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

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

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

```r
dat %<>%
  filter(`RH Include?`=="YES")
##We dedcided to filter this becuase 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$p + 1.96*COVID19$S.E.
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 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 = CO
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>
```

Study	Events	Total	Proportion	95%–CI	Weight (fixed)	Weight (random)
Measurement Type = Objective						
Moein et al.	59	60	0.98	[0.91; 1.00]	0.3%	2.9%
Hornuss et al.	38	45	0.84	[0.71; 0.92]	0.2%	2.9%
Iravani et al.	13	16	0.81	[0.57; 0.93]	0.1%	2.7%
Vaira et al. 3	241	345	0.70	[0.65; 0.74]	1.7%	3.0%
Vaira et al. 1	44	72	0.61	[0.50; 0.72]	0.4%	2.9%
Vaira et al. 2	17	33	0.52	[0.35; 0.67]	0.2%	2.9%
Fixed effect model	**412**	**571**	**0.74**	**[0.70; 0.77]**	**2.9%**	**––**
Random effects model			**0.77**	**[0.61; 0.89]**	**––**	**17.3%**
Heterogeneity: $I^2 = 91\%$, $\tau^2 = 0.0354$, $p < 0.01$						
Measurement Type = Subjective						
Parma et al.	3749	4039	0.93	[0.92; 0.94]	20.4%	3.0%
Lechien et al.	357	417	0.86	[0.82; 0.89]	2.1%	3.0%
Luers et al.	53	72	0.74	[0.62; 0.82]	0.4%	2.9%
Yan et al. 1	40	59	0.68	[0.55; 0.78]	0.3%	2.9%
Roland et al.	95	145	0.66	[0.57; 0.73]	0.7%	3.0%
Menni et al.	4668	7178	0.65	[0.64; 0.66]	36.3%	3.0%
Haehner et al.	22	34	0.65	[0.48; 0.79]	0.2%	2.9%
Spinato et al.	130	202	0.64	[0.58; 0.71]	1.0%	3.0%
Boscolo...Rizzo et al	34	54	0.63	[0.50; 0.75]	0.3%	2.9%
Speth et al.	63	103	0.61	[0.52; 0.70]	0.5%	3.0%
Yan et al. 2	75	128	0.59	[0.50; 0.67]	0.7%	3.0%
Gelardi et al.	42	72	0.58	[0.47; 0.69]	0.4%	2.9%
Paderno et al.	284	508	0.56	[0.52; 0.60]	2.6%	3.0%
De Maria et al.	48	95	0.51	[0.41; 0.60]	0.5%	3.0%
Klopfenstein et al.	54	114	0.47	[0.38; 0.56]	0.6%	3.0%
Dawson et al.	18	42	0.43	[0.29; 0.58]	0.2%	2.9%
Levinson et al.	15	42	0.36	[0.23; 0.51]	0.2%	2.9%
Beltran–Corbellini et al.	25	79	0.32	[0.22; 0.43]	0.4%	2.9%
Shoer et al.	136	498	0.27	[0.24; 0.31]	2.5%	3.0%
Ji Yun Noh et al.	52	199	0.26	[0.21; 0.33]	1.0%	3.0%
Trubiano et al.	7	28	0.25	[0.13; 0.43]	0.1%	2.8%
Giacomelli et al.	14	59	0.24	[0.15; 0.36]	0.3%	2.9%
Wee et al.	35	154	0.23	[0.17; 0.30]	0.8%	3.0%
Lee et al.	488	3191	0.15	[0.14; 0.17]	16.1%	3.0%
Merza et al.	2	15	0.13	[0.04; 0.38]	0.1%	2.7%
Liu et al.	42	321	0.13	[0.10; 0.17]	1.6%	3.0%
Gudbjartsson et al.	119	1113	0.11	[0.09; 0.13]	5.6%	3.0%
Mao et al.	11	214	0.05	[0.03; 0.09]	1.1%	3.0%
Fixed effect model	**10678**	**19175**	**0.57**	**[0.56; 0.57]**	**97.1%**	**––**
Random effects model			**0.45**	**[0.31; 0.59]**	**––**	**82.7%**
Heterogeneity: $I^2 = 100\%$, $\tau^2 = 0.1409$, $p = 0$						
Fixed effect model	**11090**	**19746**	**0.57**	**[0.56; 0.58]**	**100.0%**	**––**
Random effects model			**0.50**	**[0.38; 0.63]**	**––**	**100.0%**
Heterogeneity: $I^2 = 100\%$, $\tau^2 = 0.1366$, $p = 0$						
Residual heterogeneity: $I^2 = 100\%$, $p = 0$			0.2 0.4 0.6 0.8			

