

```

2022-09-16 16:52:45 [Main thread] INFO EHDENCOVIDUseCase2 execute Running CohortMethod analyses
2022-09-16 16:52:45 [Main thread] TRACE CohortMethod loadCmAnalysisList Loading cmAnalysisList from
/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/renv/library/R-4.0/x86_64-pc-
linux-gnu/EHDENCOVIDUseCase2/settings/cmAnalysisList.json
2022-09-16 16:52:46 [Main thread] INFO CohortMethod runCmAnalyses *** Creating cohortMethodData objects
***
2022-09-16 16:52:46 [Main thread] INFO CohortMethod runCmAnalyses *** Creating study populations ***
2022-09-16 16:52:46 [Main thread] TRACE CohortMethod runCmAnalyses Initiating cluster with 3 threads
2022-09-16 16:52:53 [Thread 1] TRACE Thread 1 initiated
2022-09-16 16:52:53 [Thread 2] TRACE Thread 2 initiated
2022-09-16 16:52:53 [Thread 3] TRACE Thread 3 initiated
2022-09-16 16:52:53 [Thread 3] TRACE AndromedateTempFolder set to
/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/andromedaTemp
2022-09-16 16:52:53 [Thread 2] TRACE AndromedateTempFolder set to
/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/andromedaTemp
2022-09-16 16:52:53 [Thread 1] TRACE AndromedateTempFolder set to
/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/andromedaTemp
2022-09-16 16:52:54 [Thread 1] WARN CohortMethod createStudyPopulation The addExposureDaysToStart argument is
deprecated. Please use the startAnchor argument instead.
2022-09-16 16:52:54 [Thread 3] WARN CohortMethod createStudyPopulation The addExposureDaysToStart argument is
deprecated. Please use the startAnchor argument instead.
2022-09-16 16:52:54 [Thread 2] WARN CohortMethod createStudyPopulation The addExposureDaysToStart argument is
deprecated. Please use the startAnchor argument instead.
2022-09-16 16:52:54 [Thread 1] WARN CohortMethod createStudyPopulation The addExposureDaysToEnd argument is
deprecated. Please use the endAnchor argument instead.
2022-09-16 16:52:54 [Thread 3] WARN CohortMethod createStudyPopulation The addExposureDaysToEnd argument is
deprecated. Please use the endAnchor argument instead.
2022-09-16 16:52:54 [Thread 1] TRACE CohortMethod createStudyPopulation Creating study population for outcome ID
1779680
2022-09-16 16:52:54 [Thread 3] TRACE CohortMethod createStudyPopulation Creating study population for outcome ID
1779682
2022-09-16 16:52:54 [Thread 2] WARN CohortMethod createStudyPopulation The addExposureDaysToEnd argument is
deprecated. Please use the endAnchor argument instead.
2022-09-16 16:52:54 [Thread 2] TRACE CohortMethod createStudyPopulation Creating study population for outcome ID
1779681
2022-09-16 16:52:54 [Thread 1] INFO CohortMethod createStudyPopulation Removing subjects with prior outcomes (if
any)
2022-09-16 16:52:54 [Thread 3] INFO CohortMethod createStudyPopulation Removing subjects with prior outcomes (if
any)
2022-09-16 16:52:54 [Thread 2] INFO CohortMethod createStudyPopulation Removing subjects with prior outcomes (if
any)
2022-09-16 16:52:54 [Thread 3] INFO CohortMethod createStudyPopulation Censoring time at risk of recurrent subjects
at start of new time at risk

```

| | | | |
|--------------------------------------|--------------------|-----------------------|--|
| 2022-09-16 16:52:54 [Thread 1] INFO | CohortMethod | createStudyPopulation | Censoring time at risk of recurrent subjects at start of new time at risk |
| 2022-09-16 16:52:54 [Thread 3] FATAL | CohortMethod | createStudyPopulation | only 0's may be mixed with negative subscripts |
| 2022-09-16 16:52:54 [Thread 1] FATAL | CohortMethod | createStudyPopulation | only 0's may be mixed with negative subscripts |
| 2022-09-16 16:52:54 [Thread 2] INFO | CohortMethod | createStudyPopulation | Censoring time at risk of recurrent subjects at start of new time at risk |
| 2022-09-16 16:52:54 [Thread 2] FATAL | CohortMethod | createStudyPopulation | only 0's may be mixed with negative subscripts |
| 2022-09-16 16:52:54 [Main thread] | ERROR CohortMethod | runCmAnalyses | Thread 3 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779665_c1779670.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = FALSE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 30, n firstExposureOnly = FALSE, outcomelid = 1779682), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s1_t1779665_c1779670_o1779682.rds") |
| 2022-09-16 16:52:54 [Main thread] | ERROR CohortMethod | runCmAnalyses | Thread 1 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779665_c1779670.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = FALSE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 30, n firstExposureOnly = FALSE, outcomelid = 1779680), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s1_t1779665_c1779670_o1779680.rds") |
| 2022-09-16 16:52:54 [Thread 3] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 3] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead. |
| 2022-09-16 16:52:54 [Main thread] | ERROR CohortMethod | runCmAnalyses | Thread 2 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779665_c1779670.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = FALSE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 30, n firstExposureOnly = FALSE, outcomelid = 1779681), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s1_t1779665_c1779670_o1779681.rds") |
| 2022-09-16 16:52:54 [Thread 3] TRACE | CohortMethod | createStudyPopulation | Creating study population for outcome ID 1779684 |
| 2022-09-16 16:52:54 [Thread 1] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 1] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 2] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead. |

| | | | |
|--|--------------------|-----------------------|---|
| 2022-09-16 16:52:54 [Thread 1] TRACE | CohortMethod | createStudyPopulation | Creating study population for outcome ID 1779685 |
| 2022-09-16 16:52:54 [Thread 2] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 2] TRACE | CohortMethod | createStudyPopulation | Creating study population for outcome ID 1779686 |
| 2022-09-16 16:52:54 [Thread 3] INFO any) | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |
| 2022-09-16 16:52:54 [Thread 1] INFO any) | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |
| 2022-09-16 16:52:54 [Thread 2] INFO any) | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |
| 2022-09-16 16:52:54 [Thread 3] INFO at start of new time at risk | CohortMethod | createStudyPopulation | Censoring time at risk of recurrent subjects |
| 2022-09-16 16:52:54 [Thread 1] INFO at start of new time at risk | CohortMethod | createStudyPopulation | Censoring time at risk of recurrent subjects |
| 2022-09-16 16:52:54 [Thread 2] INFO at start of new time at risk | CohortMethod | createStudyPopulation | Censoring time at risk of recurrent subjects |
| 2022-09-16 16:52:54 [Main thread] | ERROR CohortMethod | runCmAnalyses | Thread 3 returns error: "only 0's may be mixed with negative subscrip |
| ts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779665_c1779670.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = FALSE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 30, n firstExposureOnly = FALSE, outcomeId = 1779684), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s1_t1779665_c1779670_o1779684.rds") | | | |
| 2022-09-16 16:52:54 [Main thread] | ERROR CohortMethod | runCmAnalyses | Thread 1 returns error: "only 0's may be mixed with negative subscrip |
| ts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779665_c1779670.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = FALSE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 30, n firstExposureOnly = FALSE, outcomeId = 1779685), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s1_t1779665_c1779670_o1779685.rds") | | | |
| 2022-09-16 16:52:54 [Main thread] | ERROR CohortMethod | runCmAnalyses | Thread 2 returns error: "only 0's may be mixed with negative subscrip |
| ts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779665_c1779670.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = FALSE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 30, n firstExposureOnly = FALSE, outcomeId = 1779686), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s1_t1779665_c1779670_o1779686.rds") | | | |
| 2022-09-16 16:52:54 [Thread 3] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 3] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead. |

| | | | |
|--------------------------------------|--------------------|-----------------------|---|
| 2022-09-16 16:52:54 [Thread 3] TRACE | CohortMethod | createStudyPopulation | Creating study population for outcome ID 1779680 |
| 2022-09-16 16:52:54 [Thread 1] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 1] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 2] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 1] TRACE | CohortMethod | createStudyPopulation | Creating study population for outcome ID 1779681 |
| 2022-09-16 16:52:54 [Thread 2] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 2] TRACE | CohortMethod | createStudyPopulation | Creating study population for outcome ID 1779682 |
| 2022-09-16 16:52:54 [Thread 3] INFO | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |
| 2022-09-16 16:52:54 [Thread 1] INFO | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |
| 2022-09-16 16:52:54 [Thread 2] INFO | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |
| 2022-09-16 16:52:54 [Thread 3] INFO | CohortMethod | createStudyPopulation | Censoring time at risk of recurrent subjects at start of new time at risk |
| 2022-09-16 16:52:54 [Thread 1] INFO | CohortMethod | createStudyPopulation | Censoring time at risk of recurrent subjects at start of new time at risk |
| 2022-09-16 16:52:54 [Thread 2] INFO | CohortMethod | createStudyPopulation | Censoring time at risk of recurrent subjects at start of new time at risk |
| 2022-09-16 16:52:54 [Main thread] | ERROR CohortMethod | runCmAnalyses | Thread 3 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779673_c1779943.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = FALSE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 30, n firstExposureOnly = FALSE, outcomeId = 1779680), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s1_t1779673_c1779943_o1779680.rds") |
| 2022-09-16 16:52:54 [Main thread] | ERROR CohortMethod | runCmAnalyses | Thread 1 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779673_c1779943.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = FALSE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 30, n firstExposureOnly = FALSE, outcomeId = 1779681), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s1_t1779673_c1779943_o1779681.rds") |
| 2022-09-16 16:52:54 [Thread 3] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 3] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead. |

2022-09-16 16:52:54 [Main thread] ERROR CohortMethod runCmAnalyses Thread 2 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779673_c1779943.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = FALSE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 30, n firstExposureOnly = FALSE, outcomeId = 1779682), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s1_t1779673_c1779943_o1779682.rds")

2022-09-16 16:52:54 [Thread 3] TRACE CohortMethod createStudyPopulation Creating study population for outcome ID 1779684

2022-09-16 16:52:54 [Thread 3] INFO CohortMethod createStudyPopulation Removing subjects with prior outcomes (if any)

2022-09-16 16:52:54 [Thread 3] INFO CohortMethod createStudyPopulation Censoring time at risk of recurrent subjects at start of new time at risk

2022-09-16 16:52:54 [Main thread] ERROR CohortMethod runCmAnalyses Thread 3 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779673_c1779943.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = FALSE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 30, n firstExposureOnly = FALSE, outcomeId = 1779684), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s1_t1779673_c1779943_o1779684.rds")

2022-09-16 16:52:54 [Thread 3] WARN CohortMethod createStudyPopulation The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead.

