Understanding Society
THE UK HOUSEHOLD LONGITUDINAL STUDY

closer
Cohort & Longitudinal Studies Enhancement Resources

Why do social surveys have biomarker and genetic data?

Meena Kumari
Professor of Biological and Social Epidemiology
ISER, University of Essex

New sources of data for social science research
15th January 2018

An initiative by the Economic and Social Research Council, with scientific leadership by the Institute for Social and Economic Research, University of Essex, and survey delivery by the National Centre for Social Research.

Overview

- Use of biomarkers in social surveys - Me
- Overview of biomarker data available from secondary data resources - Me

- The use of biomarker data in social science research including examples demonstrating country-specific effects within the UK - you

The value of biomarker data in social surveys

The biomedical literature has generally treated socioeconomic position as a unitary construct. Likewise, the social science literature has tended to treat health as a unitary construct. To advance our understanding of the relationship between socioeconomic position and health, and ultimately to foster appropriate policies and practices to improve population health, a more nuanced approach is required—one that differentiates theoretically and empirically among dimensions of both socioeconomic position and health.

Herd et al 2007, p.223

What is a biomarker?

- *a characteristic that is objectively measured and evaluated as an indicator of normal biological processes, pathogenic processes, or pharmacologic responses to a therapeutic intervention.*

- National Institute of Health Biomarkers Definitions Working Group (1998)

Why are biomarkers useful for social science research?

- Earlier and more precise measures of health and illness
- The clinical iceberg
- Understanding the pathways by which social factors are associated with health
- ‘Objective’ assessment of health

Criteria for choice of biomarkers

- Environmental (socioeconomic, physical, psychosocial) and/or behavioural effect on marker
- Evidence of pathways to important health outcomes
- Affects reasonable proportion of general population
- Has reasonable prevalence among those affected
- Can be measured given the way our blood was collected and stored

- Core markers for main diseases
- Useful as individual measures and/or in combined risk scores
- Some novel markers – around biological ageing and stress

