Minireview Article

**The Intimate Read: Nanopore Sequencing and the Philosophical Recalibration of Life's Code**



**ABSTRACT**

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| Nanopore sequencing represents a paradigm shift in how we read and interpret the genetic and epigenetic information of living organisms. Unlike traditional sequencing methods that rely on amplification and fragmentation, nanopore sequencing enables the direct, real-time analysis of native DNA and RNA molecules, preserving structural integrity and epigenetic modifications. This technical advancement redefines biological epistemology by offering a more direct, individualized, and contextualized reading of genetic information. Long-read sequencing provides unprecedented insight into genome architecture, transcript diversity, and epigenetic states, challenging traditional notions of a static reference genome and instead revealing the dynamic, fluid nature of genetic expression.  Beyond its technical implications, nanopore sequencing provokes profound philosophical and ethical considerations. It alters our understanding of genetic identity, highlighting molecular individuality and the variability inherent in life’s code. Its portability democratizes access to sequencing, enabling decentralized applications in medicine, ecology, and forensic science, yet also raising concerns about data interpretation, privacy, and the equitable distribution of sequencing resources. The immediacy of real-time sequencing shifts scientific temporality, fostering rapid decision-making in fields such as clinical diagnostics and epidemiology while also posing risks associated with premature or incomplete analyses.  This fusion of biological and digital realms underscores the transformative potential of nanopore sequencing not just as a tool for molecular biology, but as a reconfiguration of how we perceive, interact with, and ultimately govern biological information. As this technology continues to evolve, its broader implications—ontological, ethical, and epistemological—demand critical examination to navigate the responsibilities that come with our newfound ability to read life’s code with unprecedented intimacy and speed. |

*Keywords:Nanopore sequencing Epistemology of genomics Real-time molecular analysis Genetic individuality*

**1. INTRODUCTION**

Imagine holding a thread, impossibly fine, pulled from the intricate tapestry of life itself. Imagine drawing this thread – a single molecule of DNA or RNA – through a pore no wider than a few billionths of a meter (Kasianowicz et al., 1996). As it passes, you decipher its pattern, not by shattering it into fragments and painstakingly reconstructing the message, but by listening, in real-time, to the subtle electrical whispers generated by each constituent bead. This is not science fiction; it is the essence of nanopore sequencing, a technology that, in its current state of maturity and proliferation (as of March 2025), is doing more than just accelerating biological discovery (Deamer et al., 2016). Since the commercial introduction of Oxford Nanopore Technologies in 2014 (ONT), it is acting as a profound philosophical catalyst, compelling us to re-examine our conceptions of biological information, the dynamic nature of the genome, the very temporality of scientific observation, and the ethical contours of knowledge and control in the age of molecular intimacy. Nanopore sequencing has evolved from a proof-of-concept technology with error rates between ∼5% and 40% error (Goodwin, et al., 2015) to a clinically viable platform achieving >99.9% precision (Su et al., 2025)

ONT itself fundamentally from its predecessors. Sanger sequencing, the meticulous craftsman, reads short stretches with high fidelity but low throughput. High-throughput short-read sequencing (like Illumina), the industrial powerhouse, generates billions of accurate snippets but requires complex assembly, often losing long-range context and struggling with repetitive regions (van Dijk et al., 2018). Nanopore, in contrast, offers the "long read." By threading native, often unamplified, single molecules through a protein or solid-state pore embedded in a membrane, it generates reads tens or hundreds of thousands, even millions, of bases long (Jain et al., 2018a). It can do this in real-time, on devices ranging from benchtop behemoths to palm-sized units plugged into a laptop (Jain et al., 2016), and crucially, it can directly sequence RNA and detect base modifications without laborious chemical treatments (Garalde et al., 2018; Simpson et al., 2017).

These technical capabilities are not mere incremental improvements; they represent qualitative shifts that ripple outwards, challenging long-held assumptions and opening new philosophical vistas (Leggett & Clark, 2017). We must ask: What does it mean to know the code of life in this way? How does this intimate, dynamic, and contextualized reading change our understanding of what life is? And what responsibilities arise when the ability to perform this reading becomes increasingly portable, immediate, and pervasive?

