

COVID-19 Review and Meta-Analysis

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6/5/2020

```
## Loading required package: tidyverse
## -- Attaching packages ----- tidyverse 1.3.0 --
## v ggplot2 3.3.0      v purrr  0.3.3
## v tibble  2.1.3      v dplyr  0.8.3
## v tidyr   1.0.2      v stringr 1.4.0
## v readr   1.3.1      v forcats 0.4.0

## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()

## Loading required package: magrittr
##
## Attaching package: 'magrittr'
##
## The following object is masked from 'package:purrr':
##
##   set_names
##
## The following object is masked from 'package:tidyr':
##
##   extract

## Loading required package: meta
## Warning: package 'meta' was built under R version 3.6.2
## Loading 'meta' package (version 4.12-0).
## Type 'help(meta)' for a brief overview.
## Loading required package: metaviz
## Warning: package 'metaviz' was built under R version 3.6.2
## Loading required package: readxl
```

Removing Unnecessary Data

```
dat<-read_excel("Review_Data.xlsx")
```

```
## New names:
## * notes -> notes...16
## * `` -> ...17
## * `` -> ...18
## * notes -> notes...19
```

```
dat %<>%
  filter(`RH Include?`=="YES")
##We dedcided to filter this becuae it was not in english
dat %<>% filter(`Author Name`!= "Bocksberger et al.")
COVID19 <- dat %>% select(`Article Number`, `Author Name`, DOI, `Number of subjects`, Cases, Type, Measured)
```

```
write_csv(COVID19,"COVID19_REVIEW_DATA_.csv")
rm(dat)
```

Compute some statistics

```
COVID19$p<- COVID19$Cases/COVID19$`Number of subjects`

COVID19$S.E.<- sqrt((COVID19$p*(1-COVID19$p))/COVID19$`Number of subjects`)
COVID19$CI_Lower<-COVID19$p - 1.96*COVID19$S.E.
COVID19$CI_Upper<- COVID19$p
COVID19 <- COVID19[order(COVID19$p,decreasing = T),]
summary_COVID_Obj<-data.frame(Name="Summary (Objective)",Subjects=sum(COVID19[COVID19$Type=="Objective"]
summary_COVID_Sub<-data.frame(Name="Summary (Subjective)",Subjects=sum(COVID19[COVID19$Type=="Subjective"]

summary_COVID<-bind_rows(summary_COVID_Obj,summary_COVID_Sub)

## Warning in bind_rows_(x, .id): Unequal factor levels: coercing to character
## Warning in bind_rows_(x, .id): binding character and factor vector,
## coercing into character vector

## Warning in bind_rows_(x, .id): binding character and factor vector,
## coercing into character vector
COVID19$`Measure Type`<-as.factor(COVID19$Type)
```