Earlier, more precise measures of health & illness

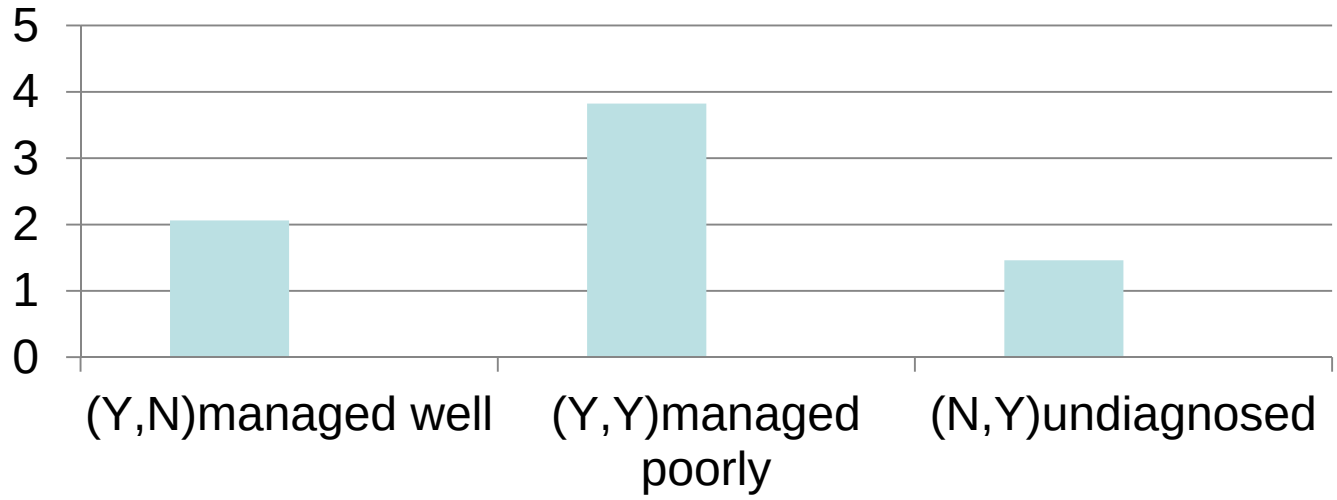
Specific conditions

Undiagnosed illness

Pre-disease risk factors

Effectiveness of treatment

Self-report diabetes and Hba1c defined disease



Davillas et al., unpublished

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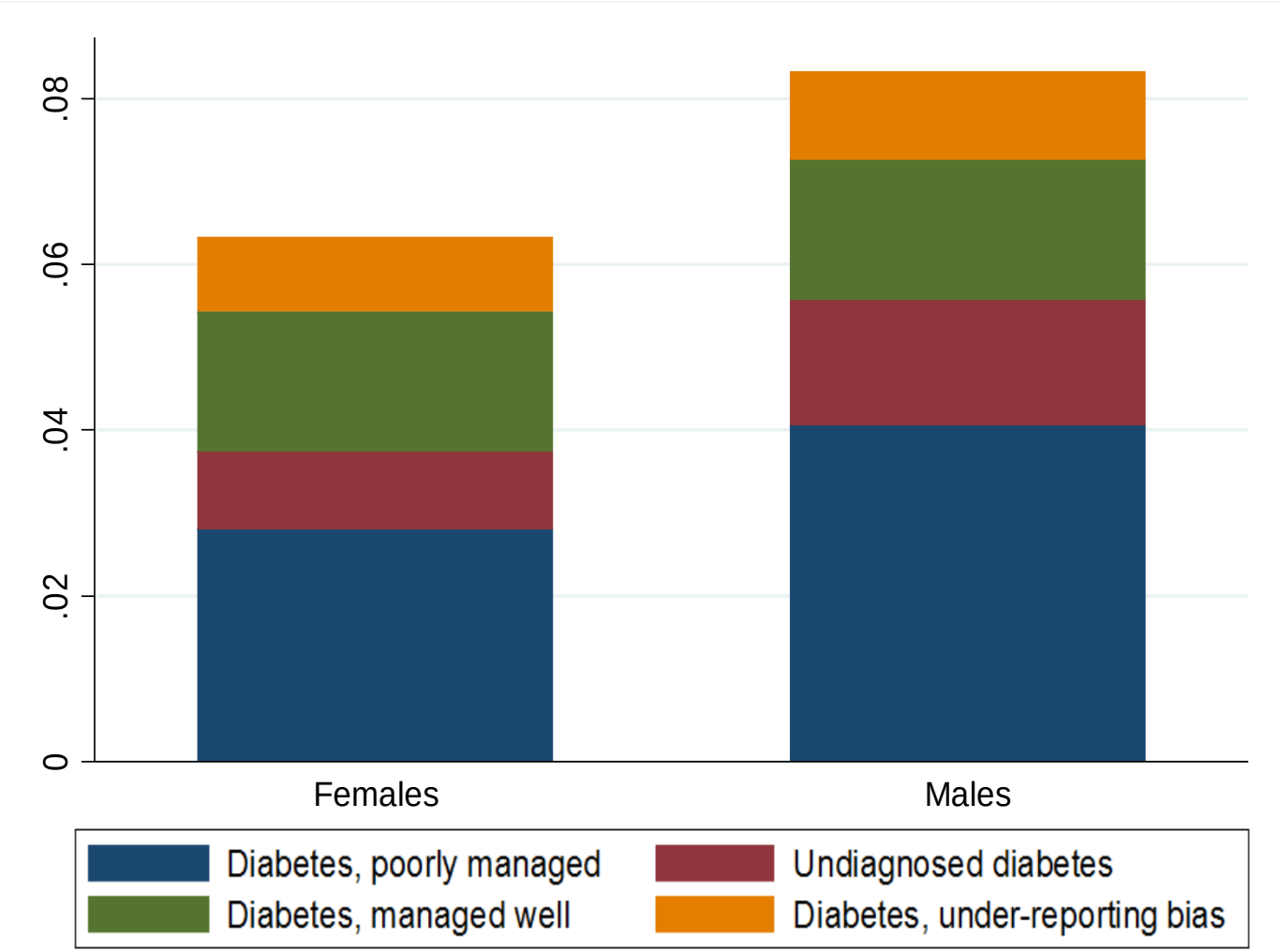
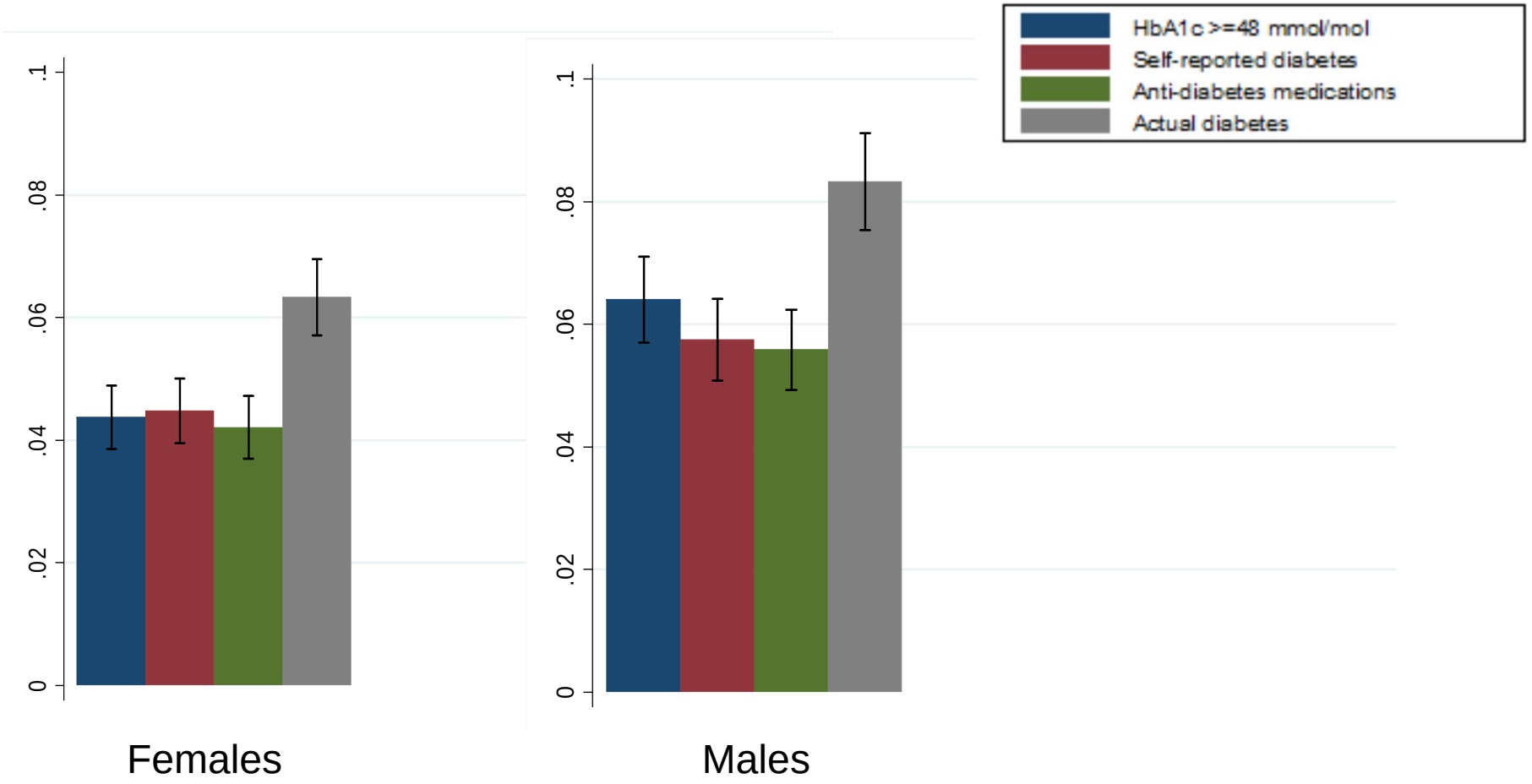
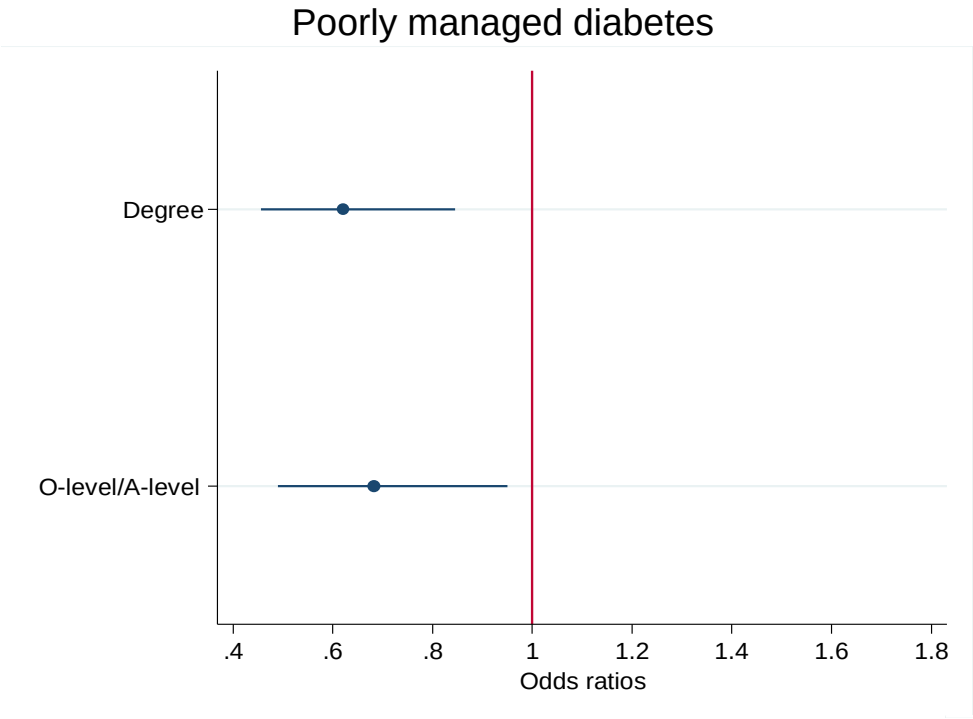
Decomposing the “actual diabetes” prevalence

