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อุตสาหกรรมยุทธศาสตร์ของประเทศ**

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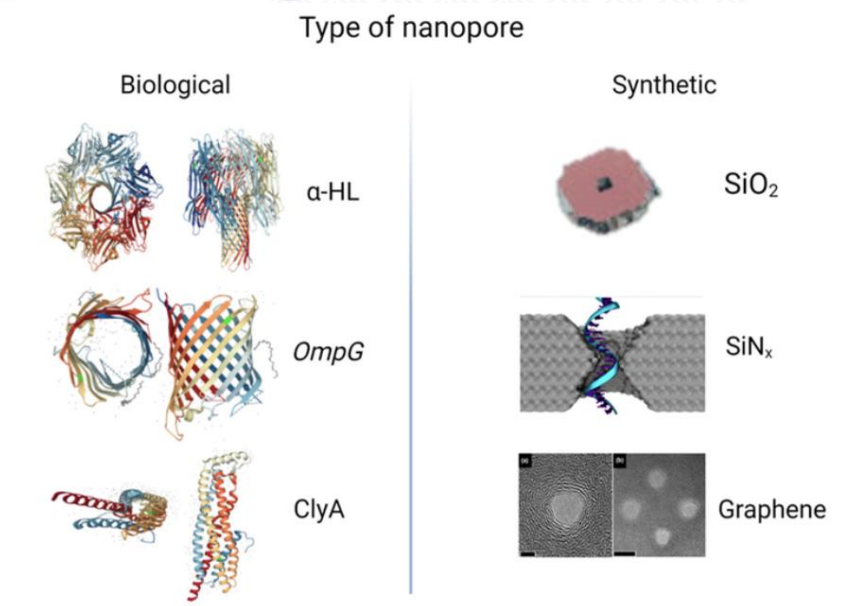
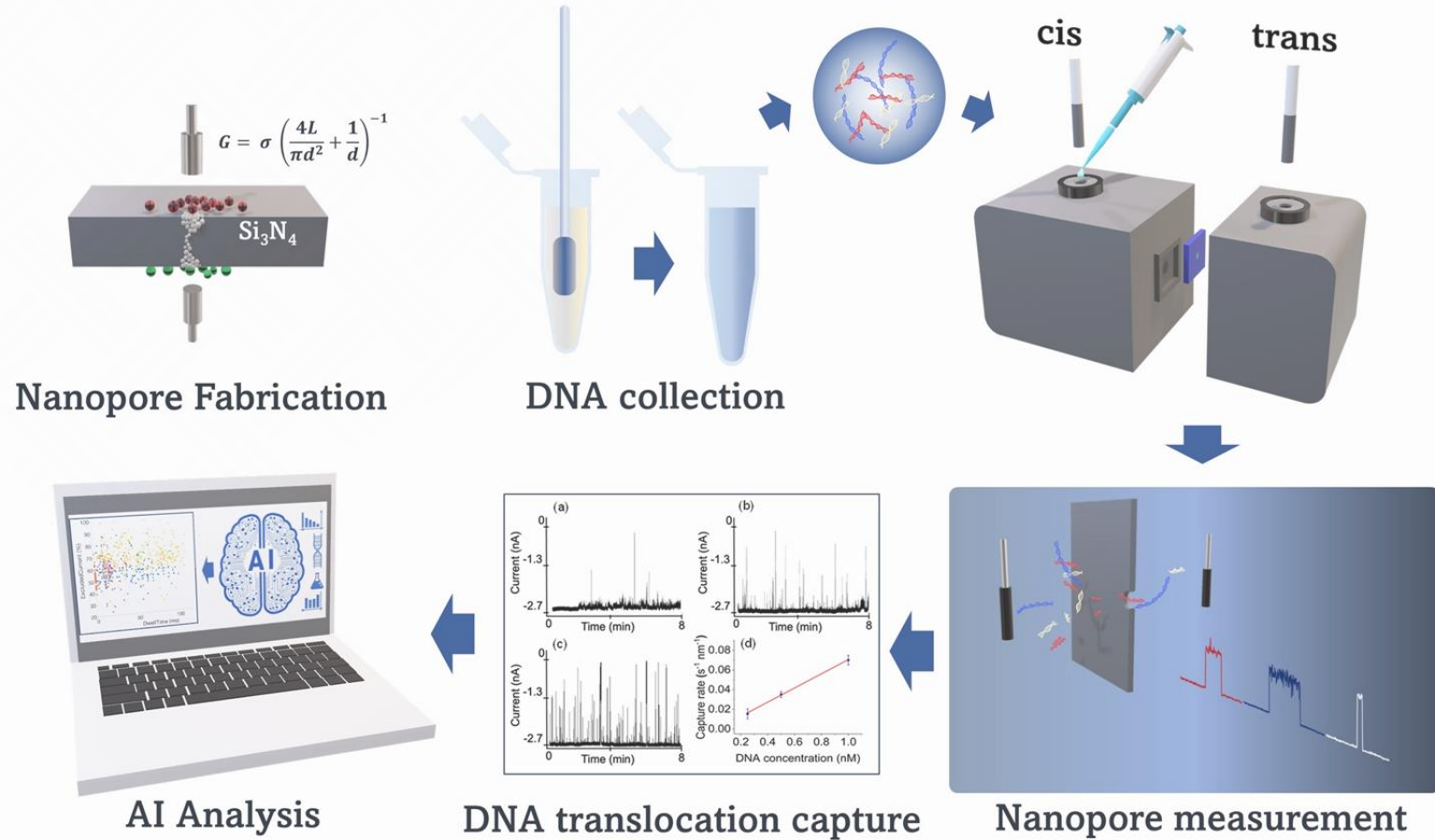
สำนักงานพัฒนาวิทยาศาสตร์และเทคโนโลยีแห่งชาติ



Advancements in Nanopore Technology: Interrogating DNA, Unveiling Proteins, and Predicting Disease with Machine Learning

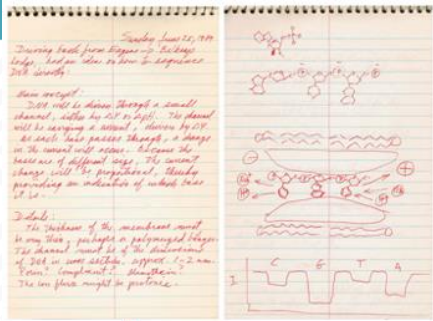
Dr. Ibrar Alam
National Nanotechnology Center,
NSTDA

Introduction to Nanopore



Șoldănescu, I.; Lobiuc, A.; Covașă, M.; Dimian, M. Detection of Biological Molecules Using Nanopore Sensing Techniques. *Biomedicines* **2023**, *11*, 1625. <https://doi.org/10.3390/biomedicines11061625>

Brief History



Church, Deamer, and Branton file patent for Nanopore Sequencing

1995

First DNA translocation through alpha-hemolysin nanopore

1996

Purine and Pyrimidine segments are distinguished in a single RNA molecules

1999

Solid state nanopore are produced and used to detect DNA

2001

E.Coli genome assembled denovo with 99.4% accuracy with MinION

2015

ONT releases MinION device for early users

2014

DNA sequencing with Phi 29 polymerase and MspA nanopore
MinION device was developed

2012

Single molecule of DNA was detected with MspA nanopore

2008

Single nucleobase are distinguished
Oxford Nanopore Technology was founded

2005

CRISPR-Cas9 is combined with nanopore technology for precise DNA editing and sequencing.

