COVID-19 Review and Meta-Analysis

Vicente Ramirez 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
          1.3.1 v forcats 0.4.0
## v readr
## -- 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 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$CI_Lower<-COVID19$p + 1.96*COVID19$p.)/COVID19$ Number of subjects`)

COVID19$CI_Lower<-COVID19$p - 1.96*COVID19$p.E.

COVID19$CI_Upper<- COVID19$p + 1.96*COVID19$p.E.

COVID19 <- COVID19[order(COVID19$p,decreasing = T),]

summary_COVID_Obj<-data.frame(Name="Summary (Objective)",Subjects=sum(COVID19$Type=="Objective" summary_COVID_Sub<-data.frame(Name="Summary (Subjective)",Subjects=sum(COVID19[COVID19$Type=="Subjective" summary_COVID_Sub<-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

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$`Author Name`,byvar = C
#pdf(sprintf("Forestplot_%s",d))
forest(ma.INV,col.by = "black",pooled.events = T,bylab = "Measurement Type")
## Warning in grid.Call(C_textBounds, as.graphicsAnnot(x$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,
```

xy, : 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	<u> </u>	0.98	[0.91; 1.00]	0.3%	2.9%				
Hornuss et al.	38	45			[0.71; 0.92]	0.2%	2.9%				
Iravani et al.	13	16	<u> </u>		[0.57; 0.93]	0.1%	2.7%				
Vaira et al. 3	241	345			[0.65; 0.74]	1.7%	3.0%				
Vaira et al. 1	44	72	! 		[0.50; 0.72]	0.4%	2.9%				
Vaira et al. 2	17	33			[0.35; 0.67]	0.2%	2.9%				
Fixed effect model	412	571	♦		[0.70; 0.77]	2.9%					
Random effects mode					[0.61; 0.89]		17.3%				
Heterogeneity: $I^2 = 91\%$,	$\tau^2 = 0.0354$, <i>p</i> < 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			[0.82; 0.89]	2.1%	3.0%				
Luers et al.	53	72			[0.62; 0.82]	0.4%	2.9%				
Yan et al. 1	40	59	<u>i</u>		[0.55; 0.78]	0.3%	2.9%				
Roland et al.	95	145			[0.57; 0.73]	0.7%	3.0%				
Menni et al.	4668	7178	+		[0.64; 0.66]	36.3%	3.0%				
Haehner et al.	22	34			[0.48; 0.79]	0.2%	2.9%				
Spinato et al.	130	202			[0.58; 0.71]	1.0%	3.0%				
BoscoloRizzo et al	34	54	<u>: i </u>	0.63	[0.50; 0.75]	0.3%	2.9%				
Speth et al.	63	103			[0.52; 0.70]	0.5%	3.0%				
Yan et al. 2	75	128	<u> </u>	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	- !		[0.41; 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.		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			[0.13; 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			[0.17; 0.30]	0.8%	3.0%				
Lee et al.	488	3191	+		[0.14; 0.17]	16.1%	3.0%				
Merza et al.	2	15 -	'		[0.04; 0.38]	0.1%	2.7%				
Liu et al.	42	321	+		[0.10; 0.17]	1.6%	3.0%				
Gudbjartsson et al.	119	1113	#		[0.09; 0.13]	5.6%	3.0%				
Mao et al.	11	214 →	-		[0.03; 0.09]	1.1%	3.0%				
Fixed effect model	10678	19175	•		[0.56; 0.57]	97.1%					
Random effects mode Heterogeneity: $I^2 = 100\%$		9, <i>p</i> = 0		0.45	[0.31; 0.59]		82.7%				
Fixed effect model	11090	19746	• •	0.57	[0.56; 0.58]	100.0%					
Random effects mode					[0.38; 0.63]		100.0%				
Heterogeneity: $I^2 = 100\%$		6. $p = 0$		2.30							
Residual heterogeneity: I	$r^2 = 100\%, \mu$	$\rho = 0$	0.2 0.4 0.6 0.8								
#den off()											

#dev.off()

 $\#\#\#\mathrm{GLMM}$ 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 =

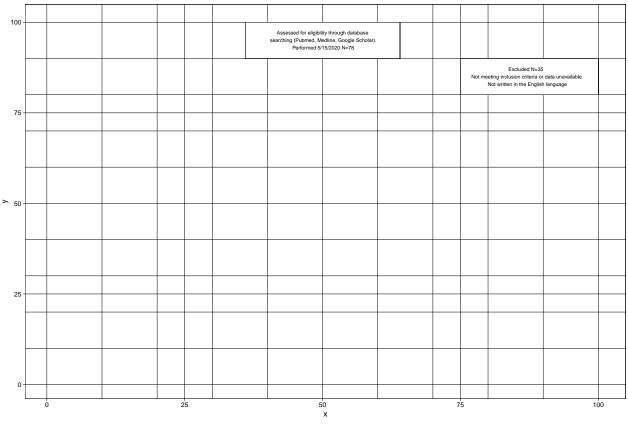
```
## Warning in grid.Call(C_textBounds, as.graphicsAnnot(x$label), x$x,
## x$y, : conversion failure on 'Boscolo-Rizzo et al' in 'mbcsToSbcs': dot
## substituted for <e2>
## Warning in grid.Call(C_textBounds, as.graphicsAnnot(x$label), x$x,
## x$y, : conversion failure on 'Boscolo-Rizzo et al' in 'mbcsToSbcs':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

