Code used in the video vignette

A short demonstration of the EvidenceSynthesis package

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This vignette contains the code used in a short video on the EvidenceSynthesis package: https://youtu.be/dho7E97vpgQ.

Simulate data

Simulate 10 sites:

```
simulationSettings <- createSimulationSettings(
  nSites = 10,
  n = 10000,
  treatedFraction = 0.8,
  nStrata = 5,
  hazardRatio = 2,
  randomEffectSd = 0.5
)
set.seed(1)
populations <- simulatePopulations(simulationSettings)

head(populations[[1]])
```

```
##   rowId stratumId x time y
## 1     1         5 1   10 0
## 2     2         2 1  113 0
## 3     3         4 1  135 0
## 4     4         2 1   27 0
## 5     5         2 1  104 0
## 6     6         3 1  342 0
```

```
table(populations[[1]][, c("x", "y")])
```

```
##    y
## x      0    1
##   0 1998    2
##   1 7981   19
```

Fit a model locally

Assume we are at site 1:

```
library(Cyclops)
```

```
population <- populations[[1]]

cyclopsData <- createCyclopsData(Surv(time, y) ~ x + strata(stratumId),
  data = population,
  modelType = "cox"
)
cyclopsFit <- fitCyclopsModel(cyclopsData)

# Hazard ratio:
exp(coef(cyclopsFit))
```

```
##        x
## 2.378318
```

```
# 95% confidence interval:
exp(confint(cyclopsFit, parm = "x")[2:3])
```

```
## [1]  0.6888127 14.9382268
```

Approximate the likelihood function at one site

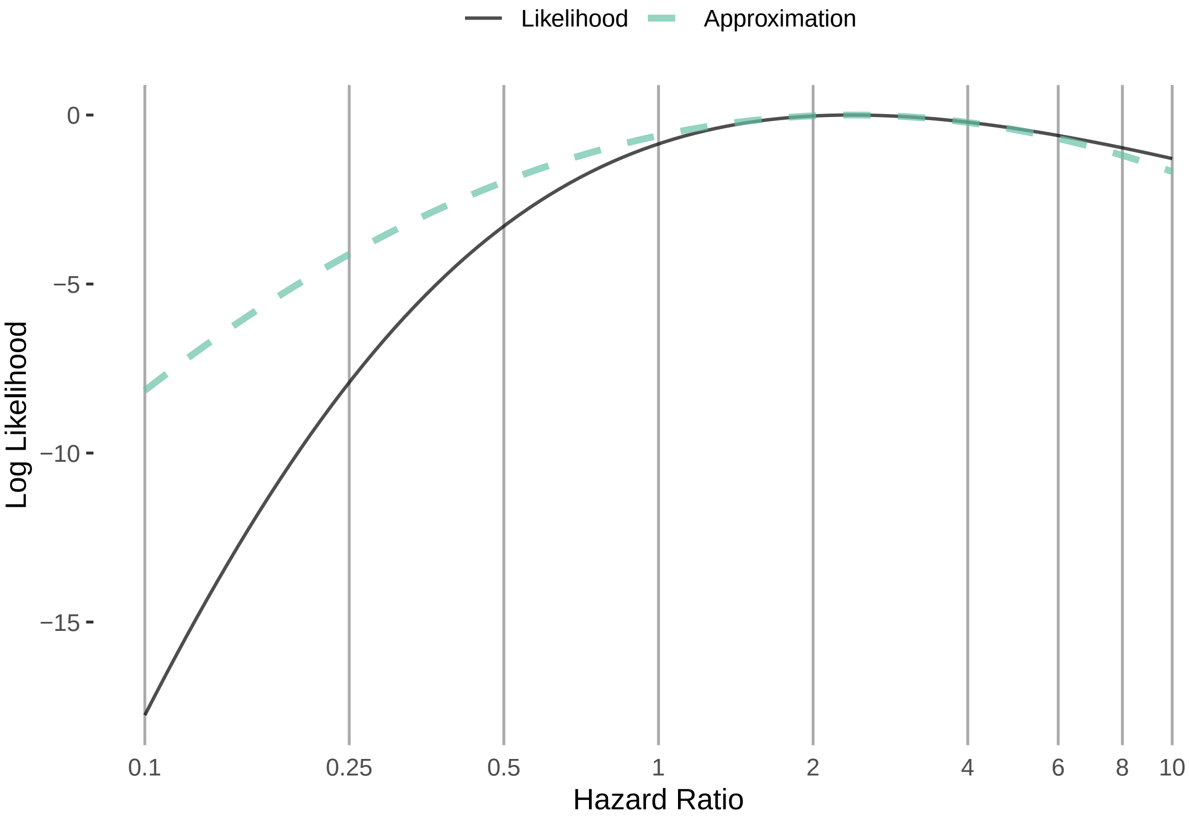
Normal approximation

```
normalApproximation <- approximateLikelihood(
  cyclopsFit = cyclopsFit,
  parameter = "x",
  approximation = "normal"
)
normalApproximation
```

```
##         rr    ci95Lb   ci95Ub     logRr   seLogRr
## x 2.378318 0.6888127 14.93823 0.8663934 0.7848893
```

```
plotLikelihoodFit(
  approximation = normalApproximation,
  cyclopsFit = cyclopsFit,
  parameter = "x"
)
```

```
## Detected data following normal distribution
```