2016

Introduction of the PromethION, a high-throughput nanopore sequencer

2017

Development of nanopore-based diagnostic tests for infectious diseases

2019

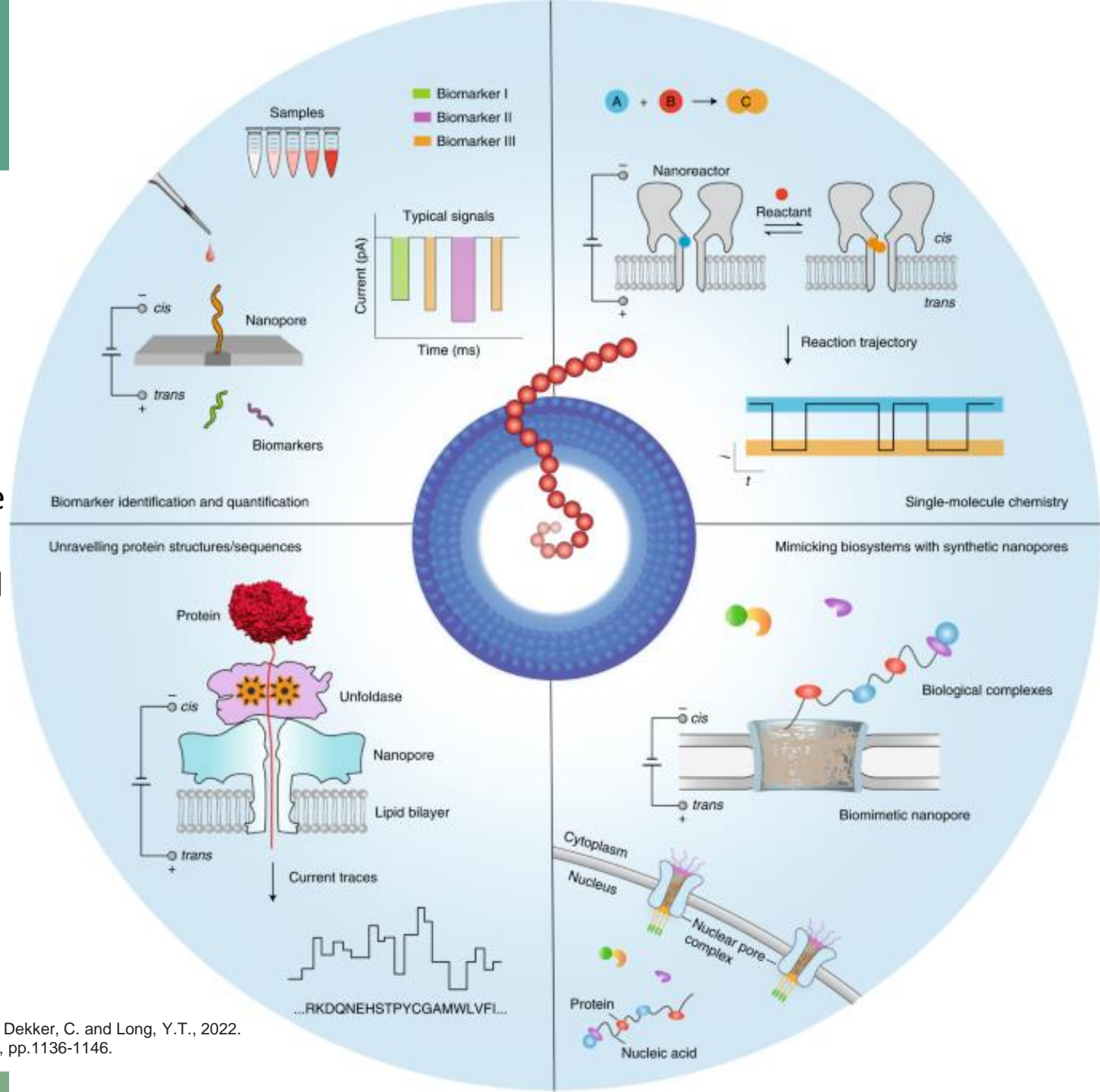
Advances in machine learning enable real-time base calling and analysis of nanopore sequencing data

2020

Expanded Applications
Clinical Adoption
Miniaturization and Portability
Integration with Other Technologies