2022-09-16 16:52:54 [Thread 3] WARN CohortMethod createStudyPopulation The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead.

2022-09-16 16:52:54 [Thread 3] TRACE CohortMethod createStudyPopulation Creating study population for outcome ID 1779680

2022-09-16 16:52:54 [Thread 3] INFO CohortMethod createStudyPopulation Removing subjects with prior outcomes (if any)

2022-09-16 16:52:54 [Thread 3] INFO CohortMethod createStudyPopulation Censoring time at risk of recurrent subjects at start of new time at risk

2022-09-16 16:52:54 [Main thread] ERROR CohortMethod runCmAnalyses Thread 3 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779675_c1779944.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = FALSE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 30, n firstExposureOnly = FALSE, outcomeId = 1779680), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s1_t1779675_c1779944_o1779680.rds")

2022-09-16 16:52:54 [Thread 3] WARN CohortMethod createStudyPopulation The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead.

2022-09-16 16:52:54 [Thread 3] WARN CohortMethod createStudyPopulation The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead.

2022-09-16 16:52:54 [Thread 3] TRACE CohortMethod createStudyPopulation Creating study population for outcome ID 1779681

| | | | |
|--------------------------------------|--------------|-----------------------|---|
| 2022-09-16 16:52:54 [Thread 3] INFO | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |
| 2022-09-16 16:52:54 [Thread 1] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 2] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 2] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 1] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 2] TRACE | CohortMethod | createStudyPopulation | Creating study population for outcome ID 1779686 |
| 2022-09-16 16:52:54 [Thread 1] TRACE | CohortMethod | createStudyPopulation | Creating study population for outcome ID 1779685 |
| 2022-09-16 16:52:54 [Thread 3] INFO | CohortMethod | createStudyPopulation | Censoring time at risk of recurrent subjects at start of new time at risk |
| 2022-09-16 16:52:54 [Main thread] | ERROR | CohortMethod | runCmAnalyses Thread 3 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779675_c1779944.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = FALSE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 30, n firstExposureOnly = FALSE, outcomeId = 1779681), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s1_t1779675_c1779944_o1779681.rds") |
| 2022-09-16 16:52:54 [Thread 3] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 3] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 2] INFO | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |
| 2022-09-16 16:52:54 [Thread 1] INFO | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |
| 2022-09-16 16:52:54 [Thread 3] TRACE | CohortMethod | createStudyPopulation | Creating study population for outcome ID 1779682 |
| 2022-09-16 16:52:54 [Thread 3] INFO | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |
| 2022-09-16 16:52:54 [Thread 2] INFO | CohortMethod | createStudyPopulation | Censoring time at risk of recurrent subjects at start of new time at risk |
| 2022-09-16 16:52:54 [Thread 1] INFO | CohortMethod | createStudyPopulation | Censoring time at risk of recurrent subjects at start of new time at risk |
| 2022-09-16 16:52:54 [Main thread] | ERROR | CohortMethod | runCmAnalyses Thread 1 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779673_c1779943.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = FALSE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 30, n firstExposureOnly = FALSE, outcomeId = 1779685), minimizeFileSizes = |

NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s1_t1779673_c1779943_o1779685.rds")

2022-09-16 16:52:54 [Main thread] ERROR CohortMethod runCmAnalyses Thread 2 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779673_c1779943.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = FALSE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 30, n firstExposureOnly = FALSE, outcomeId = 1779686), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s1_t1779673_c1779943_o1779686.rds")

2022-09-16 16:52:54 [Thread 3] INFO CohortMethod createStudyPopulation Censoring time at risk of recurrent subjects at start of new time at risk

2022-09-16 16:52:54 [Thread 1] WARN CohortMethod createStudyPopulation The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead.

2022-09-16 16:52:54 [Thread 1] WARN CohortMethod createStudyPopulation The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead.

2022-09-16 16:52:54 [Main thread] ERROR CohortMethod runCmAnalyses Thread 3 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779675_c1779944.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = FALSE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 30, n firstExposureOnly = FALSE, outcomeId = 1779682), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s1_t1779675_c1779944_o1779682.rds")

2022-09-16 16:52:54 [Thread 1] TRACE CohortMethod createStudyPopulation Creating study population for outcome ID 1779684

2022-09-16 16:52:54 [Thread 2] WARN CohortMethod createStudyPopulation The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead.

2022-09-16 16:52:54 [Thread 2] WARN CohortMethod createStudyPopulation The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead.

2022-09-16 16:52:54 [Thread 2] TRACE CohortMethod createStudyPopulation Creating study population for outcome ID 1779685

2022-09-16 16:52:54 [Thread 3] WARN CohortMethod createStudyPopulation The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead.

2022-09-16 16:52:54 [Thread 3] WARN CohortMethod createStudyPopulation The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead.

2022-09-16 16:52:54 [Thread 3] TRACE CohortMethod createStudyPopulation Creating study population for outcome ID 1779686

2022-09-16 16:52:54 [Thread 1] INFO CohortMethod createStudyPopulation Removing subjects with prior outcomes (if any)

2022-09-16 16:52:54 [Thread 2] INFO CohortMethod createStudyPopulation Removing subjects with prior outcomes (if any)

2022-09-16 16:52:54 [Thread 3] INFO CohortMethod createStudyPopulation Removing subjects with prior outcomes (if any)

2022-09-16 16:52:54 [Thread 1] INFO CohortMethod createStudyPopulation Censoring time at risk of recurrent subjects at start of new time at risk

| | | | |
|---|--------------|-----------------------|---|
| 2022-09-16 16:52:54 [Thread 3] INFO | CohortMethod | createStudyPopulation | Censoring time at risk of recurrent subjects at start of new time at risk |
| 2022-09-16 16:52:54 [Thread 2] INFO | CohortMethod | createStudyPopulation | Censoring time at risk of recurrent subjects at start of new time at risk |
| 2022-09-16 16:52:54 [Main thread] ERROR | CohortMethod | runCmAnalyses | Thread 1 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779675_c1779944.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = FALSE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 30, n firstExposureOnly = FALSE, outcomeId = 1779684), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s1_t1779675_c1779944_o1779684.rds") |
| 2022-09-16 16:52:54 [Main thread] ERROR | CohortMethod | runCmAnalyses | Thread 2 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779675_c1779944.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = FALSE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 30, n firstExposureOnly = FALSE, outcomeId = 1779685), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s1_t1779675_c1779944_o1779685.rds") |
| 2022-09-16 16:52:54 [Main thread] ERROR | CohortMethod | runCmAnalyses | Thread 3 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779675_c1779944.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = FALSE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 30, n firstExposureOnly = FALSE, outcomeId = 1779686), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s1_t1779675_c1779944_o1779686.rds") |
| 2022-09-16 16:52:54 [Thread 1] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 1] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 2] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 1] TRACE | CohortMethod | createStudyPopulation | Creating study population for outcome ID 1779680 |
| 2022-09-16 16:52:54 [Thread 2] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 3] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 2] TRACE | CohortMethod | createStudyPopulation | Creating study population for outcome ID 1779681 |
| 2022-09-16 16:52:54 [Thread 3] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 3] TRACE | CohortMethod | createStudyPopulation | Creating study population for outcome ID 1779682 |

| | | | |
|---|--------------------|-----------------------|---|
| 2022-09-16 16:52:54 [Thread 1] INFO | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |
| 2022-09-16 16:52:54 [Thread 2] INFO | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |
| 2022-09-16 16:52:54 [Thread 3] INFO | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |
| 2022-09-16 16:52:54 [Thread 1] INFO at start of new time at risk | CohortMethod | createStudyPopulation | Censoring time at risk of recurrent subjects |
| 2022-09-16 16:52:54 [Thread 2] INFO at start of new time at risk | CohortMethod | createStudyPopulation | Censoring time at risk of recurrent subjects |
| 2022-09-16 16:52:54 [Thread 3] INFO at start of new time at risk | CohortMethod | createStudyPopulation | Censoring time at risk of recurrent subjects |
| 2022-09-16 16:52:54 [Main thread] | ERROR CohortMethod | runCmAnalyses | Thread 1 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779677_c1779676.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = FALSE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 30, n firstExposureOnly = FALSE, outcomeld = 1779680), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s1_t1779677_c1779676_o1779680.rds") |
| 2022-09-16 16:52:54 [Main thread] | ERROR CohortMethod | runCmAnalyses | Thread 2 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779677_c1779676.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = FALSE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 30, n firstExposureOnly = FALSE, outcomeld = 1779681), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s1_t1779677_c1779676_o1779681.rds") |
| 2022-09-16 16:52:54 [Thread 1] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 1] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead. |
| 2022-09-16 16:52:54 [Main thread] | ERROR CohortMethod | runCmAnalyses | Thread 3 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779677_c1779676.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = FALSE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 30, n firstExposureOnly = FALSE, outcomeld = 1779682), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s1_t1779677_c1779676_o1779682.rds") |
| 2022-09-16 16:52:54 [Thread 1] TRACE 1779684 | CohortMethod | createStudyPopulation | Creating study population for outcome ID 1779684 |
| 2022-09-16 16:52:54 [Thread 2] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 2] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead. |

