OBJECTIVES: To compare homogeneous (HMM) versus non-homogeneous Markov models (NHMM) for cost-effectiveness analysis (CEA) of routine use of transparent dressings containing a chlorhexidine gluconate gel versus standard transparent dressings. The antimicrobial dressing protects central vascular accesses reducing the risk of catheter-related bloodstream infections (CRBSIs) in intensive care units (ICU). The impact of the modeling approach on the decision of adopting alternative dressings for critically ill patients is discussed.

RESULTS: Comparative clinical efficacy data from a multicentre randomised controlled trial (RCT) enrolling 1,879 patients and economical data from micro and macro-costing studies with NHMM models were compared to those using the same sources. The statistical unit was the ICU patient and the ICU perspective was chosen. Probabilistic sensitivity analyses (PSA) were conducted for both models for comparing the robustness of the CEA results.

RESULTS: The differences between each dressing groups were statistically significant with both models while cost differences were not. The PSA with the NHMM resulted in 11.8 infections avoided per 1,000 patients (95%CI: [3.85; 19.64]) and a mean extra cost of €141 per patient (95%CI: [€97; €215]) when using antimicrobial dressing. The PSA with the HMM resulted in 6.4 infections avoided per 1,000 patients (95%CI: [0.15; 12.75]) and the mean extra cost of €252 per patient (95%CI: [€92; €412]).

CONCLUSIONS: The antimicrobial dressings are cost-effectively efficacious in preventing CRBSIs whatever the model used. The HMM is less sensitive to simulate the real life of the ICU patients. Regardless of the model chosen the antimicrobial strategy is more efficacious than the control, but its probability of being cost-effective is relatively comparatively reduced with the HMM. Time dependent approach (NHMM) seems to be better adapted to model rare events as CRBSIs.

PM118 DEVELOPMENT OF A MODEL TO PREDICT DISEASE PROGRESSION IN AUTOSOMAL DOMINANT POLYCYSTIC KIDNEY DISEASE (ADPKD)

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OBJECTIVES: Autosomal dominant polycystic kidney disease (ADPKD) is a major cause of end-stage renal disease (ESRD) affecting approximately 4 per 10,000 people in Europe. There is a paucity of research regarding the natural history of ADPKD progression. This study aimed to utilise a systematic literature review and characterising predictors of ADPKD progression to construct a natural history disease model for ADPKD.

METHODS: An individual patient-level lifetime simulation was developed in TreeAge Pro. The model is driven by baseline age and time-dependent age, estimated glomerular filtration rate (eGFR) and total kidney volume (TKV). Rates of progression were informed by a large naturalistic study. Dialysis modality, transplant status and osimertinib mortality were also modelled. ADPKD complications were stratified by chronic kidney disease stages. Modification of disease progression rate was investigated in order to assess the potential of the model for evaluating treatment interventions.

RESULTS: On visual inspection, modelled and published projections for the change in eGFR and TKV were consistent (median age at ESRD of approximately 55 years). When patients are stratified by baseline TKV the model predicts variable rates of progression to ESRD, aligning with the assertion that the baseline TKV is the most important prognostic indicator for ADPKD progression. Modification of the risk equations to incorporate the impact of an intervention has shown promise to estimate important outcomes such as delay to ESRD.

CONCLUSIONS: The model has demonstrated both face and predictive validity and is capable of predicting outcomes consistent with those reported in the ADPKD literature. It represents the first model capable of informing on important clinical outcomes relevant to both clinicians and patients, such as time to ESRD, with the potential to evaluate the long-term impact of treatment interventions on ADPKD progression.

PM119 FORECASTING CANCER INCIDENCE USING GROSS DOMESTIC PRODUCT

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OBJECTIVES: To use the change in domestic changes in gross domestic product (GDP) as a proxy for forecasting change in cancer risk. METHODS: Using data from the International Agency for Research on Cancer (IARC) and GDP data from the World Bank, we investigated the change in incidence between the IARC 2002-2007 and the IARC 2012-2017. The GDP-based forecasts were compared to a control assuming no change in incidence from the IARC incidence data for 1998-2002 (midyear 2000). The two forecast estimates with the actual reported IARC 2002-2007 incidence data were compared. RESULTS: Overall, the GDP-based method correctly forecasts the directional change in incidence in 75% (95% confidence interval 67-83%) of instances compared with the control method (25%, 95% CI 17-33%). Among 83% (95% CI 76-91%) of positively-GDP-associated cancers compared with 17% (95% CI 9-24%) for the control method. There was no significant difference between the two methods for negatively-GDP-associated cancers. In terms of the relative magnitude of change compared to the actual incidences, there was no significant difference between the GDP-based forecast incidences and the control (mean magnitude difference 3.8%, 95% CI -3.5% - 11.0%).

CONCLUSIONS: During epidemiological transition, cancer incidence is unlikely to remain static and the GDP-based forecast model can be used to predict the impact of GDP changes. Using GDP as a proxy variable is preferable to the alternative of projecting historical values forward unchanged in terms of directional effect. However, our study found no significant difference in terms of relative magnitude of the change over time. This result may be due to a small sample size of registries, indicating a need for further research.