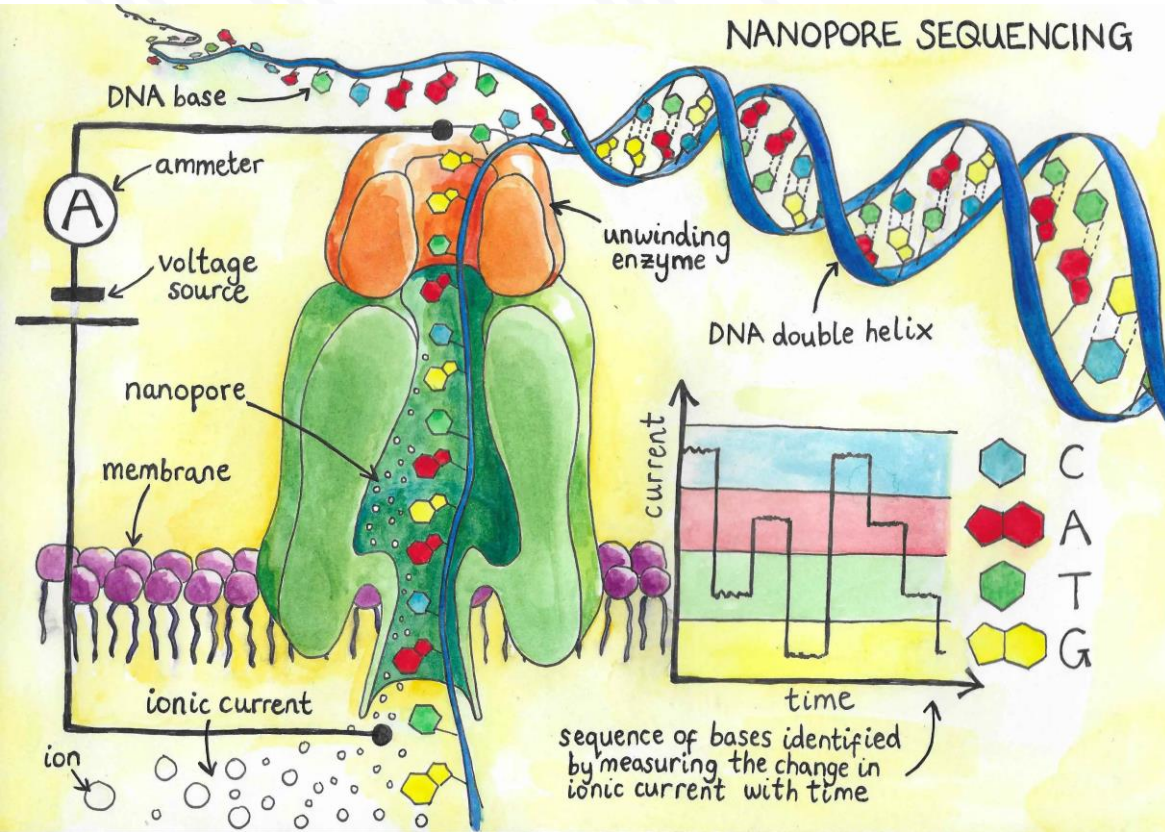
Importance in Biological Research

- Nanopore technology revolutionized DNA sequencing, enabling rapid and cost-effective analysis of DNA.
- It allows for real-time, single-molecule analysis, providing insights into biological processes at a level of detail previously unattainable.
- Nanopores have diverse applications beyond DNA sequencing, including protein analysis, drug discovery, and biomarker detection.



Nanopore Sequencing of DNA

Principle of DNA sequencing using nanopores



Advantages Over Traditional Sequencing Methods

- Real-Time Analysis:** Eliminating the need for time-consuming library preparation and post-sequencing processing.
- Single-Molecule Sensitivity:** Detection of rare mutations and structural variations that may be missed by bulk sequencing methods.
- Portability and Accessibility:** Expanding the reach of genomic research and diagnostics.
- Long Read Lengths:** Assembly of complex genomes and the analysis of repetitive regions.
- Cost-Effectiveness:** More accessible to researchers and clinicians with limited budgets.
- Versatility:** Amino acids, nucleic acids, including DNA, RNA, and modified bases, offering versatility for various research and diagnostic applications.

Single-Molecule Analysis of SARS-CoV-2 Double-Stranded Polynucleotides Using Solid-State Nanopore with AI-Assisted Detection and Classification: Implications for Understanding Disease Severity

Ibrar Alam, Thitikorn Boonkoom, Harit Pitakjakpipop, Poramin Boonbanjong, Kawin Loha, Thanaya Saeyang, Jarunee Vanichtanankul, and Deanpen Japrunng*



Cite This: <https://doi.org/10.1021/acsabm.3c00998>



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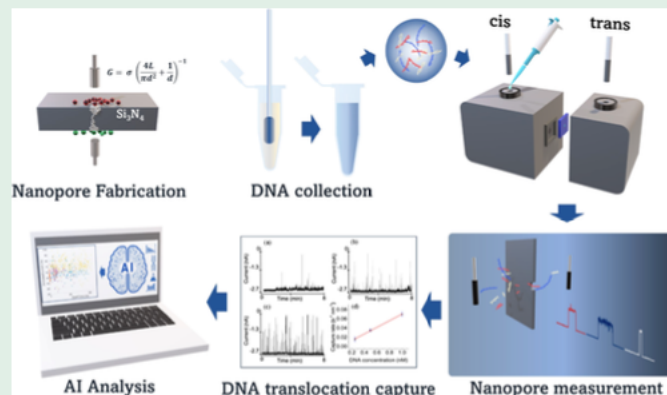
Metrics & More

Article Recommendations

Supporting Information

ABSTRACT: This study utilized solid-state nanopores, combined with artificial intelligence (AI), to analyze the double-stranded polynucleotides encoding angiotensin-converting enzyme 2, receptor-binding domain, and N protein, important parts of SARS-CoV-2 infection. By examining ionic current signals during DNA translocation, we revealed the dynamic interactions and structural characteristics of these nucleotide sequences and also quantified their abundance. Nanopores of sizes 3 and 10 nm were efficiently fabricated and characterized, ensuring an optimal experimental approach. Our results showed a clear relationship between DNA capture rates and concentration, proving our method's effectiveness. Notably, longer DNA sequences had higher capture rates, suggesting their importance for potential disease marker analysis. The 3 nm nanopore demonstrated superior performance in our DNA analysis. Using dwell time measurements and excluded currents, we were able to distinguish the longer DNA fragments, paving the way for a DNA length-based analysis. Overall, our research underscores the potential of nanopore technology, enhanced with AI, in analyzing COVID-19-related DNA and its implications for understanding disease severity. This provides insight into innovative diagnostic and treatment strategies.

KEYWORDS: *solid-state nanopore, SARS-CoV-2, single-molecule analysis, DNA translocation, capture rate, excluded current*



Highlights

- Nanopore technology and artificial intelligence (AI) used to investigate double-stranded polynucleotides of ACE2, RBD, and N protein
- Analysis of ionic current signals reveals interactions and structures of these DNA sequences
- AI enhances accuracy and depth of observations, determining prevalence of specific sequences
- Findings provide foundation for developing new diagnostic and treatment strategies for COVID-19

Alam, I., Boonkoom, T., Pitakjakpipop, H., Boonbanjong, P., Loha, K., Saeyang, T., Vanichtanankul, J. and Japrunng, D., 2024. Single-Molecule Analysis of SARS-CoV-2 Double-Stranded Polynucleotides Using Solid-State Nanopore with AI-Assisted Detection and Classification: Implications for Understanding Disease Severity. *ACS Applied Bio Materials*, 7(2), pp.1017-1027.