| | | | | |
|-----------------------------------|-------|--------------|-----------------------|---|
| 2022-09-16 16:52:54 [Thread 3] | WARN | CohortMethod | createStudyPopulation | The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 2] | TRACE | CohortMethod | createStudyPopulation | Creating study population for outcome ID 1779685 |
| 2022-09-16 16:52:54 [Thread 3] | WARN | CohortMethod | createStudyPopulation | The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 3] | TRACE | CohortMethod | createStudyPopulation | Creating study population for outcome ID 1779686 |
| 2022-09-16 16:52:54 [Thread 1] | INFO | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |
| 2022-09-16 16:52:54 [Thread 2] | INFO | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |
| 2022-09-16 16:52:54 [Thread 3] | INFO | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |
| 2022-09-16 16:52:54 [Thread 1] | INFO | CohortMethod | createStudyPopulation | Censoring time at risk of recurrent subjects at start of new time at risk |
| 2022-09-16 16:52:54 [Thread 2] | INFO | CohortMethod | createStudyPopulation | Censoring time at risk of recurrent subjects at start of new time at risk |
| 2022-09-16 16:52:54 [Thread 3] | INFO | CohortMethod | createStudyPopulation | Censoring time at risk of recurrent subjects at start of new time at risk |
| 2022-09-16 16:52:54 [Main thread] | ERROR | CohortMethod | runCmAnalyses | Thread 1 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779677_c1779676.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = FALSE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 30, n_firstExposureOnly = FALSE, outcomeId = 1779684), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s1_t1779677_c1779676_o1779684.rds") |
| 2022-09-16 16:52:54 [Main thread] | ERROR | CohortMethod | runCmAnalyses | Thread 2 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779677_c1779676.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = FALSE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 30, n_firstExposureOnly = FALSE, outcomeId = 1779685), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s1_t1779677_c1779676_o1779685.rds") |
| 2022-09-16 16:52:54 [Main thread] | ERROR | CohortMethod | runCmAnalyses | Thread 3 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779677_c1779676.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = FALSE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 30, n_firstExposureOnly = FALSE, outcomeId = 1779686), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s1_t1779677_c1779676_o1779686.rds") |
| 2022-09-16 16:52:54 [Thread 1] | WARN | CohortMethod | createStudyPopulation | The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead. |

| | | | | |
|-----------------------------------|-------|--------------|-----------------------|---|
| 2022-09-16 16:52:54 [Thread 1] | WARN | CohortMethod | createStudyPopulation | The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 1] | TRACE | CohortMethod | createStudyPopulation | Creating study population for outcome ID 1779680 |
| 2022-09-16 16:52:54 [Thread 2] | WARN | CohortMethod | createStudyPopulation | The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 2] | WARN | CohortMethod | createStudyPopulation | The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 2] | TRACE | CohortMethod | createStudyPopulation | Creating study population for outcome ID 1779681 |
| 2022-09-16 16:52:54 [Thread 3] | WARN | CohortMethod | createStudyPopulation | The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 3] | WARN | CohortMethod | createStudyPopulation | The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 3] | TRACE | CohortMethod | createStudyPopulation | Creating study population for outcome ID 1779682 |
| 2022-09-16 16:52:54 [Thread 1] | INFO | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |
| 2022-09-16 16:52:54 [Thread 2] | INFO | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |
| 2022-09-16 16:52:54 [Thread 3] | INFO | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |
| 2022-09-16 16:52:54 [Thread 1] | INFO | CohortMethod | createStudyPopulation | Censoring time at risk of recurrent subjects at start of new time at risk |
| 2022-09-16 16:52:54 [Thread 2] | INFO | CohortMethod | createStudyPopulation | Censoring time at risk of recurrent subjects at start of new time at risk |
| 2022-09-16 16:52:54 [Thread 3] | INFO | CohortMethod | createStudyPopulation | Censoring time at risk of recurrent subjects at start of new time at risk |
| 2022-09-16 16:52:54 [Main thread] | ERROR | CohortMethod | runCmAnalyses | Thread 1 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779677_c1779946.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = FALSE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 30, n firstExposureOnly = FALSE, outcomeId = 1779680), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s1_t1779677_c1779946_o1779680.rds") |
| 2022-09-16 16:52:54 [Main thread] | ERROR | CohortMethod | runCmAnalyses | Thread 2 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779677_c1779946.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = FALSE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 30, n firstExposureOnly = FALSE, outcomeId = 1779681), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s1_t1779677_c1779946_o1779681.rds") |
| 2022-09-16 16:52:54 [Thread 1] | WARN | CohortMethod | createStudyPopulation | The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead. |

| | | | | |
|-----------------------------------|-------|--------------|-----------------------|---|
| 2022-09-16 16:52:54 [Thread 1] | WARN | CohortMethod | createStudyPopulation | The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead. |
| 2022-09-16 16:52:54 [Main thread] | ERROR | CohortMethod | runCmAnalyses | Thread 3 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779677_c1779946.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = FALSE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 30, n firstExposureOnly = FALSE, outcomeId = 1779682), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s1_t1779677_c1779946_o1779682.rds") |
| 2022-09-16 16:52:54 [Thread 1] | TRACE | CohortMethod | createStudyPopulation | Creating study population for outcome ID 1779684 |
| 2022-09-16 16:52:54 [Thread 2] | WARN | CohortMethod | createStudyPopulation | The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 2] | WARN | CohortMethod | createStudyPopulation | The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 3] | WARN | CohortMethod | createStudyPopulation | The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 2] | TRACE | CohortMethod | createStudyPopulation | Creating study population for outcome ID 1779685 |
| 2022-09-16 16:52:54 [Thread 3] | WARN | CohortMethod | createStudyPopulation | The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 3] | TRACE | CohortMethod | createStudyPopulation | Creating study population for outcome ID 1779686 |
| 2022-09-16 16:52:54 [Thread 1] | INFO | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |
| 2022-09-16 16:52:54 [Thread 2] | INFO | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |
| 2022-09-16 16:52:54 [Thread 3] | INFO | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |
| 2022-09-16 16:52:54 [Thread 1] | INFO | CohortMethod | createStudyPopulation | Censoring time at risk of recurrent subjects at start of new time at risk |
| 2022-09-16 16:52:54 [Thread 2] | INFO | CohortMethod | createStudyPopulation | Censoring time at risk of recurrent subjects at start of new time at risk |
| 2022-09-16 16:52:54 [Thread 3] | INFO | CohortMethod | createStudyPopulation | Censoring time at risk of recurrent subjects at start of new time at risk |
| 2022-09-16 16:52:54 [Main thread] | ERROR | CohortMethod | runCmAnalyses | Thread 1 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779677_c1779946.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = FALSE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 30, n firstExposureOnly = FALSE, outcomeId = 1779684), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s1_t1779677_c1779946_o1779684.rds") |
| 2022-09-16 16:52:54 [Main thread] | ERROR | CohortMethod | runCmAnalyses | Thread 2 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread- |

EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779677_c1779946.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = FALSE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 30, n firstExposureOnly = FALSE, outcomeId = 1779685), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s1_t1779677_c1779946_o1779685.rds")

2022-09-16 16:52:54 [Main thread] ERROR CohortMethod runCmAnalyses Thread 3 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779677_c1779946.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = FALSE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 30, n firstExposureOnly = FALSE, outcomeId = 1779686), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s1_t1779677_c1779946_o1779686.rds")

2022-09-16 16:52:54 [Thread 1] WARN CohortMethod createStudyPopulation The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead.

2022-09-16 16:52:54 [Thread 2] WARN CohortMethod createStudyPopulation The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead.

2022-09-16 16:52:54 [Thread 1] WARN CohortMethod createStudyPopulation The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead.

2022-09-16 16:52:54 [Thread 1] TRACE CohortMethod createStudyPopulation Creating study population for outcome ID 1779680

2022-09-16 16:52:54 [Thread 2] WARN CohortMethod createStudyPopulation The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead.

2022-09-16 16:52:54 [Thread 2] TRACE CohortMethod createStudyPopulation Creating study population for outcome ID 1779681

2022-09-16 16:52:54 [Thread 1] INFO CohortMethod createStudyPopulation Removing subjects with prior outcomes (if any)

2022-09-16 16:52:54 [Thread 2] INFO CohortMethod createStudyPopulation Removing subjects with prior outcomes (if any)

2022-09-16 16:52:54 [Thread 3] WARN CohortMethod createStudyPopulation The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead.

2022-09-16 16:52:54 [Thread 3] WARN CohortMethod createStudyPopulation The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead.

2022-09-16 16:52:54 [Thread 3] TRACE CohortMethod createStudyPopulation Creating study population for outcome ID 1779682

2022-09-16 16:52:54 [Thread 3] INFO CohortMethod createStudyPopulation Removing subjects with prior outcomes (if any)

2022-09-16 16:52:54 [Thread 1] INFO CohortMethod createStudyPopulation Censoring time at risk of recurrent subjects at start of new time at risk

2022-09-16 16:52:54 [Thread 2] INFO CohortMethod createStudyPopulation Censoring time at risk of recurrent subjects at start of new time at risk

2022-09-16 16:52:54 [Main thread] ERROR CohortMethod runCmAnalyses Thread 1 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779679_c1779945.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = FALSE, priorOutcomeLookback = 30,

removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 30, n firstExposureOnly = FALSE, outcomelD = 1779680), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s1_t1779679_c1779945_o1779680.rds")

2022-09-16 16:52:54 [Main thread] ERROR CohortMethod runCmAnalyses Thread 2 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779679_c1779945.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = FALSE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 30, n firstExposureOnly = FALSE, outcomelD = 1779681), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s1_t1779679_c1779945_o1779681.rds")

2022-09-16 16:52:54 [Thread 1] WARN CohortMethod createStudyPopulation The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead.