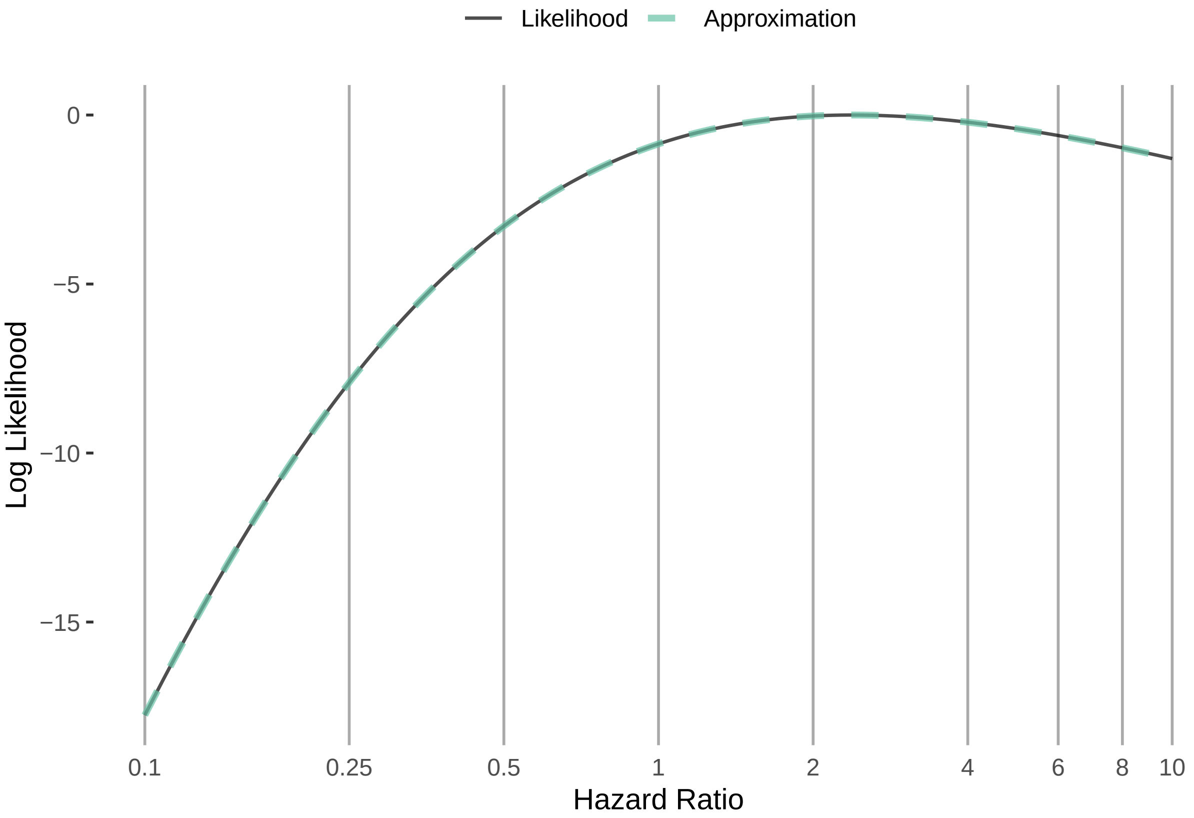
Adaptive approximation

```r
approximation <- approximateLikelihood(
  cyclopsFit = cyclopsFit,
  parameter = "x",
  approximation = "adaptive grid",
  bounds = c(log(0.1), log(10))
)
head(approximation)
```

```
## # A tibble: 6 x 2
##   point value
##   <dbl> <dbl>
## 1 -2.30 -156.
## 2 -2.29 -156.
## 3 -2.27 -156.
## 4 -2.25 -155.
## 5 -2.24 -155.
## 6 -2.22 -155.
```

```r
plotLikelihoodFit(
  approximation = approximation,
  cyclopsFit = cyclopsFit,
  parameter = "x"
)
```

```
## Detected data following adaptive grid distribution
```



