Oxford Nanopore Technologies

Taking multiomics to new lengths with Oxford Nanopore

Jonathan Mill looks beyond DNA sequence variation to better understand complex diseases, with a focus on the central nervous system. Discover why he uses Oxford Nanopore sequencing to uncover data missed with short-read sequencing.

‘The advent of long-read sequencing has really enabled us to ask new questions’[1]

Professor Jonathan Mill
University of Exeter Medical School, UK

What you’re missing matters

Ask bolder questions

Understanding both the causes and consequences of molecular variation in the human brain is key for improving our understanding of neurological disorders. A multiomic approach is required, characterising both epigenetic and transcriptional variation, but standard methods are limited in their ability to assess RNA isoforms and DNA modifications. Long, native nanopore reads can solve this problem.

Ultra-rich data

>28 million
CpG sites assessed for modification[2]

12 transcripts
linked to Alzheimer's disease[3]

11 mutations
linked to neuro-developmental disorders[4]

Thousands
of novel transcripts in the human cortex[4]

Reveal more biology

Jonathan's team have used nanopore sequencing to quantify splicing events and identify differential isoform expression during brain development[3,4] — both undetectable using short-read approaches. He has also used nanopore sequencing to detect 5-hydroxymethylcytosine (5hmC), a modification critical in regulating alternative splicing in neurons, but hard to differentiate using alternative methods[1].

'One of the real powers … is not just being able to detect DNA methylation, but also to directly read out DNA hydroxymethylation'[1]

Read more about multiomic studies with Oxford Nanopore sequencing

References

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