parameter, we also modeled the precision parameter using a regression structure. Regression coefficients and predictive accuracy from this model estimated using the Bayesian approach with vague priors were compared to those from a linear mixed effects model estimated classically. **RESULTS:** Our results indicated that beta distribution fitted the SF-6D outcome better than normal distribution. Furthermore, compared to the linear mixed effects model, the mixed beta regression model was superior in terms of predictive model accuracy. We found that mortality risk had a significant effect on both mean and precision parameters: we observed lower mean HRQoL for higher mortality risk and higher variation of health utilities for higher mortality risk. **CONCLUSIONS:** Mixed beta regression offers a superior approach for modelling the HRQoL outcome longitudinally. Furthermore, such a model can be easily implemented using freely available Bayesian software.

PRM129

EFFECT OF SAMPLE SIZE AND DATA MATURITY ON PARAMETRIC SURVIVAL MODELING PROJECTIONS IN ADVANCED CANCER

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OBJECTIVES: Parametric survival modeling (PSM) is often used in cost-effectiveness analyses of oncology treatments to aid in lifetime projections due to right censoring of data. We sought to better understand the effect of sample sizes and data maturity (follow-up time) on PSM projections to aid in the design of clinical trials and the interpretation of cost-effectiveness models. **METHODS:** We modeled overall survival (OS) for advanced colorectal cancer patients treated with first-line chemotherapy and/or a biologic using SEER-Medicare data (2004-2010). Survival was estimated using Kaplan-Meier (KM) and PSM methods. From the full cohort, we randomly drew patients to match typical sample sizes from Phase II and III clinical trials (n=50, 100, 200, and 400). Additionally, arbitrary data cutoffs were created to proxy clinical trial follow-up times (t=3, 6, 9, 12, 24, and 36 months). Using PSM methods mean survival from the full cohort was compared with survival from the combinations of sample sizes and follow-up times. **RESULTS:** Using the KM method, 6% of patients were alive at the end of the follow-up period (6.5 years). Mean OS from the full cohort was estimated to be 21.9 months using the PSM method (best fit Weibull curve). OS estimates for the sample size and follow-up time combinations ranged from 5.9-28.0 months. Minimum and maximum survival projections represented a 73% underestimation and 28% overestimation of survival compared with the full cohort projection, respectively. Projection accuracy was improved when $t \geq 6$ months and $n \geq 200$. **CONCLUSIONS:** Both sample size and data maturity have a profound effect on survival projections. Care should be taken when interpreting projections in cost-effectiveness models, especially when sample size is low and follow-up time short. In addition to power calculations, clinical trial design should account for these issues. Additional analyses in other cancer types may provide further guidance for optimum trial design.

PRM130

UNDERSTANDING REAL LIFE TREATMENT PATTERNS AMONG PATIENTS WITH HYPERTENSION: A MARKOV MODEL

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OBJECTIVES: Approximately 65% of patients diagnosed with hypertension are not well controlled and two third of patients need to be treated by two or more drugs for achieving target blood pressure. The aim of this study was to describe antihypertensive treatment patterns in real life settings by using Markov chain model. **METHODS:** Data concerning prescriptions of patients with diagnosed hypertension were obtained from a large primary care survey conducted in 2012 using CSD Longitudinal Patient Database. Patients selected were treated with sartans, prescribed alone or in combination with amlodipine and/or hydrochlorothiazide (HCT), either in free associations or in fixed combinations. A Markov chain model M1 with 4-states (A: single sartan, B: sartan+ amlodipine, C: sartan + HCT, D: sartan + amlodipine + HCT) was proposed to model transitions from one treatment to another over time. A second chain, M2, with 6 states was also studied, in which dual-therapies were divided into two states depending on whether the combination was free or fixed. Age and sex were included as covariates. R packages and MSM DIAGRAM were used. **RESULTS:** 11,976 patients were selected, 49% were men, aged 69 years on average (SD = 11), suffering from hypertension for 7 years on average, 35% had diabetes, 5% renal failure and 31% a previous cardiovascular event. At the time of selection, the distribution between the states was as follows: A: N = 5187 (43.3%), B: N = 1060 (8.9%), C: N = 5120 (42.8%), D: N = 609 (5%). At the end of one year, > 93% of patients had remained in the same state of M1. The M2 model showed substantial transitions from free to fixed associations. Age and sex did not change the coefficients. **CONCLUSIONS:** The Markov chains used to visually describe the evolution of treatment regimens are useful for analyzing large longitudinal databases of prescriptions.

PRM131

THE PROPORTIONAL ODDS MODEL IS MORE EFFICIENT THAN THE MULTINOMIAL LOGISTIC MODEL FOR NETWORK META-ANALYSES OF ORDERED OUTCOMES

