Competing risk regression models in cohort studies with the R package CohortMethod

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INTRODUCTION

- **CohortMethod** performs comparative cohort studies in the Observational Medical Outcomes Partnership (OMOP) common data model. Capabilities include:
    - Propensity models
    - Logistic, Poisson, Cox regression
- We extend **CohortMethod** to include the Fine and Gray model, which extends the Cox proportional hazards model with subdistribution hazard function:

$$\lambda_k(t) = \lim_{\Delta t \to 0} \frac{\text{Prob}(t \leq T < t + \Delta t, D = k | T \geq t \cup (T < t \cap K \neq k))}{\Delta t}$$

where λ_k is the instantaneous rate of experience the event of interest $D=k$ for subjects, given they have survival to time t without experiencing any competing events $K \neq k$ for observed failure time T.

METHODS

- Kawaguchi, Shen, Li, and Suchard (2019) use a novel forward-backward scan algorithm to linearize computations to reduce complexity from $O(n^2)$ to $O(n)$:
    - Log-pseudo likelihood
    - Gradient
    - Hessian diagonal
- We develop function **combineCompetingStudyPopulations** that combines two study populations, with the outcome of interest and competing event to generate a population with information on subjects experience either outcome
- We include option **riskId** in the function **createFitOutcomeModelArgs** where we specify the competing risk outcome concept ID to fit Fine Gray in the multiple analysis framework
- Regression modelling is fitted using **Cyclops**

We are able to extend **CohortMethod** to perform comparative cohort studies in an observational database using Fine and Gray regression models for competing risks with fast and scalable computational methods.

Take a picture to view the GitHub repository for **OHDSI/CohortMethod@finegray**

RESULTS

- We apply **CohortMethod** to study the relative risk of hospitalization with heart failure for new users under angiotensin-converting enzyme (ACE) inhibitors and thiazide diuretics (THZs).

```
studyPopOutcome <- createStudyPopulation(cohortMethodData = cmData,
                                         outcomeId = 7368,
                                         firstExposureOnly = FALSE,
                                         riskWindowStart = 0,
                                         riskWindowEnd = 9999)

studyPopRisk <- createStudyPopulation(cohortMethodData = cmData,
                                      outcomeId = 7364,
                                      firstExposureOnly = FALSE,
                                      riskWindowStart = 0,
                                      riskWindowEnd = 9999)

studyPopCombined <- combineCompetingStudyPopulations( ### New function
  mainPopulation = studyPopOutcome,
  competingRiskPopulation = studyPopRisk,
  removeSubjectsWithSimultaneousEvents = TRUE
)

ps <- createPs(cohortMethodData = cmData,
               population = studyPopCombined)

matchedPop <- matchOnPs(population = ps,
                        caliper = 0.2)
```

Figure 1. Generating combined study population for both outcomes and performing one-to-one matching on propensity scores.

```
outcome <- fitOutcomeModel(population = matchedPop, ### Updated for multi-type events
                           modelType = "fgr")
outcome
```

```
## Model type: fgr
## Stratified: FALSE
## Use covariates: FALSE
## Use inverse probability of treatment weighting: FALSE
## Status: OK
##
##            Estimate lower .95 upper .95    logRr seLogRr
## treatment  0.942060  0.873580  1.015845 -0.059686  0.0385
```

Figure 2. Fitting Fine and Gray model on our one-to-one matched population.

REFERENCES

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