groupedHG

The goal of **groupedHG** is to estimate probability mass function (PMF) for grouped hypergeometric distribution considering adjustment for sensitivity and specificity of the test. The sensitivity and specificity can be considered at the item and group level. In addition to this, Fisher Information (FI) of the total number of contaminated items in the population (denoted as T_x) can be calculated using two alternative methods - analytic derivative (AD) and PMF-based. The PMF-based FI calculation is based on the Sánchez-Moreno, Yánez and Dehesa (2009) work.

Installation

You can install the development version of `groupedHG` like so:

```r
install.packages("devtools")
devtools::install_github("sumon148/groupedHG")
```

Example

Let assume a population containing N items of which Tx are contaminated. We can calculate PMF of having ty contaminated groups of size $barN$ after inspecting a sample of b groups as below assuming group-level imperfect sensitivity ($\Delta = 0.7$) and specificity ($\Lambda = 0.8$).

```r
library(groupedHG)
b = 4
ty.values <- c(0:b)
PRty.HG.group <- sapply(ty.values, function(ty) pmfHG.imperfect.group(ty,
    N = 100, barN = 4, Tx = 20, b = b, delta = 0.7, lambda = 0.8,
    verbose = FALSE))
plot(0:b, PRty.HG.group, type = "l", col = "black", xlab = expression(paste("Number of group detections
    t[y])), ylab = "Probability mass", main = "Grouped Hypergeometric model",
    lty = 2)
points(0:b, PRty.HG.group, type = "b", pch = 19, col = "black")
```

Grouped Hypergeometric model
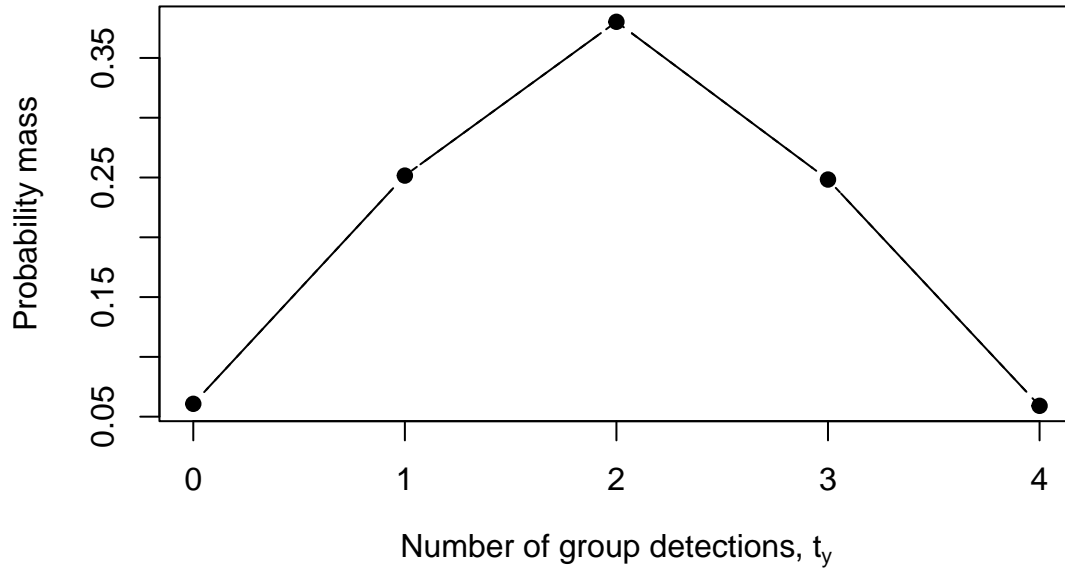
In the similar way, the PMF can be calculated assuming item-level imperfect test as below:

```
PRty.HG.item <- sapply(ty.values, function(ty) pmfHG.imperfect.item(ty,
    N = 100, barN = 4, Tx = 20, b = b, delta = 0.7, lambda = 0.8,
    verbose = FALSE))
PRty.HG.item
#> [1] 0.002993711 0.040346066 0.198811210 0.424987223 0.332861789
```