2022-09-16 16:52:54 [Thread 1] WARN CohortMethod createStudyPopulation The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead.

2022-09-16 16:52:54 [Thread 1] TRACE CohortMethod createStudyPopulation Creating study population for outcome ID 1779684

2022-09-16 16:52:54 [Thread 2] WARN CohortMethod createStudyPopulation The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead.

2022-09-16 16:52:54 [Thread 2] WARN CohortMethod createStudyPopulation The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead.

2022-09-16 16:52:54 [Thread 2] TRACE CohortMethod createStudyPopulation Creating study population for outcome ID 1779685

2022-09-16 16:52:54 [Thread 3] INFO CohortMethod createStudyPopulation Censoring time at risk of recurrent subjects at start of new time at risk

2022-09-16 16:52:54 [Main thread] ERROR CohortMethod runCmAnalyses Thread 3 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779679_c1779945.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = FALSE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 30, n firstExposureOnly = FALSE, outcomelD = 1779682), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s1_t1779679_c1779945_o1779682.rds")

2022-09-16 16:52:54 [Thread 3] WARN CohortMethod createStudyPopulation The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead.

2022-09-16 16:52:54 [Thread 3] WARN CohortMethod createStudyPopulation The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead.

2022-09-16 16:52:54 [Thread 1] INFO CohortMethod createStudyPopulation Removing subjects with prior outcomes (if any)

2022-09-16 16:52:54 [Thread 3] TRACE CohortMethod createStudyPopulation Creating study population for outcome ID 1779686

2022-09-16 16:52:54 [Thread 2] INFO CohortMethod createStudyPopulation Removing subjects with prior outcomes (if any)

2022-09-16 16:52:54 [Thread 3] INFO CohortMethod createStudyPopulation Removing subjects with prior outcomes (if any)

2022-09-16 16:52:54 [Thread 1] INFO CohortMethod createStudyPopulation Censoring time at risk of recurrent subjects at start of new time at risk

2022-09-16 16:52:54 [Thread 2] INFO CohortMethod createStudyPopulation Censoring time at risk of recurrent subjects at start of new time at risk

2022-09-16 16:52:54 [Main thread] ERROR CohortMethod runCmAnalyses Thread 1 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779679_c1779945.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = FALSE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 30, n firstExposureOnly = FALSE, outcomeId = 1779684), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s1_t1779679_c1779945_o1779684.rds")

2022-09-16 16:52:54 [Main thread] ERROR CohortMethod runCmAnalyses Thread 2 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779679_c1779945.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = FALSE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 30, n firstExposureOnly = FALSE, outcomeId = 1779685), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s1_t1779679_c1779945_o1779685.rds")

2022-09-16 16:52:54 [Thread 3] INFO CohortMethod createStudyPopulation Censoring time at risk of recurrent subjects at start of new time at risk

2022-09-16 16:52:54 [Main thread] ERROR CohortMethod runCmAnalyses Thread 3 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779679_c1779945.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = FALSE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 30, n firstExposureOnly = FALSE, outcomeId = 1779686), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s1_t1779679_c1779945_o1779686.rds")

2022-09-16 16:52:54 [Thread 1] WARN CohortMethod createStudyPopulation The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead.

2022-09-16 16:52:54 [Thread 1] WARN CohortMethod createStudyPopulation The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead.

2022-09-16 16:52:54 [Thread 1] TRACE CohortMethod createStudyPopulation Creating study population for outcome ID 1779680

2022-09-16 16:52:54 [Thread 2] WARN CohortMethod createStudyPopulation The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead.

2022-09-16 16:52:54 [Thread 2] WARN CohortMethod createStudyPopulation The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead.

2022-09-16 16:52:54 [Thread 2] TRACE CohortMethod createStudyPopulation Creating study population for outcome ID 1779681

2022-09-16 16:52:54 [Thread 3] WARN CohortMethod createStudyPopulation The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead.

2022-09-16 16:52:54 [Thread 3] WARN CohortMethod createStudyPopulation The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead.

2022-09-16 16:52:54 [Thread 3] TRACE CohortMethod createStudyPopulation Creating study population for outcome ID 1779682

| | | | |
|--|--------------------|-----------------------|---|
| 2022-09-16 16:52:54 [Thread 1] INFO any) | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |
| 2022-09-16 16:52:54 [Thread 2] INFO any) | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |
| 2022-09-16 16:52:54 [Thread 3] INFO any) | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |
| 2022-09-16 16:52:54 [Thread 3] INFO at start of new time at risk | CohortMethod | createStudyPopulation | Censoring time at risk of recurrent subjects |
| 2022-09-16 16:52:54 [Main thread] | ERROR CohortMethod | runCmAnalyses | Thread 3 returns error: "only 0's may be mixed with negative subscrip |
| ts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779946_c1779676.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = FALSE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 30, n firstExposureOnly = FALSE, outcomeId = 1779682), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s1_t1779946_c1779676_o1779682.rds") | | | |
| 2022-09-16 16:52:54 [Thread 3] WARN deprecated. Please use the startAnchor argument instead. | CohortMethod | createStudyPopulation | The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 3] WARN deprecated. Please use the endAnchor argument instead. | CohortMethod | createStudyPopulation | The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 3] TRACE 1779684 | CohortMethod | createStudyPopulation | Creating study population for outcome ID 1779684 |
| 2022-09-16 16:52:54 [Thread 1] INFO at start of new time at risk | CohortMethod | createStudyPopulation | Censoring time at risk of recurrent subjects |
| 2022-09-16 16:52:54 [Thread 2] INFO at start of new time at risk | CohortMethod | createStudyPopulation | Censoring time at risk of recurrent subjects |
| 2022-09-16 16:52:54 [Main thread] | ERROR CohortMethod | runCmAnalyses | Thread 1 returns error: "only 0's may be mixed with negative subscrip |
| ts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779946_c1779676.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = FALSE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 30, n firstExposureOnly = FALSE, outcomeId = 1779680), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s1_t1779946_c1779676_o1779680.rds") | | | |
| 2022-09-16 16:52:54 [Thread 1] WARN deprecated. Please use the startAnchor argument instead. | CohortMethod | createStudyPopulation | The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead. |
| 2022-09-16 16:52:54 [Main thread] | ERROR CohortMethod | runCmAnalyses | Thread 2 returns error: "only 0's may be mixed with negative subscrip |
| ts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779946_c1779676.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = FALSE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 30, n firstExposureOnly = FALSE, outcomeId = 1779681), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s1_t1779946_c1779676_o1779681.rds") | | | |
| 2022-09-16 16:52:54 [Thread 1] WARN deprecated. Please use the endAnchor argument instead. | CohortMethod | createStudyPopulation | The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead. |

| | | | |
|--|--------------|-----------------------|---|
| 2022-09-16 16:52:54 [Thread 1] TRACE | CohortMethod | createStudyPopulation | Creating study population for outcome ID 1779685 |
| 2022-09-16 16:52:54 [Thread 3] INFO | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |
| 2022-09-16 16:52:54 [Thread 1] INFO | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |
| 2022-09-16 16:52:54 [Thread 3] INFO | CohortMethod | createStudyPopulation | Censoring time at risk of recurrent subjects at start of new time at risk |
| 2022-09-16 16:52:54 [Main thread] | ERROR | CohortMethod | runCmAnalyses Thread 3 returns error: "only 0's may be mixed with negative subscrip |
| ts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779946_c1779676.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = FALSE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 30, n firstExposureOnly = FALSE, outcomeld = 1779684), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s1_t1779946_c1779676_o1779684.rds") | | | |
| 2022-09-16 16:52:54 [Thread 1] INFO | CohortMethod | createStudyPopulation | Censoring time at risk of recurrent subjects at start of new time at risk |
| 2022-09-16 16:52:54 [Main thread] | ERROR | CohortMethod | runCmAnalyses Thread 1 returns error: "only 0's may be |
| mixed with negative subscrip | | | |
| ts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779946_c1779676.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = FALSE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 30, n firstExposureOnly = FALSE, outcomeld = 1779685), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s1_t1779946_c1779676_o1779685.rds") | | | |
| 2022-09-16 16:52:54 [Thread 3] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 3] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 3] TRACE | CohortMethod | createStudyPopulation | Creating study population for outcome ID 1779680 |
| 2022-09-16 16:52:54 [Thread 3] INFO | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |
| 2022-09-16 16:52:54 [Thread 3] INFO | CohortMethod | createStudyPopulation | Censoring time at risk of recurrent subjects at start of new time at risk |
| 2022-09-16 16:52:54 [Main thread] | ERROR | CohortMethod | runCmAnalyses Thread 3 returns error: "only 0's may be |
| mixed with negative subscrip | | | |
| ts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779665_c1779670.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = TRUE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 0, n firstExposureOnly = FALSE, outcomeld = 1779680), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s2_t1779665_c1779670_o1779680.rds") | | | |
| 2022-09-16 16:52:54 [Thread 3] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead. |