Solid-state nanopore fabrication and DNA translocation experiment

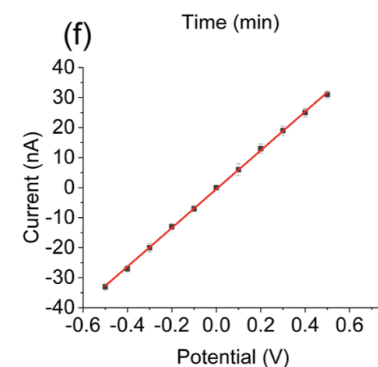
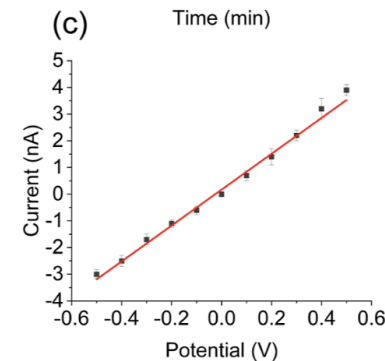
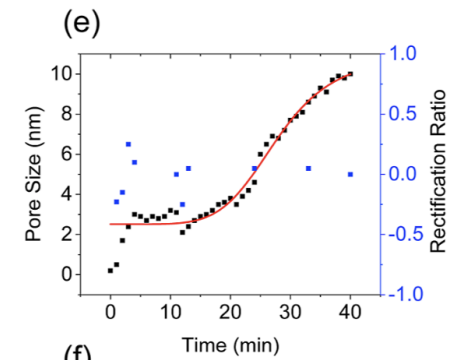
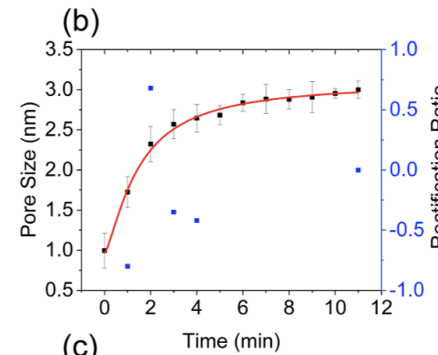
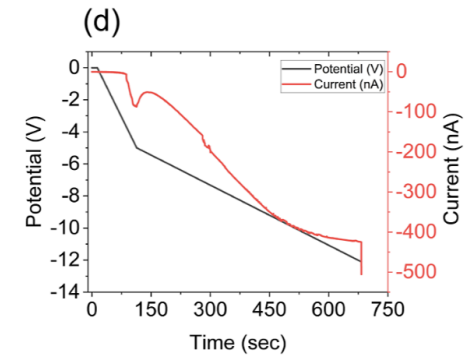
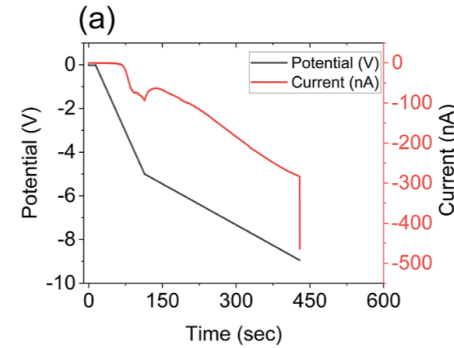
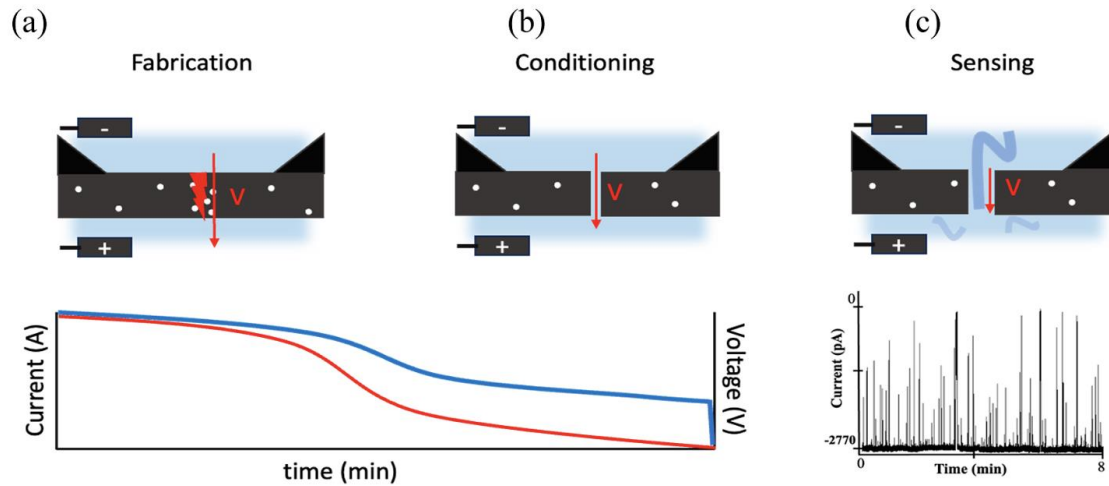
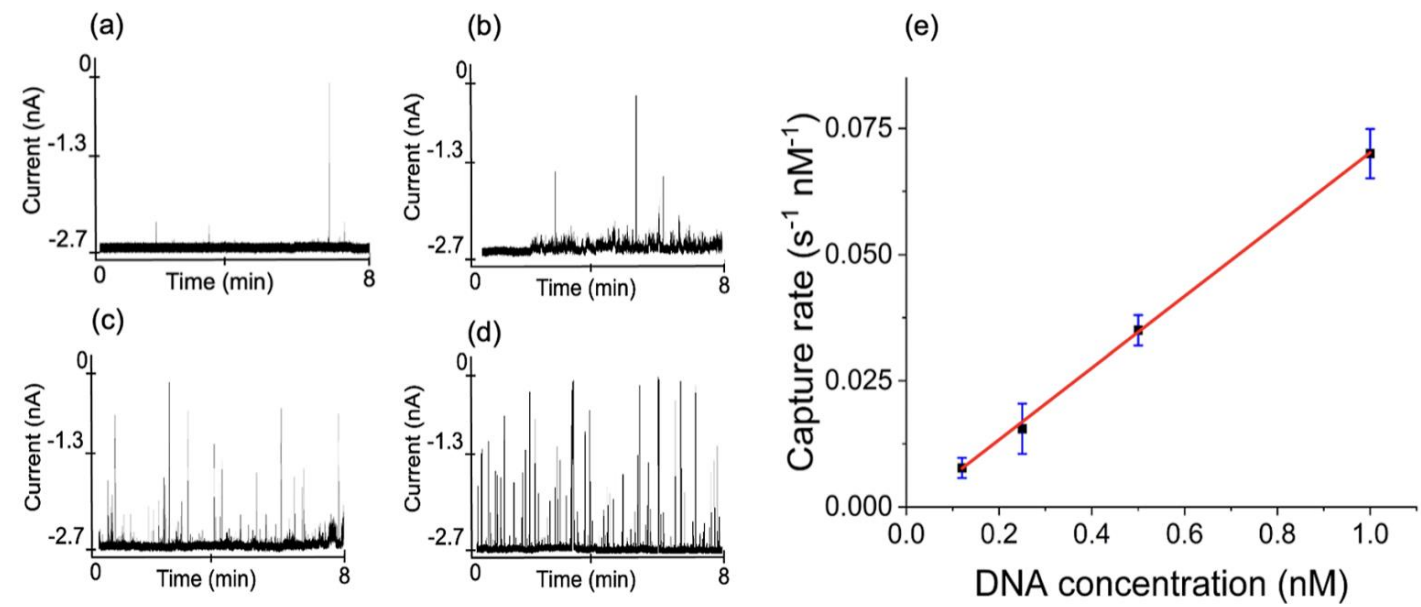


Table 1. Summary of Prepared Double-Stranded Polynucleotides for ACE2, RBD, and N Protein

DNA fragment	Encoded protein	Base pair length (bp)	% GC content
ACE2-PD	peptidase domain of ACE2 protein	1836	54.96
RBD	spike protein RBD	846	54.61
NTD	N-terminal domain of N protein	450	59.55
CTD	C-terminal domain of N protein	414	56.28