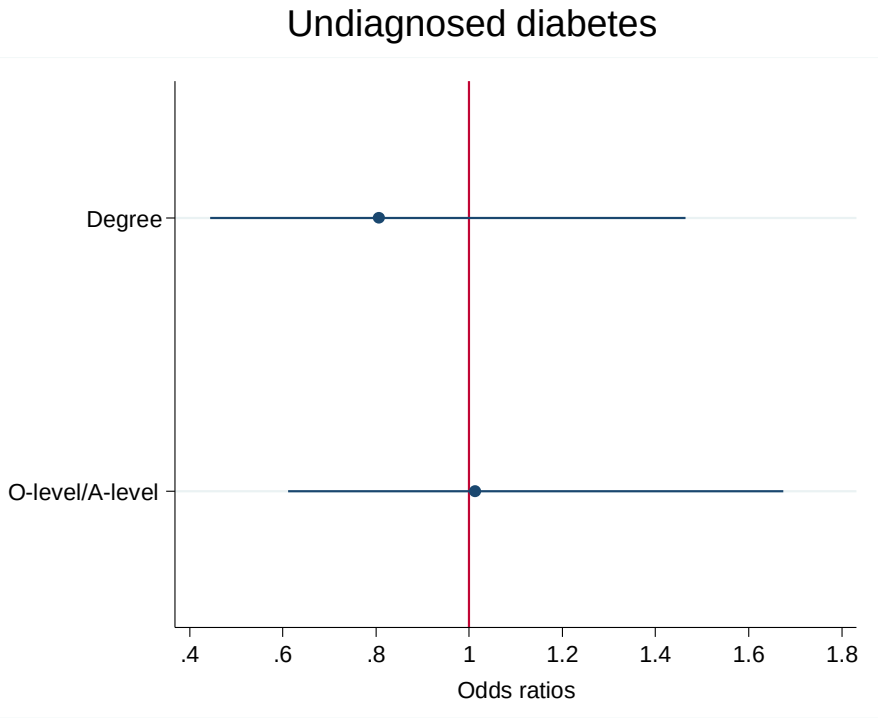


Combining the three measures



Associations with SEP (educational level attained)