**2. The Epistemological Aperture: Knowing Life Directly, Individually, and Contextually**

At its heart, science is a knowledge-generating project – a way of knowing. Nanopore sequencing reshapes biological epistemology in several key ways. Firstly, it introduces a profound sense of directness. While all sequencing involves transduction – converting molecular properties into interpretable signals – nanopore minimizes the intermediate steps of fragmentation, amplification (which can introduce bias), and chemical conversion (like bisulfite treatment for methylation) (Branton et al., 2008). Reading the fluctuating ionic current as a native molecule traverses the pore feels conceptually closer to observing the molecule itself (Akeson et al., 1999). This fosters an intuition of less mediated knowledge, even though the interpretation of the complex electrical "squiggle" into discrete bases remains a sophisticated computational challenge, itself a form of mediation.

Secondly, nanopore champions the individual molecule. Previous dominant methods largely relied on consensus sequences derived from millions of amplified fragments. This yielded a valuable, statistically robust picture but inherently averaged out variation, obscured haplotype phasing (which parent contributed which set of variants), and struggled to represent the heterogeneity within a population of molecules (e.g., different RNA isoforms or modification patterns on individual DNA strands) (Byrne et al., 2017). Nanopore, by sequencing single strands, brings individuality to the forefront (Jain et al., 2018a). It reveals the unique mosaic of variations on a single chromosome arm, the specific combination of edits on a particular RNA molecule (Volden et al., 2018). This shifts the epistemological focus from an idealized, averaged "genome" or "transcriptome" towards a recognition of the inherent, and often functional, diversity at the molecular level. The "reference genome" becomes less of a static Platonic ideal and more of a navigational chart for exploring a sea of individual variations (Seo et al., 2016).

Thirdly, the long read provides unprecedented context. Short reads are like understanding a novel by reading isolated words; long reads are like reading complete sentences, paragraphs, even chapters (Goodwin et al., 2015). This allows for the resolution of complex genomic structures – large-scale rearrangements, insertions, deletions, and crucially, repetitive regions that were previously intractable "dark matter" (Sedlazeck et al., 2018). It enables the direct phasing of haplotypes across long distances, revealing the combined effect of variants inherited together (Edge & Bansal, 2019; Cretu Stancu et al., 2017). In the transcriptome, it allows for the characterization of full-length RNA isoforms, capturing the complete splicing pattern in a single read rather than inferring it computationally from fragments (Kovaka et al., 2019). This contextual knowledge is not just additive; it changes the kind of understanding we can achieve, moving from a linear parts list towards appreciating the genome and transcriptome as complex, structured entities (Miga et al., 2020).

However, this new epistemology is not without its nuances and limitations. The raw nanopore signal is inherently "analog" – a continuous stream of electrical data influenced by multiple bases within the pore, the speed of translocation, and background noise (Deamer et al., 2016). Converting this rich, but noisy, signal into a discrete sequence of A, C, G, and T/U involves sophisticated basecalling algorithms, often powered by deep learning (Wick et al., 2019; Teng et al., 2018). These algorithms are themselves interpretive frameworks, constantly improving but still prone to characteristic error patterns (particularly indels), although accuracy has dramatically increased (Rang et al., 2018). Furthermore, the interpretation of modification signals is complex, requiring distinct models and often comparative analysis (Liu et al., 2019d; Yuen et al., 2021). Thus, while conceptually direct, the knowledge gained is still computationally constructed, carrying the imprint of the algorithms used. The challenge shifts from purely experimental limitations to a blend of experimental and bioinformatic interpretation (Magi et al., 2018).

Moreover, the increasing portability and accessibility, exemplified by the MinION and its successors, democratizes who can generate sequence data (Jain et al., 2016). Field researchers tracking viral outbreaks in remote locations, clinicians potentially performing rapid diagnostics at the bedside, even researchers sequencing in microgravity – this decentralization is powerful (McIntyre et al., 2016; Quick & Loman, 2019). But it also raises epistemological questions about data quality standards (Leger & Leonardi, 2019), interpretation expertise, and the potential for generating vast amounts of data disconnected from robust analytical pipelines or contextual understanding (Amarasinghe et al., 2020). Knowledge generation becomes more distributed, but potentially more fragmented and uneven in quality.

