Epigenomic Insights into Human Health & Disease

Presenting Author: Christopher G. Bell
William Harvey Research Institute, Barts and The London Faculty of Medicine, Queen Mary University of London, Charterhouse Square, London, EC1M 6BQ, United Kingdom
Contact@E-mail: c.bell@qmul.ac.uk

Abstract

The epigenome—the direct chemical modifications added to DNA as well as the chromatin-related protein packaging of the genome—enables the same genetic template to be activated or repressed in different cellular settings. These mechanisms enable cell-type specific function.
DNA methylation (5mC), the major epigenetic DNA modification in the human genome, is now recognized as a biomarker of immense clinical potential [1]. This is due to this ability to delineate precisely cell-type, as well as to quantitate both internal and external exposures. Furthermore, it can track chronological and 'biological' components of the ageing process via machine learning (ML) derived DNA methylation 'clocks' [2-3].
This talk will cover the current state of epigenomics: its ability to bring novel insights into disease pathogenesis as well as its role as a surrogate biomarker of traits and disease [4].

References

[1] Christofidou P. & Bell C.G., 'The analytical power of profiling the DNA methylome in human health and disease.' *Epigenomics* (2025) 17:9; 599-610.
[2] Bell C.G. 'Quantifying stochasticity in the aging DNA methylome' *Nature Aging* (2024) 4; 755–758
[3] Bell C.G. *et al*. 'DNA methylation ageing clocks: challenges & recommendations' *Genome Biology* (2019) 20:1; 1-24
[4] Bell C.G., 'Epigenomic Insights into Common Human Disease Pathology' *Cellular & Molecular Life Sciences* (2024) 81:178; 1-29.

Figure

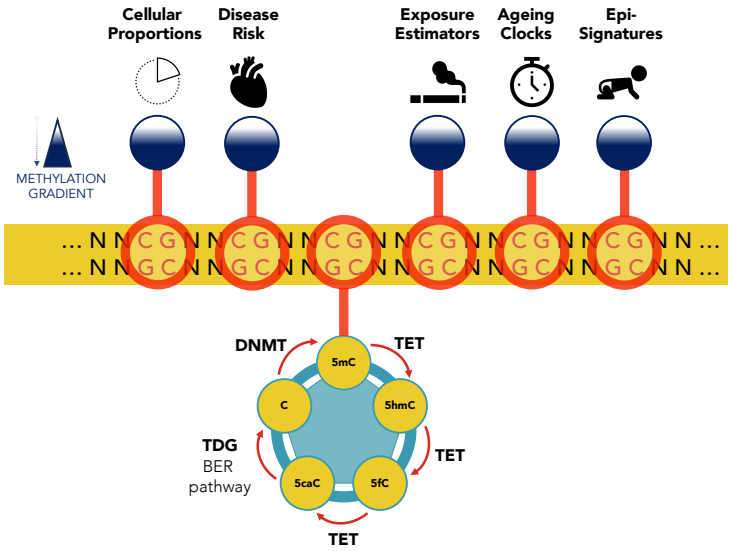

Figure 1: DNA methylation (DNAm) biomarkers and the DNAm cycle (from Ref [1] Christofidou & Bell, 2025).