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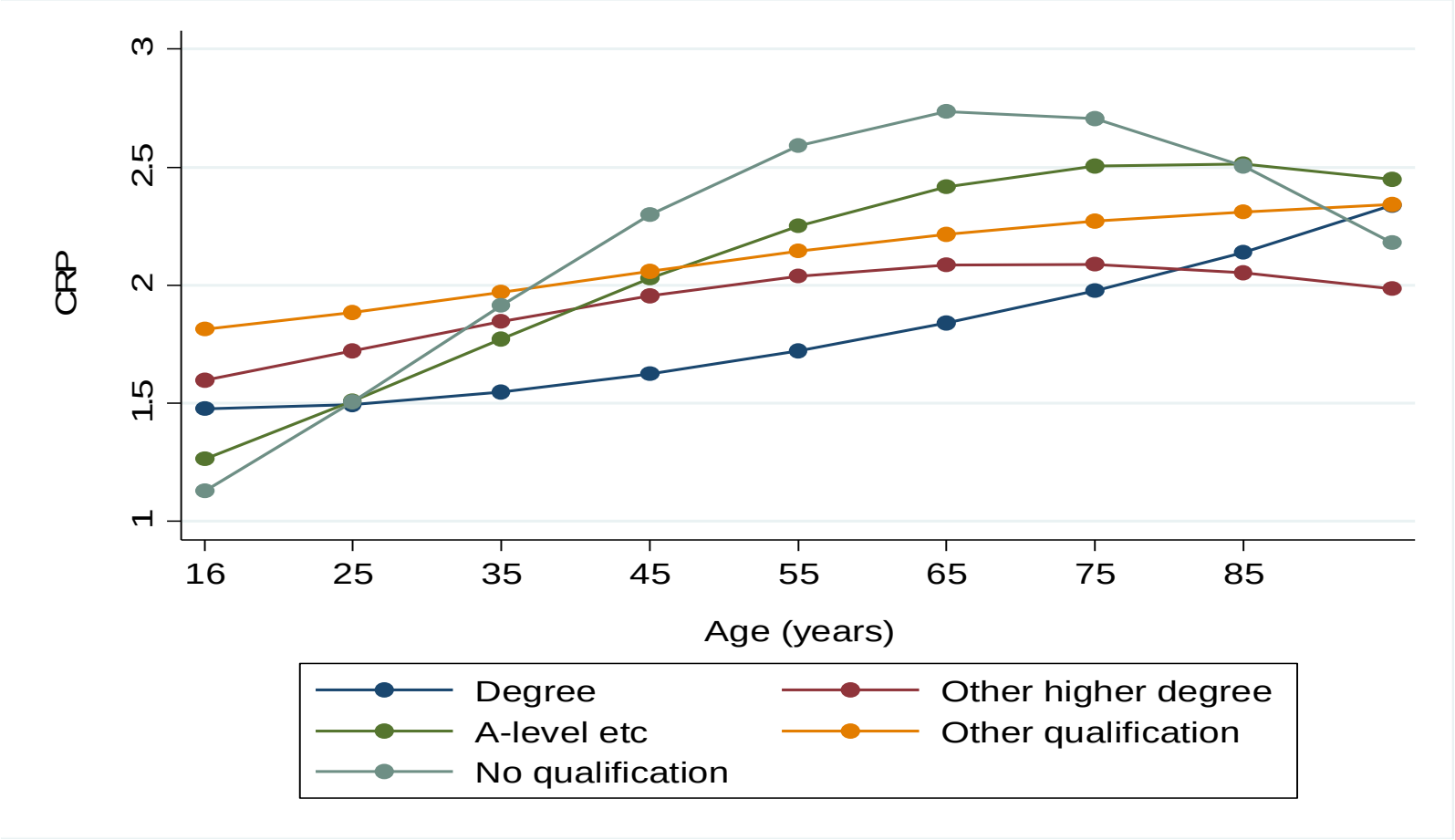
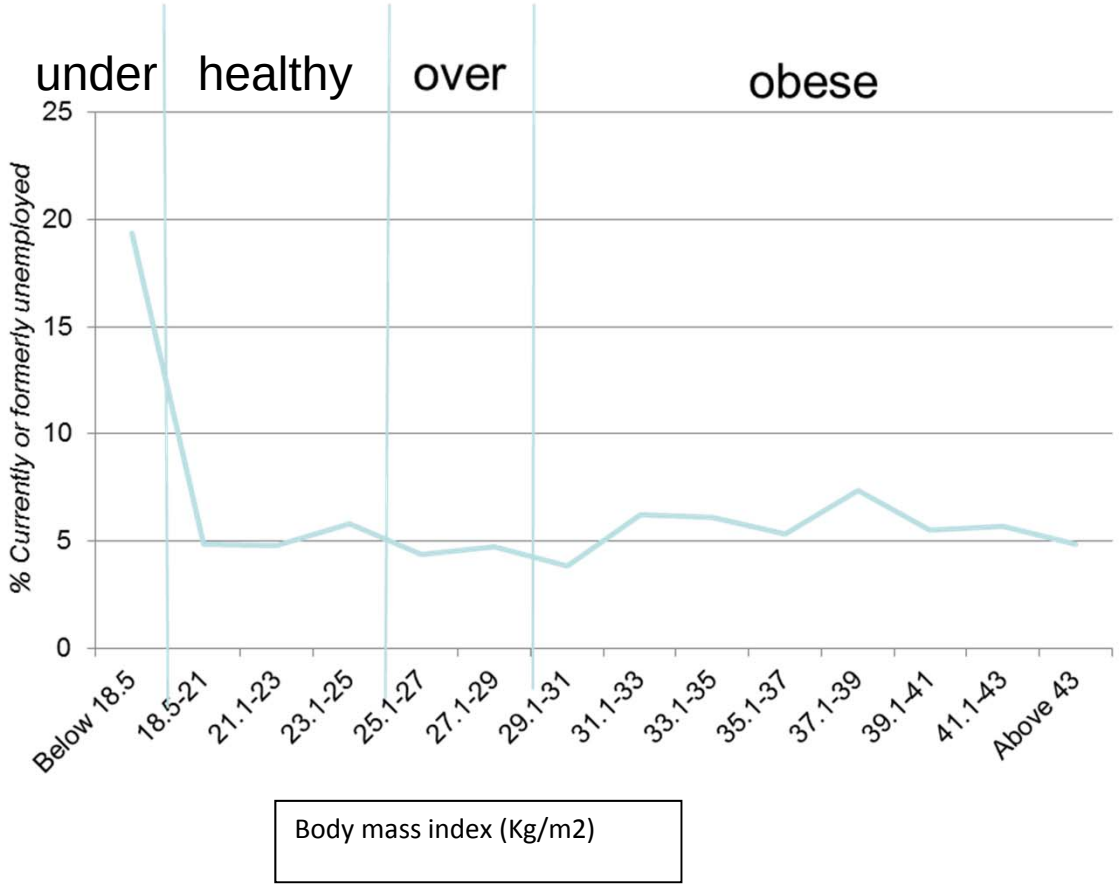
Biomarkers help us understand the pathways by which the environment gets under the skin



Davillas, Benzeval, Kumari, Scientific Reports, 2017

Unemployment by Body Mass Index in waves 1 and 2 of *Understanding Society*

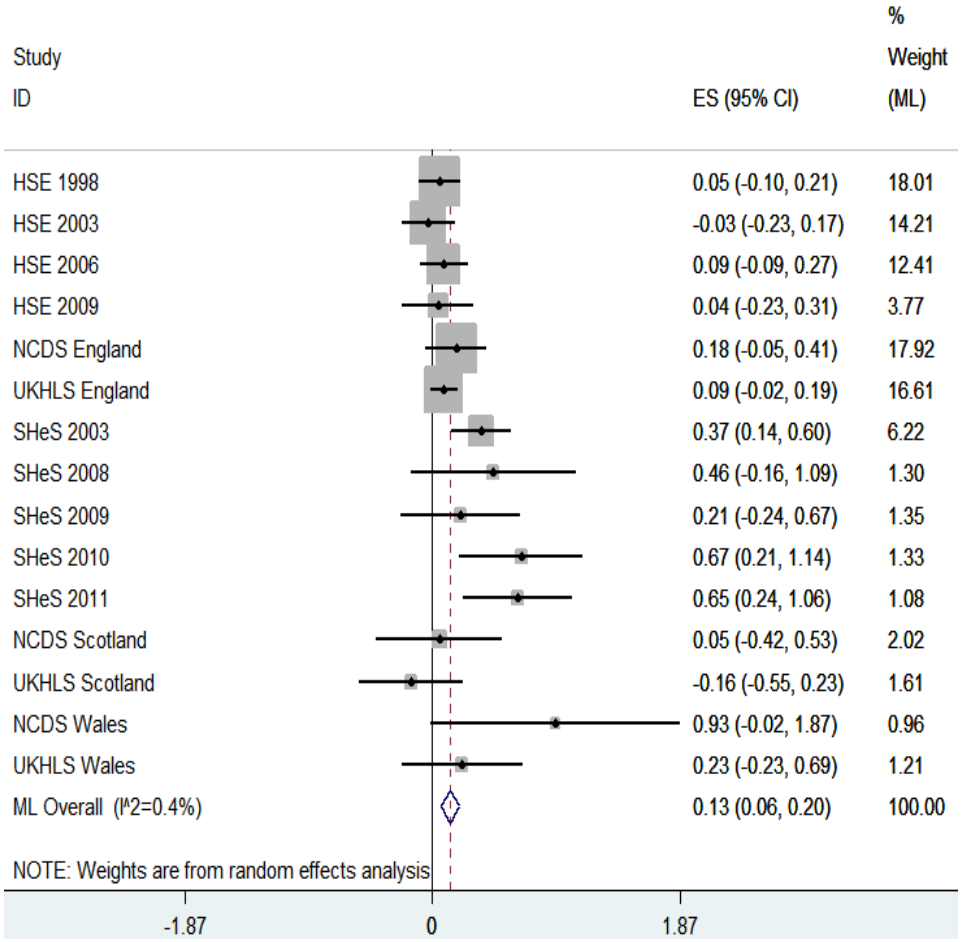
Weight=



quadratic term for centred BMI and current unemployment, p=0.004

From Hughes and Kumari, Prev. Med. 2017

Unemployment and CRP: country specific associations



COUNTRY STRATIFICATION				
Log-transformed CRP	Coeff	CI	p	Within-strata I^2
ENGLAND	0.08	-0.00-0.16	0.06	0.3%
SCOTLAND	0.33	0.13-0.53	0.001	3.0%
WALES	0.50	-0.05-1.05	0.08	7.2%
CRP>3mg/L	OR	CI	p	Within-strata I^2
ENGLAND	1.24	1.02- 1.51	0.03	n/a*
SCOTLAND	2.04	1.17-3.57	0.01	n/a
WALES	1.96	0.63-6.04	0.24	n/a

