discrimination and calibration for performance of a model. Framingham risk score (FRS) for cardiovascular disease is a widely used one which has been validated in different countries but its clinical usefulness has been neglected.

Methods We checked discrimination of FRS and so its calibration and clinical usefulness before and after recalibration in a population based cohort, Tehran lipid and glucose study, of 2640 men and 3584 women aged 30–74 years. To check clinical usefulness, we used decision curve analysis (DCA) and calculated net benefit of treatment for patients with ≥20% of 10 year probability of disease according to FRS model.

Results The area under the curve for FRS model, was 0.794 and 0.838 for men and women respectively. The original model had a poor calibration but got a good one after recalibration (Hosmer-Lemeshow χ^2 statistic of 16.8 for men and 18.4 for women). Based on DCA, FRS was clinically useful in cut points of 10%–30%, as threshold probability of disease that a patient should be treated, before and after recalibration. The net benefit of model to treat patients at cut point of 20% did not differ significantly before and after recalibration in both men and women (p>0.3 based on bootstrap resampling).

Conclusion Original FRS has a good discrimination and poor calibration in Iran but considering clinical usefulness, it can be used even without recalibration.

P1-32 | **TESTING LIFE COURSE MODELS TO INVESTIGATE THE EFFECT OF SOCIOECONOMIC POSITION ON CRYSTALLISED COGNITIVE FUNCTION IN OLDER AGE, ACCOUNTING FOR MISSING DATA**

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Objective To investigate how lifetime socioeconomic position (SEP) is associated with later-life crystallised cognitive function, accounting for different missing data mechanisms.

Participants A nationally representative population sample born in 1946 (MRC National Survey of Health and Development; NSHD, N=5362), and a sample of British civil servants (Whitehall II; WHII, N=10 308).

Methods Novel structured statistical approach to distinguish between accumulation and sensitive period life course models using SEP measures from childhood, early-adulthood and midlife. Results of complete case (CC) (assuming missing completely at random), multiple imputation (MI) (missing at random) and a Heckman selection model (missing not at random) were compared.

Outcomes National Adult Reading Test, age 53 (NSHD); Mill Hill Test, age 55–79 (WHII).

Results NSHD: After adjusting for childhood cognitive function, the best fitting model was an accumulation model allowing SEP at each time point to have its own estimate. However estimates varied by missing data method (women: childhood SEP: CC: coefficient=1.11 (95% CI 0.15 to 2.06), MI: coefficient=1.82 (95% CI 0.87 to 2.76), Heckman: coefficient=0.70 (95% CI −0.38 to 1.78)). WHII (not adjusted for childhood cognition): the best fitting model represented accumulation in adulthood only, with childhood SEP not significant.

Conclusion Despite adjustment for childhood cognitive score, childhood SEP remains important in NSHD, whereas in Whitehall II childhood SEP was not associated with cognitive function. These differences may be due to recall bias of early SEP in WHII. Our findings demonstrate the utility of the method for distinguishing models of how SEP across the life course influences cognition and the importance of dealing with missing data.

P1-33 | **ADULT DNA METHYLATION IN RELATION TO PRENATAL NUTRITION AND RISK FACTORS FOR CARDIO-VASCULAR DISEASE**

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Epigenetic changes may play an important role in the development of adult disease. Exposure to a prenatal famine environment has been associated with a persistent decrease in DNA methylation of the IGF2 gene, and other early life factors like birthweight with adult genomic DNA methylation. We evaluated genomic DNA methylation in relation to prenatal nutrition and CVD risk factors. Our study includes 353 births from three clinics with prenatal exposure to the Dutch famine of 1944–1945, 296 before-or-after the famine births as unexposed time controls, and 311 same-sex siblings of either group as unexposed family controls. All study subjects underwent medical examinations and DNA collections at a mean age of ∼58 years. We used Luminometric methylation (LUMA) and LINE-1 (Long Interspersed Nucleotide Element 1) pyrosequencing assays to quantify genomic DNA methylation. Mean DNA methylation by LUMA was 75.5% (SD 2.2) and by LINE-1 77.1% (SD 2.5). Neither was associated with prenatal famine exposure. Using all controls, famine exposure showed a decline of 0.12 % (95% CI −0.42 to 0.18; p=0.44) by LUMA and an increase of 0.05 % (−0.33 to 0.21; p=0.68) by LINE-1. Using family controls, the increases were 0.36 % (LUMA) and 0.16 % (LINE-1). Neither assay was associated with adult cholesterol, blood pressure, body size, type 2 diabetes mellitus, gender or age. Our results suggest that these genomic DNA methylation markers may not be associated with prenatal famine; further work should target regions in the genome that may be differentially methylated in response to early life exposures.

P1-34 | **CAN ASSOCIATIONS BETWEEN PRENATAL NUTRITION AND BODY MASS INDEX BE EXPLAINED BY COMMON GENETIC VARIANTS? FINDINGS FROM THE DUTCH HUNGER WINTER FAMILIES STUDY**

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Genome wide association (GWAS) studies have identified single nucleotide polymorphisms (SNPs) related to body mass index (BMI: kg/m^2). Associations have also been reported between fetal malnutrition and BMI. We use the circumstances of the Dutch Hunger Winter of 1944–1945 to further examine these relations. We studied 348 adult men and women born in affected cities in the western Netherlands who had been exposed to famine during pregnancy, 294 born before or after the famine as time-controls, and 305 same-sex unexposed siblings of above groups as family controls. Mean age at examination was 58 years. We evaluated common variants in the FTO, TMEM18, MC4R, GNPDA2, BDNF, SEC16B, NEGR1, SH2B1, SFRS10, MTCH2, and KCTD15 genes related to BMI. A genetic risk score was calculated for each individual by summing the number of risk alleles in these genes. Scores were also weighted using recent GWAS estimates of gene specific changes in BMI per risk allele. Institutional ethics committees gave the appropriate approvals for the study. Genetic risk scores had a mean of 11.4 (SD 2.2) and were not related to prenatal famine. Adult BMI was 1.34 units higher among famine exposed (95% CI 0.73 to 1.94) and further adjustments for risk score had little effect. There was no statistical