

## NanoOK: a portable, rapid, low-cost DNA sequencing tool

Nanopore's MinION sequencer has been combined with an open-source, sequence alignment-based genome analysis tool called 'NanoOK'. NanoOK is the first open-source tool that provides comprehensive alignment-based quality control and error profile analysis for the MinION platform. NanoOK's main output is a detailed PDF report featuring graphs and tables of sample analysis data.



*Oxford Nanopore's MinION™ USB-attached miniature sensing device*

The tool currently supports four popular Nanopore aligners which is extensible through a Java programming interface. It also handles metagenomic sampling, due to support for multiple reference sequences and the output report PDF benefits from programming language R's graphical capabilities, for at-a-glance reporting of large data volumes.

The MinION is a compact, portable device, smaller than a typical TV remote control and produces long reads in the kilobase length range. A USB-connected device, its compact size and portability makes it ideal for low-cost research fieldwork. NanoOK's comprehensive alignment-based error profiling enables researchers to understand data quality, the effect of different alignment tools and to understand the effect of updates to the MinION's chemistry and software.

Dr Richard Leggett, the project leader, in the Data Infrastructure & Algorithms Group at The Genome Analysis Centre (TGAC), Norwich said that the speed of change within the Minlon Access Programme (MAP) is rapid and a tool such as NanoOK can help researchers to understand and evaluate changes. This will be crucial as anticipated updates are rolled out, such as the 'fast run mode' announced at Oxford Nanopore's 'May London Calling event'.

The paper, titled "NanoOK: Multi-reference alignment analysis of nanopore sequencing data, quality and error profiles" has been published in Oxford Journals *Bioinformatics*, 2015.

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