Full adjustment: age, age squared, gender, education, long-term illness, BMI, smoking status

Hughes et al., Brain, Behavior, Immunity.2017

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Objective is better than subjective

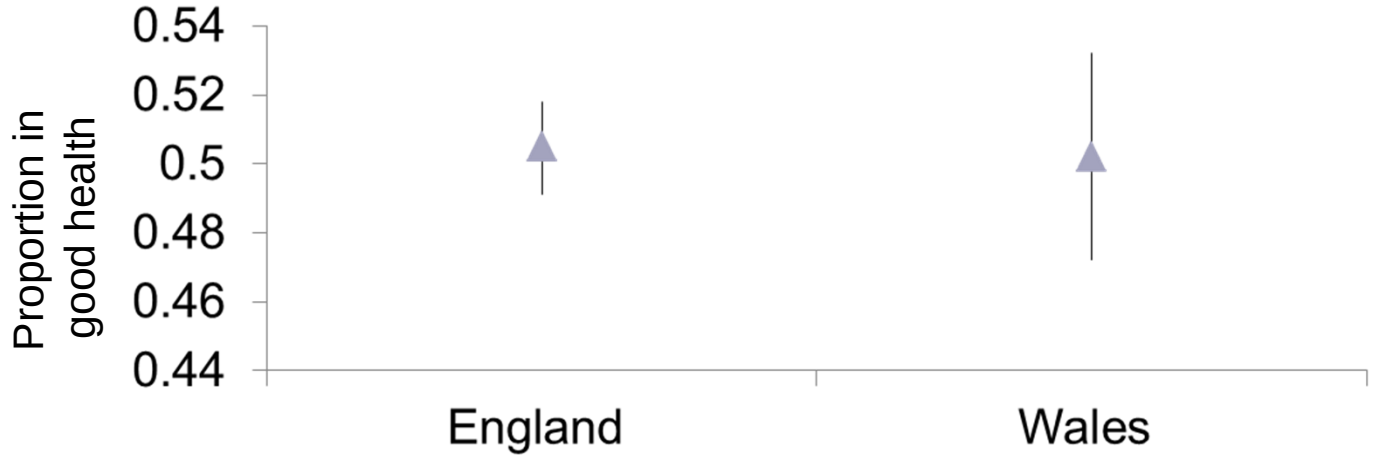
Income tertile	England	US
1	40.1	32.9
2	25.5	14.4
3	13.2	8.9
total	25.4	17.6
from Banks et al., 2009, IFS comparing men aged 55-64 in ELSA and HRS		
Education tertile	CRP (% above 3 mg/l)	
1	40.2	57.8
2	28.7	44.3
3	25.0	34.6
	Fibrinogen (% above 400mg/dl/)	
1	14.1	37.1
2	8.8	26.6
3	8.6	20.1
From Banks et al., 2007 NEJM		

Self reported ‘bad health’ in England vs. US suggests that health in poorer in England than in the US.

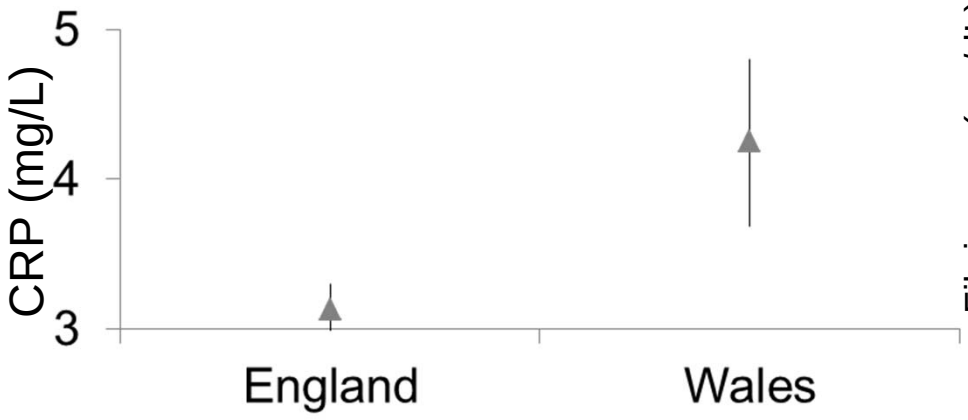
Objective data present the opposite picture

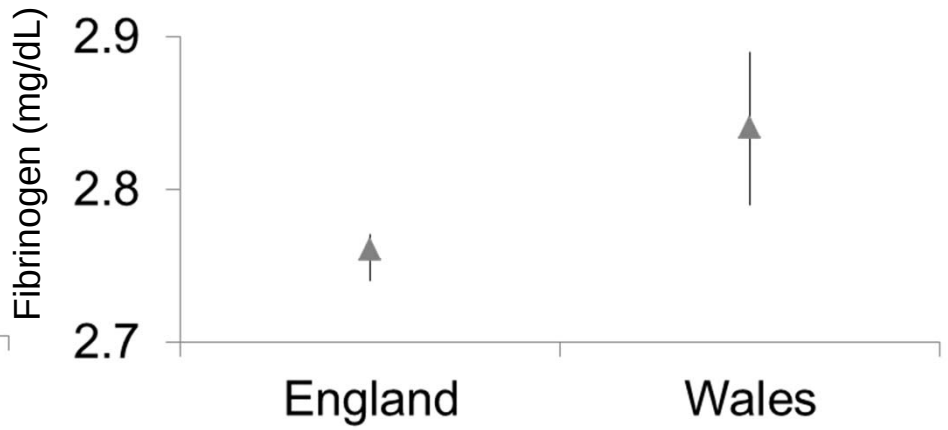
Objective and subjective measures

Self reported health in England and Wales suggests that 'health' is similar in the two countries.