Ontological Reconfigurations: The Fluidity and Annotation of the Living Code

If epistemology is about how we know, ontology is about what fundamentally is. Nanopore sequencing prompts a subtle but significant ontological shift in our understanding of the genome and transcriptome. For decades, the "genome" was largely conceived as a static, linear digital code – the A's, C's, G's, and T's constituting the blueprint of life. While the discovery of epigenetics complicated this picture, methods for studying modifications like methylation often required treatments (like bisulfite sequencing) that destroyed the original molecule and couldn't easily be combined with standard sequencing (Saletore et al., 2012). Nanopore's ability to directly detect methylation (5mC, 6mA, and others) and RNA modifications (m6A, pseudouridine, etc.) on the same molecule being sequenced integrates these layers of information ontologically (Simpson et al., 2017; Liu et al., 2019a; Jenjaroenpun et al., 2020). Modifications are no longer mere "annotations" on a primary sequence; they are revealed as intrinsic features of the molecule itself, part of its identity and state at a given moment (Rand et al., 2017). The technology encourages us to view the genome not just as a sequence, but as a physically modified object, and the transcriptome as a dynamic, chemically diverse population of molecules (Begik et al., 2021). The "code" is multi-layered, context-dependent, and far more analog than the simple digital metaphor suggests.

The focus on single molecules and long reads also reinforces the understanding of the genome as a physical structure. Resolving complex rearrangements and mapping chromatin accessibility (e.g., via methylation patterns like those explored by Nanopore-DamID) provides a clearer picture of how the genome is folded and organized in three dimensions, which is crucial for its function (Chaisson et al., 2019; Cheetham et al., 2021b). The linear sequence, while foundational, is insufficient; its physical embodiment and regulation are equally part of its being (Wang et al., 2019).

Furthermore, direct RNA sequencing captures the transcriptome not as a static collection of inferred transcripts, but as a snapshot of ongoing cellular activity (Workman et al., 2019). It reveals the diversity of isoforms, including partially processed or transient molecules, offering a glimpse into the flux of genetic information expression (Soneson et al., 2019). This reinforces an ontology of life as fundamentally processual rather than solely based on static blueprints (Keller et al., 2018). The transcriptome, as read by nanopore, is less like a finished library and more like a busy, noisy workshop floor.

This richer, more dynamic ontology challenges simplistic reductionism. While sequencing inherently focuses on the molecular level, the ability to capture context – long-range structure, modifications, isoform diversity, individual variation – pushes back against the idea that life can be fully understood by its smallest parts alone (Amarasinghe et al., 2020). Nanopore provides tools to see how these parts interact and are modified within a larger, dynamic system (Ewing et al., 2020).

**3. Real-Time Revelation: Temporality, Immediacy, and Intervention**

Perhaps one of the most philosophically striking aspects of nanopore sequencing is its real-time nature. Data streams off the sequencer as the molecules pass through the pores, allowing for concurrent analysis (Cao et al., 2016). Basecalling and preliminary analysis can occur concurrently (Loman & Quinlan, 2014). This collapses the timeframe between experiment and insight, contrasting sharply with the batch-processing nature of previous high-throughput methods (Mason & Elemento, 2012).

This immediacy has profound implications. In pathogen surveillance, it allows for rapid identification of infectious agents and tracking of their evolution during an outbreak, informing public health responses within hours or days rather than weeks (Lu et al., 2020; Moore et al., 2020). In clinical settings, it holds the promise of rapid diagnostics – identifying resistance genes in bacterial infections or characterizing cancer mutations quickly enough to influence immediate treatment decisions (Ashton et al., 2015; Pitt et al., 2020).

This introduces a new temporality to biological investigation. Research becomes less retrospective, more observational in the present moment. We can, in principle, "watch" molecular processes unfold over time by sequentially sampling and sequencing, such as monitoring DNA replication dynamics (Hennion et al., 2020). This changes the relationship between observer and observed, making it more interactive and immediate.