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

###GLMM Next we compute using the GLMM method. We ultimately do no use this in the paper.

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

```r
forest(ma.GLMM,,col.by = "black",pooled.events = T,bylab = "Measurement Type")
```
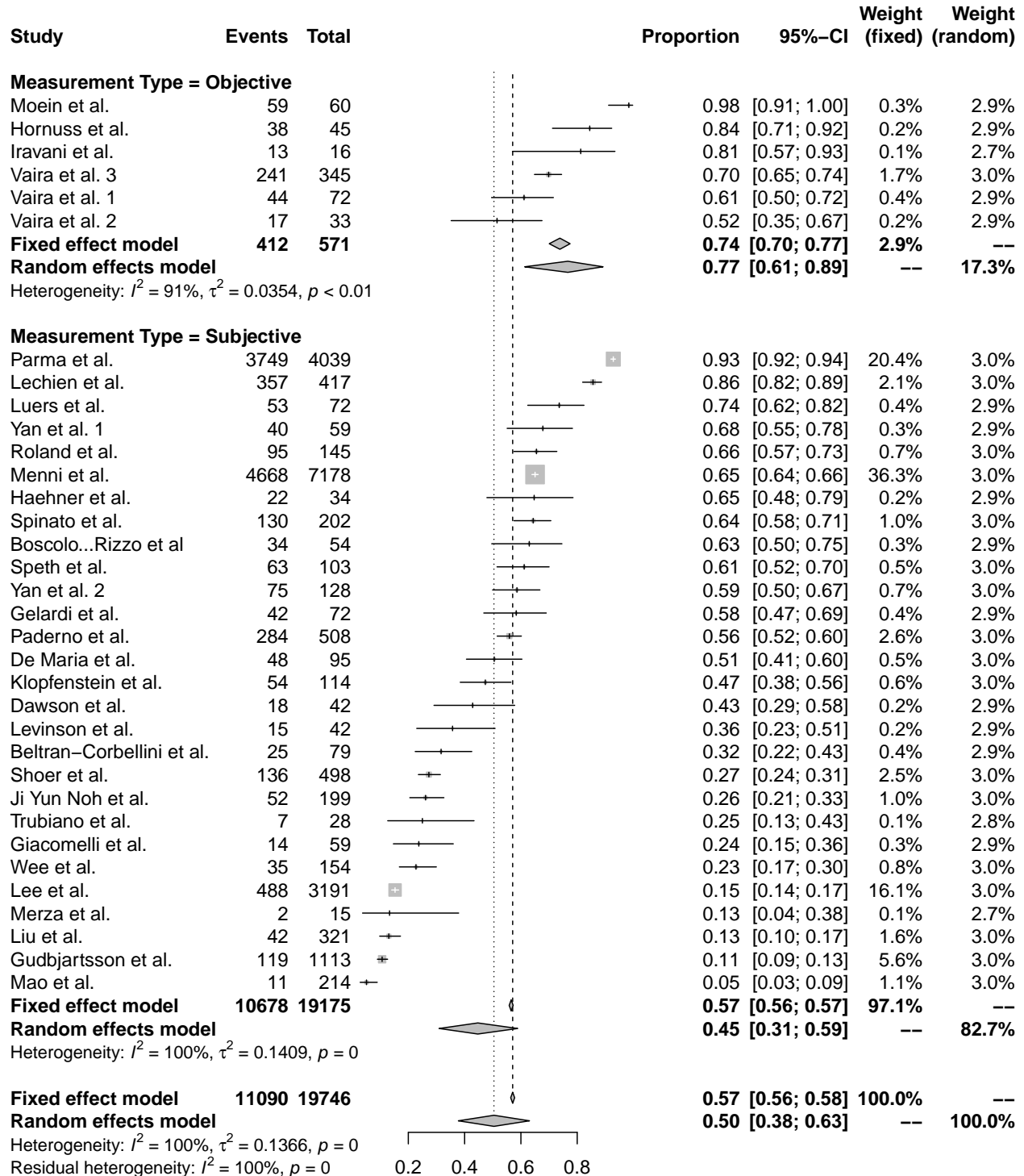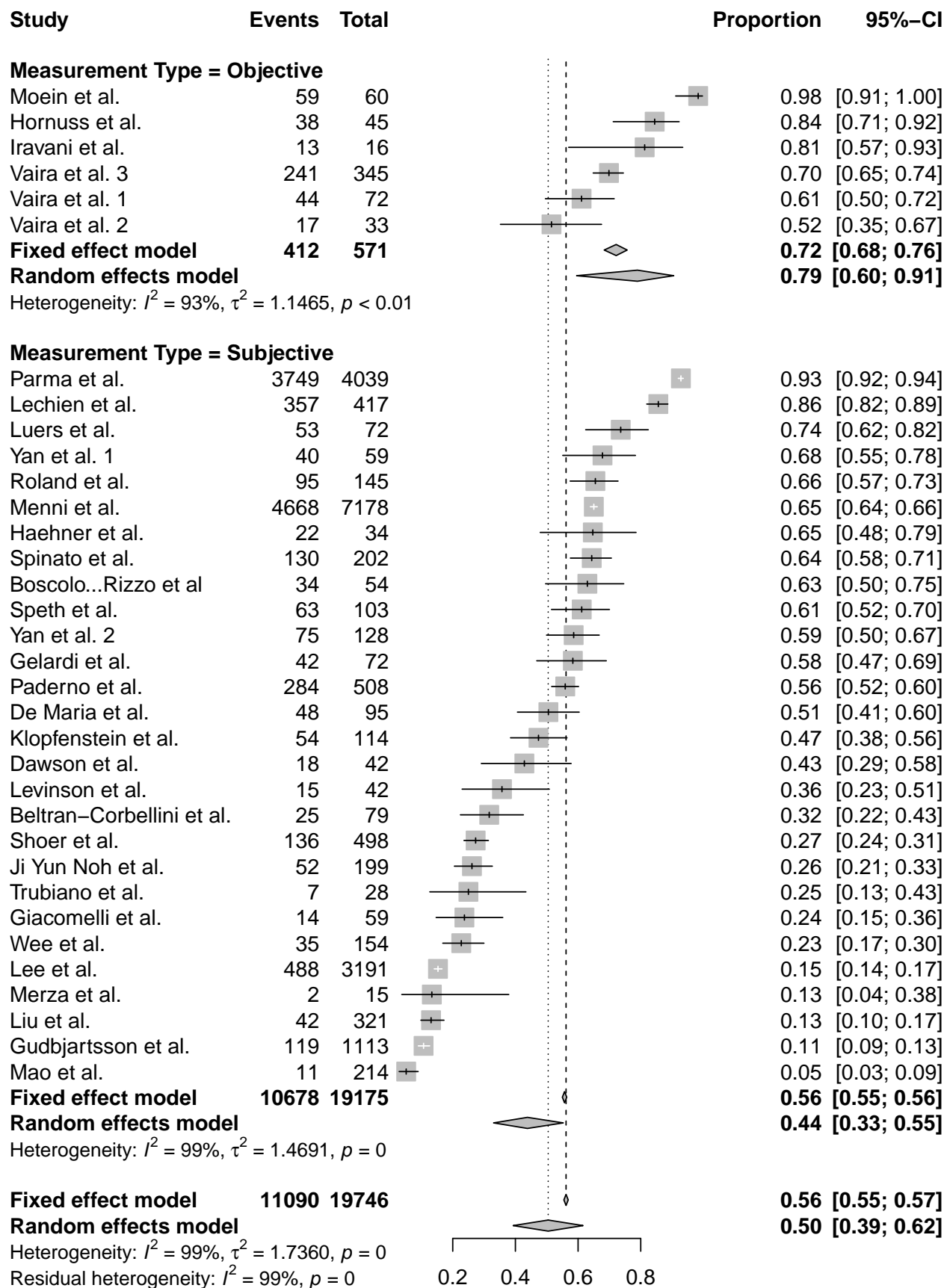
```
## Warning in grid.Call(C_textBounds, as.graphicsAnnot(x$label), x$x,
## x$y, : conversion failure on 'Boscolo-Rizzo et al' in 'mbcsToSbcs': dot
## substituted for <e2>

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