Objective measures suggest better health in England





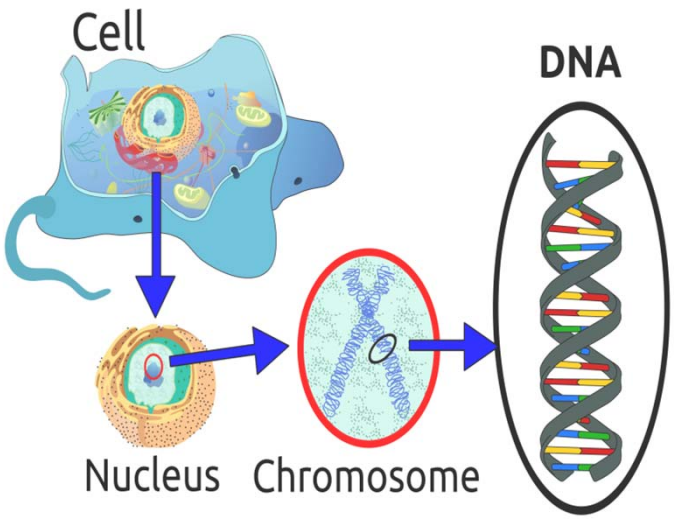
Understanding Society, unpublished

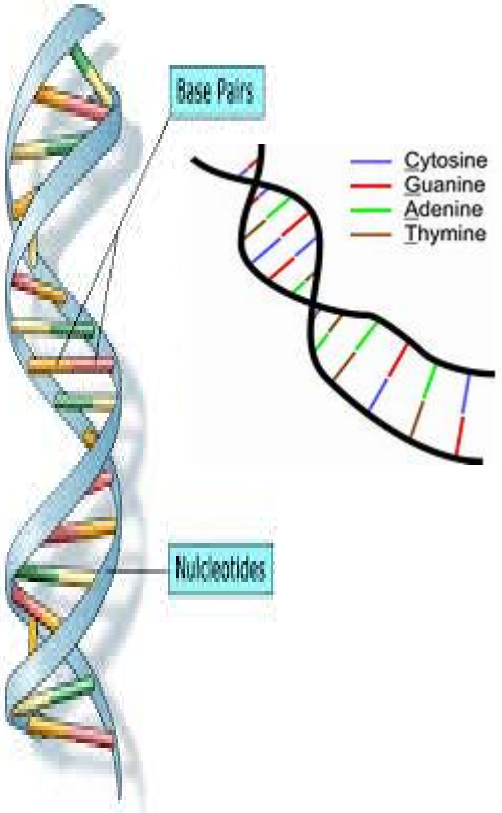
Why are genetic data useful for social science research?

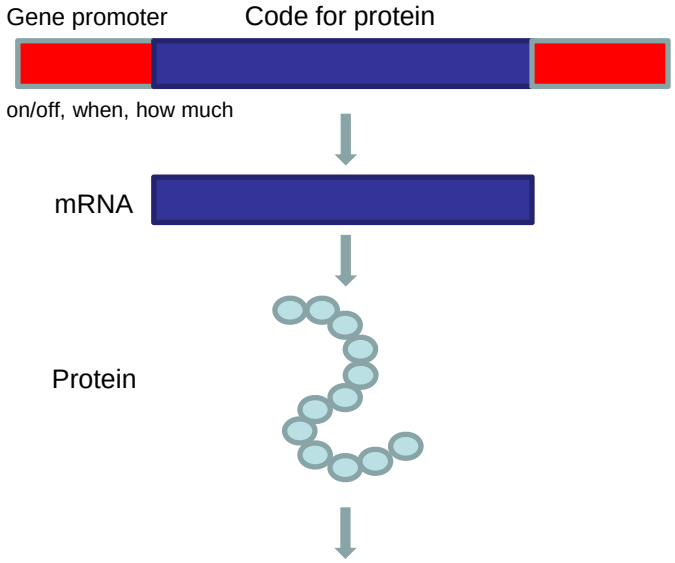
- Understanding the biological underpinnings of social phenotypes
- Better understand causation
- Gene-environment interactions
- Understanding how the environment gets under the skin

Genetics:

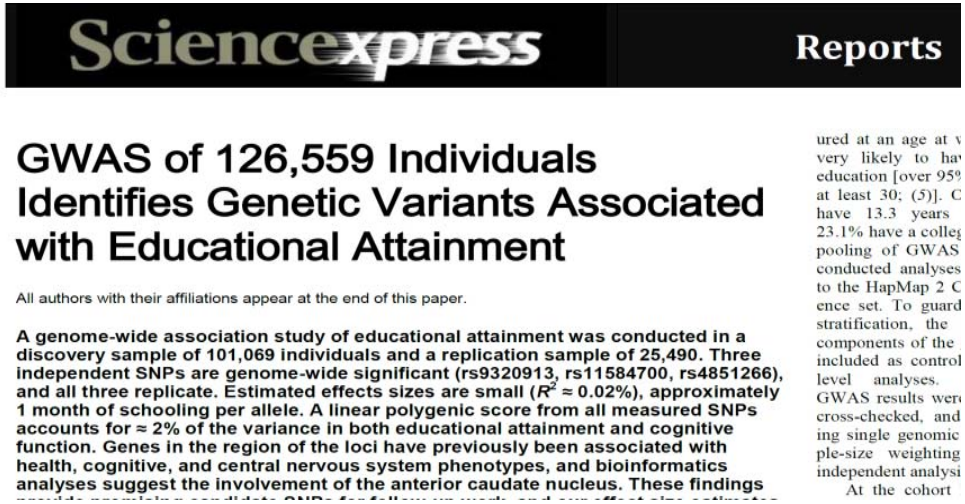
Genes, which are made up of DNA, act as instructions to make molecules called proteins.
In humans, genes vary in size from a few hundred DNA bases to more than 2 million bases.
The Human Genome Project has estimated that humans have between 20,000 and 25,000 genes.







Genetics: attempts to a better understand of the biological underpinnings of social phenotypes



Sciencexpress Reports

GWAS of 126,559 Individuals Identifies Genetic Variants Associated with Educational Attainment

All authors with their affiliations appear at the end of this paper.

A genome-wide association study of educational attainment was conducted in a discovery sample of 101,069 individuals and a replication sample of 25,490. Three independent SNPs are genome-wide significant (rs9320913, rs11584700, rs4851266), and all three replicate. Estimated effects sizes are small ($R^2 \approx 0.02\%$), approximately 1 month of schooling per allele. A linear polygenic score from all measured SNPs accounts for ≈ 2% of the variance in both educational attainment and cognitive function. Genes in the region of the loci have previously been associated with health, cognitive, and central nervous system phenotypes, and bioinformatics analyses suggest the involvement of the anterior caudate nucleus. These findings

ured at an age at v
very likely to hav
education [over 95%
at least 30; (5)]. C
have 13.3 years
23.1% have a colleg
pooling of GWAS
conducted analyses
to the HapMap 2 C
ence set. To guard
stratification, the
components of the
included as control
level analyses.
GWAS results were
cross-checked, and
ing single genomic
ple-size weighting
independent analysi
At the cohort

- Educational Attainment GWAS
  - ‘Neural SNPs’
  - Associated with phenotypes downstream and upstream of educational attainment?