Computing Detailed Meta-Analysis of Proportions

IVM

First we compute using the Inverse Variance Method

```
ma.INV<-metaprop(COVID19$Cases,n=COVID19$`Number of subjects`,studlab = COVID19$`Author Name`,byvar = COVID19$`Measure Type`,
d=date())
#pdf(sprintf("Forestplot_%s",d))
forest(ma.INV,col.by = "black",pooled.events = T,bylab = "Measurement Type")

## Warning in grid.Call(C_textBounds, as.graphicsAnnot(x$label), x$x,
## x$y, : conversion failure on 'Boscolo-Rizzo et al' in 'mbcsToSbcs': dot
## substituted for <e2>

## Warning in grid.Call(C_textBounds, as.graphicsAnnot(x$label), x$x,
## x$y, : conversion failure on 'Boscolo-Rizzo et al' in 'mbcsToSbcs': dot
## substituted for <80>

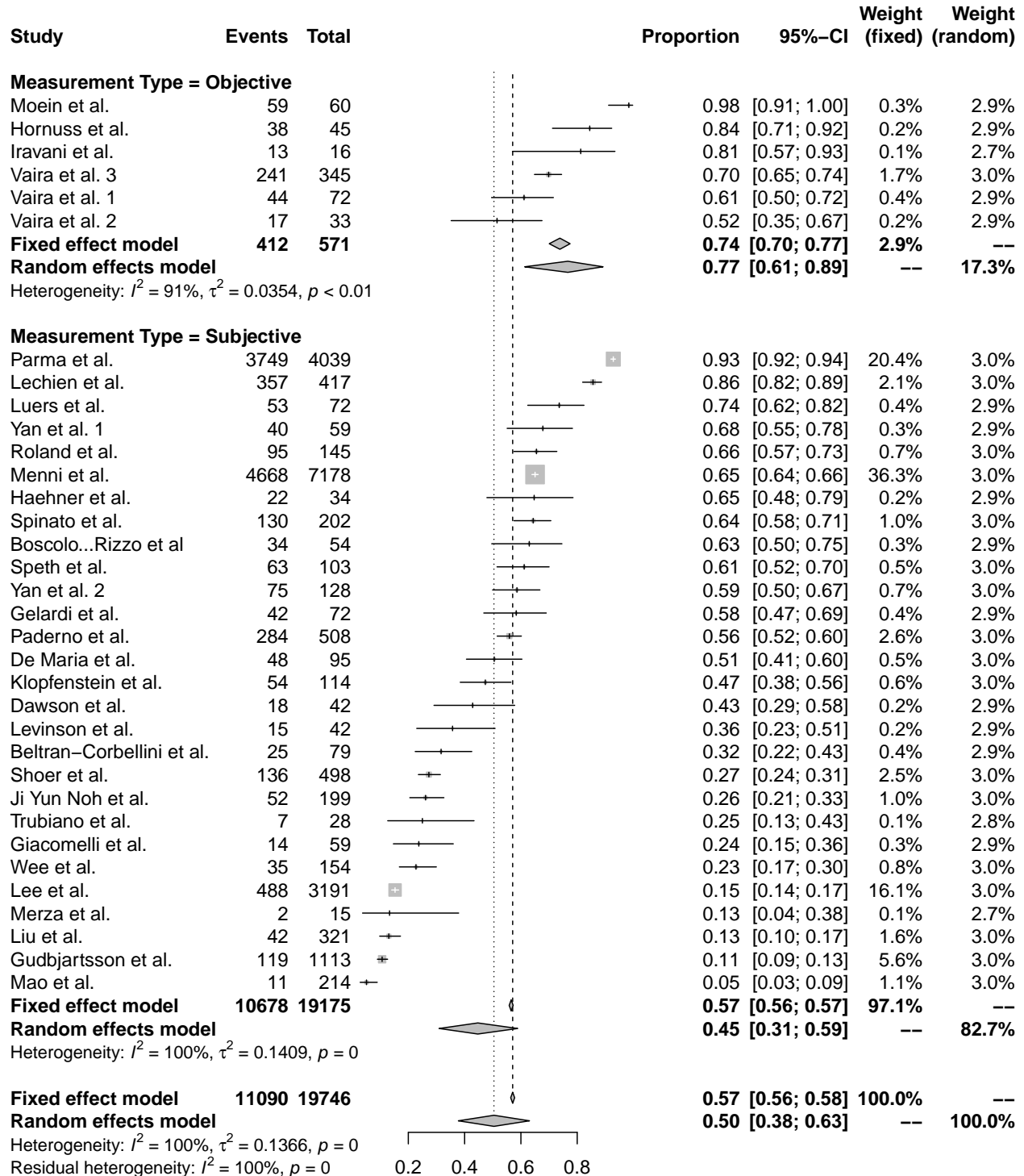
## Warning in grid.Call(C_textBounds, as.graphicsAnnot(x$label), x$x,
## x$y, : conversion failure on 'Boscolo-Rizzo et al' in 'mbcsToSbcs': dot
## substituted for <91>

## Warning in grid.Call.graphics(C_text, as.graphicsAnnot(x$label), x$x,
## x$y, : conversion failure on 'Boscolo-Rizzo et al' in 'mbcsToSbcs': dot
## substituted for <e2>

## Warning in grid.Call.graphics(C_text, as.graphicsAnnot(x$label), x$x,
## x$y, : conversion failure on 'Boscolo-Rizzo et al' in 'mbcsToSbcs': dot
## substituted for <80>

## Warning in grid.Call.graphics(C_text, as.graphicsAnnot(x$label), x$x,
```

```
## x$y, : conversion failure on 'Boscolo-Rizzo et al' in 'mbcsToSbcs': dot
## substituted for <91>
```



