

Improvements in epigenomic sequencing technologies could enhance cancer diagnostics

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An international research collaboration led by UCL scientists has developed ways to improve the quality and accuracy of information harvested from epigenome sequencing datasets in two new research papers published jointly in *Nature Biotechnology* and *Nature Communications* today. According to the studies, epigenome sequencing technologies can allow for more comprehensive analysis of cancers - a key component in the development of targeted approaches to combat cancer.

Epigenetics is a relatively new and rapidly evolving area of [cancer](#) research and refers to chemical modifications to DNA that turn genes 'on' or 'off'. These modifications do not change the DNA sequence itself but the way it functions. In this way, epigenetic modifications help determine cellular identity i.e. what distinguishes a skin cell from a brain or other type of cell. Currently, sophisticated technologies exist that can be used to detect epigenetic changes in tissue samples. In many cancers, epigenetic variants are more frequent than genetic variants, so can therefore provide vital information for understanding how cancers develop and progress.

A key question for the researchers involved in the studies was whether epigenome sequencing technologies could be improved to detect such modifications much more comprehensively and efficiently.

"Our studies focused on measuring one of the most commonly known epigenetic modifications: DNA Methylation. This is a chemical 'tag' that attaches to the genetic material (DNA) of a cell, which can alter the behaviour of that cell," explains Dr Emanuele Libertini, UCL Cancer Institute Research Associate and lead author of the studies. "We are looking at what information can be extracted from DNA Methylation using whole-genome bisulfite sequencing (WGBS) technology. WGBS has been widely used to generate reference methylomes since 2010 and our improvements empower researchers to obtain additional information that could not be obtained before."

"To achieve this, we've developed a tool that dynamically segments WGBS methylomes into blocks of comethylation (COMETs) from which previously undetected information can be recovered. Given the high cost of WGBS, there is a clear benefit to extracting as much information as possible from a given dataset - our algorithms allow us to extract information that is not available to standard analysis. Essentially, we are offering a way to get more for less."

Professor Stephan Beck, Head of the Medical Genomics Research Group at UCL Cancer Institute, says: "This exciting new technology will advance our ability to understand phenotypic plasticity in health and disease, an important aspect of cancer research".

More information: *Nature Biotechnology*, [DOI: 10.1038/nbt.3605](https://doi.org/10.1038/nbt.3605)

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