Why are genetic data useful for social science research?

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Better understand causation: using genes as instruments in instrumental variable analyses

- Better adapt traditional econometric methodology to Mendelian randomisation

American Journal of Epidemiology

Vol. 173, No. 4
DOI: 10.1093/aje/kwq444
Advance Access publication: January 19, 2011

Original Contribution

Examining Overweight and Obesity as Risk Factors for Common Mental Disorders Using Fat Mass and Obesity-Associated (*FTO*) Genotype-Instrumented Analysis

The Whitehall II Study, 1985–2004

Mika Kivimäki*, Markus Jokela, Mark Hamer, John Geddes, Klaus Ebmeier, Meena Kumari, Archana Singh-Manoux, Aroon Hingorani, and G. David Batty

* Correspondence to Dr. Mika Kivimäki, Department of Epidemiology and Public Health, Faculty of Biomedical Sciences, University College London, 1-19 Torrington Place, London WC1E 6BT, United Kingdom (e-mail: m.kivimaki@ucl.ac.uk).

Initially submitted January 11, 2010; accepted for publication May 10, 2010.

Why are genetic data useful for social science research?

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Gene-environment interactions

- Issues in measurement of ‘environment’
- Greater than the usual issues around power

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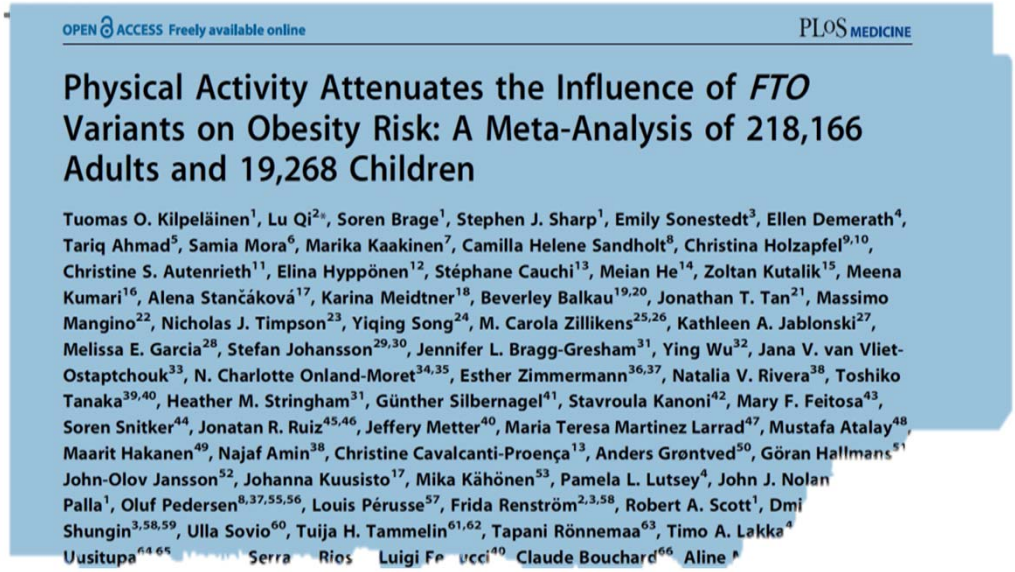

OPEN ACCESS Freely available online PLoS MEDICINE

Physical Activity Attenuates the Influence of *FTO* Variants on Obesity Risk: A Meta-Analysis of 218,166 Adults and 19,268 Children

Tuomas O. Kilpeläinen[1], Lu Qi[2*], Soren Brage[1], Stephen J. Sharp[1], Emily Sonestedt[3], Ellen Demerath[4], Tariq Ahmad[5], Samia Mora[6], Marika Kaakinen[7], Camilla Helene Sandholt[8], Christina Holzapfel[9,10], Christine S. Autenrieth[11], Elina Hyppönen[12], Stéphane Cauchi[13], Meian He[14], Zoltan Kutalik[15], Meena Kumari[16], Alena Stančáková[17], Karina Meidtner[18], Beverley Balkau[19,20], Jonathan T. Tan[21], Massimo Mangino[22], Nicholas J. Timpson[23], Yiqing Song[24], M. Carola Zillikens[25,26], Kathleen A. Jablonski[27], Melissa E. Garcia[28], Stefan Johansson[29,30], Jennifer L. Bragg-Gresham[31], Ying Wu[32], Jana V. van Vliet-Ostaptchouk[33], N. Charlotte Onland-Moret[34,35], Esther Zimmermann[36,37], Natalia V. Rivera[38], Toshiko Tanaka[39,40], Heather M. Stringham[31], Günther Silbernagel[41], Stavroula Kanoni[42], Mary F. Feitosa[43], Soren Snitker[44], Jonatan R. Ruiz[45,46], Jeffery Metter[40], Maria Teresa Martinez Larrad[47], Mustafa Atalay[48], Maarit Hakanen[49], Najaf Amin[38], Christine Cavalcanti-Proença[13], Anders Grøntved[50], Göran Hallmans[51], John-Olov Jansson[52], Johanna Kuusisto[17], Mika Kähönen[53], Pamela L. Lutsey[4], John J. Nolan, Palla[1], Oluf Pedersen[8,37,55,56], Louis Pérusse[57], Frida Renström[2,3,58], Robert A. Scott[1], Dmi Shungin[3,58,59], Ulla Sovio[60], Tuija H. Tammelin[61,62], Tapani Rönnemaa[63], Timo A. Lakka[4], Uusitupa[64,65], Serra Rios, Luigi Fe ucci[40], Claude Bouchard[66], Aline

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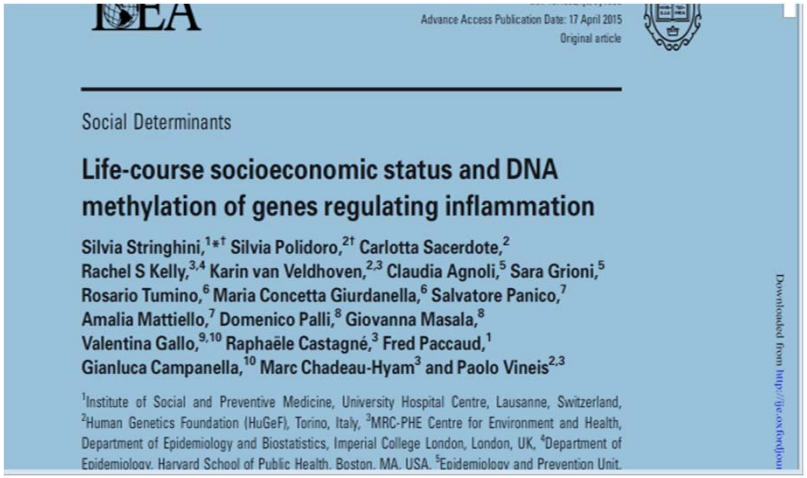
Environment and genome: modification of genetic expression