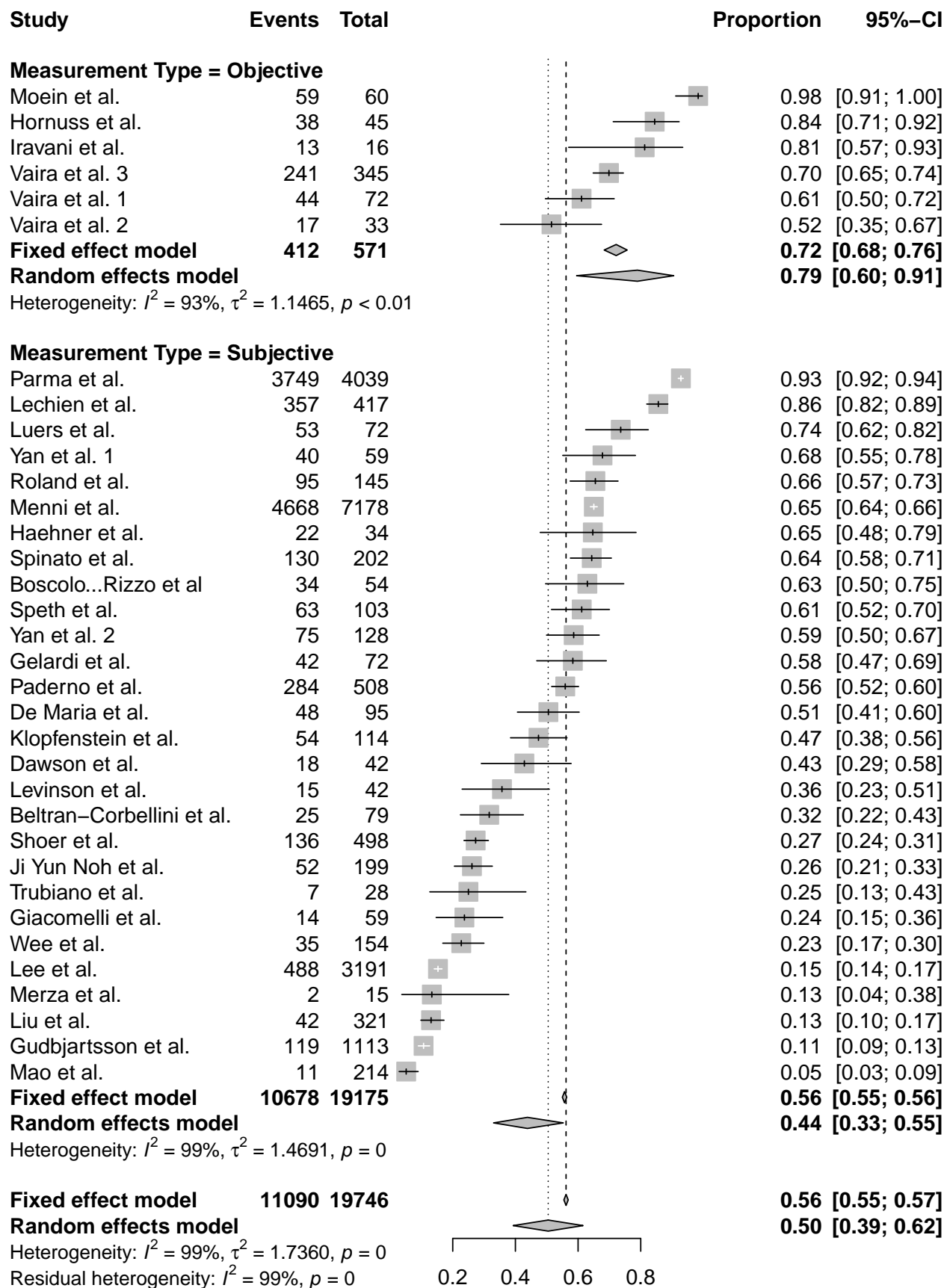
```
#dev.off()
```

```
###GLMM Next we compute using the GLMM method. We ultimately do not use this in the paper.
```

```
ma.GLMM<-metaprop(COVID19$Cases,n=COVID19$`Number of subjects`,studlab = COVID19$`Author Name`,byvar = )
```

```
forest(ma.GLMM,,col.by = "black",pooled.events = T,bylab = "Measurement Type")
```

```
## Warning in grid.Call(C_textBounds, as.graphicsAnnot(x$label), x$x,  
## x$y, : conversion failure on 'Boscolo-Rizzo et al' in 'mbcsToSbcs': dot  
## substituted for <e2>  
  
## Warning in grid.Call(C_textBounds, as.graphicsAnnot(x$label), x$x,  
## x$y, : conversion failure on 'Boscolo-Rizzo et al' in 'mbcsToSbcs': dot  
## substituted for <80>  
  
## Warning in grid.Call(C_textBounds, as.graphicsAnnot(x$label), x$x,  
## x$y, : conversion failure on 'Boscolo-Rizzo et al' in 'mbcsToSbcs': dot  
## substituted for <91>  
  
## Warning in grid.Call.graphics(C_text, as.graphicsAnnot(x$label), x$x,  
## x$y, : conversion failure on 'Boscolo-Rizzo et al' in 'mbcsToSbcs': dot  
## substituted for <e2>  
  
## Warning in grid.Call.graphics(C_text, as.graphicsAnnot(x$label), x$x,  
## x$y, : conversion failure on 'Boscolo-Rizzo et al' in 'mbcsToSbcs': dot  
## substituted for <80>  
  
## Warning in grid.Call.graphics(C_text, as.graphicsAnnot(x$label), x$x,  
## x$y, : conversion failure on 'Boscolo-Rizzo et al' in 'mbcsToSbcs': dot  
## substituted for <91>
```



