and improving the accuracy of genomic and epigenomic annotations (Akbari et al. 2021).

Methylation deconvolution of individual reads could harness the single-molecule resolution of LRS to disentangle complex methylation patterns within heterogeneous samples. By analyzing methylation signals at the level of individual molecules, it could be possible to identify cell-type-specific methylation signatures and quantify allele-specific methylation variations. Such methods could leverage the read length of LRS to capture contiguous methylation states across entire genomic regions, potentially enabling the precise reconstruction of methylation landscapes often obscured in bulk analyses. Advanced computational tools are required to interpret these high-resolution methylation profiles accurately, which could offer new insights into epigenetic regulation and disease mechanisms.

Improved mappability through repeats and other hard-to-map regions is a significant advantage of LRS technologies (Ebbert et al. 2018; Giesselmann et al. 2019; Stevanovski et al. 2022; Dolzhenko et al. 2024). LRS platforms, such as ONT and PacBio, produce reads that span thousands of base pairs, allowing for the accurate sequencing of complex regions like tandem repeats, segmental duplications, and regions with low SNP density.

Unlike short-read sequencing, which struggles with these regions, LRS provides a clearer and more comprehensive view of the genome. This capability is particularly valuable for detecting variations within repeats, such as those found in repeat expansion disorders, and for achieving precise haplotype phasing. Enhanced mappability improves variant detection and epigenetic profiling, facilitating a deeper understanding of genetic and epigenetic mechanisms underlying various diseases.

Accurate haplotype assignment and phasing tools continue to evolve, combining both genetic and epigenetic data. Tools like NanoMethPhase (Akbari et al. 2021) (for ONT), PRINCESS (Mahmoud et al. 2021) (for both ONT and PacBio), and csmeth (Ni et al. 2023) (for PacBio) leverage SNPs and methylation for phasing, enabling accurate, haplotype-resolved variant and methylation calls. While these approaches face challenges in heterogeneous tissue samples with different methylation profiles, they also could offer unique advantages, particularly in determining haplotype parent-of-origin without requiring trio sequencing data. Tools like MethPhaser (Fu et al. 2024) attempt to extend phase blocks using methylation data, though improvements may be modest in regions with few allele-specific methylation sites.

The potential of LRS remains constrained by the need for specialized tools and methodologies, particularly those focused on haplotype-aware analysis and noise reduction. Both standardization and benchmarking are essential for LRS to become a routine clinical tool. Although core technologies and algorithms are steadily improving the accuracy of LRS data, clinical laboratories require stable workflows to comply with stringent regulatory requirements. Additionally the current reliance on high-quality DNA, often obtained from frozen blood samples, presents logistical challenges for clinics without freezer storage. Other tissue specimens (e.g., biopsies) may also not offer the micrograms required for LRS methods. Thus, validating LRS in more readily accessible samples, such as saliva or buccal tissue, is crucial for broader clinical adoption.

Competing interest statement

The authors declare no competing interests.

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