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Fixed effect model	**412**	**571**		**0.72**	**[0.68; 0.76]**
Random effects model				**0.79**	**[0.60; 0.91]**
Heterogeneity: $I^2 = 93\%$, $\tau^2 = 1.1465$, $p < 0.01$					
Measurement Type = Subjective					
Parma et al.	3749	4039		0.93	[0.92; 0.94]
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Haehner et al.	22	34		0.65	[0.48; 0.79]
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Liu et al.	42	321		0.13	[0.10; 0.17]
Gudbjartsson et al.	119	1113		0.11	[0.09; 0.13]
Mao et al.	11	214		0.05	[0.03; 0.09]
Fixed effect model	**10678**	**19175**		**0.56**	**[0.55; 0.56]**
Random effects model				**0.44**	**[0.33; 0.55]**
Heterogeneity: $I^2 = 99\%$, $\tau^2 = 1.4691$, $p = 0$					
Fixed effect model	**11090**	**19746**		**0.56**	**[0.55; 0.57]**
Random effects model				**0.50**	**[0.39; 0.62]**
Heterogeneity: $I^2 = 99\%$, $\tau^2 = 1.7360$, $p = 0$					
Residual heterogeneity: $I^2 = 99\%$, $p = 0$					

0.2 0.4 0.6 0.8

##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)
```
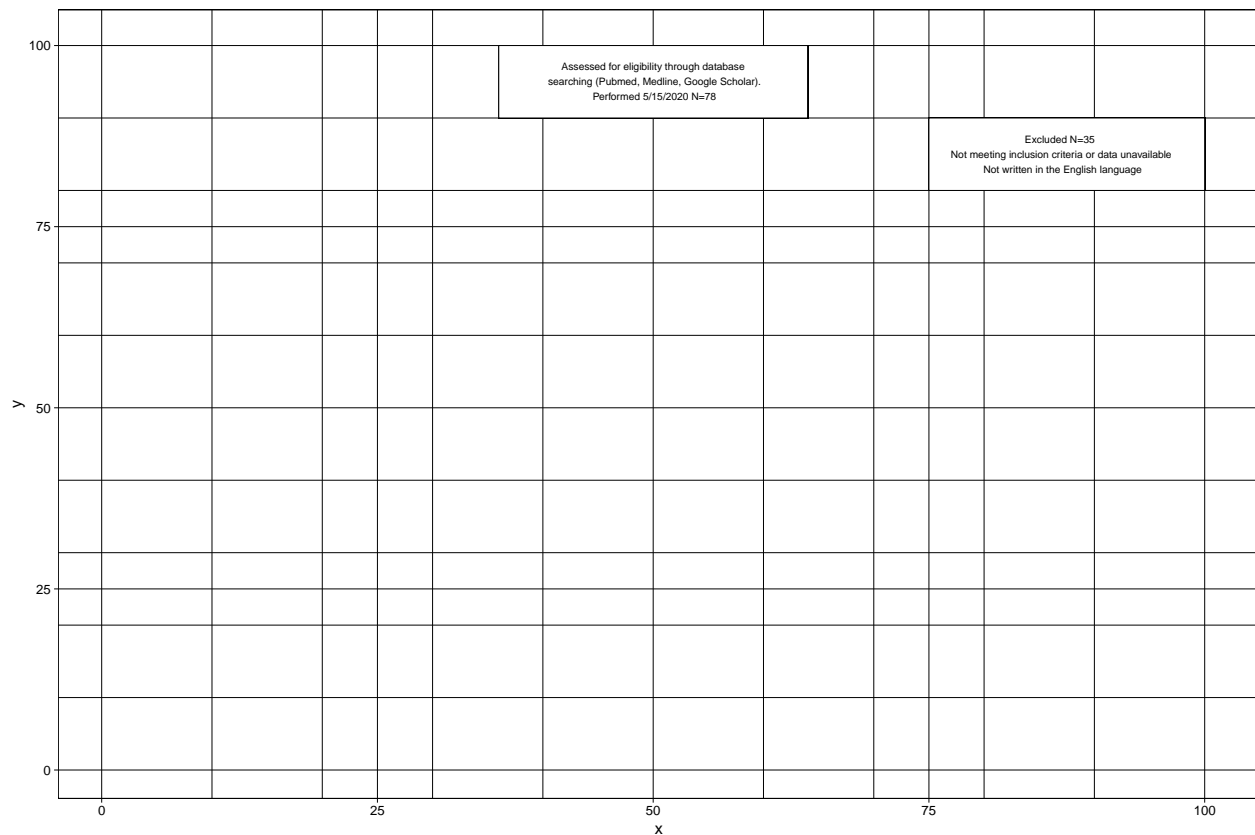
```
## Warning: Duplicated aesthetics after name standardisation: size
```

```
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
```