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OBJECTIVES: Network meta-analysis (NMA) techniques have been developed to study relative treatment effects for several outcome types (e.g. time-to-event outcomes). No literature exists comparing models of NMA for ordered categorical data, though models are available with different characteristics. This study compared the proportional odds (PO) and multinomial logistic (ML) model for NMA in ordered categorical datasets based on model fit and qualitative characteristics. **METHODS:** To contrast model performance, two extreme datasets were simulated, one which exactly satisfied the PO assumption (POA dataset), and one which did not (nPOA dataset). The models were also tested in a clinical dataset including ordered response categories for four different treatments in psoriasis patients. Both fixed and random effects models were studied. **RESULTS:** In the POA dataset, the PO fixed effects model had the lowest residual deviance (54.8 versus 58.9 for the ML model) and uncertainty of treatment effects (49% lower standard error (SE)). In the nPOA dataset, the predictions of the PO model were biased, and the ML model had the lowest residual deviance (52.7 versus 271.0 for the PO model). Visual inspection indicated a partial violation of the PO assumption in the psoriasis data. Analyses of the psoriasis data, showed that the PO fixed effects model had the lowest residual deviance (18.1 versus 20.9) and uncertainty (62% lower SE). However, PO model predictions were biased for treatment responses which violated the PO assumption. **CONCLUSIONS:** Statistical selection of NMA models for ordered outcomes should be based on the PO assumption and deviance measures. If data satisfies the PO assumption, the PO model differentiated treatment effects better as a result of lower uncertainty. In terms of flexibility, the PO model can handle data from studies that use different cut-offs for response categories and the ML model can be applied to datasets violating the PO assumption.

PRM132

EVALUATING THE EFFECT OF IMMUNOTHERAPY IN ADVANCED NON-SMALL-CELL LUNG CANCER PATIENTS USING TWO COMPONENTS MIXTURE MODEL

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OBJECTIVES: The aim of the study was to assess the effect of an immunotherapy for the treatment of advanced non–small-cell lung cancer (NSCLC). **METHODS:** Data from a phase III, multicenter, randomized, open-label trial evaluating the efficacy of one EGF-based cancer vaccine (CIMAvaxEGF) as switch maintenance in patients with advanced NSCLC, were used. Survival analysis using Kaplan Meier estimates was performed. Weighted log-rank was conducted to assess the later effect of the immunotherapy. Additionally, a finite mixture model to the primary endpoint (Overall Survival, OS) was fitted. Weibull distribution was assumed for the overall survival and a mixture model consists of one, two or three components was fitted.. All analysis was conducted using the NLMIXED procedure in SAS. The Akaike Information Criterion (AIC) was used for model selection. **RESULTS:** Intention-to-treat (ITT) analysis showed 1.44 months of OS benefit for vaccinated patients with confirmed delayed-separation phenomena (OS: Vaccine arm, 10.37 months vs. Control arm, 8.93 months; p= 0.043). The mixture model with the best goodness to fit to the data consists of two components (AIC=3097.7). The two mixture components represent short-term and long-term survival subpopulations. The proportions of the subpopulations are estimated to be equal to 0.89 and 0.11 respectively. The median OS was estimated to be equal to 9.59 and 60.32 for short- and long- term survival populations, respectively. 23.26% and 76.74% from the patients who were classified into long-term survival subpopulation were from the control and vaccinated group, respectively. From them, 7 (70%) patients in the control group and 25 (75%) patients in the treated group were still alive at the end of the study. **CONCLUSIONS:** The results confirm that the vaccination with CIMAvaxEGF prolongs the survival of the advanced NSCLC patients. Mixture models allow assessing the efficacy/effectiveness of vaccines and biological products in the presence of heterogeneous populations.

PRM133

PREDICTIVE MODELLING: PREDICTING HOSPITALISATION AND ESTIMATING THE COST AND RISK TO THE THIRD PARTY FUNDER

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PREDICTIVE MODELLING: PREDICTING HOSPITALISATION AND ESTIMATING THE COST AND RISK TO THE THIRD PARTY FUNDER R CELLIERS (MsC. (Mathematical Statistics) University of Pretoria)

OBJECTIVES: In the third party funder environment most analyses focus on retrospective claims analyses; the aim of predictive modelling is to estimate future claims or current risk, based on the probability of a hospital event using historical data. **METHODS:** A logistic regression approach is followed where the likelihood of a hospitalisation event is established and mapped to a cost estimate. The modelling process involved establishing a development and validation sample, identifying the predictor variables, building and lastly validating the sample. During the model building process the development and validation population consisted of 149 416 and 47623 beneficiaries respectively; where the data was obtained from a third party funder consisting of 3 years of data. During the building process the dependant variable (*Y=Logg (odds)*) takes on the value 1 or 0 depending on whether or not a hospital event occurred. To calculate the cost per beneficiary a weighted probability was multiplied by the average cost of a hospital authorisation. Beneficiaries were classified as high risk if *log (odds)* >=0.7. **RESULTS:** The final model is: *Log (odds)* $=-0.11X_1+0.00576X_2+0.409X_3+0.179X_4+0.614X_5$ where X_1-X_5 denotes the predictor variables. X_1 denotes an indicator variable for gender, X_2 the predictor variable for age, X_3 the HIV indicator variable, X_4 the diabetes indicator variable and X_5 the chronic indicator variable. The strongest predictors were the chronic indicator variable and age. The validation process resulted in 79% of the beneficiaries being correctly classified and the cost estimation resulted in totals within 3-5% of the actual values. **CONCLUSIONS:** The proposed model predicts hospitalisation efficiently at a beneficiary level and can be implemented to monitor risk and the associated cost (hospital or total) for individuals, employer group or the third party funder. Third party risk management and cost estimation are other applications of the model.

PRM134

JOINT MODELLING OF THE CHANGE IN TUMOR SIZE AND OVERALL SURVIVAL; A PARAMETRIC MODEL CONSIDERING PATIENT HETEROGENEITY NOT OBSERVED AT BASELINE

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