| | | | |
|--------------------------------------|--------------------|-----------------------|---|
| 2022-09-16 16:52:54 [Thread 3] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 3] TRACE | CohortMethod | createStudyPopulation | Creating study population for outcome ID 1779682 |
| 2022-09-16 16:52:54 [Thread 3] INFO | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |
| 2022-09-16 16:52:54 [Thread 2] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 2] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 2] TRACE | CohortMethod | createStudyPopulation | Creating study population for outcome ID 1779686 |
| 2022-09-16 16:52:54 [Thread 3] INFO | CohortMethod | createStudyPopulation | Censoring time at risk of recurrent subjects at start of new time at risk |
| 2022-09-16 16:52:54 [Main thread] | ERROR CohortMethod | runCmAnalyses | Thread 3 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779665_c1779670.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = TRUE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 0, n_firstExposureOnly = FALSE, outcomeId = 1779682), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s2_t1779665_c1779670_o1779682.rds") |
| 2022-09-16 16:52:54 [Thread 3] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 3] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 3] TRACE | CohortMethod | createStudyPopulation | Creating study population for outcome ID 1779684 |
| 2022-09-16 16:52:54 [Thread 2] INFO | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |
| 2022-09-16 16:52:54 [Thread 3] INFO | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |
| 2022-09-16 16:52:54 [Thread 2] INFO | CohortMethod | createStudyPopulation | Censoring time at risk of recurrent subjects at start of new time at risk |
| 2022-09-16 16:52:54 [Main thread] | ERROR CohortMethod | runCmAnalyses | Thread 2 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779946_c1779676.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = FALSE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 30, n_firstExposureOnly = FALSE, outcomeId = 1779686), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s1_t1779946_c1779676_o1779686.rds") |
| 2022-09-16 16:52:54 [Thread 1] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 1] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead. |

| | | | |
|--------------------------------------|--------------|-----------------------|---|
| 2022-09-16 16:52:54 [Thread 1] TRACE | CohortMethod | createStudyPopulation | Creating study population for outcome ID 1779681 |
| 2022-09-16 16:52:54 [Thread 2] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 3] INFO | CohortMethod | createStudyPopulation | Censoring time at risk of recurrent subjects at start of new time at risk |
| 2022-09-16 16:52:54 [Thread 2] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 2] TRACE | CohortMethod | createStudyPopulation | Creating study population for outcome ID 1779685 |
| 2022-09-16 16:52:54 [Main thread] | ERROR | CohortMethod | runCmAnalyses Thread 3 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779665_c1779670.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = TRUE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 0, n firstExposureOnly = FALSE, outcomeId = 1779684), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s2_t1779665_c1779670_o1779684.rds") |
| 2022-09-16 16:52:54 [Thread 3] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 3] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 1] INFO | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |
| 2022-09-16 16:52:54 [Thread 3] TRACE | CohortMethod | createStudyPopulation | Creating study population for outcome ID 1779686 |
| 2022-09-16 16:52:54 [Thread 2] INFO | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |
| 2022-09-16 16:52:54 [Thread 3] INFO | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |
| 2022-09-16 16:52:54 [Thread 1] INFO | CohortMethod | createStudyPopulation | Censoring time at risk of recurrent subjects at start of new time at risk |
| 2022-09-16 16:52:54 [Main thread] | ERROR | CohortMethod | runCmAnalyses Thread 1 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779665_c1779670.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = TRUE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 0, n firstExposureOnly = FALSE, outcomeId = 1779681), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s2_t1779665_c1779670_o1779681.rds") |
| 2022-09-16 16:52:54 [Thread 2] INFO | CohortMethod | createStudyPopulation | Censoring time at risk of recurrent subjects at start of new time at risk |
| 2022-09-16 16:52:54 [Main thread] | ERROR | CohortMethod | runCmAnalyses Thread 2 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779665_c1779670.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = TRUE, priorOutcomeLookback = 30, |

removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 0, n firstExposureOnly = FALSE, outcomeId = 1779685), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s2_t1779665_c1779670_o1779685.rds")

2022-09-16 16:52:54 [Thread 1] WARN CohortMethod createStudyPopulation The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead.

2022-09-16 16:52:54 [Thread 1] WARN CohortMethod createStudyPopulation The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead.

2022-09-16 16:52:54 [Thread 1] TRACE CohortMethod createStudyPopulation Creating study population for outcome ID 1779680

2022-09-16 16:52:54 [Thread 3] INFO CohortMethod createStudyPopulation Censoring time at risk of recurrent subjects at start of new time at risk

2022-09-16 16:52:54 [Main thread] ERROR CohortMethod runCmAnalyses Thread 3 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779665_c1779670.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = TRUE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 0, n firstExposureOnly = FALSE, outcomeId = 1779686), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s2_t1779665_c1779670_o1779686.rds")

2022-09-16 16:52:54 [Thread 2] WARN CohortMethod createStudyPopulation The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead.

2022-09-16 16:52:54 [Thread 2] WARN CohortMethod createStudyPopulation The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead.

2022-09-16 16:52:54 [Thread 2] TRACE CohortMethod createStudyPopulation Creating study population for outcome ID 1779681

2022-09-16 16:52:54 [Thread 1] INFO CohortMethod createStudyPopulation Removing subjects with prior outcomes (if any)

2022-09-16 16:52:54 [Thread 2] INFO CohortMethod createStudyPopulation Removing subjects with prior outcomes (if any)

2022-09-16 16:52:54 [Thread 1] INFO CohortMethod createStudyPopulation Censoring time at risk of recurrent subjects at start of new time at risk

2022-09-16 16:52:54 [Main thread] ERROR CohortMethod runCmAnalyses Thread 1 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779673_c1779943.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = TRUE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 0, n firstExposureOnly = FALSE, outcomeId = 1779680), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s2_t1779673_c1779943_o1779680.rds")

2022-09-16 16:52:54 [Thread 1] WARN CohortMethod createStudyPopulation The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead.

2022-09-16 16:52:54 [Thread 1] WARN CohortMethod createStudyPopulation The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead.

2022-09-16 16:52:54 [Thread 1] TRACE CohortMethod createStudyPopulation Creating study population for outcome ID 1779684

2022-09-16 16:52:54 [Thread 2] INFO CohortMethod createStudyPopulation Censoring time at risk of recurrent subjects at start of new time at risk

2022-09-16 16:52:54 [Main thread] ERROR CohortMethod runCmAnalyses Thread 2 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779673_c1779943.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = TRUE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 0, n firstExposureOnly = FALSE, outcomeId = 1779681), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s2_t1779673_c1779943_o1779681.rds")

2022-09-16 16:52:54 [Thread 2] WARN CohortMethod createStudyPopulation The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead.

2022-09-16 16:52:54 [Thread 2] WARN CohortMethod createStudyPopulation The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead.

2022-09-16 16:52:54 [Thread 2] TRACE CohortMethod createStudyPopulation Creating study population for outcome ID 1779685

2022-09-16 16:52:54 [Thread 1] INFO CohortMethod createStudyPopulation Removing subjects with prior outcomes (if any)

2022-09-16 16:52:54 [Thread 2] INFO CohortMethod createStudyPopulation Removing subjects with prior outcomes (if any)

2022-09-16 16:52:54 [Thread 1] INFO CohortMethod createStudyPopulation Censoring time at risk of recurrent subjects at start of new time at risk

2022-09-16 16:52:54 [Main thread] ERROR CohortMethod runCmAnalyses Thread 1 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779673_c1779943.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = TRUE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 0, n firstExposureOnly = FALSE, outcomeId = 1779684), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s2_t1779673_c1779943_o1779684.rds")

2022-09-16 16:52:54 [Thread 1] WARN CohortMethod createStudyPopulation The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead.

2022-09-16 16:52:54 [Thread 1] WARN CohortMethod createStudyPopulation The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead.

2022-09-16 16:52:54 [Thread 1] TRACE CohortMethod createStudyPopulation Creating study population for outcome ID 1779686

2022-09-16 16:52:54 [Thread 2] INFO CohortMethod createStudyPopulation Censoring time at risk of recurrent subjects at start of new time at risk

2022-09-16 16:52:54 [Main thread] ERROR CohortMethod runCmAnalyses Thread 2 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779673_c1779943.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = TRUE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 0, n firstExposureOnly = FALSE, outcomeId = 1779685), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s2_t1779673_c1779943_o1779685.rds")

2022-09-16 16:52:54 [Thread 1] INFO CohortMethod createStudyPopulation Removing subjects with prior outcomes (if any)

| | | | | |
|-----------------------------------|-------|--------------|-----------------------|---|
| 2022-09-16 16:52:54 [Thread 2] | WARN | CohortMethod | createStudyPopulation | The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 2] | WARN | CohortMethod | createStudyPopulation | The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 2] | TRACE | CohortMethod | createStudyPopulation | 1779680 Creating study population for outcome ID |
| 2022-09-16 16:52:54 [Thread 2] | INFO | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |
| 2022-09-16 16:52:54 [Thread 1] | INFO | CohortMethod | createStudyPopulation | at start of new time at risk Censoring time at risk of recurrent subjects |
| 2022-09-16 16:52:54 [Main thread] | ERROR | CohortMethod | runCmAnalyses | Thread 1 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779673_c1779943.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = TRUE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 0, n firstExposureOnly = FALSE, outcomeId = 1779686), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s2_t1779673_c1779943_o1779686.rds") |
| 2022-09-16 16:52:54 [Thread 2] | INFO | CohortMethod | createStudyPopulation | at start of new time at risk Censoring time at risk of recurrent subjects |
| 2022-09-16 16:52:54 [Thread 1] | WARN | CohortMethod | createStudyPopulation | The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 1] | WARN | CohortMethod | createStudyPopulation | The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 1] | TRACE | CohortMethod | createStudyPopulation | 1779681 Creating study population for outcome ID |
| 2022-09-16 16:52:54 [Main thread] | ERROR | CohortMethod | runCmAnalyses | Thread 2 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779675_c1779944.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = TRUE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 0, n firstExposureOnly = FALSE, outcomeId = 1779680), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s2_t1779675_c1779944_o1779680.rds") |
| 2022-09-16 16:52:54 [Thread 3] | WARN | CohortMethod | createStudyPopulation | The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 3] | WARN | CohortMethod | createStudyPopulation | The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 2] | WARN | CohortMethod | createStudyPopulation | The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 3] | TRACE | CohortMethod | createStudyPopulation | 1779682 Creating study population for outcome ID |
| 2022-09-16 16:52:54 [Thread 2] | WARN | CohortMethod | createStudyPopulation | The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 2] | TRACE | CohortMethod | createStudyPopulation | 1779682 Creating study population for outcome ID |