Assessed for eligibility through database searching (Pubmed, Medline, Google Scholar). Performed 5/15/2020 N=78

Excluded N=35
Not meeting inclusion criteria or data unavailable
Not written in the English language

Final Version

```r
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

```r
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 Pap
          size=2.5)
```

Warning: Duplicated aesthetics after name standardisation: size

```r
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()
```

```
┌─────────────────────────────────────┐
│ Assessed for eligibility through    │
│ database searching (Pubmed, Medline,│
│ Google Scholar).                    │
│ Performed 5/15/2020 N=78            │
└─────────────────────────────────────┘
                │
                │                        ┌──────────────────────────────────────────┐
                ├───────────────────────▶│ Excluded N=35                              │
                │                        │ Not meeting inclusion criteria or data     │
                │                        │ unavailable                                │
                │                        │ Not written in the English language        │
                ▼                        └──────────────────────────────────────────┘
┌─────────────────────────────────────┐
│ Eligible papers for inclusion       │
│ Measure of olfactory dysfunction    │
│ N=43                                │
└─────────────────────────────────────┘
                │
                │                        ┌──────────────────────────────────────────┐
                ├───────────────────────▶│ Excluded                                   │
                │                        │ Not lab tested COVID N=5                   │
                │                        │ Recruitment of Patients With Smell Loss N=3│
                │                        │ Papers with Overlapping Samples N=1        │
                ▼                        └──────────────────────────────────────────┘
┌─────────────────────────────────────┐
│ Full text screened for prevalence   │
│ rate                                │
│ N=34                                │
└─────────────────────────────────────┘
                │
                ▼
┌─────────────────────────────────────┐
│ Data extracted N=34                 │
│ Two authors extracted data          │
│ Two authors confirmed data extracted│
└─────────────────────────────────────┘
                │
                ▼
┌─────────────────────────────────────┐
│ Articles included                   │
│ N=34                                │
└─────────────────────────────────────┘
```