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(</pre>
  nSites = 10,
  n = 10000,
 treatedFraction = 0.8,
 nStrata = 5,
 hazardRatio = 2,
  randomEffectSd = 0.5
)
set.seed(1)
populations <- simulatePopulations(simulationSettings)</pre>
head(populations[[1]])
##
     rowId stratumId x time y
## 1
       1
                  5 1
                       10 0
## 2
        2
                   2 1 113 0
       3
                  4 1 135 0
## 4
        4
                  2 1
                        27 0
                   2 1 104 0
## 5
         5
                   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:

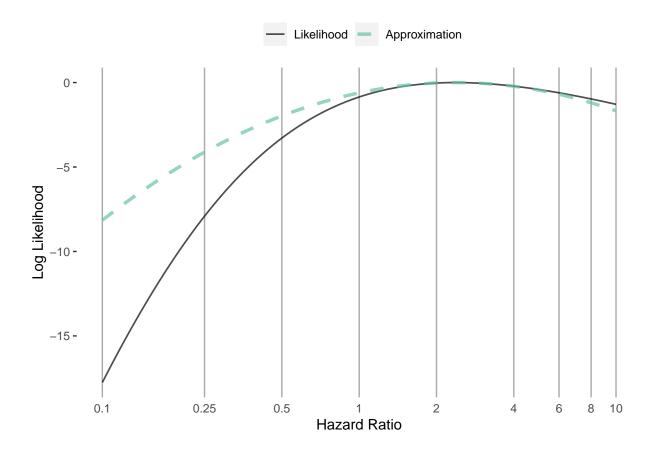
```
library(Cyclops)
```

[1] 0.6888127 14.9382268

Approximate the likelihood function at one site

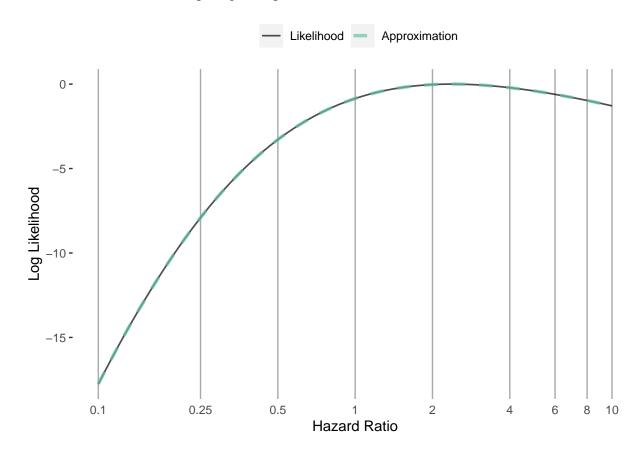
Normal approximation

Detected data following normal distribution



Adaptive approximation

```
approximation <- approximateLikelihood(</pre>
  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.
plotLikelihoodFit(
 approximation = approximation,
  cyclopsFit = cyclopsFit,
  parameter = "x"
)
```



Approximate at all sites

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

```
)
normalApproximations <- do.call(rbind, (normalApproximations))
```

Synthesize evidence

Fixed-effects

```
Gold standard (pooling data):
```

```
fixedFxPooled <- computeFixedEffectMetaAnalysis(populations)
fixedFxPooled</pre>
```

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

Normal approximation:

```
fixedFxNormal <- computeFixedEffectMetaAnalysis(normalApproximations)</pre>
```

```
## Warning: Estimate(s) with NA seLogRr 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</pre>
```

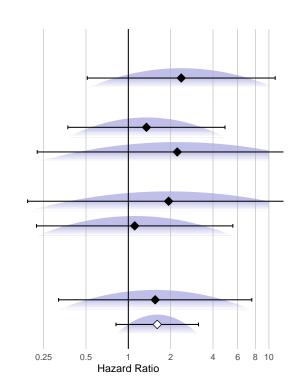
```
## rr lb ub logRr seLogRr
## 1 2.448437 1.376857 4.792428 0.8954498 0.3181777
```

Visualization

Normal approximation:

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

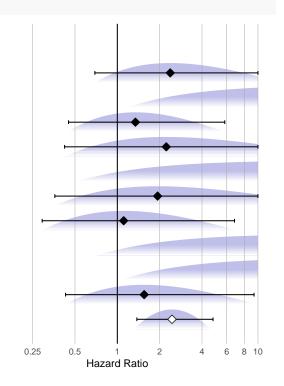
Source	Hazard Ratio (95% CI)
Site 1	2.38 (0.51 – 11.08)
Site 2	-
Site 3	1.34 (0.37 – 4.87)
Site 4	2.23 (0.22 – 22.08)
Site 5	-
Site 6	1.93 (0.19 – 19.45)
Site 7	1.11 (0.22 – 5.54)
Site 8	-
Site 9	-
Site 10	1.55 (0.32 – 7.55)
Summary	1.61 (0.82 – 3.15)



Adaptive grid approximation:

```
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)



0.1

0.1

Random-effects

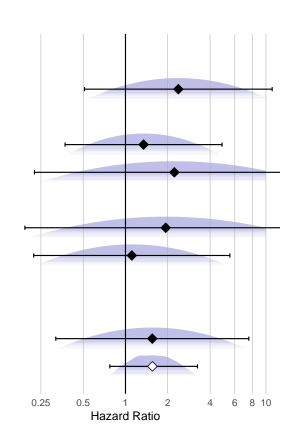
```
Gold standard (pooling data):
randomFxPooled <- computeBayesianMetaAnalysis(populations)</pre>
exp(randomFxPooled[, 1:3])
                mu95Lb
                          mu95Ub
           mu
## 1 2.594023 1.326203 5.272257
Normal approximation:
randomFxNormal <- computeBayesianMetaAnalysis(normalApproximations)</pre>
## Warning: Estimate(s) with NA seLogRr detected. Removing before computing
## meta-analysis.
exp(randomFxNormal[, 1:3])
##
          mu
                mu95Lb
                          mu95Ub
## 1 1.55483 0.7732428 3.254443
Adaptive grid approximation:
randomFxAdaptiveGrid <- computeBayesianMetaAnalysis(adaptiveGridApproximations)</pre>
exp(randomFxAdaptiveGrid[, 1:3])
               mu95Lb
                       mu95Ub
          mu
## 1 2.66668 1.329153 5.255041
```

Visualization

Normal approximation:

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

Source	Hazard Ratio (95% CI)
Site 1	2.38 (0.51 – 11.08)
Site 2	-
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	-
Site 10	1.55 (0.32 – 7.55)
Summary (tau = 0.25)	1.55 (0.77 – 3.25)

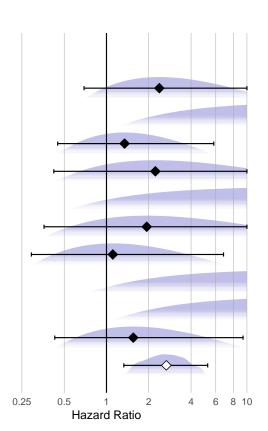


Adaptive grid approximation:

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

0.1

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 = 0.28)	2.67 (1.33 – 5.26)



0.1