README

A design and analytic strategy for monitoring disease positivity and case characteristics in accessible closed populations

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Illustrate calculations for case count and continuous mean estimations with a simulated dataset

The data was simulated under the anchor stream design with the setting in which ($N_{\text{tot}} = 500$, selection probability into the random sample $\psi = 0.1$, prevalence p = 0.2).

The simulated dataset has 196 observations, each observation includes a continuous random variable (x) representing a hypothetical biomarker level, indicators of capture status $(y_1$ for Stream 1, and y_2 for Stream 2), symptom (sympt), and disease (case). For the continuous random variable, it was drawn from a mixture of normal distributions with the mean and the variance differing according to symptom status and disease status. Specifically, normal distributions used for generating data are given by

	symptom =1	symptom = 0
case=1	$N(10, 0.75^2)$	$N(5, 0.5^2)$
case=0	$N(2.5, 1.2^2)$	$N(1, 1.5^2)$

read in self-defined functions and the simulated dataset

```
source("FUN_AnchorStream.R")
load("toydata.rda")
```

take a look of the simulated inidividual-level data

```
y1 y2 case sympt
## 1
     1
       1
             0
                      0.5010140
             0
                   0 -1.7333531
## 3 1 1
             0
                   0 3.1168936
## 4 1 1
             0
                   0 -0.2563737
             0
                   0 -0.6856442
                   0 5.5656488
```

observed cell counts

n1	n2	n3	n4	n5	n6	n7
6	5	100	46	33	6	304

case count estimates based on the simulated data

```
Ntot = 500
p2 = 0.1
re.counts <- AnchorStream_CaseCount(dat.obs = dat.obs,</pre>
                                      Ntot = Ntot, p2 = p2,
                                      num.post = 10000,
                                      seed = 1234,
                                      data.type = "individual",
                                       cellcounts.vec = NULL)
results from using random sample alone
re.counts$pointest$Nhat.RS
## [1] 110
re.counts$SE$SE.RS.FPC
## [1] 28.07061
re.counts$CI$CI.RS.Jeffreys
## [1] 63.47027 171.54453
results from using the estiamtor \hat{N}_{\psi}
re.counts$pointest$Nhat.psi
## [1] 111
re.counts$SE$SE.Nhat.psi
## [1] 23.2379
re.counts$CI$CI.Nhat.psi.Diri
## [1] 76.01301 166.25019
results from using the estiamtor \hat{N}_{\hat{n}^*}
re.counts$pointest$Nhat.psihatstar
## [1] 103.7692
re.counts$SE$SE.Nhat.psihatstar
## [1] 21.94541
re.counts$CI$CI.Nhat.psihatstar.Diri
## [1] 71.86727 162.77501
continuous mean estimates based on the simulated data
```

```
re.continuous <- AnchorStream_Continuous(dat.obs = dat.obs,

Ntot = Ntot, seed = 12345,

nboot = 1000)
```

results of estimating overall mean

re.continuous\$overall

```
## est se lci uci
## xbarldot 3.378704 NA NA NA
## xbar2dot 2.765692 0.4898039 1.830166 3.722037
## muhatx 2.552818 0.3188371 1.965768 3.194178
```

results of estimating continuous mean among cases

re.continuous\$cases

```
## est se lci uci
## xbarldot.cases 7.471739 0.3651921 6.782233 8.195105
## xbar2dot.cases 8.581201 0.8525923 6.771870 10.165044
## muhatx.cases 7.692362 0.5977918 6.529768 8.786034
```

results of estimating continuous mean among non-cases

re.continuous\$noncases

```
## est se lci uci

## xbar1dot.noncases 1.409414 0.1610869 1.0859128 1.707119

## xbar2dot.noncases 1.125420 0.2890897 0.5713258 1.699620

## muhatx.noncases 1.206818 0.2090333 0.7799455 1.631326
```

results of estimating continuous mean difference for cases relative to non-cases

re.continuous\$difference

```
## est se lci uci
## xbarldot.diff 6.062325 0.3996517 5.279764 6.815613
## xbar2dot.diff 7.455780 0.9088060 5.518571 9.238345
## muhatx.diff 6.485544 0.6343667 5.230512 7.656846
```