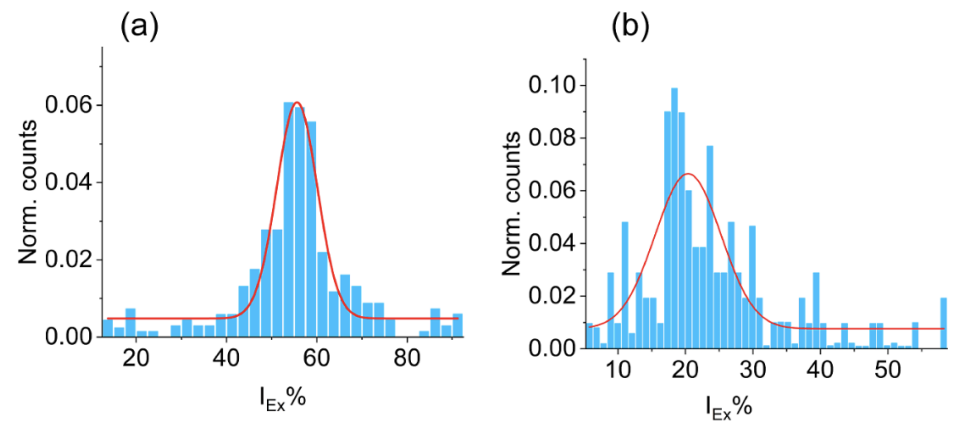
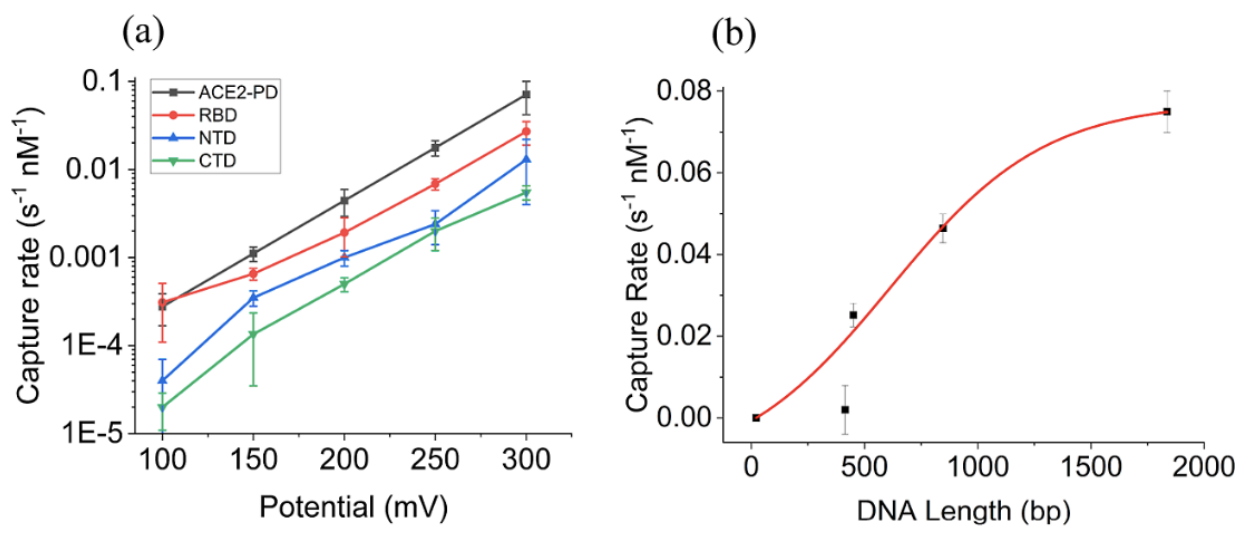
Nanopore Analysis of Double-Stranded Polynucleotides Encoded for ACE2, RBD, and N Protein



$$G = \sigma \left(\frac{4L}{\pi d^2} + \frac{1}{d} \right)^{-1}$$

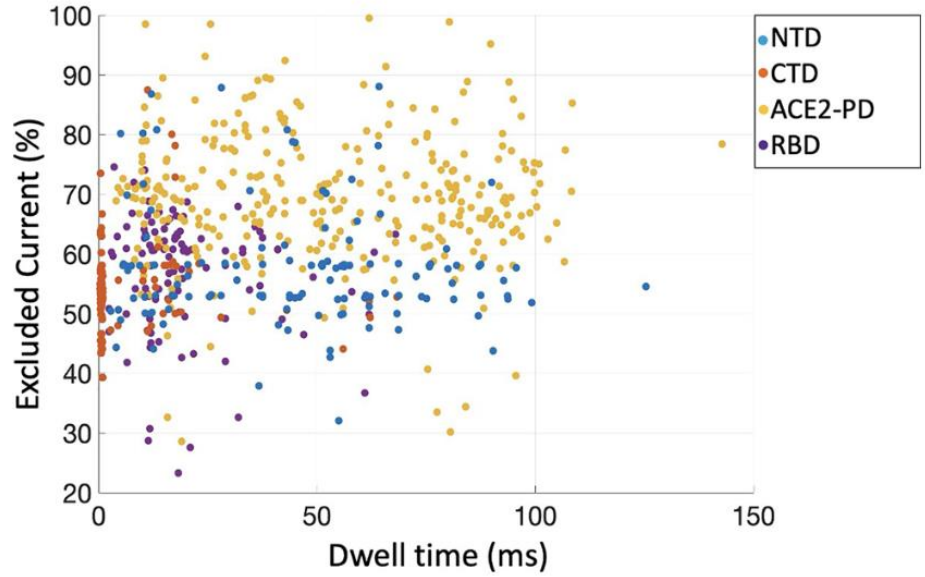
$$\text{Capture rate} \propto e^{(\alpha V)}$$

