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interventions in the social care sector. As interest in implementation science increases, it is important that health economists are equipped to study the costs and effects of implementing these studies. We hope that this paper will help guide future economic evaluations in order to inform policy-makers of the costs and benefits of implementing home visiting interventions.

PNS201
A SIMPLE METHOD OF SAMPLING ORDERED BOUNDED PARAMETERS IN PROBABILISTIC SENSITIVITY ANALYSIS
Litkiewicz M1, Nikolaki M1, Behnke M1
1Federica, London, UK, 2Modelling and Simulation, Evidera, London, UK

Objectives: Probabilistic sensitivity analysis (PSA) in economic models involves sampling of model parameters from probability distributions and often assumes their independence. For parameters with known order, such as utilities or costs by disease severity, PSA may lead to inconsistent samples. In such cases, the recent ISPOR guidelines on health-state utilities recommend using the difference method. This method is cumbersome to implement as it requires additional sampling to obtain the required sampling parameters. We present an alternative method for sampling ordered bounded parameters that does not present such difficulty. Methods: Assuming two ordered and bounded random variables \( X_1 \) and \( X_2 \), with \( \text{E}(X_1) \geq \text{E}(X_2) \), an ancillary random variable \( Y \) is introduced as the ratio of the lower \((X_2)\) to the higher \((X_1)\) variable. This variable is bounded in \([0,1]\), with mean and variance calculated on the span and varia of the \( X_1 \) and \( X_2 \) samples. Samples of \( X_2 \) can then be generated by sampling \( X_1 \) and \( Y \) independently and setting \( X_2 = X_1 \cdot Y \). We tested this method under a range of scenarios, discussed its applicability, accuracy and limitations, and compared it both with independent sampling and with the difference method. Results: The method was able to match the mean and variance of the sampled parameters across all scenarios. No correlation between parameters other than that imposed by the ordering was detected in a visual inspection of their joint distributions. For certain combinations of means and variances (small differences in means but large differences in variances), a minor adjustment of the method was required. Conclusions: The proposed method generates PSA samples in accordance to the bounds, order, and summary statistics of the sampled parameters. In comparison to the difference method, this method is easier to implement, as all distribution parameters can be calculated analytically, and no additional sampling is required.

PNS203
MACHINE LEARNING FOR SUBPOPULATION ANALYSIS IN DATASETS WITHOUT CONTROL ARM
Wang Y1, Wei G1, Wang Y1, Behnke M1, Reiner E1, Chaudhuri K1,4,5, Reed E1, McKerney A1, Oliveira C1, Reynolds M1
1IQVIA, Plymouth Meeting, PA, USA, 2IQVIA, Overland Park, KS, USA, 3IQVIA, Pound Ridge, NY, USA, 4IQVIA, Ambler, PA, USA, 5IQVIA, Durham, NC, USA, 6IQVIA, New York, NY, USA, 7IQVIA, Reading, UK

Objectives: Develop machine learning (ML) and predictive analysis models to identify patient attributes and biomarkers predictive of a particular outcome desirable or undesirable. This can be used in one arm clinical trials and real world data towards various outcomes including disease-free survival and adverse events. Methods: Methods to rank the top biomarkers using ML and validated them using hypothesis tests. We used these to develop ML models predicting the mortality of sepsis patients. 10-fold cross-validation was performed using the best parameters from the grid search to predict the study outcome. The decision tree has at least 30 samples on each node and returns the biomarkers splitting criterion of each node until maximum depth reaches five. We used Reincer Operating Characteristic (ROC) to assess model performance. Results: The decision tree method returned three sub-groups with differentiated outcomes, and the information gain increased by an average of 0.2 for each one. Analysis of splitting criteria and Cox Regression models showed statistical significance of the outcome of the optimal sub-group vs. the rest. Conclusions: The decision tree method returns optimal sub-groups with differentiated outcomes, and the information gain increased by an average of 0.2 for each one. These calculations enable analysis of potential costs and time savings with and without the Custom Pak®.

