and the true treatment effects were used to compare the scenarios. For the two largest networks, meta-regressions were also conducted to adjust partially on the heterogeneity. ***Results:*** From scenarios 1 to 3, including additional studies in the networks while increasing the heterogeneity level reduced the MRDs when conducting standard NMAs (respectively 48.2%, 21.3% and 18.6%). However, a higher MRD was obtained for the largest network (scenario 4: 24.4%) compared to scenarios 2 and 3. Conducting meta-regressions markedly reduced the MRDs for the scenario 3 (7.2% with meta-regression vs. 18.6%) and scenario 4 (9.1% with meta-regression vs. 24.4%). ***Conclusions:*** This simulation study shows that including additional studies in case of a small network in a NMA context can be relevant, especially if it allows for a meta-regression to be conducted.

Oncology Studies

CN1
PATTERNS OF UTILIZATION AND IMPLEMENTATION EXPERIENCES OF ONCOLOGY MONOCLONAL ANTIBODIES (MABS) BIOSIMILARS IN THE U.S.: FROM BOTH PAYERS AND HEALTHCARE PROFESSIONALS (HCPS) PERSPECTIVES

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Objectives: Biosimilars are highly similar to an originator biologic, with no clinically meaningful differences in safety or efficacy. The adoption of biosimilars might provide an opportunity to lower costs and increase patient access to biologics. The current study sought to understand real-world implementation experiences associated with oncology MAbs biosimilars (trastuzumab, rituximab, and bevacizumab) from both payer and healthcare professional (HCP) perspectives. ***Methods:*** In-depth qualitative telephone interviews with 20 each of US HCPs (including 3 practice managers) and payers were conducted. The HCPs were either affiliated with a healthcare network or were community-based. They specialized in hematology/oncology and had experience prescribing oncology biosimilars. Participating payers included Managed Care Organizations (MCOs), Integrated Delivery Networks (IDNs) and Pharmacy Benefit Managers (PBMs). Audio transcripts of the interviews were coded using MaxQDA software. ***Results:*** Over 80% of HCPs interviewed perceived biosimilars to be highly comparable to originators in efficacy and safety. About 70% of HCPs reported using biosimilars in $\geq$50% of their treatment-naïve patients and were comfortable with use of biosimilars in all approved indications. To encourage utilization, approximately 75% of MCO/PBM payers preferred biosimilars over originators in treatment-naïve patients, which was implemented through step therapy. HCP involvement in choosing a biosimilar for their patients was minimal, and biosimilars were often automatically ordered by pharmacists or administrators based on practice protocols or patients' cost due to insurance preferences. The major factor that influenced both payers' coverage decisions and HCP adoption of biosimilars was potential cost savings. Moreover, payers considered HCPs' clinical confidence with biosimilars as a factor influencing their biosimilar coverage decisions. ***Conclusions:*** Both HCPs and payers in the US have favorable views of oncology MAbs biosimilars, particularly among treatment-naïve patients. A framework for biosimilars integration into oncology practice is developing, which is primarily driven by insurance coverage policy, contracting, and cost benefits.