$$\text{Capture rate} \propto e^{(\alpha V)} \times L^\beta$$

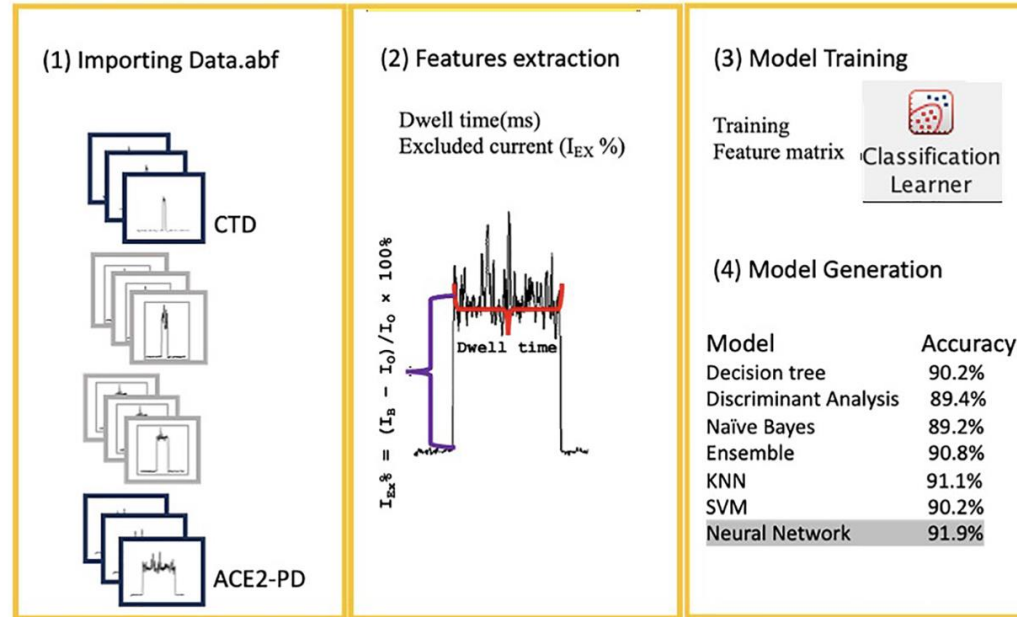


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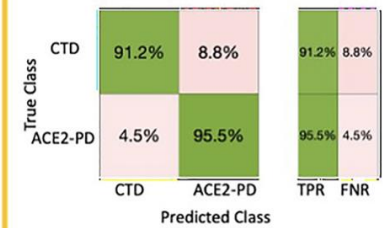
AI-Assisted Dwell Time Analysis of DNA Interactions and Translocations through the Nanopore.



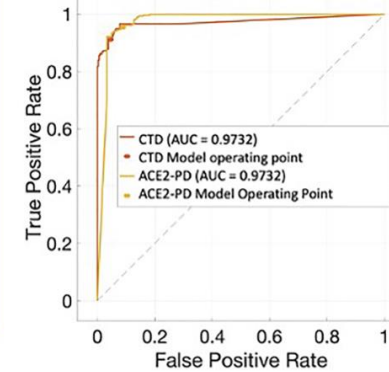
(a) Training process



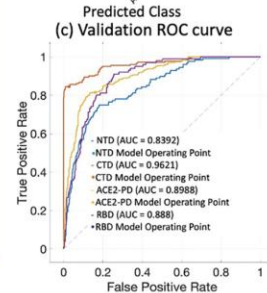
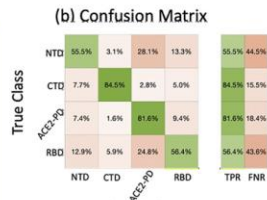
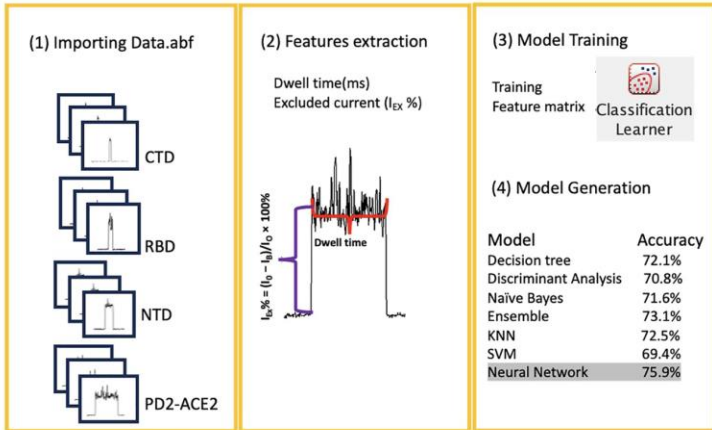
(b) Confusion Matrix



(c) Validation ROC curve

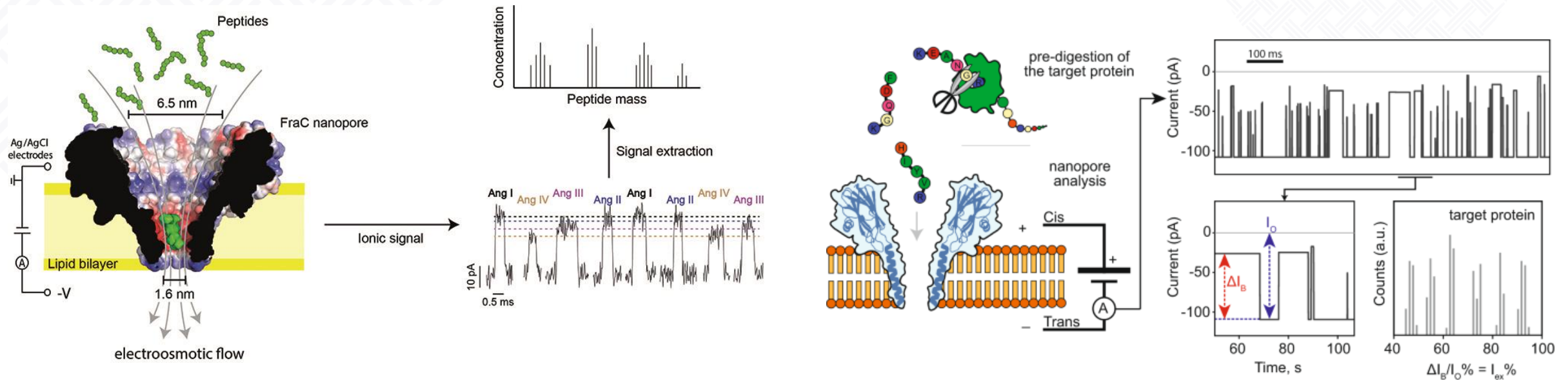


(a) Training process



$$\text{Number of polynucleotide molecules} = \frac{\text{capture rate} \times \text{total number of molecules}}{\text{capture efficiency}}$$