| | | | |
|--|--------------------|-----------------------|---|
| 2022-09-16 16:52:54 [Thread 1] INFO any) | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |
| 2022-09-16 16:52:54 [Thread 3] INFO any) | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |
| 2022-09-16 16:52:54 [Thread 2] INFO any) | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |
| 2022-09-16 16:52:54 [Thread 1] INFO at start of new time at risk | CohortMethod | createStudyPopulation | Censoring time at risk of recurrent subjects |
| 2022-09-16 16:52:54 [Main thread] | ERROR CohortMethod | runCmAnalyses | Thread 1 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779675_c1779944.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = TRUE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 0, n firstExposureOnly = FALSE, outcomeId = 1779681), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s2_t1779675_c1779944_o1779681.rds") |
| 2022-09-16 16:52:54 [Thread 3] INFO at start of new time at risk | CohortMethod | createStudyPopulation | Censoring time at risk of recurrent subjects |
| 2022-09-16 16:52:54 [Thread 2] INFO at start of new time at risk | CohortMethod | createStudyPopulation | Censoring time at risk of recurrent subjects |
| 2022-09-16 16:52:54 [Thread 1] WARN deprecated. Please use the startAnchor argument instead. | CohortMethod | createStudyPopulation | The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead. |
| 2022-09-16 16:52:54 [Main thread] | ERROR CohortMethod | runCmAnalyses | Thread 3 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779673_c1779943.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = TRUE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 0, n firstExposureOnly = FALSE, outcomeId = 1779682), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s2_t1779673_c1779943_o1779682.rds") |
| 2022-09-16 16:52:54 [Thread 1] WARN deprecated. Please use the endAnchor argument instead. | CohortMethod | createStudyPopulation | The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 1] TRACE 1779684 | CohortMethod | createStudyPopulation | Creating study population for outcome ID 1779684 |
| 2022-09-16 16:52:54 [Main thread] | ERROR CohortMethod | runCmAnalyses | Thread 2 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779675_c1779944.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = TRUE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 0, n firstExposureOnly = FALSE, outcomeId = 1779682), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s2_t1779675_c1779944_o1779682.rds") |
| 2022-09-16 16:52:54 [Thread 2] WARN deprecated. Please use the startAnchor argument instead. | CohortMethod | createStudyPopulation | The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 2] WARN deprecated. Please use the endAnchor argument instead. | CohortMethod | createStudyPopulation | The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead. |

| | | | |
|--------------------------------------|--------------|-----------------------|---|
| 2022-09-16 16:52:54 [Thread 2] TRACE | CohortMethod | createStudyPopulation | Creating study population for outcome ID 1779686 |
| 2022-09-16 16:52:54 [Thread 3] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 3] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 3] TRACE | CohortMethod | createStudyPopulation | Creating study population for outcome ID 1779685 |
| 2022-09-16 16:52:54 [Thread 1] INFO | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |
| 2022-09-16 16:52:54 [Thread 2] INFO | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |
| 2022-09-16 16:52:54 [Thread 3] INFO | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |
| 2022-09-16 16:52:54 [Thread 1] INFO | CohortMethod | createStudyPopulation | Censoring time at risk of recurrent subjects at start of new time at risk |
| 2022-09-16 16:52:54 [Main thread] | ERROR | CohortMethod | runCmAnalyses Thread 1 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779675_c1779944.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = TRUE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 0, n firstExposureOnly = FALSE, outcomeId = 1779684), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s2_t1779675_c1779944_o1779684.rds") |
| 2022-09-16 16:52:54 [Thread 2] INFO | CohortMethod | createStudyPopulation | Censoring time at risk of recurrent subjects at start of new time at risk |
| 2022-09-16 16:52:54 [Main thread] | ERROR | CohortMethod | runCmAnalyses Thread 2 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779675_c1779944.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = TRUE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 0, n firstExposureOnly = FALSE, outcomeId = 1779686), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s2_t1779675_c1779944_o1779686.rds") |
| 2022-09-16 16:52:54 [Thread 3] INFO | CohortMethod | createStudyPopulation | Censoring time at risk of recurrent subjects at start of new time at risk |
| 2022-09-16 16:52:54 [Main thread] | ERROR | CohortMethod | runCmAnalyses Thread 3 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779675_c1779944.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = TRUE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 0, n firstExposureOnly = FALSE, outcomeId = 1779685), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s2_t1779675_c1779944_o1779685.rds") |
| 2022-09-16 16:52:54 [Thread 2] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead. |

| | | | | |
|-----------------------------------|-------|--------------|-----------------------|---|
| 2022-09-16 16:52:54 [Thread 2] | WARN | CohortMethod | createStudyPopulation | The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 2] | TRACE | CohortMethod | createStudyPopulation | Creating study population for outcome ID 1779681 |
| 2022-09-16 16:52:54 [Thread 3] | WARN | CohortMethod | createStudyPopulation | The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 3] | WARN | CohortMethod | createStudyPopulation | The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead. |
| 2022-09-16 16:52:54 [Thread 3] | TRACE | CohortMethod | createStudyPopulation | Creating study population for outcome ID 1779682 |
| 2022-09-16 16:52:54 [Thread 2] | INFO | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |
| 2022-09-16 16:52:54 [Thread 3] | INFO | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |
| 2022-09-16 16:52:55 [Thread 2] | INFO | CohortMethod | createStudyPopulation | Censoring time at risk of recurrent subjects at start of new time at risk |
| 2022-09-16 16:52:55 [Main thread] | ERROR | CohortMethod | runCmAnalyses | Thread 2 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779677_c1779676.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = TRUE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 0, n firstExposureOnly = FALSE, outcomeId = 1779681), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s2_t1779677_c1779676_o1779681.rds") |
| 2022-09-16 16:52:55 [Thread 2] | WARN | CohortMethod | createStudyPopulation | The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead. |
| 2022-09-16 16:52:55 [Thread 3] | INFO | CohortMethod | createStudyPopulation | Censoring time at risk of recurrent subjects at start of new time at risk |
| 2022-09-16 16:52:55 [Thread 2] | WARN | CohortMethod | createStudyPopulation | The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead. |
| 2022-09-16 16:52:55 [Thread 2] | TRACE | CohortMethod | createStudyPopulation | Creating study population for outcome ID 1779684 |
| 2022-09-16 16:52:55 [Main thread] | ERROR | CohortMethod | runCmAnalyses | Thread 3 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779677_c1779676.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = TRUE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 0, n firstExposureOnly = FALSE, outcomeId = 1779682), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s2_t1779677_c1779676_o1779682.rds") |
| 2022-09-16 16:52:55 [Thread 3] | WARN | CohortMethod | createStudyPopulation | The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead. |
| 2022-09-16 16:52:55 [Thread 3] | WARN | CohortMethod | createStudyPopulation | The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead. |
| 2022-09-16 16:52:55 [Thread 3] | TRACE | CohortMethod | createStudyPopulation | Creating study population for outcome ID 1779685 |

| | | | |
|--------------------------------------|--------------------|-----------------------|---|
| 2022-09-16 16:52:55 [Thread 2] INFO | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |
| 2022-09-16 16:52:55 [Thread 3] INFO | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |
| 2022-09-16 16:52:55 [Thread 2] INFO | CohortMethod | createStudyPopulation | Censoring time at risk of recurrent subjects at start of new time at risk |
| 2022-09-16 16:52:55 [Main thread] | ERROR CohortMethod | runCmAnalyses | Thread 2 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779677_c1779676.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = TRUE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 0, n firstExposureOnly = FALSE, outcomeld = 1779684), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s2_t1779677_c1779676_o1779684.rds") |
| 2022-09-16 16:52:55 [Thread 3] INFO | CohortMethod | createStudyPopulation | Censoring time at risk of recurrent subjects at start of new time at risk |
| 2022-09-16 16:52:55 [Thread 2] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead. |
| 2022-09-16 16:52:55 [Thread 2] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead. |
| 2022-09-16 16:52:55 [Main thread] | ERROR CohortMethod | runCmAnalyses | Thread 3 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779677_c1779676.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = TRUE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 0, n firstExposureOnly = FALSE, outcomeld = 1779685), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s2_t1779677_c1779676_o1779685.rds") |
| 2022-09-16 16:52:55 [Thread 2] TRACE | CohortMethod | createStudyPopulation | Creating study population for outcome ID 1779686 |
| 2022-09-16 16:52:55 [Thread 2] INFO | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |
| 2022-09-16 16:52:55 [Thread 2] INFO | CohortMethod | createStudyPopulation | Censoring time at risk of recurrent subjects at start of new time at risk |
| 2022-09-16 16:52:55 [Main thread] | ERROR CohortMethod | runCmAnalyses | Thread 2 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779677_c1779676.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = TRUE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 0, n firstExposureOnly = FALSE, outcomeld = 1779686), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s2_t1779677_c1779676_o1779686.rds") |
| 2022-09-16 16:52:55 [Thread 1] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead. |
| 2022-09-16 16:52:55 [Thread 1] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead. |

