

Polishing the Oxford Nanopore long-read assemblies of bacterial pathogens with Illumina short reads to improve genomic analyses

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- Illumina sequencing:

A technique used to determine the series of base pairs in DNA, also known as DNA Sequencing. It was developed by [Shankar Balasubramanian](#) and [David Klenerman](#) of Cambridge University, who subsequently founded Solexa, a company later acquired by [Illumina](#). This sequencing method is based on reversible dye-terminators that enable the identification of single nucleotides as they are washed over DNA strands. It can also be used for whole-genome and region sequencing, [transcriptome](#) analysis, [metagenomics](#), small [RNA](#) discovery, [methylation](#) profiling, and genome-wide [protein-nucleic acid](#) interaction analysis.

- Bacterial genomes:

By studying the genomes of bacteria we are able to better understand their metabolic capabilities, their ability to cause disease and also their capacity to survive in extreme environments. Many of the well-studied bacterial model organisms, such as *E. coli*, have a single circular chromosome.

- Antimicrobial resistance:

The QIAGEN CLC Microbial Genomics Module provides extensive tools to support advanced bioinformatics and genomics analysis of antimicrobial resistance (AMR) genes and markers. The tools specifically developed for AMR include those for analysis of both assembled isolate genomes or metagenomes, as well as tools for the assembly-free detection of AMR markers directly from your FASTQ data.

- Bacillus Megaterium:

A rod-like, Gram positive, mainly aerobic spore forming bacterium found in widely diverse habitats. *Megaterium* is amongst the biggest known bacteria. The cells often occur in pairs and chains, where the cells are joined together by polysaccharides on the cell walls

Megaterium was the main model organism among Gram-positive bacteria for intensive studies on biochemistry, sporulation and bacteriophages. Recently, its popularity has started increasing in the field of biotechnology for its recombinant protein production capacity.