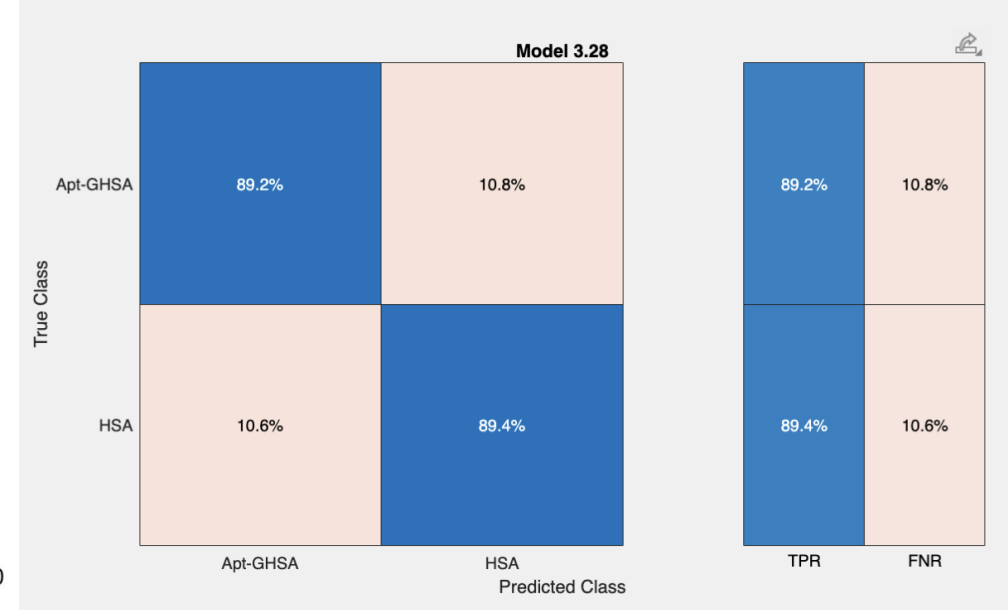
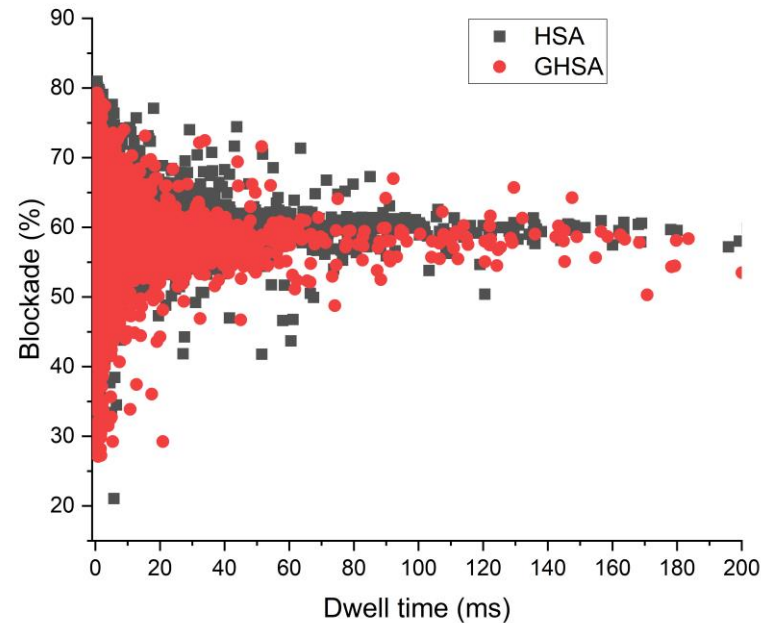
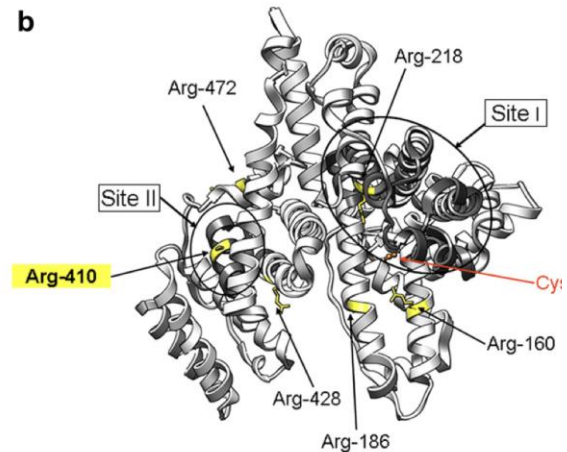
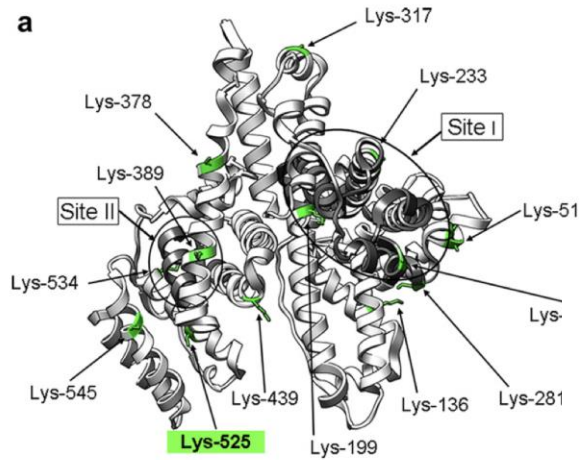
Protein Analysis with Nanopores



