

# Calculating missing values

Spatially targeted systematic review

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*Table of Contents:*

## Contents

1. Background . . . . .	1
2. Set-up . . . . .	1
3. Define functions . . . . .	1
4. Goswami2012 paper HIV . . . . .	2
5. Goswami2012 paper TB . . . . .	2
6. Fatima2016 paper TB . . . . .	2
7. Barreto2015 Leprosy . . . . .	2
6. Srivastava 2009 paper Malaria . . . . .	3
8. Morris 2018 Malaria . . . . .	3
X. Reproducibility . . . . .	4

## 1. Background

## 2. Set-up

Load all required packages for analysis.

## 3. Define functions

```
prop_CI_to_n <- function(prop,c1,c2){
  n = round((prop*(1-prop))/(((c2-c1)/4)^2))
}

prop_std_error <- function(prop,n){
  std_er = ((prop*(1-prop)/n))^(1/2)
}

prop_to_CI <- function(prop, prop_stderror){
  low_ci = prop - 2*prop_stderror
  upper_ci = prop + 2*prop_stderror
  list(low_ci,upper_ci)
}

poisson_to_prop <- function(x1,x2){
  prop = x1/(x1 + x2)
}
```

#### 4. Goswami2012 paper HIV

```
N_total = prop_CI_to_n(0.004,0.005,0.003)
n_cases = round(N_total*0.004)
glue::glue("Total number of cases N:{N_total} ", "Number of positive cases n:{n_cases}")
```

```
## Total number of cases N:15936 Number of positive cases n:64
```

#### 5. Goswami2012 paper TB

```
N_total = prop_CI_to_n(0.06,0.066,0.056)
n_cases = round(N_total*0.06)
glue::glue("Total number of cases N:{N_total} ", "Number of positive cases n:{n_cases}")
```

```
## Total number of cases N:9024 Number of positive cases n:541
```

#### 6. Fatima2016 paper TB

```
prop = poisson_to_prop(100384,108341)
prop
```

```
## [1] 0.480939
```

```
prop_std = prop_std_error(prop, (100384 +108341))
prop_std
```

```
## [1] 0.001093621
```

```
glue::glue("The prop:{prop} prop std error: {prop_std} the test statistic {(0.5-prop)/prop_std}")
```

```
## The prop:0.480939034614924 prop std error: 0.00109362130915856 the test statistic 17.4292190774353
```

```
low_upper_ci = prop_to_CI(prop,prop_std)
```

```
glue::glue("The prop: {1/(prop)-1}, lowerCI: {1/(low_upper_ci[[1]])-1}, upperCI: {1/(low_upper_ci[[2]])}")
```

```
## The prop: 1.07926562001913, lowerCI: 1.08876502755124, upperCI: 1.0698522252335
```

#### 7. Barreto2015 Leprosy

```
#Start with the hotspot children
prop = 11/134
```

```
prop_std = prop_std_error(prop, 134)
prop_std
```

```
## [1] 0.02371328
```

```
glue::glue("The prop:{prop} prop std error: {prop_std}")
```

```
## The prop:0.082089552238806 prop std error: 0.0237132838979372
```

```
low_upper_ci = prop_to_CI(prop,prop_std)
```

```
glue::glue("The prop%: {100*prop}, lowerCI%: {100*low_upper_ci[[1]]}, upperCI%: {100*low_upper_ci[[2]]}")
```

```
## The prop%: 8.2089552238806, lowerCI%: 3.46629844429316, upperCI%: 12.951612003468
```

```
#Second with the randomly selected children children
```

```
prop = 63/1592
```

```
prop_std = prop_std_error(prop, 1592)
```

```
prop_std
```

```
## [1] 0.004886067
```

```
glue::glue("The prop:{prop} prop std error: {prop_std}")
```

```
## The prop:0.039572864321608 prop std error: 0.00488606704957417
```

```
low_upper_ci = prop_to_CI(prop,prop_std)
```

```
glue::glue("The prop%: {100*prop}, lowerCI%: {100*low_upper_ci[[1]]}, upperCI%: {100*low_upper_ci[[2]]}")
```

```
## The prop%: 3.9572864321608, lowerCI%: 2.98007302224597, upperCI%: 4.93449984207564
```

## 6. Srivastava 2009 paper Malaria

```
prop = poisson_to_prop(90829,96042)
```

```
prop
```

```
## [1] 0.4860519
```

```
prop_std = prop_std_error(prop, (90829 +96042))
```

```
prop_std
```

```
## [1] 0.001156192
```

```
glue::glue("The prop:{prop} prop std error: {prop_std} the test statistic {(0.5-prop)/prop_std}")
```

```
## The prop:0.486051875357867 prop std error: 0.00115619210527176 the test statistic 12.0638469840221
```

```
low_upper_ci = prop_to_CI(prop,prop_std)
```

```
glue::glue("The prop: {1/(prop)-1}, lowerCI: {1/(low_upper_ci[[1]])-1}, upperCI: {1/(low_upper_ci[[2]])}")
```

```
## The prop: 1.05739356372965, lowerCI: 1.06722837043595, upperCI: 1.04765189181482
```