##Flow Chart This code was adapted from Peter Higgins post on <https://rpubs.com/phiggins/461686>

```
data <- tibble(x= 1:100, y= 1:100)
head(data)
```

```
## # A tibble: 6 x 2
##       x     y
##   <int> <int>
## 1     1     1
## 2     2     2
## 3     3     3
## 4     4     4
## 5     5     5
## 6     6     6
```

```
p<- data %>%
  ggplot(aes(x, y)) +
  scale_x_continuous(minor_breaks = seq(0, 100, 10)) +
  scale_y_continuous(minor_breaks = seq(0, 100, 10)) +
  theme_linedraw()

p <- p +
  geom_rect(xmin = 36, xmax=64, ymin=90, ymax=100, color='black',
            fill='white', size=0.25, size=0.25) +
  annotate('text', x= 50, y=95,label=
            'Assessed for eligibility through database\n searching (Pubmed, Medline, Google Scholar).\n'
            size=2.5)
```

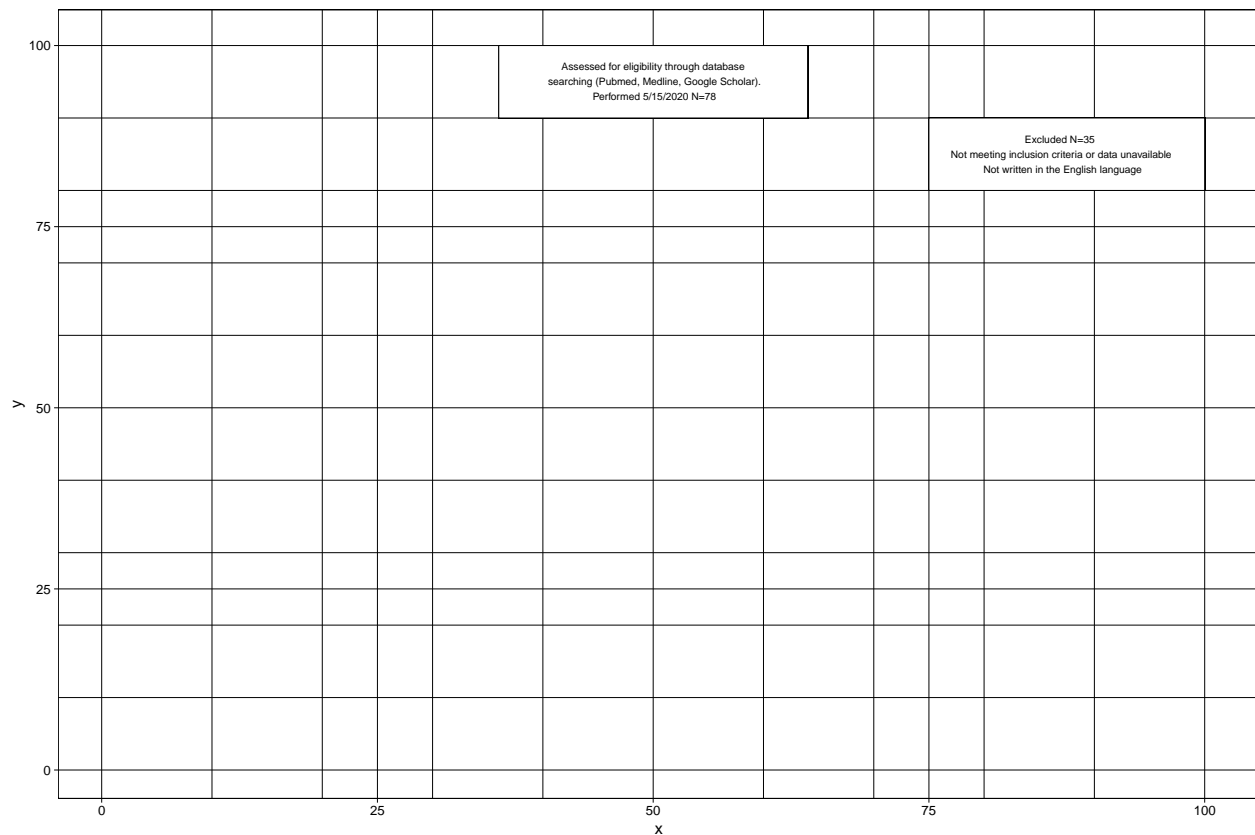
Warning: Duplicated aesthetics after name standardisation: size

```
p<- p +
  geom_rect(xmin = 75, xmax=100, ymin=80, ymax=90, color='black',
            fill='white', size=0.25, size=0.25) +
  annotate('text', x= 87, y=85,label=
            'Excluded N=35 \n Not meeting inclusion criteria or data unavailable \n Not written in the'
            size=2.5)
```

