Conclusions: Our study provided probabilities of lossFU and death in HIV patients. ARTs and health coverage were preventive-factors whereas males, old-age, OI, and shopping-around hospital were risk factors of loss-FU and death.

P3.1.189

New insights on therapy choices in non-small cell lung cancer using a flexible extension of the standard Cox's model

W Wynant[1], M Abrahamowicz[1], I Gioulbasanis[2], G Kasymjanova[3], JS Agulnik[3], B Gagnon[4]
[1]McGill University, Montreal, Canada, [2]University Hospital of Larissa, Larissa, Greece, [3]Jewish General Hospital, Montreal, Canada, [4]Laval University, Quebec, Canada

Non-small cell lung (NSCL) cancer accounts for about 80% of all cases of lung cancer. Most of the patients present with advanced-stage disease at diagnosis and have a poor prognosis. Moreover, chemotherapy confers a modest survival improvement, compared with supportive care alone.
Therefore, probability of survival conditional on patient characteristics is a meaningful metric for prognosis and therapy choices. In NSCL cancer, this could guide treatment by recognizing patients at high risk for poor survival who might be considered to earlier intervention and could help for optimal clinical management.
We estimated survival probabilities from data on 269 patients with NSCL cancer. As misspecification of covariates' effects can have a huge impact, we extended the standard Cox´s model to allow (i) non-linear effects of the covariates on the logarithm of the hazard and (ii) covariates effects to change over time. We also considered a flexible modeling of the baseline hazard to avoid step functions, biologically implausible.
Our results emphasize the importance of taking into account the potential time-dependent and non-linear effects of biomarkers and new insights obtained from survival curves. For example, our survival probability estimate at 6 months after chemotherapy, for patients who smoke, had a double-agent chemotherapy but with low blood levels of albumin and C-reactive protein and average level of various other biomarkers (including neutrophil counts and alkaline phosphatise) was only 40%, whereas the estimate from the widespread standard Cox´s model was 85%.
This highlights a profile of patients who may be targeted to earlier intervention.

P3.1.191

Heterogeneous M/M/1 type queuing models

S Yiu[1]
[1]MRC Biostatistics Unit, Cambridge, United Kingdom

Motivated by the need to account for unobserved heterogeneity from a missing important covariate in a longitudinal reversible count data setting, this work presents three M/M/1 type queuing models with random effects.
The standard M/M/1 queuing model is considered with and without an absorbing state, followed by the M/M/1 queuing model with one modified transition intensity. By convenient choice of mixing distributions, closed form expressions for the marginal likelihoods are available, thereby providing tractability.
The methodology is illustrated with an application to a psoriatic arthritis data set where modelling the number of active joints is of interest.

P3.2 Diagnostic studies

P3.2.91

Sample size calculations for confidence limits of prevalence of disease adjusted for estimated sensitivity and specificity

Z Lang[1], J Reiczigel[1]
[1]Szent István University, Faculty of Veterinary Science, Budapest, Hungary

Prevalence of a disease or other characteristic of a target population is frequently estimated by diagnostic tests. Lang and Reiczigel (2014) constructed approximate confidence intervals for prevalence when apparent prevalence, sensitivity and specificity were estimated from independent binomial samples. When the sample sizes are small, the confidence intervals obtained may prove to be too wide to cope with a required precision. The solution for this problem is to calculate suitable sample sizes based on preliminary diagnostic parameter estimates stemming from earlier studies or estimated from the actual data and draw new samples from both the target population and the populations to re-estimate sensitivity, specificity and prevalence. In this presentation we provide sample size formulas e.g. when the planned length of the confidence interval of prevalence is prescribed and the estimated values of the diagnostic parameters remain unchanged.
When the variances of the estimates of sensitivity or specificity are poor it is advisable to re-estimate them from larger new independent samples. If prevalence is small then the variance of specificity has to be reduced first of all.
Analogously, when prevalence is close to 1 the variance of sensitivity is advised to be controlled.

P3.2.95

Systematic review and meta-analysis of diagnostic accuracy of FDG-PET in dementia and Alzheimer's disease

YE Lee[1], JE Choi[1], J-Y Kim[1], YH Yoo[2], DY Lee[3], S-H Park[1], S-K Son[1], Y-K Lee[1], E Shin[1], CH Ryu[2], C-H Sohn[3], J-Y Lee[4], Y Kim[4]
[1]National Evidence-based Healthcare Collaborating Agency, Seoul, Republic of Korea, [2]Department of Nuclear Medicine, Gangnam Severance Hospital, Seoul, Republic of Korea, [3]Seoul National University Hospital, Seoul, Republic of Korea, [4]SMG-SNU Boramae Medical Center, Seoul, Republic of Korea

As aging population is rapidly increasing, it is estimated that prevalence of dementia among older adults would be doubled every twenty years and number of patients would increase by one million until 2027. Dementia would lead to a burden of care on family members, care-givers, and even societies due to social and economic cost. Therefore, early diagnosis of dementia is important step to prevent further worsening of disease and improve quality of life of dementia patients and their family. In this study, we assessed diagnostic accuracy of FDG-PET in evaluation of dementia, which known as a tool for detecting reduced glucose metabolism in patient's brain even before the development of dementia symptoms.
To evaluate diagnostic accuracy in early detection of dementia and Alzheimer's disease, we conducted systematic reviews of published articles, and identified 9 cross-sectional studies and 13 delayed cross-sectional studies. Bivariate Meta-analysis of 9 cross-sectional studies resulted in a pooled sensitivity(SN) of 0.61(95% CI: 0.42-0.79), a pooled specificity(SP) of 0.81(95% CI: 0.55-1.07). In 13 delayed cross-section studies, it resulted in a pooled SN of 0.81(95% CI: 0.72-0.91), and a pooled SP of 0.78(95% CI: 0.65-0.92). With subgroup analyses in amnestic mild cognitive impairment(MCI) patients, the result suggested a pooled SN of 0.92(95% CI: 0.75-1.00), a pooled SP of 0.88(95% CI: 0.77-0.98). These results indicate that FDG-PET among amnestic MCI patients was most accurate in the aspects of pooled SN and SP in delayed cross-sectional studies.