## 8. Morris 2018 Malaria

```
#Start with the control clusters
```

```
prop = 52/12307
```

```
prop_std = prop_std_error(prop, 12307)
```

```
prop_std
```

```
## [1] 0.0005846959
```

```
glue::glue("The prop:{prop} prop std error: {prop_std}")
```

```
## The prop:0.00422523766961892 prop std error: 0.000584695873375013
```

```

low_upper_ci = prop_to_CI(prop,prop_std)

glue::glue("The prop per 1000: {1000*prop}, lowerCI per 1000: {1000*low_upper_ci[[1]]}, upperCI per 1000: {1000*upper_upper_ci[[1]]}")

## The prop per 1000: 4.22523766961892, lowerCI per 1000: 3.05584592286889, upperCI per 1000: 5.39462941155801
#The intervention clusters
prop = 43/10944

prop_std = prop_std_error(prop, 10944)
prop_std

## [1] 0.0005980029

glue::glue("The prop:{prop} prop std error: {prop_std}")

## The prop:0.00392909356725146 prop std error: 0.000598002873774306

low_upper_ci = prop_to_CI(prop,prop_std)

glue::glue("The prop per 1000: {1000*prop}, lowerCI per 1000: {1000*low_upper_ci[[1]]}, upperCI per 1000: {1000*upper_upper_ci[[1]]}")

## The prop per 1000: 3.92909356725146, lowerCI per 1000: 2.73308781970285, upperCI per 1000: 5.12509931155801

```

## X. Reproducibility

This reproduction of the analysis was run by:

keyName	value
sysname	Windows
release	10 x64
version	build 17134
nodename	LAPT2176
machine	x86-64
login	lsh1805281
user	lsh1805281
effective_user	lsh1805281

Analysis was run at **2020-03-11 11:56:11**, and using the following Session Info:

```

R version 3.6.1 (2019-07-05)
Platform: x86_64-w64-mingw32/x64 (64-bit)
Running under: Windows 10 x64 (build 17134)

```

Matrix products: default

```

locale:
[1] LC_COLLATE=English_United Kingdom.1252
[2] LC_CTYPE=English_United Kingdom.1252
[3] LC_MONETARY=English_United Kingdom.1252
[4] LC_NUMERIC=C
[5] LC_TIME=English_United Kingdom.1252

```

attached base packages:

```
[1] stats      graphics  grDevices utils      datasets  methods   base
```

other attached packages:

```
[1] knitr_1.23          pmthemes_0.0.0.9000 forcats_0.4.0
[4] stringr_1.4.0       dplyr_0.8.99.9000  purrr_0.3.3
[7] readr_1.3.1         tidyr_1.0.2        tibble_2.99.99.9014
[10] ggplot2_3.2.1       tidyverse_1.3.0
```

loaded via a namespace (and not attached):

```
[1] tidyselect_1.0.0.9000 xfun_0.8          haven_2.2.0
[4] lattice_0.20-38      colorspace_1.4-1  vctrs_0.2.99.9005
[7] generics_0.0.2       htmltools_0.3.6   yaml_2.2.0
[10] rlang_0.4.4          pillar_1.4.3.9000 withr_2.1.2
[13] glue_1.3.1           DBI_1.0.0         dbplyr_1.4.2
[16] modelr_0.1.5         readxl_1.3.1      lifecycle_0.1.0
[19] munsell_0.5.0        gtable_0.3.0      cellranger_1.1.0
[22] rvest_0.3.5          evaluate_0.14     fansi_0.4.0
[25] highr_0.8            broom_0.5.5       Rcpp_1.0.2
[28] backports_1.1.4      scales_1.0.0      jsonlite_1.6
[31] lobstr_1.1.1         fs_1.3.1          hms_0.5.3
[34] digest_0.6.20        stringi_1.4.3     grid_3.6.1
[37] cli_2.0.2            tools_3.6.1       magrittr_1.5
[40] lazyeval_0.2.2       crayon_1.3.4      pkgconfig_2.0.2
[43] zeallot_0.1.0        xml2_1.2.2        reprex_0.3.0
[46] lubridate_1.7.4      assertthat_0.2.1  rmarkdown_1.14
[49] httr_1.4.1           rstudioapi_0.11   R6_2.4.0
[52] nlme_3.1-140         compiler_3.6.1
```