

```
plpData <- getPlpData(  
  sampleSize = NULL,  
  connectionDetails = connectionDetails,  
  cdmDatabaseSchema = cdmDatabaseSchema,  
  cohortDatabaseSchema = resultsDatabaseSchema,  
  cohortTable = cohortTable,  
  cohortId = 158,  
  outcomeDatabaseSchema = resultsDatabaseSchema,  
  outcomeTable = cohortTable,  
  outcomeIds = 157,  
  cdmVersion = 5,  
  covariateSettings = cs  
)  
  
#####  
  
populationSettings <- PatientLevelPrediction::createStudyPopulation(  
  plpData = plpData,  
  washoutPeriod = 0,  
  firstExposureOnly = T,  
  removeSubjectsWithPriorOutcome = F,  
  priorOutcomeLookback = 0,  
  outcomeId = 157,  
  riskWindowStart = 180,  
  riskWindowEnd = 1065,  
  minTimeAtRisk = 0,  
  startAnchor = 'cohort start',  
  endAnchor = 'cohort start',  
  requireTimeAtRisk = T,  
  includeAllOutcomes = TRUE,  
  restrictTarToCohortEnd = T  
)  
  
cox <- setCoxModel(variance = 0.01,  
  seed = 2021)  
  
coxResults <- runPlp(population = populationSettings,  
  plpData = plpData,  
  modelSettings = cox,  
  testSplit='subject',  
  testFraction=0.25,  
  nfold=3,  
  splitSeed = 2021,  
  minCovariateFraction = 0.001,  
  normalizeData = T)
```