Expectation and variance of the grouped HG distribution for the number of contaminated groups can be obtained as below:

```
ExpVarHG.imperfect.item <- ExpVarHG.imperfect(N = 100, Tx = 20,
    barN = 4, b = 4, delta = 0.7, lambda = 0.8, type = "item")
ExpVarHG.imperfect.item$expectation
#> [1] 3.044377
ExpVarHG.imperfect.item$variance
#> [1] 0.7180313

ExpVarHG.perfect.group <- ExpVarHG.imperfect(N = 100, Tx = 20,
    barN = 4, b = 4, delta = 1, lambda = 1, type = "group")
ExpVarHG.perfect.group$expectation
#> [1] 2.386647
ExpVarHG.perfect.group$variance
#> [1] 0.8797255
```

The Fisher Information for the number of contaminated items in the population T_x can be calculated as below assuming group and item level imperfect sensitivity and specificity:

```
Tx_values <- c(0:80)
# Different cases: Item level sensitivity
FI_case1_AD_Based_group <- sapply(Tx_values, function(Tx) FIpmfHG.Tx.imperfect(Tx,
```

```
    N = 100, b = 4, barN = 4, delta = 1, lambda = 1, method = "AD",
    type = "group", verbose = FALSE))
FI_case1_AD_Based_Item <- sapply(Tx_values, function(Tx) FIpmfHG.Tx.imperfect(Tx,
    N = 100, b = 4, barN = 4, delta = 1, lambda = 1, method = "AD",
    type = "item", verbose = FALSE))
plot(Tx_values, FI_case1_AD_Based_group, type = "l", col = "black",
    xlab = expression(paste("Number of Contaminated Items, ",
        T[x])), ylab = "Fisher Information: Hypergeometric",
    main = "FI under HG: Group and item level imperfect test",
    lty = 2)
lines(Tx_values, FI_case1_AD_Based_Item, type = "l", lty = 2,
    col = "blue")
legend("topright", legend = c("Group", "Item"), col = c("black",
    "blue"), lty = c(1, 2), bty = "n")
```
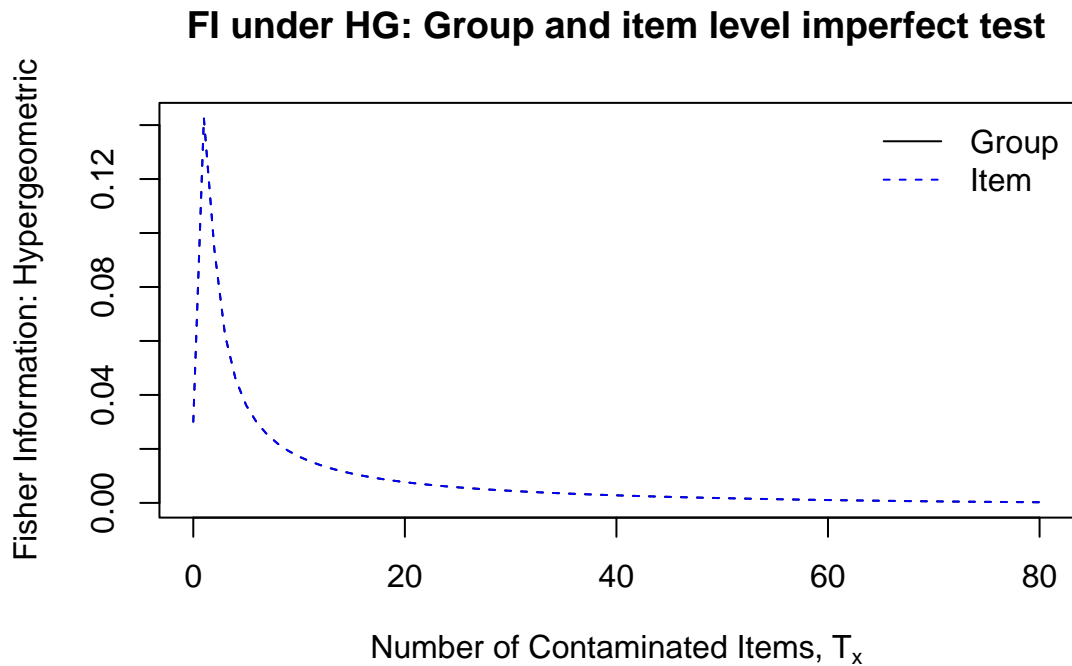

Reference

Sánchez-Moreno, P., Yánez, R. J., & Dehesa, J. S. (2009, October). Discrete densities and Fisher information. In Proceedings of the 14th International Conference on Difference Equations and Applications. Difference Equations and Applications. Istanbul, Turkey: Bahçesehir University Press (pp. 291-298).