But this temporal compression is double-edged. The liberation from waiting brings the pressure of instant analysis and decision-making (Quick & Loman, 2019). The potential for rapid intervention based on real-time data is powerful but also fraught with the risk of acting on incomplete or misinterpreted information. Does the immediacy foster a deeper understanding, or does it encourage reactive responses over reflective analysis? Furthermore, the concept of biological processes being observable in real-time raises questions about biological surveillance at a molecular level. If portable sequencers become ubiquitous (Jain et al., 2016), the potential exists for continuous or near-continuous monitoring of individuals or environments. This capability could be used for health monitoring, but also potentially for more invasive forms of tracking or control. The "present moment" revealed by nanopore is not neutral; it is a space of potential action and, potentially, intrusion.

**4. The Ethical Landscape: Access, Equity, Privacy, and the Burden of Knowledge**

The technical capabilities and shifting philosophical perspectives engendered by nanopore sequencing inevitably raise critical ethical questions that society must grapple with today. The democratization offered by lower-cost, handheld sequencing devices like the MinION are often valued (Jain et al., 2016). It potentially empowers researchers in low-resource settings and enables new forms of citizen science. However, true access requires more than just the sequencer; it demands robust computational infrastructure, bioinformatics expertise for analysis, and resources for sample preparation – elements that remain unevenly distributed globally (Senol Cali et al., 2019). Does nanopore risk creating a new digital divide, where generating data is easy but interpreting it meaningfully remains the purview of the well-resourced? The potential for personalized medicine driven by individual genomic and epigenomic profiles is exciting, but raises urgent questions about equity (Magi et al., 2018). Will these advances benefit all, or primarily those in wealthy nations who can afford the analyses and tailored treatments?

Privacy concerns, already significant with genomic data, are amplified. The ability to sequence long fragments, potentially revealing structural variations and modification patterns linked to health status or environmental exposures, generates deeply personal information (Rand et al., 2017; Cretu Stancu et al., 2017). The portability of the technology increases the scenarios where such data could be collected, perhaps even surreptitiously (McIntyre et al., 2016). Who owns the sequence data generated on a portable device? How is consent managed in field research or rapid diagnostic settings? How do we protect individuals from genetic discrimination based not only on their sequence but also their epigenetic profile, which might reveal lifestyle factors or disease predispositions (Stoiber et al., 2016)?

The detection of modifications adds another ethical layer. Epigenetic marks can reflect not just inherited predispositions but also environmental exposures, diet, stress, and aging (Ewing et al., 2020). This information could be highly sensitive, potentially used by insurers or employers (Simpson et al., 2017). Furthermore, the ability to read these marks raises questions about their potential manipulation – the prospect of "epigenetic editing" looms, with its own complex ethical considerations (Fang et al., 2012).

Finally, there is the "burden of knowledge." As sequencing becomes more comprehensive and accessible, individuals may face difficult choices about what they want to know about their own predispositions or current health state, especially when effective interventions are lacking (Leggett & Clark, 2017). The immediacy of real-time sequencing could exacerbate this, delivering potentially life-altering information with little time for preparation or counseling (Cao et al., 2016).

Bridging Worlds – The Nanopore as Metaphor

Nanopore sequencing often involves a biological component – a precisely structured protein pore like α-hemolysin or MspA – integrated into an artificial membrane and connected to sophisticated electronic sensors (Kasianowicz et al., 1996; Butler et al., 2008). This hybridity, blurring the lines between the natural and the artificial, serves as a potent metaphor. The technology physically bridges the molecular world of biology with the digital world of information technology.

This bridge facilitates an extraordinary flow of information across scales, from the conformation of a single molecule within the pore to vast digital datasets stored in the cloud (Payne et al., 2019). The nanopore itself acts as a transducer, a gatekeeper, translating the language of molecular structure and dynamics into the language of electrical signals, which are then further translated by basecalling algorithms into digital sequence data (Teng et al., 2018). Reflecting on this process prompts philosophical questions about translation itself: What is preserved, what is lost, and what is inevitably altered when biological reality is converted into digital representation (Rang et al., 2018)? Does the nature of the tool – the specific properties of the pore and the algorithms used for interpretation – shape the questions we ask and the biological phenomena we are able to perceive?

