

SUPPORTIVE ENVIRONMENTS FOR **PHYSICAL & SOCIAL ACTIVITY, HEALTHY AGEING & COGNITIVE HEALTH** 

WP4 **Interrogating biological** pathways to understand how environment exposure influence cognitive health/ageing

This work was supported by UK Research and Innovation [ES/V016075/1]





**Healthy Ageing Challenge** Social, Behavioural and Design Research

SPACE | Queen's University Belfast (qub.ac.uk)



## **OUR HEALTH IS LINKED TO THE ENVIRONMENT** where we are born, live, and work

How do factors in our external environment get 'under the skin' to change our biology and affect health outcomes?



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# WHAT IS EPIGENETICS?

- *Epi* = on top of
- *Genetics* = your genes that are typically inherited from parents
- Epigenetics describes the influence of chemical changes to DNA that lead to modifications in gene expression
- Epigenetics explains how a person's environment interacts with their genetics

#### **DNA METHYLATION**

- regulates gene expression like dimmer switch without altering DNA sequences
- is the most studied and therefore the best understood epigenetic modification



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# **DNA METHYLATION (DNAm) AGE**

- Epigenetic clocks are biomarker signatures that estimate biological age compared to years of life.
- Eleven epigenetic clocks have been generated for NICOLA.
- These clocks will help to demonstrate what environmental features lead to accelerated biological ageing & poor health outcomes.





### HOW CAN EPIGENETIC CLOCKS BE USED TO UNDERSTAND ENVIRONMENTAL INFLUENCE ON OUR DNA?



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### **MENDELIAN RANDOMISATION (MR)**

- MR can be used to find causal associations between a particular exposure (such as pollution) (X) and an outcome (such as dementia) (Y).
- This is possible because our genetic make-up does not change over our life course, so we are able to determine genetic correlations between an exposure and an outcome.
- A fundamental basis of MR is that our genetic make-up in • defined at conception, before the influence of **confounders** (U/C).
- Our epigenetic make-up does change over our lifetime, so we can't use epigenetic markers (X) directly in MR analysis. However, we can use the genetic changes that we know alter particular epigenetic changes (Z) as substitutes.

#### Key:

- Z Instrumental variable/Genetic variant (SNP)
- X Exposure (DNA methylation site as a consequence of air pollution exposure)
- Y Outcome (cognitive impairment or dementia)



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U/C - Unmeasured and measured confounders (sex, age, weight, physical activity)



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# Thank you

#### Figures created with Biorender.com

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