- DNA methylation

and gene expression

are socially patterned



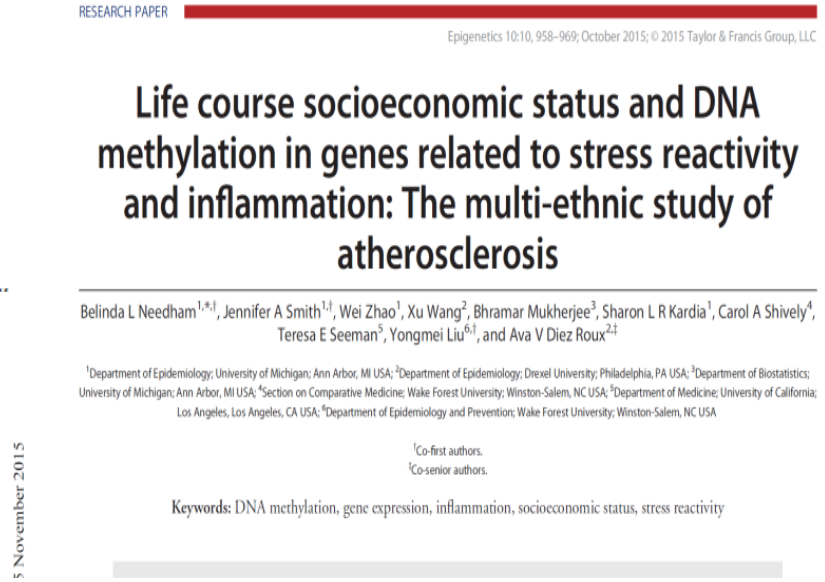
Advance Access Publication Date: 17 April 2015
Original article

Social Determinants

Life-course socioeconomic status and DNA methylation of genes regulating inflammation

Silvia Stringhini,[1]*† Silvia Polidoro,[2]† Carlotta Sacerdote,[2] Rachel S Kelly,[3,4] Karin van Veldhoven,[2,3] Claudia Agnoli,[5] Sara Grioni,[5] Rosario Tumino,[6] Maria Concetta Giurdanella,[6] Salvatore Panico,[7] Amalia Mattiello,[7] Domenico Palli,[8] Giovanna Masala,[8] Valentina Gallo,[9,10] Raphaële Castagné,[3] Fred Paccaud,[1] Gianluca Campanella,[10] Marc Chadeau-Hyam[3] and Paolo Vineis[2,3]

[1]Institute of Social and Preventive Medicine, University Hospital Centre, Lausanne, Switzerland, [2]Human Genetics Foundation (HuGeF), Torino, Italy, [3]MRC-PHE Centre for Environment and Health, Department of Epidemiology and Biostatistics, Imperial College London, London, UK, [4]Department of Epidemiology, Harvard School of Public Health, Boston, MA, USA, [5]Epidemiology and Prevention Unit,



RESEARCH PAPER

Epigenetics 10:10, 958–969; October 2015; © 2015 Taylor & Francis Group, LLC

Life course socioeconomic status and DNA methylation in genes related to stress reactivity and inflammation: The multi-ethnic study of atherosclerosis

Belinda L Needham[1,*,†], Jennifer A Smith[1,†], Wei Zhao[1], Xu Wang[2], Bhramar Mukherjee[3], Sharon L R Kardia[1], Carol A Shively[4], Teresa E Seeman[5], Yongmei Liu[6,†], and Ava V Diez Roux[2,‡]

[1]Department of Epidemiology; University of Michigan; Ann Arbor, MI USA; [2]Department of Epidemiology; Drexel University; Philadelphia, PA USA; [3]Department of Biostatistics; University of Michigan; Ann Arbor, MI USA; [4]Section on Comparative Medicine; Wake Forest University; Winston-Salem, NC USA; [5]Department of Medicine; University of California; Los Angeles, Los Angeles, CA USA; [6]Department of Epidemiology and Prevention; Wake Forest University; Winston-Salem, NC USA

[†]Co-first authors.
[‡]Co-senior authors.

Keywords: DNA methylation, gene expression, inflammation, socioeconomic status, stress reactivity

5 November 2015

Data sources: biomarkers

- UKDA
  - *Understanding Society*
  - English Longitudinal Study of Ageing
  - Health Survey for England
  - Scottish Health surveys
  - NCDS (1958 birth cohort)
  - BCS70 (1970 birth cohort)*

*forthcoming

Data sources: biomarkers

- CLOSER
  - ALSPAC (children of the ‘90s)
  - Hertfordshire Cohort Study
  - NCDS (1958 British birth cohort)
  - NSHD (1946 British birth cohort)
  - BCS70 (1970 birth cohort)
  - Southampton Women’s Survey
  - *Understanding Society*: UKHLS

Data sources: genetic and genomic data

- DNA
  - *Understanding Society*
  - English Longitudinal Study of Ageing
  - NCDS (1958 birth cohort)
  - BCS70 (1970 birth cohort)*
  - ALSPAC (children of the ‘90s)
  - Hertfordshire Cohort Study
  - NSHD (1946 British birth cohort)
  - Southampton Women’s Survey
- Epigenetic
  - *Understanding Society*
  - NCDS (1958 birth cohort)*
  - BCS70 (1970 birth cohort)*

} Metadac.ac.uk

} Closer.ac.uk

Data information

- CLOSER: catalogue of the biomarker data

https://www.closer.ac.uk/wp-content/uploads/A-guide-to-the-biomarker-data-in-the-CLOSER-studies-FINAL.compressed.pdf

Over 50 biomarkers in over 50,000 participants

- *Understanding Society*

https://www.understandingsociety.ac.uk/documentation/health-assessment

21 biomarkers in 13,000 participants

Thanks!

- (How) can we incorporate biomarkers into your work?

Useful websites for further information

- www.understandingsociety.ac.uk
- www.closer.ac.uk
- www.ukdataservice.ac.uk
- www.metadac.ac.uk

Meena Kumari

mkumari@essex.ac.uk

https://www.iser.essex.ac.uk/people/mkumari