**5. The 2025 Nanopore Landscape: Pushing Towards Temporal Omics and Macromolecule Sequencing**The evolution of nanopore sequencing technologies has catalyzed breakthroughs across molecular biology, driven by innovations in RNA modification detection, temporal omics resolution, and environmental DNA analysis. Early foundational work by Arzumanian et al. (2023) demonstrated the utility of Oxford Nanopore Technology (ONT) for identifying N6-methyladenosine (m6A) modifications in HepG2 cell lines, establishing a framework for direct RNA epigenetics profiling. Building on this, Yu et al. (2024) advanced the field with m6ATM, a deep learning algorithm that deciphers m6A epitranscriptomic landscapes using long-read RNA-seq data, resolving isoform-specific methylation patterns with unprecedented accuracy. These studies laid the groundwork for 2025’s focus on temporal and single-molecule resolution, where Li et al. (2025) have pioneered nanopore-based approaches to track dynamic molecular interactions—such as protein-RNA binding events and post-translational modifications—in real time, offering insights into cellular processes with millisecond precision. Concurrently, methodological refinements in sample preparation, exemplified by Cousson et al. (2024), have enabled the extraction of ultra-pure high-molecular-weight DNA from soil microbiomes, expanding nanopore metagenomics to resolve previously inaccessible environmental microbial communities.

By 2025, nanopore technology has transcended its original genomic applications, now addressing interdisciplinary challenges in cancer diagnostics, food safety, and adaptive sequencing. For instance, Su et al. (2025) leverage ONT’s single-molecule capabilities to detect rare oncogenic fusion transcripts and tumor-specific epigenetic alterations, enabling non-invasive liquid biopsy platforms for early cancer detection. In parallel, Sharma et al. (2025) utilize rapid nanopore workflows to identify foodborne pathogens like Salmonella and Listeria within hours, revolutionizing outbreak containment in global supply chains. However, scaling these applications requires overcoming persistent technical hurdles. Li et al. (2025) emphasize the need for improved signal-to-noise ratios in temporal omics, particularly when analyzing low-abundance macromolecules, while Munro et al. (2025) highlight computational limitations in adaptive sampling algorithms when processing terabase-scale PromethION datasets. Nevertheless, innovations such as Cousson et al.’s (2024) soil DNA extraction protocols and Yu et al.’s (2024) machine learning frameworks provide a roadmap for addressing these challenges, ensuring nanopore sequencing remains a versatile, transformative tool for both basic research and industrial applications.

**6. Conclusion: Reading Between the Lines of Life**

Nanopore sequencing, as it stands today, is far more than a sophisticated tool for reading DNA and RNA. It is a philosophical instrument tuning our understanding of life's code (van Dijk et al., 2018). It pushes us towards an epistemology that values directness, individuality, and context, while acknowledging the mediating role of computation (Magi et al., 2018). It encourages an ontology that embraces the multi-layered, dynamic, and structurally complex nature of the genome and transcriptome, integrating sequence with modification and form with function (Workman et al., 2019; Simpson et al., 2017). It introduces a novel temporality of real-time observation, collapsing the delay between biological event and human knowledge, bringing both immense power and potential peril (Lu et al., 2020).

The journey of the single molecule through the nanopore becomes a metaphor for our own scientific journey – navigating the intricate passages of biological complexity. The technology forces us to confront fundamental questions about the nature of information, the definition of biological identity, the ethics of knowing, and the responsibilities that attend the power to read life's script with unprecedented intimacy and speed (Nurk et al., 2021; Miga et al., 2020). As nanopore technology continues to evolve – improving accuracy, throughput, and analytical methods (Amarasinghe et al., 2020) – its philosophical resonance will only deepen.

It challenges us not merely to sequence more, faster, and cheaper, but to think more deeply about what it means to read the code of life and what we intend to do with that knowledge. The intimate read offered by the nanopore (Deamer et al., 2016) demands an equally intimate form of reflection on its meaning for science, society, and our place within the biological world we are now deciphering, one molecule at a time. As nanopore technology continues to evolve – with emerging frameworks now decoding protein sequences atom-by-atom (Deshpande et al., 2025) – its philosophical resonance will only deepen.

**Competing interests**

“Authors have declared that no competing interests exist. ”The author affirms that no generative artificial intelligence tools—including but not limited to large language models (e.g., ChatGPT, Gemini, Copilot) or text-to-image systems—were employed in the drafting, revision, or conceptual development of this manuscript. All content reflects original human intellectual wor.

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Details of the AI usage are given below:

1.

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