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#### COMPARISON OF FIVE, WITH AND WITHOUT TIME-DEPENDENT COVARIATES, SURVIVAL MODELS AS DESCRIPTORS FOR CULLING DISTRIBUTIONS IN DAIRY COWS

doi:10.1136/jech.2011.142976c.44

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**Introduction** This paper presents the results of a study to evaluate survival analysis the effect of treated diseases on the culling rate (remove from herd) in dairy cows.

Methods Five different models, with and without time-dependent covariates, using Gompertz distribution were studied. Model 1 treated diseases as a binary and time-independent covariates. Models 2 through 5 treated diseases as time-dependent covariates. For each observation, we split follow-up time in intervals each corresponding to a different lactation month. In other words, each observation from study entry until culling or censoring was split into several one-month observations by Lexis expansion of the original dataset. Model 2 assumed an animal experience a certain disease from the beginning of the occurrence of that disease by the end of follow-up period. Model 3 assumed cows are at risk from the begging of the study until the disease occurred (inverse of model 2). In model 4 and 5 an animal was assumed to experience a certain disease for 1 month if the disease occurred during this period. The only difference is in model 4 assumed diseases occurred only one time and in model 5 multiple disease occurrences at different months were considered as different episodes.

**Results** According to Akaike's Information Criterion (AIC) value and Cox-Snell residuals model 5 was the best model.

**Conclusion** A comparison of culling models with and without time-dependent covariates found that models without time dependency tended to seriously underestimate the risk of a disease on culling.

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## THE IMPLICATIONS OF USING DIFFERENT METHODS TO MEASURE ETHNICITY IN A COHORT STUDY

doi:10.1136/jech.2011.142976c.45

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**Introduction** Maori, the indigenous population of New Zealand, have the right to good health, healthy conditions and high quality epidemiological data. Consistent, comprehensive ethnicity data are crucial for appropriate representation of Maori health status and in order to monitor governmental progress towards equity in health. Maori have been undercounted in health datasets in the past and different methods of adjusting for this undercount have been developed and used in the calculation of population rates. This study investigates the implications of using four different methods to measure ethnicity in a cohort study.

**Methods** Using a cohort of patients with ischaemic heart disease (IHD), a sensitivity analysis was applied to determine the impact of four different methods of measuring Maori ethnicity on outcomes that determine disparities in both mortality and receipt of procedures, between Maori and non-Maori with IHD.

**Results** There was some slight variation in results with the use of different methods to measure ethnicity. Overall however, the interpretation of the results would remain largely unchanged with the use of the different methods. These implications will be discussed. This study has wider considerations for the measurement

of ethnicity in a cohort study, the right of indigenous populations to high quality ethnicity data, and the ongoing critique and development of an epidemiology that is responsive to the needs and aspirations of Maori in New Zealand.

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## COLLIDER-STRATIFICATION BIAS COMPLICATES ESTIMATION OF THE STRENGTH OF RISK FACTORS OF DISEASE RECURRENCE

doi:10.1136/jech.2011.142976c.46

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Knowledge of factors influencing recurrence risk is essential in the prevention of disease recurrence. In this paper, we show that correct estimation of the strength of such factors is, however, troublesome. We performed a simulation study of the recurrence risk of a fictional pregnancy-related disorder, Y. We assumed that there were four component causes of Y, X1 representing the determinant under study, X2 and X3 representing unmeasured determinants, and X4 representing pregnancy as a necessary condition for developing Y. We stipulated that each woman would become pregnant twice. RR of disease during the first pregnancy for X1+ (presence) vs X1-(absence) was 19.0. Attributable risk (AR) was 0.18. RR of recurrent disease for X1+ vs X1- during the second pregnancy, calculated among women with previous disease, was apparently 1.0, and AR was apparently 0.00. However, we show that real RR and AR were considerably higher (19.0 and 0.95, respectively). Our simulation shows that selection of a study population on the basis of previous disease can lead to underestimation of the strength of recurrence risk factors. The bias involved is a form of collider-stratification bias. We urge for extra caution in the interpretation of studies of recurrence risk factors.

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## EXPOSURE EFFECT ESTIMATES DIFFER SUBSTANTIALLY BETWEEN MARGINAL STRUCTURAL MODELS AND CONVENTIONAL MODELS: RESULTS OF A SYSTEMATIC REVIEW

doi:10.1136/jech.2011.142976c.47

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**Introduction** Marginal structural models (MSMs) were developed to address time-varying confounding in nonrandomized exposure effect studies. It is unclear how estimates from MSMs to conventional models differ in real settings and how the MSMs are implemented in the literature.

**Methods** We systematically reviewed the literature of MSMs since 2000 retrieving papers from both PubMed and ISI Web of Knowledge databases.

**Results** Data to compare MSMs and conventional models were obtained from 65 papers reporting 164 exposure-outcome associations. In 18 (11.0%), the two techniques resulted in estimates with opposite interpretations, and in 58 (39.7%) estimates differed by at

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least 20%. The SEs of the MSM associations were in median 19.4% greater than the respective conventional SEs (IQR: 2.4% to 47.5%) in the 156 available associations. In 88 papers, MSMs were used to analyse real data; only 53 (60.2%) of these papers reported that stabilised inverse-probability weights (IPWs) were used, and only 28 (31.8%) reported that they verified that the mean of the stabilised IPWs was close to one.