| | | | |
|--------------------------------------|--------------------|-----------------------|---|
| 2022-09-16 16:52:55 [Thread 1] TRACE | CohortMethod | createStudyPopulation | Creating study population for outcome ID 1779680 |
| 2022-09-16 16:52:55 [Thread 1] INFO | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |
| 2022-09-16 16:52:55 [Thread 1] INFO | CohortMethod | createStudyPopulation | Censoring time at risk of recurrent subjects at start of new time at risk |
| 2022-09-16 16:52:55 [Main thread] | ERROR CohortMethod | runCmAnalyses | Thread 1 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIdUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779677_c1779676.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = TRUE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 0, n firstExposureOnly = FALSE, outcomeld = 1779680), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIdUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s2_t1779677_c1779676_o1779680.rds") |
| 2022-09-16 16:52:55 [Thread 1] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead. |
| 2022-09-16 16:52:55 [Thread 1] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead. |
| 2022-09-16 16:52:55 [Thread 1] TRACE | CohortMethod | createStudyPopulation | Creating study population for outcome ID 1779682 |
| 2022-09-16 16:52:55 [Thread 1] INFO | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |
| 2022-09-16 16:52:55 [Thread 3] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead. |
| 2022-09-16 16:52:55 [Thread 3] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead. |
| 2022-09-16 16:52:55 [Thread 3] TRACE | CohortMethod | createStudyPopulation | Creating study population for outcome ID 1779680 |
| 2022-09-16 16:52:55 [Thread 1] INFO | CohortMethod | createStudyPopulation | Censoring time at risk of recurrent subjects at start of new time at risk |
| 2022-09-16 16:52:55 [Main thread] | ERROR CohortMethod | runCmAnalyses | Thread 1 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIdUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779677_c1779946.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = TRUE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 0, n firstExposureOnly = FALSE, outcomeld = 1779682), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIdUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s2_t1779677_c1779946_o1779682.rds") |
| 2022-09-16 16:52:55 [Thread 1] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead. |
| 2022-09-16 16:52:55 [Thread 1] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead. |
| 2022-09-16 16:52:55 [Thread 1] TRACE | CohortMethod | createStudyPopulation | Creating study population for outcome ID 1779684 |
| 2022-09-16 16:52:55 [Thread 3] INFO | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |

| | | | |
|---|--------------|-----------------------|---|
| 2022-09-16 16:52:55 [Thread 1] INFO | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |
| 2022-09-16 16:52:55 [Thread 2] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead. |
| 2022-09-16 16:52:55 [Thread 2] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead. |
| 2022-09-16 16:52:55 [Thread 2] TRACE | CohortMethod | createStudyPopulation | Creating study population for outcome ID 1779681 |
| 2022-09-16 16:52:55 [Thread 3] INFO | CohortMethod | createStudyPopulation | Censoring time at risk of recurrent subjects at start of new time at risk |
| 2022-09-16 16:52:55 [Main thread] ERROR | CohortMethod | runCmAnalyses | Thread 3 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779677_c1779946.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = TRUE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 0, n firstExposureOnly = FALSE, outcomeld = 1779680), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s2_t1779677_c1779946_o1779680.rds") |
| 2022-09-16 16:52:55 [Thread 3] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead. |
| 2022-09-16 16:52:55 [Thread 3] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead. |
| 2022-09-16 16:52:55 [Thread 3] TRACE | CohortMethod | createStudyPopulation | Creating study population for outcome ID 1779685 |
| 2022-09-16 16:52:55 [Thread 2] INFO | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |
| 2022-09-16 16:52:55 [Thread 1] INFO | CohortMethod | createStudyPopulation | Censoring time at risk of recurrent subjects at start of new time at risk |
| 2022-09-16 16:52:55 [Main thread] ERROR | CohortMethod | runCmAnalyses | Thread 1 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779677_c1779946.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = TRUE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 0, n firstExposureOnly = FALSE, outcomeld = 1779684), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s2_t1779677_c1779946_o1779684.rds") |
| 2022-09-16 16:52:55 [Thread 1] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead. |
| 2022-09-16 16:52:55 [Thread 1] WARN | CohortMethod | createStudyPopulation | The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead. |
| 2022-09-16 16:52:55 [Thread 1] TRACE | CohortMethod | createStudyPopulation | Creating study population for outcome ID 1779686 |
| 2022-09-16 16:52:55 [Thread 3] INFO | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |
| 2022-09-16 16:52:55 [Thread 1] INFO | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |

2022-09-16 16:52:55 [Thread 2] INFO CohortMethod createStudyPopulation Censoring time at risk of recurrent subjects at start of new time at risk

2022-09-16 16:52:55 [Main thread] ERROR CohortMethod runCmAnalyses Thread 2 returns error: "only 0's may be mixed with negative subscripsts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779677_c1779946.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = TRUE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 0, n firstExposureOnly = FALSE, outcomeId = 1779681), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s2_t1779677_c1779946_o1779681.rds")

2022-09-16 16:52:55 [Thread 3] INFO CohortMethod createStudyPopulation Censoring time at risk of recurrent subjects at start of new time at risk

2022-09-16 16:52:55 [Main thread] ERROR CohortMethod runCmAnalyses Thread 3 returns error: "only 0's may be mixed with negative subscripsts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779677_c1779946.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = TRUE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 0, n firstExposureOnly = FALSE, outcomeId = 1779685), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s2_t1779677_c1779946_o1779685.rds")

2022-09-16 16:52:55 [Thread 2] WARN CohortMethod createStudyPopulation The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead.

2022-09-16 16:52:55 [Thread 2] WARN CohortMethod createStudyPopulation The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead.

2022-09-16 16:52:55 [Thread 2] TRACE CohortMethod createStudyPopulation Creating study population for outcome ID 1779680

2022-09-16 16:52:55 [Thread 1] INFO CohortMethod createStudyPopulation Censoring time at risk of recurrent subjects at start of new time at risk

2022-09-16 16:52:55 [Thread 3] WARN CohortMethod createStudyPopulation The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead.

2022-09-16 16:52:55 [Thread 3] WARN CohortMethod createStudyPopulation The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead.

2022-09-16 16:52:55 [Thread 3] TRACE CohortMethod createStudyPopulation Creating study population for outcome ID 1779681

2022-09-16 16:52:55 [Main thread] ERROR CohortMethod runCmAnalyses Thread 1 returns error: "only 0's may be mixed with negative subscripsts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779677_c1779946.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = TRUE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 0, n firstExposureOnly = FALSE, outcomeId = 1779686), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s2_t1779677_c1779946_o1779686.rds")

2022-09-16 16:52:55 [Thread 2] INFO CohortMethod createStudyPopulation Removing subjects with prior outcomes (if any)

2022-09-16 16:52:55 [Thread 1] WARN CohortMethod createStudyPopulation The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead.

| | | | | |
|-----------------------------------|-------|--------------|-----------------------|---|
| 2022-09-16 16:52:55 [Thread 1] | WARN | CohortMethod | createStudyPopulation | The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead. |
| 2022-09-16 16:52:55 [Thread 1] | TRACE | CohortMethod | createStudyPopulation | Creating study population for outcome ID 1779682 |
| 2022-09-16 16:52:55 [Thread 3] | INFO | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |
| 2022-09-16 16:52:55 [Thread 2] | INFO | CohortMethod | createStudyPopulation | Censoring time at risk of recurrent subjects at start of new time at risk |
| 2022-09-16 16:52:55 [Thread 1] | INFO | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |
| 2022-09-16 16:52:55 [Main thread] | ERROR | CohortMethod | runCmAnalyses | Thread 2 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779679_c1779945.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = TRUE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 0, n firstExposureOnly = FALSE, outcomeId = 1779680), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s2_t1779679_c1779945_o1779680.rds") |
| 2022-09-16 16:52:55 [Thread 2] | WARN | CohortMethod | createStudyPopulation | The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead. |
| 2022-09-16 16:52:55 [Thread 2] | WARN | CohortMethod | createStudyPopulation | The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead. |
| 2022-09-16 16:52:55 [Thread 2] | TRACE | CohortMethod | createStudyPopulation | Creating study population for outcome ID 1779684 |
| 2022-09-16 16:52:55 [Thread 3] | INFO | CohortMethod | createStudyPopulation | Censoring time at risk of recurrent subjects at start of new time at risk |
| 2022-09-16 16:52:55 [Main thread] | ERROR | CohortMethod | runCmAnalyses | Thread 3 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779679_c1779945.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = TRUE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 0, n firstExposureOnly = FALSE, outcomeId = 1779681), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s2_t1779679_c1779945_o1779681.rds") |
| 2022-09-16 16:52:55 [Thread 3] | WARN | CohortMethod | createStudyPopulation | The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead. |
| 2022-09-16 16:52:55 [Thread 3] | WARN | CohortMethod | createStudyPopulation | The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead. |
| 2022-09-16 16:52:55 [Thread 3] | TRACE | CohortMethod | createStudyPopulation | Creating study population for outcome ID 1779685 |
| 2022-09-16 16:52:55 [Thread 2] | INFO | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |
| 2022-09-16 16:52:55 [Thread 1] | INFO | CohortMethod | createStudyPopulation | Censoring time at risk of recurrent subjects at start of new time at risk |
| 2022-09-16 16:52:55 [Main thread] | ERROR | CohortMethod | runCmAnalyses | Thread 1 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread- |

```

EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779679_c1779945.zip", args =
list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE,
riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = TRUE, priorOutcomeLookback = 30,
removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 0, n firstExposureOnly = FALSE, outcomeId = 1779682), minimizeFileSizes =
NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-
EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s2_t1779679_c1779945_o1779682.rds")

2022-09-16 16:52:55 [Thread 1] WARN CohortMethod createStudyPopulation The addExposureDaysToStart argument is
deprecated. Please use the startAnchor argument instead.

2022-09-16 16:52:55 [Thread 3] INFO CohortMethod createStudyPopulation Removing subjects with prior outcomes (if
any)

2022-09-16 16:52:55 [Thread 1] WARN CohortMethod createStudyPopulation The addExposureDaysToEnd argument is
deprecated. Please use the endAnchor argument instead.

2022-09-16 16:52:55 [Thread 1] TRACE CohortMethod createStudyPopulation Creating study population for outcome ID
1779686

2022-09-16 16:52:55 [Thread 2] INFO CohortMethod createStudyPopulation Censoring time at risk of recurrent subjects
at start of new time at risk

2022-09-16 16:52:55 [Thread 1] INFO CohortMethod createStudyPopulation Removing subjects with prior outcomes (if
any)

2022-09-16 16:52:55 [Main thread] ERROR CohortMethod runCmAnalyses Thread 2 returns error: "only 0's may be
mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile =
"/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-
EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779679_c1779945.zip", args =
list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE,
riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = TRUE, priorOutcomeLookback = 30,
removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 0, n firstExposureOnly = FALSE, outcomeId = 1779684), minimizeFileSizes =
NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-
EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s2_t1779679_c1779945_o1779684.rds")

2022-09-16 16:52:55 [Thread 3] INFO CohortMethod createStudyPopulation Censoring time at risk of recurrent subjects
at start of new time at risk

2022-09-16 16:52:55 [Main thread] ERROR CohortMethod runCmAnalyses Thread 3 returns error: "only 0's may be
mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile =
"/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-
EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779679_c1779945.zip", args =
list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE,
riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = TRUE, priorOutcomeLookback = 30,
removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 0, n firstExposureOnly = FALSE, outcomeId = 1779685), minimizeFileSizes =
NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-
EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s2_t1779679_c1779945_o1779685.rds")

2022-09-16 16:52:55 [Thread 2] WARN CohortMethod createStudyPopulation The addExposureDaysToStart argument is
deprecated. Please use the startAnchor argument instead.

2022-09-16 16:52:55 [Thread 2] WARN CohortMethod createStudyPopulation The addExposureDaysToEnd argument is
deprecated. Please use the endAnchor argument instead.

2022-09-16 16:52:55 [Thread 2] TRACE CohortMethod createStudyPopulation Creating study population for outcome ID
1779680

2022-09-16 16:52:55 [Thread 3] WARN CohortMethod createStudyPopulation The addExposureDaysToStart argument is
deprecated. Please use the startAnchor argument instead.

2022-09-16 16:52:55 [Thread 3] WARN CohortMethod createStudyPopulation The addExposureDaysToEnd argument is
deprecated. Please use the endAnchor argument instead.

2022-09-16 16:52:55 [Thread 3] TRACE CohortMethod createStudyPopulation Creating study population for outcome ID
1779681

