



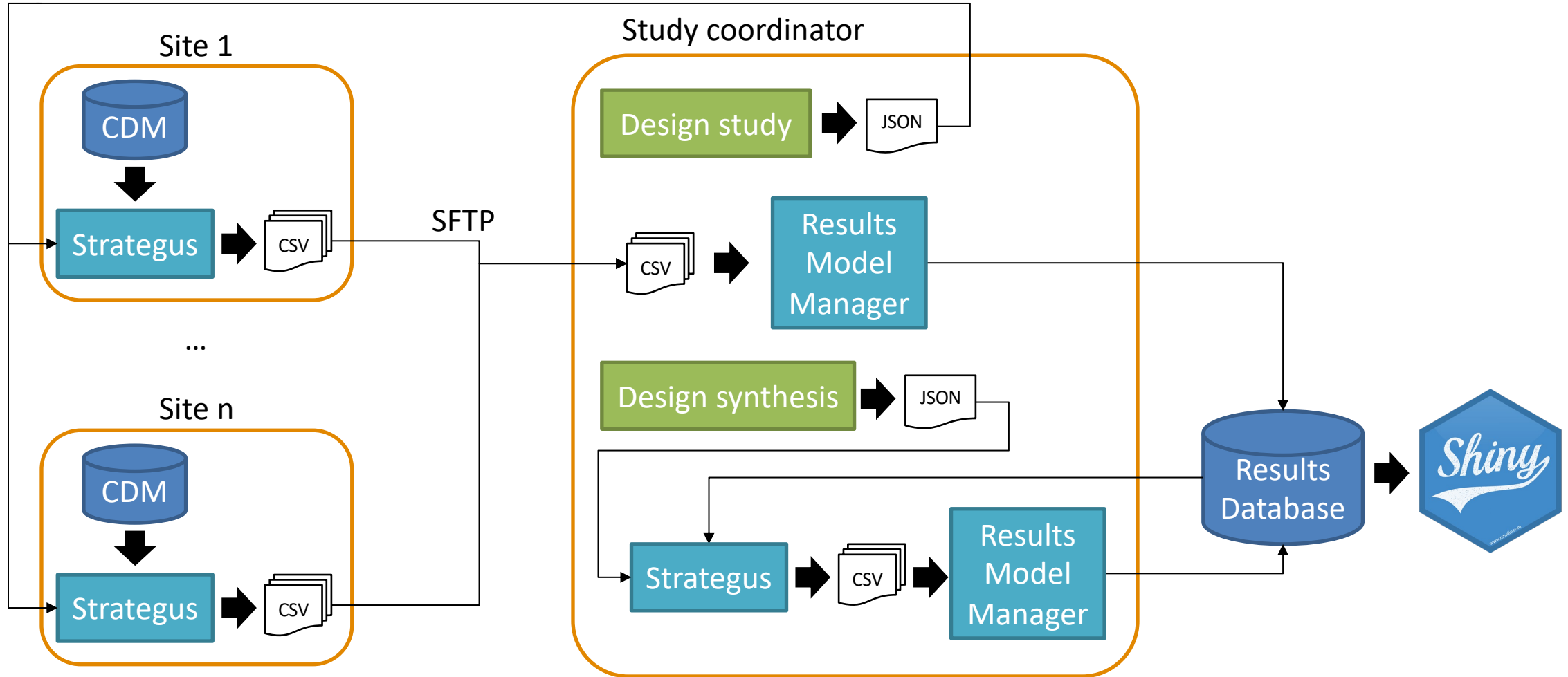
Evidence Synthesis in practice

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Overview



— Firewall



EvidenceSynthesis using Strategus

Read along: go to <https://github.com/ohdsi-studies/AntiVegfKidneyFailure> and find the EvidenceSynthesis.R file

ohdsi-studies / AntiVegfKidneyFailure Public

generated from ohdsi-studies/StudyRepoTemplate

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Documents	updated version and date	5 days ago
docs	compiled protocol to html	5 days ago
inst	Update analysis specification script and JSON to be...	2 weeks ago
.gitignore	Initial commit	2 months ago
AntiVegfKidneyFailure.Rp...	Re-including R setup, commenting out cohort defin...	last month
EvidenceSynthesis.R	Adding code to run evidence synthesis	3 days ago
KeyringSetup.R	Update KeyringSetup.R	2 weeks ago

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Creating analysis specifications

```
source("https://raw.githubusercontent.com/ohdsi/EvidenceSynthesisModule/v0.1.3/SettingsFunctions.R")

evidenceSynthesisSourceCm <- createEvidenceSynthesisSource(sourceMethod = "CohortMethod",
                                                           likelihoodApproximation = "adaptive grid")
metaAnalysisCm <- createBayesianMetaAnalysis(evidenceSynthesisAnalysisId = 1,
                                             alpha = 0.05,
                                             evidenceSynthesisDescription = "Bayesian random-effects",
                                             evidenceSynthesisSource = evidenceSynthesisSourceCm)

evidenceSynthesisSourceSccs <- createEvidenceSynthesisSource(sourceMethod = "SelfControlledCaseSeries",
                                                            likelihoodApproximation = "adaptive grid")
metaAnalysisSccs <- createBayesianMetaAnalysis(evidenceSynthesisAnalysisId = 2,
                                              alpha = 0.05,
                                              evidenceSynthesisDescription = "Bayesian random-effects",
                                              evidenceSynthesisSource = evidenceSynthesisSourceSccs)

evidenceSynthesisAnalysisList <- list(metaAnalysisCm, metaAnalysisSccs)
analysisSpecifications <- createEvidenceSynthesisModuleSpecifications(evidenceSynthesisAnalysisList)
analysisSpecifications <- createEmptyAnalysisSpecifications() %>%
addModuleSpecifications(evidenceSynthesisAnalysisSpecifications)
```



Creating execution settings

```
library(Strategus)

resultsDatabaseConnectionDetails <- DatabaseConnector::createConnectionDetails(
  dbms = "postgresql",
  port = 5432,
  server = paste(keyring::key_get("antiVegfStudyServer"), keyring::key_get("antiVegfStudyDatabase"), sep = "/"),
  user = keyring::key_get("antiVegfStudyUser"),
  password = keyring::key_get("antiVegfStudyPassword")
)
resultsDatabaseSchema <- keyring::key_get("antiVegfStudySchema")
outputLocation <- "D:/AntiVegfKidneyFailure"

storeConnectionDetails(connectionDetails = resultsDatabaseConnectionDetails,
  connectionDetailsReference = "antiVegfResultsConnectionDetailsRef")

resultsExecutionSettings <- createResultsExecutionSettings(
  resultsConnectionDetailsReference = "antiVegfResultsConnectionDetailsRef",
  resultsDatabaseSchema = resultsDatabaseSchema,
  workFolder = file.path(outputLocation, "work"),
  resultsFolder = file.path(outputLocation, "results"),
  minCellCount = 5)
```



Running EvidenceSynthesis in Strategus: Running analyses

```
execute(analysisSpecifications = analysisSpecifications,  
        executionSettings = executionSettings)
```



View results

<https://data.ohdsi.org/AntiVegfKidneyFailure/>