CN2
ELICITING UNREPORTED SUBGROUP-SPECIFIC SURVIVAL FROM AGGREGATE RANDOMIZED CONTROLLED TRIAL DATA

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Objectives: Subgroup analyses are vital components of health technology assessments but randomized controlled trials (RCTs) do not commonly report survival distributions for subgroups. This study developed an analytical framework to elicit unreported subgroup-specific survival information from aggregate RCT data. ***Methods:*** Assuming exponentially-distributed subgroup survival times, we developed an optimization model which aimed to approximate the restricted mean survival time (RMST) for the overall population via weighted average of the RMSTs of two mutually exclusive and exhaustive subgroups in each arm. Reported hazard ratios from the forest plots between the arms were used to enforce the relationship among subgroups' hazard rates in the model. The performance of the model was tested in a case study consisting of 8 RCTs in advanced stage gastrointestinal tumors (3 in hepatocellular carcinoma, 3 in gastric/gastroesophageal junction/esophageal cancer and 2 in colorectal cancer) which also reported Kaplan-Meier (KM) curves for overall survival (OS) for 40 subgroups in total. For each subgroup, predicted median survival, OS rates and the RMSTs were compared against the actual OS rates, median survival and the RMSTs as well as their 95% confidence intervals (CIs). ***Results:*** - Predicted median survivals and RMSTs were within the 95% CIs of the reported values in 32 and 35 out of 40 subgroups, respectively. In 8 of the subgroups, the gap between the estimated RMSTs from the predicted and the reported survival curves was less than 5%. In 6 of the subgroups, predicted survival curves laid within the 95% CIs of reported KM-curves in at least 90% of the time. Across all subgroups, on average, predicted survival curves laid within the 95% CIs of reported KM-curves in 71% of the time. ***Conclusions:*** Our study offers a useful and reliable approach for extracting subgroup-specific survival from aggregate RCT data to better inform economic and comparative effectiveness analyses for subgroups.

CN3
IT'S ALL IN THE FAMILY: MICROSIMULATION MODELLING OF GENETIC TESTING

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Objectives: Around 20-25% of ovarian cancers and 5-10% of breast cancers are due to an inherited predisposition. The primary clinical and economic benefit of hereditary breast and ovarian cancer (HBOC) testing is from preventing cancers in unaffected relatives who present for predictive/cascade testing for a known pathogenic variant in the family. Population-based genetic testing (GT) as an alternative to current practice has been gaining momentum, as it enables identification of high-risk women before they develop cancer. Existing evaluations of population-based GT mostly rely on heavily simplified comparators, and are based on selected point estimates for probabilities of identifying relatives and cascade testing uptake. This likely overestimates the benefit of population-based testing. ***Methods:*** We developed a microsimulation model for evaluating HBOC testing that includes individuals linked within family structures (thus a more sophisticated cascade testing component). Family structures are modelled using an analysis of 11,143 pedigrees from an Australian genetics clinic. The genetic component includes Mendelian inheritance of pathogenic variants for eight high- and moderate-risk genes. HBOC risk associated with single nucleotide polymorphisms was incorporated through polygenic risk scores. Life histories for individuals are generated, considering their gender, age, and genetic risk. ***Results:*** This microsimulation model, called NEEMO, more accurately reflects current practice using a simulated family-based approach. It has been validated for gene-specific cancer incidence, mortality, pathology, and uptake of cancer risk management. It has also been validated for genetic testing referral rates, and uptake of predictive GT in relatives. ***Conclusions:*** Modelling GT presents challenges due to the nature of inheritance and interaction between individuals. Clinical genetics is complex and highly specialised, with a commonly cited barrier to GT being a lack of awareness or understanding in non-genetics specialists around eligibility and management. The NEEMO model will be useful for evaluating changes in risk assessment, target GT populations, and modifying cancer prevention strategies.

CN4
PATIENT-REPORTED OUTCOMES FROM THE PHASE 3, RANDOMIZED STUDY OF ACALABRUTINIB WITH OR WITHOUT OBINUTUZUMAB VERSUS CHLORAMBUCIL PLUS OBINUTUZUMAB FOR TREATMENT-NAÏVE CHRONIC LYMPHOCYTIC LEUKEMIA (ELEVATE-TN)

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Objectives: Report patient-reported outcomes of fatigue and health-related quality of life (HRQoL) from the randomized, phase 3, ELEVATE-TN study (NCT02475681) in patients with treatment-naïve chronic lymphocytic leukemia (CLL). ***Methods:*** Patients received acalabrutinib alone (A), A plus obinutuzumab (AO), or chlorambucil plus obinutuzumab (CO). Assessments included the FACIT-Fatigue Global Fatigue Score (GFS) (scale: 0–52; lower score=worse outcome [clinically meaningful improvement: $\geq$+3]) and the EORTC QLQ-C30