```

| | | | | |
|-----------------------------------|-------|--------------|-----------------------|---|
| 2022-09-16 16:52:55 [Thread 1] | INFO | CohortMethod | createStudyPopulation | Censoring time at risk of recurrent subjects at start of new time at risk |
| 2022-09-16 16:52:55 [Thread 2] | INFO | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |
| 2022-09-16 16:52:55 [Main thread] | ERROR | CohortMethod | runCmAnalyses | Thread 1 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779679_c1779945.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = TRUE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 0, n_firstExposureOnly = FALSE, outcomeId = 1779686), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s2_t1779679_c1779945_o1779686.rds") |
| 2022-09-16 16:52:55 [Thread 3] | INFO | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |
| 2022-09-16 16:52:55 [Thread 1] | WARN | CohortMethod | createStudyPopulation | The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead. |
| 2022-09-16 16:52:55 [Thread 1] | WARN | CohortMethod | createStudyPopulation | The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead. |
| 2022-09-16 16:52:55 [Thread 1] | TRACE | CohortMethod | createStudyPopulation | Creating study population for outcome ID 1779682 |
| 2022-09-16 16:52:55 [Thread 2] | INFO | CohortMethod | createStudyPopulation | Censoring time at risk of recurrent subjects at start of new time at risk |
| 2022-09-16 16:52:55 [Main thread] | ERROR | CohortMethod | runCmAnalyses | Thread 2 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779946_c1779676.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = TRUE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 0, n_firstExposureOnly = FALSE, outcomeId = 1779680), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s2_t1779946_c1779676_o1779680.rds") |
| 2022-09-16 16:52:55 [Thread 1] | INFO | CohortMethod | createStudyPopulation | Removing subjects with prior outcomes (if any) |
| 2022-09-16 16:52:55 [Thread 2] | WARN | CohortMethod | createStudyPopulation | The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead. |
| 2022-09-16 16:52:55 [Thread 2] | WARN | CohortMethod | createStudyPopulation | The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead. |
| 2022-09-16 16:52:55 [Thread 2] | TRACE | CohortMethod | createStudyPopulation | Creating study population for outcome ID 1779684 |
| 2022-09-16 16:52:55 [Thread 3] | INFO | CohortMethod | createStudyPopulation | Censoring time at risk of recurrent subjects at start of new time at risk |
| 2022-09-16 16:52:55 [Main thread] | ERROR | CohortMethod | runCmAnalyses | Thread 3 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779946_c1779676.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = TRUE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 0, n_firstExposureOnly = FALSE, outcomeId = 1779681), minimizeFileSizes = |

NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s2_t1779946_c1779676_o1779681.rds")

2022-09-16 16:52:55 [Thread 3] WARN CohortMethod createStudyPopulation The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead.

2022-09-16 16:52:55 [Thread 3] WARN CohortMethod createStudyPopulation The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead.

2022-09-16 16:52:55 [Thread 3] TRACE CohortMethod createStudyPopulation Creating study population for outcome ID 1779685

2022-09-16 16:52:55 [Thread 2] INFO CohortMethod createStudyPopulation Removing subjects with prior outcomes (if any)

2022-09-16 16:52:55 [Thread 1] INFO CohortMethod createStudyPopulation Censoring time at risk of recurrent subjects at start of new time at risk

2022-09-16 16:52:55 [Thread 3] INFO CohortMethod createStudyPopulation Removing subjects with prior outcomes (if any)

2022-09-16 16:52:55 [Main thread] ERROR CohortMethod runCmAnalyses Thread 1 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779946_c1779676.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = TRUE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 0, n firstExposureOnly = FALSE, outcomeld = 1779682), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s2_t1779946_c1779682.rds")

2022-09-16 16:52:55 [Thread 1] WARN CohortMethod createStudyPopulation The addExposureDaysToStart argument is deprecated. Please use the startAnchor argument instead.

2022-09-16 16:52:55 [Thread 1] WARN CohortMethod createStudyPopulation The addExposureDaysToEnd argument is deprecated. Please use the endAnchor argument instead.

2022-09-16 16:52:55 [Thread 1] TRACE CohortMethod createStudyPopulation Creating study population for outcome ID 1779686

2022-09-16 16:52:55 [Thread 2] INFO CohortMethod createStudyPopulation Censoring time at risk of recurrent subjects at start of new time at risk

2022-09-16 16:52:55 [Main thread] ERROR CohortMethod runCmAnalyses Thread 2 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779946_c1779676.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = TRUE, priorOutcomeLookback = 30, removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 0, n firstExposureOnly = FALSE, outcomeld = 1779684), minimizeFileSizes = NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s2_t1779946_c1779676_o1779684.rds")

2022-09-16 16:52:55 [Thread 1] INFO CohortMethod createStudyPopulation Removing subjects with prior outcomes (if any)

2022-09-16 16:52:55 [Thread 3] INFO CohortMethod createStudyPopulation Censoring time at risk of recurrent subjects at start of new time at risk

2022-09-16 16:52:55 [Main thread] ERROR CohortMethod runCmAnalyses Thread 3 returns error: "only 0's may be mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-EHDENCOVIDUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779946_c1779676.zip", args = list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE, riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = TRUE, priorOutcomeLookback = 30,

```
removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 0, n firstExposureOnly = FALSE, outcomeld = 1779685), minimizeFileSizes =
NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-
EHDENCOVIdUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s2_t1779946_c1779676_o1779685.rds")
```

```
2022-09-16 16:52:55 [Thread 1] INFO CohortMethod createStudyPopulation Censoring time at risk of recurrent subjects
at start of new time at risk
```

```
2022-09-16 16:52:55 [Main thread] ERROR CohortMethod runCmAnalyses Thread 1 returns error: "only 0's may be
mixed with negative subscripts" when using argument(s): list(cohortMethodDataFile =
"/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-
EHDENCOVIdUseCase2/output_15_09_22_no_positive_controls/cmOutput/CmData_l1_t1779946_c1779676.zip", args =
list(restrictToCommonPeriod = FALSE, removeDuplicateSubjects = "keep all", minDaysAtRisk = 1, addExposureDaysToStart = FALSE,
riskWindowStart = 1, washoutPeriod = 0, censorAtNewRiskWindow = TRUE, addExposureDaysToEnd = TRUE, priorOutcomeLookback = 30,
removeSubjectsWithPriorOutcome = TRUE, riskWindowEnd = 0, n firstExposureOnly = FALSE, outcomeld = 1779686), minimizeFileSizes =
NULL, studyPopFile = "/home/juanma/OHDSI/NICE/new_15_september/EhdenCovidUseCase-christinaread-
EHDENCOVIdUseCase2/output_15_09_22_no_positive_controls/cmOutput/StudyPop_l1_s2_t1779946_c1779676_o1779686.rds")
```

```
2022-09-16 16:52:55 [Main thread] FATAL CohortMethod runCmAnalyses Error in ParallelLogger::clusterApply(cluster,
objectsToCreate, createStudyPopObject) : Error(s) when calling function 'fun', see earlier messages for details
```