**Conclusions** We found important differences between MSMs and conventional models in real studies. Reporting of MSMs can be improved.

#### P1-55

### COMPARISON OF TWO CRITERIA TO EVALUATE PHYSICAL ACTIVITY PATTERN IN ADULTS

doi:10.1136/jech.2011.142976c.48

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**Background** The international literature has presented several criteria for classifying people in terms of physical activity pattern, making it difficult to compare the results.

**Objective** The study aims to evaluate the reliability between two criteria used to classify physical activity pattern, in adults living in Ribeirão Preto, SP, Brazil, in 2006.

**Methods** Using data from a cross-sectional population-based study, the International Physical Activity Questionnaire (IPAQ) and the American College of Sports Medicine/American Heart Association (ACSM/AHA) criteria were applied. The  $\kappa$  statistic estimated by point and 95% CIs, stratified by gender, age, education level and income was applied to evaluate reliability between the two criteria. **Results** The results showed an agreement close to the unity ( $\kappa\!\approx\!1$ ) between the two criteria, in both genders, with crude coefficients  $k_{male}\!=\!0.95$  (95% CI 0.83 to 1.06) and  $k_{female}\!=\!0.93$  (95% CI 0.85 to 1.01). The lowest magnitude of  $\kappa$  were found in the age group of 60 years and over in both genders [ $k_{male}\!=\!0.87$  (95% CI 0.60 to 1.15);  $k_{female}\!=\!0.88$  (95% CI 0.70 to 1.06)], and among illiterate women or with <01 year of education [ $k\!=\!0.72$  (95% CI 0.34 to 1.09)].

**Conclusions** The IPAQ and ACSM/AHA criteria showed practically the same ability to classify participants in terms of physical activity levels, allowing comparison of population-based studies that have used the IPAQ instrument to obtain information about physical activity practice. The results pointed out the higher prevalence of "actives" when the second criteria was applied and "walking" was the main practice of physical activity.

#### P1-56

### UNDERSTANDING THE NATURAL PROGRESSION IN FEV<sub>1</sub> DECLINE IN PATIENTS WITH LUNG DISEASE

doi:10.1136/jech.2011.142976c.49

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**Introduction** We outline a novel approach for longitudinal modelling of lung function with long-term follow-up in which within-patient variation over time is described by a stationary (mean-reverting) stochastic process, and apply these techniques to a unique dataset of cystic fibrosis patients in Denmark. The aim is to quantify how lung function changes in chronic lung diseases.

**Methods** The Danish CF register contains data collected on a monthly basis with up to 30 years of follow-up. Our statistical analysis framework is that of a linear mixed effects model with

longitudinally structured correlation. Using open-source software we describe how to partition the variability in the data into three components (between and within patient, and measurement error) using the empirical variogram. A parametric model for lung function decline can then be developed. We apply this approach to explore the effect of age, birth cohort and infection status on lung function decline.

**Results** The dataset contains 70 448 measures on 479 patients seen between 1960 and 2009. The empirical variogram shows slowly decaying long-term correlation (>15 years) in FEV1, with half of the variability in lung function explained by within person variation. The mean rate of lung function decline is 0.96% per year (95% CI 0.86 to 1.07). There is a significant cohort effect, and chronic infection significantly increases the rate of lung function decline.

**Conclusions** We apply a novel modelling approach to demonstrate that lung function in early life in the Danish cystic fibrosis population is correlated with lung function over 15 years later.

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## USING PARTIAL LEAST SQUARES REGRESSION FOR THE AGE-PERIOD-COHORT ANALYSIS

doi:10.1136/jech.2011.142976c.50

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**Background** Identification has been a problem with the Age-Period-Cohort analysis. Since Age + Cohort = Period, there is no unique solution using generalised linear modelling. To overcome this problem of perfect collinearity we propose to use partial least squares regression (PLSR), a dimension-reduction technique widely used in bioinformatics. Data from a large Taiwanese cohort was used to illustrate our approach.

**Methods** PLSR is a set of algorithms that aims to maximise the covariance between outcome and successively extracted orthogonal components under the constraint that the sum of squared weights is equal to unity. To assess the impact of age, birth year and year of examination on the levels of metabolic syndrome (MetS) components, we used PLSR to analyse data collected by Mei-Jaw clinics in Taiwan in years 1996 and 2006. Confounders, such as the number of years in formal education, alcohol intake, smoking history status, and betel-nut chewing were adjusted for.

**Results** As the age of individuals increased, the values of components generally increased. People born after 1970 had lower fasting plasma glucose, lower body mass index, lower diastolic blood pressure, lower triglycerides, lower low-density cholesterol lipids and greater high-density cholesterol lipids. A similar pattern between the trend in levels of metabolic syndrome components against birth year of birth and economic growth in Taiwan were also found.

**Conclusions** Our study found cohort effects in some MetS components, suggesting associations between the changing environment and health outcomes in later life. PLSR provides a flexible analytical strategy for the Age-Period-Cohort analysis.

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# THE VOLUMETRIC MEASUREMENT OF BRAIN IMAGING BIOMARKERS FOR EPIDEMIOLOGICAL STUDIES CAN BE MISLEADING IN THE VALIDATION OF IMAGE SEGMENTATION METHODS

doi:10.1136/jech.2011.142976c.51

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Large scale neuro-epidemiology studies using brain imaging need tissue segmentation methods to determine lesion or normal tissue