Warning: Duplicated aesthetics after name standardisation: size

##HERE IS ESSENTIALLY WHAT WE ARE DOING RIGHT NOW. It is ugly for now, but this is the thought process behind the code

p



##Final Version

```
p<- p +
  geom_rect(xmin = 36, xmax=64, ymin=70, ymax=80, color='black',
            fill='white', size=0.25, size=0.25) +
  annotate('text', x= 50, y=75,label=
            'Eligible papers for inclusion \nMeasure of olfactory dysfunction \nN=43',
            size=2.5)
```

Warning: Duplicated aesthetics after name standardisation: size

```
p <- p +
  geom_rect(xmin = 75, xmax=100, ymin=60, ymax=70, color='black',
            fill='white', size=0.25, size=0.25) +
  annotate('text', x= 87, y=65,label=
            'Excluded \n Not lab tested COVID N=5\n Recruitment of Patients With Smell Loss N=3 \n Paper N=3',
            size=2.5)
```

Warning: Duplicated aesthetics after name standardisation: size

```
p<- p +
  geom_rect(xmin = 36, xmax=64, ymin=50, ymax=60, color='black',
            fill='white', size=0.25, size=0.25) +
  annotate('text', x= 50, y=55,label=
            'Full text screened for prevalence rate \nN=34',
            size=2.5)
```

Warning: Duplicated aesthetics after name standardisation: size

```
p<- p +
  geom_rect(xmin = 36, xmax=64, ymin=30, ymax=40, color='black',
            fill='white', size=0.25, size=0.25) +
  annotate('text', x= 50, y=35,label=
            ' Data extracted N=34 \nTwo authors extracted data \nTwo authors confirmed data extracted'
            size=2.5)
```

Warning: Duplicated aesthetics after name standardisation: size

```
p<- p +
  geom_rect(xmin = 36, xmax=64, ymin=10, ymax=20, color='black',
            fill='white', size=0.25, size=0.25) +
  annotate('text', x= 50, y=15,label=
            'Articles included \nN=34',
            size=2.5)
```

Warning: Duplicated aesthetics after name standardisation: size

```
p <-p +
  geom_segment(
    x=50, xend=50, y=90, yend=80.3,
    size=0.10, linejoin = "mitre", lineend = "butt",
    arrow = arrow(length = unit(1, "mm"), type= "closed")) +
  geom_segment(
    x=50, xend=74.7, y=85, yend=85,
    size=0.10, linejoin = "mitre", lineend = "butt",
    arrow = arrow(length = unit(1, "mm"), type= "closed")) +
  geom_segment(
    x=50, xend=50, y=70, yend=60.3,
    size=0.10, linejoin = "mitre", lineend = "butt",
    arrow = arrow(length = unit(1, "mm"), type= "closed")) +
  geom_segment(
    x=50, xend=74.7, y=65, yend=65,
    size=0.10, linejoin = "mitre", lineend = "butt",
    arrow = arrow(length = unit(1, "mm"), type= "closed")) +
  geom_segment(
    x=50, xend=50, y=50, yend=40.3,
    size=0.10, linejoin = "mitre", lineend = "butt",
    arrow = arrow(length = unit(1, "mm"), type= "closed")) +
  geom_segment(
    x=50, xend=50, y=30, yend=20.3,
    size=0.10, linejoin = "mitre", lineend = "butt",
    arrow = arrow(length = unit(1, "mm"), type= "closed"))

p + theme_void()
```