Approximate at all sites

```
fitModelInDatabase <- function(population, approximation) {
  cyclopsData <- createCyclopsData(Surv(time, y) ~ x + strata(stratumId),
    data = population,
    modelType = "cox"
  )
  cyclopsFit <- fitCyclopsModel(cyclopsData)
  approximation <- approximateLikelihood(cyclopsFit,
    parameter = "x",
    approximation = approximation
  )
  return(approximation)
}
adaptiveGridApproximations <- lapply(
  X = populations,
  FUN = fitModelInDatabase,
  approximation = "adaptive grid"
)
normalApproximations <- lapply(
  X = populations,
  FUN = fitModelInDatabase,
  approximation = "normal"
)
normalApproximations <- do.call(rbind, (normalApproximations))
```

Synthesize evidence

Fixed-effects

Gold standard (pooling data):

```
fixedFxPooled <- computeFixedEffectMetaAnalysis(populations)
fixedFxPooled
```

```
##         rr       lb       ub     logRr  seLogRr
## x 2.432933 1.370034 4.800644 0.8890975 0.319882
```

Normal approximation:

```
fixedFxNormal <- computeFixedEffectMetaAnalysis(normalApproximations)
```

```
## Warning: Estimate(s) with NA seLogRr detected. Removing before computing
## meta-analysis.

## Warning: Estimate(s) with extremely high seLogRr (>100) detected. Removing
## before computing meta-analysis.
```

```
fixedFxNormal
```

```
##         rr        lb       ub     logRr   seLogRr
## 1 1.605267 0.8168054 3.154828 0.4732898 0.3447228
```

Adaptive grid approximation:

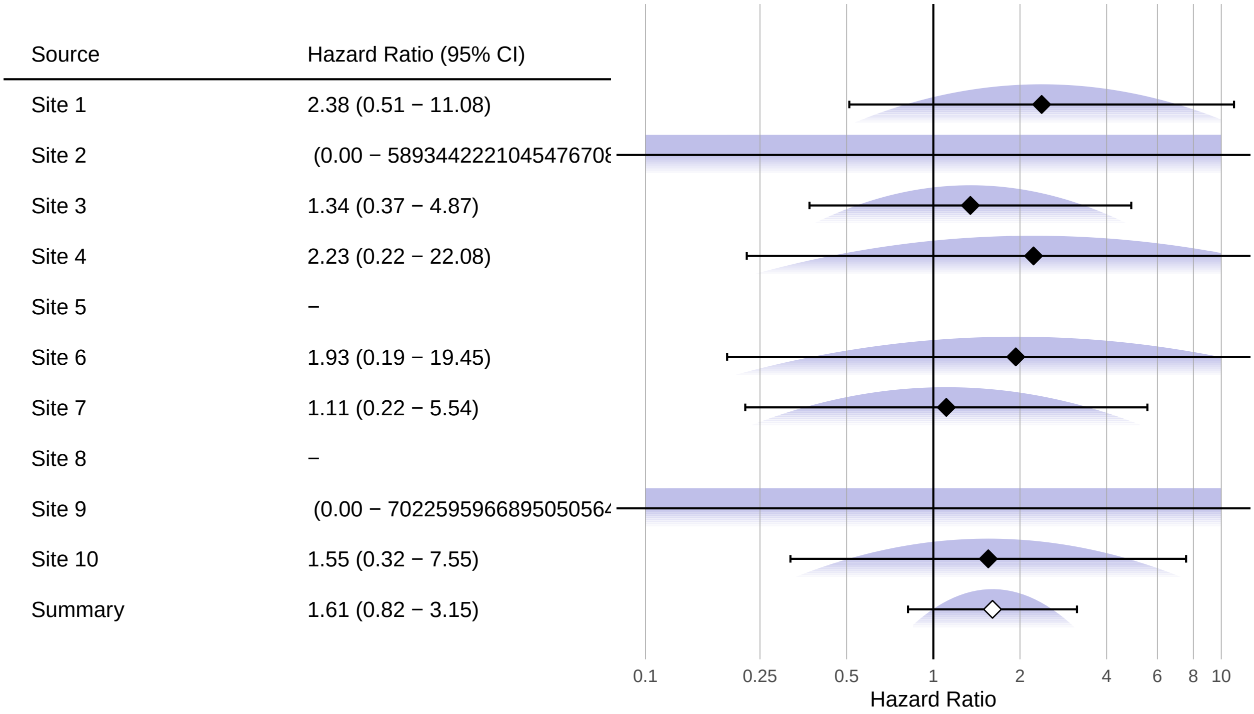
```
fixedFxAdaptiveGrid <- computeFixedEffectMetaAnalysis(adaptiveGridApproximations)
fixedFxAdaptiveGrid
```

```
##         rr       lb       ub     logRr   seLogRr
## 1 2.448437 1.376857 4.792428 0.8954498 0.3181777
```

Visualization

Normal approximation:

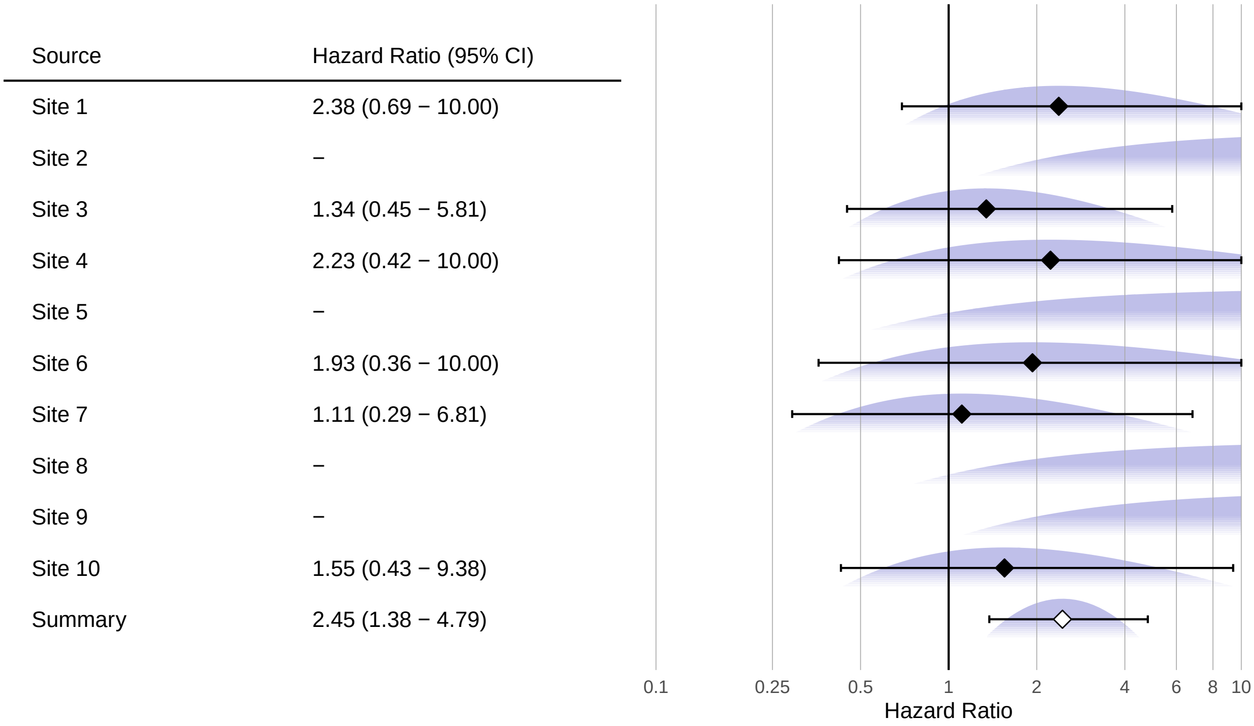
```
plotMetaAnalysisForest(
  data = normalApproximations,
  labels = paste("Site", 1:10),
  estimate = fixedFxNormal,
  xLabel = "Hazard Ratio"
)
```