PNS206
PROJECTING THE COVID-19 WEEKLY DEATHS AND HOSPITALIZATIONS FOR JEFFERSON COUNTY, KENTUCKY
Naity P1
1University of Louisville, LOUISVILLE, KY, USA

Objectives: The trends in the numbers of active hospitalizations and fatalities caused by the Covid-19 in Jefferson County, Kentucky, were projected over the period May 7 to August 20, 2020. Methods: The projections provided in this report are from a susceptible-exposed-infectious-recovered (SEIR) model. The model was calibrated using the COVID-19 transmission dynamics parameters from relevant literature and clinical dynamics parameters from the county’s data. The model was used for measuring the impact of public health policy interventions designed to contain the infection. The policy was modeled by its intervention day and impact on the transmission of the virus such that the resulted fatalities resembled those observed in Jefferson County. Results: By May 6, 2020, 1,557 cases and 109 COVID-19 deaths in Jefferson County. The average age of deceased individuals was 76.5 years—76% of them had a previous medical condition, and 28% were African American. Among the hospitalized, 53% were admitted to the ICU, and 43% used a ventilator. Projections based on the status quo showed 91 active hospitalizations and 147 total fatalities, on average, on May 14. By June 4, the average number of active hospitalizations were projected to decrease to 61, but total fatalities to increase to 195, assuming a 70% reduction in transmission of the virus was maintained since the implementation of the policy intervention. By late August, the average number of active hospitalizations and total fatalities were projected to be 12 and 269, respectively. Conclusions: Had the county practiced weaker containment strategies, it would have been on an upward path with increased hospitalization and fatalities. Therefore, decreasing the current social distancing measures without efforts regarding testing, isolating, and contact tracing can worsen the county to an unstable status.

PNS207
PATIENT AND SUB-POPULATION SIMULATION VIA MULTIDIMENSIONAL CORRELATION AND CLUSTER ANALYSIS (MCG) AND WEIGHTED K NEAREST NEIGHBORS (KNN) ALGORITHMS FOR CLINICAL TRIALS AND REAL-WORLD DATA
Wei G1, Wang Y1, Wang Y1, Behnke M1, Reiner E1, Chaudhuri K1,4,5, Reed E1, McKerney A1, Oliveira C1, Kelly B1
1IQVIA, Plymouth Meeting, PA, USA, 2IQVIA, Overland Park, KS, USA, 3IQVIA, Pound Ridge, NY, USA, 4IQVIA, Ambler, PA, USA, 5IQVIA, Durham, NC, USA, 6IQVIA, Reading, UK

Objectives: Create predictive algorithms that can approximate future treatment and control patient populations based on similarly structured prior data. Pairwise correlation and distribution and correlation of selected variables like patient demographics, disease states and biomarkers. Compare similarities between original and simulated data. Methods: Data related to Sepsis and other datasets were used. We classified related variables as Treatment, Outcome, or Covariates. For each group, we converted data to multivariate standard normal distribution. Using the correlation matrix and prescribed marginal distributions, we applied the netcdf’s standard transformation to simulate a large number of records with a specific correlation structure. Conclusions: The algorithm is useful for a training data set. The examples used for this purpose were generated using a Multidimensional Nonparametric Cramer-Cramer and Bhattacharyya Distance (BD) as the performance evaluation method. We also used a KNN and weighted KNN algorithm to simulate the study results. The distance for categorical variables was calculated by Hamming distance and Euclidean distance measures, respectively. This detected the K

PNS207
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Objectives: Probabilistic sensitivity analysis (PSA) in economic models involves sampling of model parameters from probability distributions and often assumes their independence. For parameters with known order, such as utilities or costs by disease severity, PSA may lead to inconsistent samples. In such cases, the recent ISPOR guidelines on health-state utilities recommend using the difference method. This method is cumbersome to implement as it requires additional sampling to obtain the required sampling parameters. We present an alternative method for sampling ordered bounded parameters that does not present such difficulty. Methods: Assuming two ordered and bounded random variables \( X_1 \) and \( X_2 \), with \( \text{E}(X_1) \geq \text{E}(X_2) \), an ancillary random variable \( Y \) is introduced as the ratio of the lower \((X_2)\) to the higher \((X_1)\) variable. This variable is bounded in \([0,1]\), with mean and variance calculated on the span and varia of the \( X_1 \) and \( X_2 \) samples. Samples of \( X_2 \) can then be generated by sampling \( X_1 \) and \( Y \) independently and setting \( X_2 = X_1 \cdot Y \). We tested this method under a range of scenarios, discussed its applicability, accuracy and limitations, and compared it both with independent sampling and with the difference method. Results: The method was able to match the mean and variance of the sampled parameters across all scenarios. No correlation between parameters other than that imposed by the ordering was detected in a visual inspection of their joint distributions. For certain combinations of means and variances (small differences in means but large differences in variances), a minor adjustment of the method was required. Conclusions: The proposed method generates PSA samples in accordance to the bounds, order, and summary statistics of the sampled parameters. In comparison to the difference method, this method is easier to implement, as all distribution parameters can be calculated analytically, and no additional sampling is required.