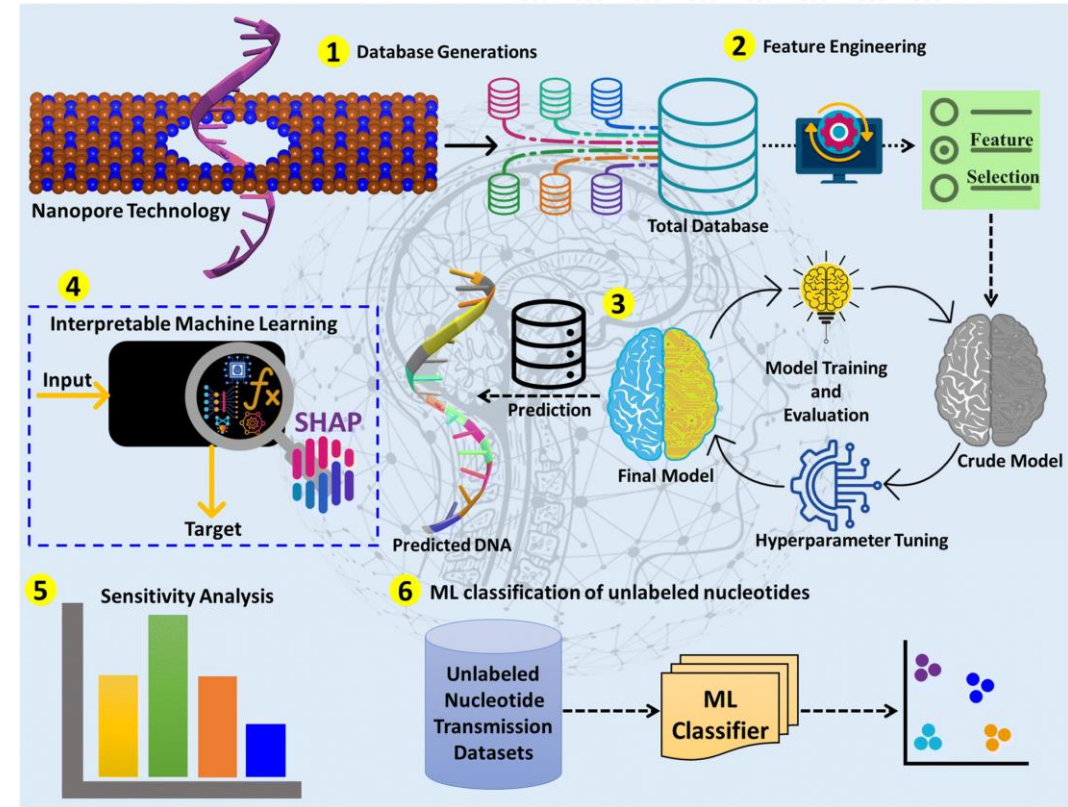
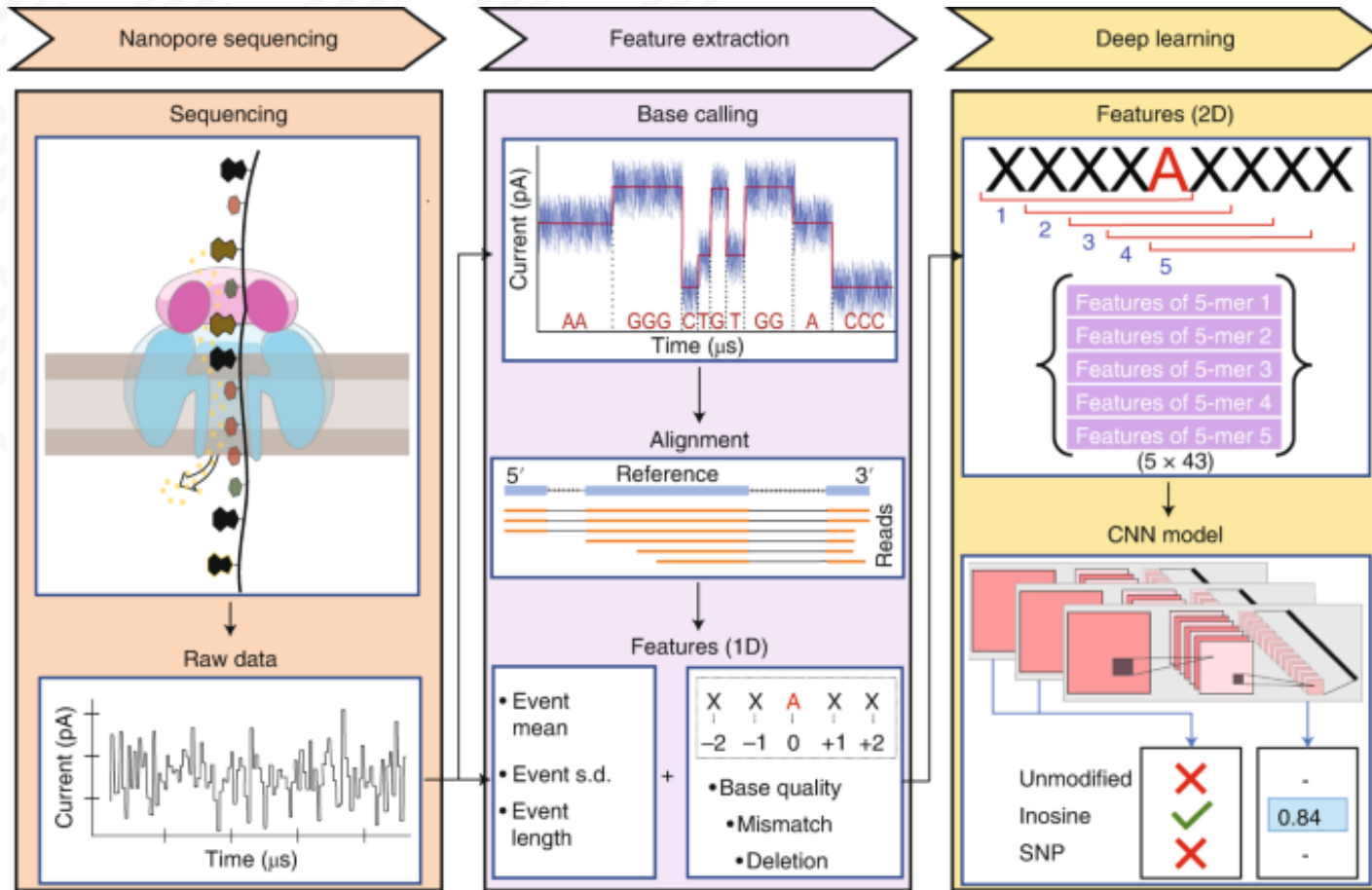
Lucas, F.L.R., Versloot, R.C.A., Yakovlieva, L. *et al.* Protein identification by nanopore peptide profiling. *Nat Commun* **12**, 5795 (2021). <https://doi.org/10.1038/s41467-021-26046-9>

Protein Analysis with Nanopores

Solid-state nanopore analysis of Human Serum /Glycated Albumin.



Machine Learning in Nanopore Technology



Jena, M.K., Mittal, S., Manna, S.S. and Pathak, B., 2023. Deciphering DNA nucleotide sequences and their rotation dynamics with interpretable machine learning integrated C 3 N nanopores. *Nanoscale*, 15(44), pp.18080-18092.

Deep learning identifies A-to-I RNA edits using nanopore sequencing data. *Nat Methods*19, 797–798 (2022). <https://doi.org/10.1038/s41592-022-01514-2>

Future perspective

Nanopore Arrays: Development of nanopore arrays for parallel sequencing, increasing throughput and reducing sequencing time.

Improved Base Calling: Advancements in base calling algorithms for higher accuracy and better handling of difficult sequences, such as repetitive regions.

Nanopore Protein Sequencing: Progress in nanopore technology for direct sequencing of proteins, enabling rapid and accurate protein analysis.

Nanopore-Based Epigenetic Analysis: Use of nanopores for studying epigenetic modifications, such as DNA methylation and histone modifications, providing insights into gene regulation.

Single-Molecule Imaging: Advancements in nanopore imaging techniques for real-time visualization of single molecules, expanding applications in structural biology and drug discovery.

Integration with Microfluidics: Further integration of nanopores with microfluidic devices for automated sample preparation and analysis, improving workflow efficiency.

Clinical Diagnostics: Continued development of nanopore-based diagnostic tools for personalized medicine, early disease detection, and monitoring of treatment responses.

Synthetic Biology Applications: Utilization of nanopores in synthetic biology for designing novel biosensors, gene editing tools, and bioinformatics applications.

Challenges and Limitations of Nanopore Technology

Current Challenges:

Accuracy: Nanopore sequencing still faces challenges in achieving the same level of accuracy as other sequencing methods, particularly in detecting repetitive sequences and base modifications.

Throughput: Despite improvements, nanopore sequencing throughput is lower compared to some high-throughput sequencing technologies, limiting its applicability in large-scale studies.

Cost: While nanopore sequencing is cost-effective for certain applications, the overall cost, including equipment and reagents, can be a barrier for widespread adoption.

Signal-to-Noise Ratio: Maintaining a high signal-to-noise ratio is crucial for accurate base calling, and noise levels can vary depending on the sample and experimental conditions.

Strategies for Overcoming Limitations:

Improving Base Calling Algorithms: Continued development of base calling algorithms to enhance accuracy, especially in challenging regions of the genome.

Enhancing Nanopore Technology: Research efforts focused on improving nanopore design and materials to increase throughput and reduce error rates.

Cost Reduction: Streamlining workflows and reducing the cost of reagents and consumables to make nanopore sequencing more affordable.

Noise Reduction: Developing methods to reduce noise levels and improve signal-to-noise ratio for more accurate sequencing results.

ขอขอบคุณผู้ให้การสนับสนุน Industrial Postdoc



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