Source	Hazard Ratio (95% CI)
Site 1	2.38 (0.51 − 11.08)
Site 2	(0.00 − 589344222104547670
Site 3	1.34 (0.37 − 4.87)
Site 4	2.23 (0.22 − 22.08)
Site 5	–
Site 6	1.93 (0.19 − 19.45)
Site 7	1.11 (0.22 − 5.54)
Site 8	–
Site 9	(0.00 − 702259596689505056
Site 10	1.55 (0.32 − 7.55)
Summary	1.61 (0.82 − 3.15)

Adaptive grid approximation:

```r
plotMetaAnalysisForest(
  data = adaptiveGridApproximations,
  labels = paste("Site", 1:10),
  estimate = fixedFxAdaptiveGrid,
  xLabel = "Hazard Ratio"
)
```



Source	Hazard Ratio (95% CI)
Site 1	2.38 (0.69 − 10.00)
Site 2	–
Site 3	1.34 (0.45 − 5.81)
Site 4	2.23 (0.42 − 10.00)
Site 5	–
Site 6	1.93 (0.36 − 10.00)
Site 7	1.11 (0.29 − 6.81)
Site 8	–
Site 9	–
Site 10	1.55 (0.43 − 9.38)
Summary	2.45 (1.38 − 4.79)

Random-effects

Gold standard (pooling data):

```
randomFxPooled <- computeBayesianMetaAnalysis(populations)
exp(randomFxPooled[, 1:3])
```

```
##          mu   mu95Lb   mu95Ub
## 1 2.705529 1.416858 5.465772
```

Normal approximation:

```
randomFxNormal <- computeBayesianMetaAnalysis(normalApproximations)
```

```
## Warning: Estimate(s) with NA seLogRr detected. Removing before computing
## meta-analysis.
```

```
## Warning: Estimate(s) with extremely high seLogRr (>100) detected. Removing
## before computing meta-analysis.
```

```
exp(randomFxNormal[, 1:3])
```

```
##          mu    mu95Lb   mu95Ub
## 1 1.597623 0.7221914 3.083936
```

Adaptive grid approximation:

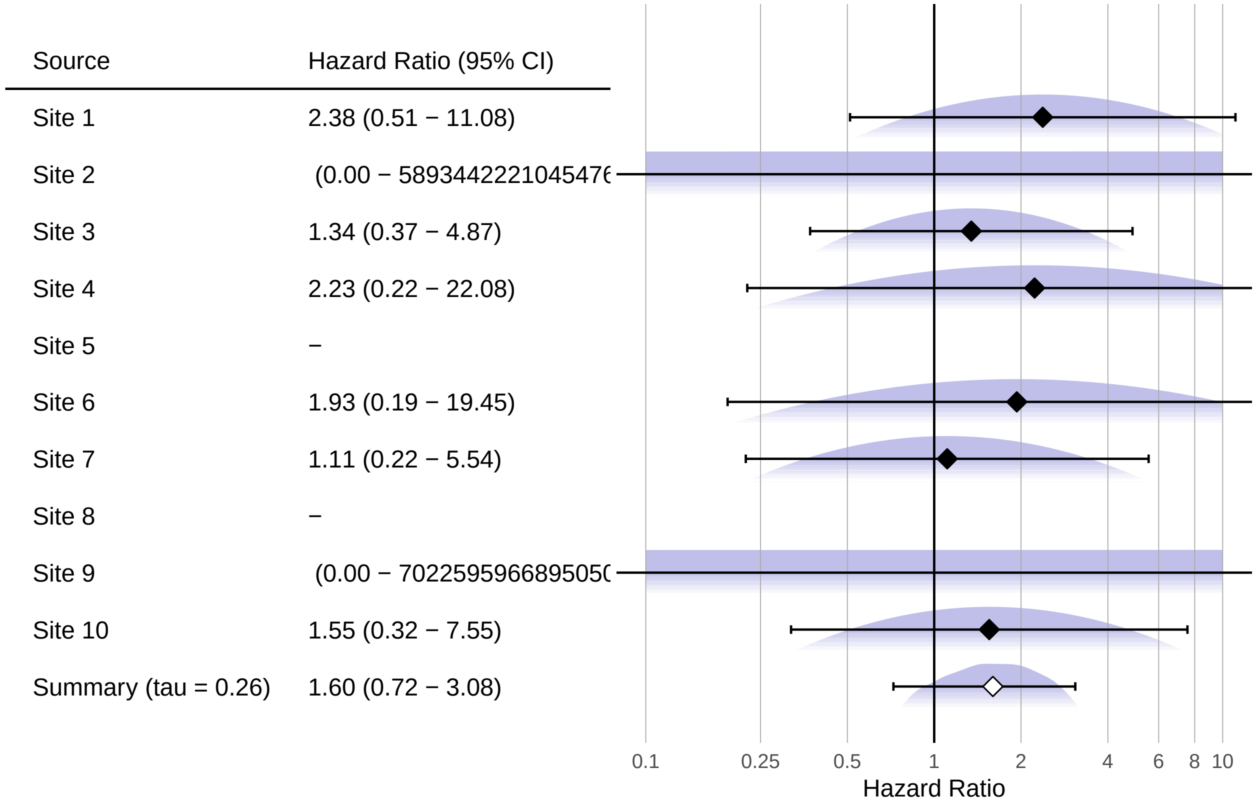
```
randomFxAdaptiveGrid <- computeBayesianMetaAnalysis(adaptiveGridApproximations)
exp(randomFxAdaptiveGrid[, 1:3])
```

```
##         mu   mu95Lb   mu95Ub
## 1 2.59455 1.283359 5.064328
```

Visualization

Normal approximation:

```
plotMetaAnalysisForest(
  data = normalApproximations,
  labels = paste("Site", 1:10),
  estimate = randomFxNormal,
  xLabel = "Hazard Ratio"
)
```



Adaptive grid approximation:

```r
plotMetaAnalysisForest(
  data = adaptiveGridApproximations,
  labels = paste("Site", 1:10),
  estimate = randomFxAdaptiveGrid,
  xLabel = "Hazard Ratio"
)
```

Source	Hazard Ratio (95% CI)
Site 1	2.38 (0.69 − 10.00)
Site 2	–
Site 3	1.34 (0.45 − 5.81)
Site 4	2.23 (0.42 − 10.00)
Site 5	–
Site 6	1.93 (0.36 − 10.00)
Site 7	1.11 (0.29 − 6.81)
Site 8	–
Site 9	–
Site 10	1.55 (0.43 − 9.38)
Summary (tau = 0.29)	2.59 (1.28 − 5.06)