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MEASURES OF SOCIO-DEMOGRAPHIC FACTORS FOR CHILD

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CUTTING EDGE METHODOLOGY

P1-6 MEASURES OF SOCIO-DEMOGRAPHIC FACTORS FOR CHILD HEALTH RESEARCH

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Background *H pylori* infection is one of the major causes of health problems with considerable morbidity and mortality. *H pylori* seroprevalence is common in populations with poor standards of sanitation and hygiene.
Methods A two-stage cluster sampling technique was employed to draw the required sample. A crowding index with three categories (low, moderate, high) was constructed by dividing the number of individuals per household by the number of the rooms. Assessment of socioeconomic status (SES) was calculated by Hollingstead Index (HI).
Results Serum of 1976 children was tested. *H pylori* seropositivity in 1–5 years were 53.5%. It increased with moderate crowding index (CRI) of 2–4 to 45.9% and to 51.2% with CRI >4. In middle SES, seropositivity was 331 (50.5%) while in lower SES 500 (47.1%). Multivariate analysis showed *H pylori* seroprevalence was high in 6–10 and 11–15 years (OR: 1.5, 95% CI 1.2 to 1.9 and OR: 1.9, 95% CI 1.56 to 2.47, respectively), in lower-middle SES (OR: 1.6, 95% CI 1.2 to 2.1 and OR: 1.5, 95% CI 1.10 to 2.0, respectively) and uneducated fathers (OR: 1.58, 95% CI 1.27 to 1.95).
Conclusion *H pylori* seropositivity increased with age, in low-middle SES and is related to father's educational status.

P1-7 INFLUENZA RECYCLING AND EPIDEMIOLOGIC EVOLUTION: AN ALTERNATIVE TO OMRAN'S EPIDEMIOLOGIC TRANSITION THEORY FOR POPULATION CHANGE

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The sustained increase in longevity initiated during the second half of the 20th Century poses huge challenges upon the public and private healthcare and pensions' systems. Current theories do not explain the observed phenomenon, what precludes predictions of its future trends. The authors goal was to go back to Omram's original project—to develop an epidemiologic theory of the demographic change—but looking for an explanation alternative to the epidemiologic transition proposed by him. The study expands upon a previous one, that showed, for the first time, a cohort association between the mortality burden of 1918 Influenza Pandemic and the 20th Century rise in CHD mortality. Based on an age-period-cohort analysis of USA and UK mortality (and natality) data (1933–2005) and on the epidemiology of influenza as we know it, it is shown that, overall, temporal changes in mortality and natality accompany the recycling of influenza A viruses, that is, the re-exposure of human populations, from time to time, to influenza A subtypes that circulated in the past. Mortality (and natality) and main causes of death change as birth cohorts (whole population and maternal) primed at early life with one (period-specific) influenza A sub-type, course through subsequent influenza A environments over time.[1] The implications of this new theory to demography and to the epidemiology of several diseases are revolutionary.

REFERENCE

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P1-8 PRINCIPAL COMPONENTS ANALYSIS OF DIET IS NOT GOOD AT IDENTIFYING FOODS THAT ARE CAUSALLY LINKED TO DISEASE: A SIMULATION STUDY

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Introduction Dietary patterns derived empirically from food frequency questionnaire (FFQ) data using principal components analysis (PCA) are widely employed for the investigation of diet-disease relationships. The aim of the study was to investigate whether PCA performed better at identifying associations between diet and disease than an analysis of each individual food in the FFQ separately after adjusting for multiple testing, a process we refer to as exhaustive single food analysis (ESFA).
Methods Using simulated data employing a known model for the associations between food intakes and disease, and a realistic joint distribution of food intakes, we investigated the performance of PCA and ESFA in correctly identifying associations between diet and disease. Performance was assessed in terms of the power with which we could identify at least one association between a food intake and disease, and the power and false discovery rate (FDR) for identifying specific food intakes that were causally linked to disease in the model.
Results ESFA had greater power than PCA to detect an association of at least one food with disease, and greater power and lower FDR for identifying specific foods causally linked to disease. With both methods FDRs increased with sample size, even using an FDR-controlling adjustment. However, when we adjusted the ESFA for foods that were significant in univariate analyses, FDRs were controlled at the specified level.
Conclusions An exhaustive analysis of single foods out-performed PCA in identifying associations between diet and disease using FFQ data.

P1-9 THE HEALTH IMPACT FUND-MEETING THE CHALLENGE OF HEALTH IMPACT ASSESSMENT

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Introduction The Health Impact Fund (HIF) is a publicly funded international agency proposed to enable pharmaceutical innovators to register a product for health impact rewards in exchange for selling it worldwide at cost. Supplementing the current patent regime, the HIF would improve incentives to research diseases concentrated among the poor. A workable HIF presupposes a consistent, predictable, and contractible method of health impact assessment.
Methods We reviewed the literature using search terms,"health impact assessment tools" and an exploratory workshop for all stakeholders was held at the National Institute for Health and Clinical Excellence in April 2010.
Results Although there are many challenges with the nature of current epidemiological data and their application to global health, there is scope for improvement and the HIF may help to trigger and sustain such enhancements. Moreover, the HIF would use much more information than the present system. The following steps in health impact assessment need to occur for each registered product: defining subgroups, establishing baseline treatments, defining incremental health impact by subgroup, measuring the numbers of patients treated in each subgroup, and a process of appeal.

P1-6 Measures of socio-demographic factors for child health research

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