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| Journal Name: | [**Asian Journal of Biochemistry, Genetics and Molecular Biology**](https://journalajbgmb.com/index.php/AJBGMB) |
| Manuscript Number: | **Ms\_AJBGMB\_134760** |
| Title of the Manuscript: | **The Intimate Read: Nanopore Sequencing and the Philosophical Recalibration of Life's Code** |
| Type of the Article | **Minireview Article** |

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| PART 1: Comments | | |
|  | Reviewer’s comment **Artificial Intelligence (AI) generated or assisted review comments are strictly prohibited during peer review.** | Author’s Feedback *(Please correct the manuscript and highlight that part in the manuscript. It is mandatory that authors should write his/her feedback here)* |
| **Please write a few sentences regarding the importance of this manuscript for the scientific community. A minimum of 3-4 sentences may be required for this part.** | The article goes beyond a technical review and combines molecular biology with philosophical and ethical reflections, making it unique and interdisciplinary. |  |
| **Is the title of the article suitable?**  **(If not please suggest an alternative title)** | It is suitable |  |
| Is the abstract of the article comprehensive? Do you suggest the addition (or deletion) of some points in this section? Please write your suggestions here. | I don't have a comment about the abstract |  |
| Is the manuscript scientifically, correct? Please write here. | Yes, i don't find errors |  |
| **Are the references sufficient and recent? If you have suggestions of additional references, please mention them in the review form.** | Most of the references cited are from 2018–2021, and do not include the latest studies on Oxford Nanopore Technologies (ONT) and long-read sequencing. It would be beneficial to incorporate more recent publications, particularly those covering the latest ONT chemistries, basecalling models, and advances in the detection of DNA and RNA modifications. For example: <https://www.nature.com/articles/s41592-024-02492-3>, <https://pubmed.ncbi.nlm.nih.gov/39846015/>, <https://pubmed.ncbi.nlm.nih.gov/39846015/>, <https://pubmed.ncbi.nlm.nih.gov/38003667/>, <https://pubmed.ncbi.nlm.nih.gov/39438075/> etc |  |
| Is the language/English quality of the article suitable for scholarly communications? | The style of the article requires a high level of preparation. The density of philosophical terms and metaphors may make it difficult for readers without the appropriate background to understand. |  |
| Optional/General comments | I would like to thank the authors for this thoughtful and philosophically rich manuscript. The article successfully explores important questions that have been debated for years in the context of sequencing technologies, especially those related to Illumina. It is refreshing to see an interdisciplinary approach that links molecular biology with epistemological, ontological, and ethical considerations.  That said, I believe the manuscript would benefit from a broader and more critical engagement with the technical and practical limitations of Oxford Nanopore Technologies (ONT), in addition to the ethical and philosophical discussions already provided.  While the authors mention certain challenges, the manuscript does not sufficiently highlight that ONT still exhibits relatively high error rates, especially in the context of single-nucleotide polymorphism (SNP) detection. This is a significant omission, as SNPs are critical for identifying disease-associated variants and personalized medicine applications. Until basecalling accuracy further improves, ONT remains limited in these clinically relevant areas.  The discussion on epigenetics may come across as overly optimistic. Although ONT can detect various epigenetic modifications, the biological interpretation of these marks remains immature, and their reliability in reflecting complex traits (e.g., stress levels, lifestyle, or socio-economic status) is still under debate. It may be premature to suggest that epigenetic data can meaningfully inform such assessments at this stage.  One of the most intriguing issues raised in the article is the question of data ownership. Yet, the manuscript only hints at this point without developing it further. I would be interested in the authors’ perspective on this issue — especially in decentralized or field-based sequencing scenarios. Who owns the data produced in such contexts? How should consent and data governance be handled? A deeper exploration would strengthen the ethical section.  I would also like to see more illustrative material - graphs, diagrams, comparisons. For example, on the volume of data generated by short and long read technologies.  And also - does the volume of data produced by ONT really continue to grow, or do Illumina and its analogues still dominate the industry? It would be useful to receive comments from the authors on this matter.  By the way, is the section "Ontological Reconfigurations: The Fluidity and Annotation of the Living Code" a new conceptual part?  While the philosophical nature of the article is appreciated, it sometimes leans too heavily into abstraction without offering actionable conclusions. In my opinion, this article would be even more impactful if the authors took clearer positions on some of the core questions they raise. |  |

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| **PART 2:** | | |
|  | Reviewer’s comment | Author’s comment *(if agreed with the reviewer, correct the manuscript and highlight that part in the manuscript. It is mandatory that authors should write his/her feedback here)* |
| **Are there ethical issues in this manuscript?** |  |  |

**Reviewer details:**

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