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

Study	Events	Total		Proportion	95%-CI						
Measurement Type = Objective											
Moein et al.	59	60	-	0.98 [0	0.91; 1.00]						
Hornuss et al.	38	45		-	0.71; 0.92]						
Iravani et al.	13	16		-	0.57; 0.93]						
Vaira et al. 3	241	345	-	-	0.65; 0.74]						
Vaira et al. 1	44	72	: 	-	0.50; 0.72]						
Vaira et al. 2	17	33		-	0.35; 0.67]						
Fixed effect model	412	571	→		0.68; 0.76]						
Random effects mode		_		-	0.60; 0.91]						
Heterogeneity: $I^2 = 93\%$, $\tau^2 = 1.1465$, $p < 0.01$											
,											
Measurement Type = \$	-		_								
Parma et al.	3749	4039			0.92; 0.94]						
Lechien et al.	357	417	_ =	-	0.82; 0.89]						
Luers et al.	53	72		_	0.62; 0.82]						
Yan et al. 1	40	59	<u> </u>	-	0.55; 0.78]						
Roland et al.	95	145	<u> </u>	-	0.57; 0.73]						
Menni et al.	4668	7178	<u>+</u>	-	0.64; 0.66]						
Haehner et al.	22	34		-	0.48; 0.79]						
Spinato et al.	130	202		-	0.58; 0.71]						
BoscoloRizzo et al	34	54	: : : -	-	0.50; 0.75]						
Speth et al.	63	103		-	0.52; 0.70]						
Yan et al. 2	75	128	-	-	0.50; 0.67]						
Gelardi et al.	42	72		-	0.47; 0.69]						
Paderno et al.	284	508	-	-	0.52; 0.60]						
De Maria et al.	48	95		_	0.41; 0.60]						
Klopfenstein et al.	54	114		-	0.38; 0.56]						
Dawson et al.	18	42		-	0.29; 0.58]						
Levinson et al.	15	42		-	0.23; 0.51]						
Beltran-Corbellini et al.	25	79		_	0.22; 0.43]						
Shoer et al.	136	498		-	0.24; 0.31]						
Ji Yun Noh et al.	52	199	-	-	0.21; 0.33]						
Trubiano et al.	7	28			0.13; 0.43]						
Giacomelli et al.	14	59		-	0.15; 0.36]						
Wee et al.	35	154		-	0.17; 0.30]						
Lee et al.	488	3191	+	-	0.14; 0.17]						
Merza et al.	2	15		-	0.04; 0.38]						
Liu et al.	42	321		-	0.10; 0.17]						
Gudbjartsson et al.	119	1113		-	0.09; 0.13]						
Mao et al.	11	214	=		0.03; 0.09]						
Fixed effect model	10678	19175	. •		0.55; 0.56]						
Random effects mode				0.44 [0	0.33; 0.55]						
Heterogeneity: $I^2 = 99\%$,	τ ⁻ = 1.4691	, p = 0									
Fixed effect model	11090	19746	\(\)	0.56 [0	0.55; 0.57]						
Random effects mode				_	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
##
     <int> <int>
## 1
        1
               1
## 2
        2
## 3
        3
               3
## 4
         4
               4
## 5
         5
               5
## 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).\
## 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



##Final Version

Warning: Duplicated aesthetics after name standardisation: size

Warning: Duplicated aesthetics after name standardisation: size

 $\hbox{\tt\#\# Warning: Duplicated aesthetics after name standardisation: size}$

```
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, x=674.7, y=85, y=685,
    size=0.10, linejoin = "mitre", lineend = "butt",
    arrow = arrow(length = unit(1, "mm"), type= "closed")) +
  geom_segment(
    x=50, x=60, y=70, y=60.3,
    size=0.10, linejoin = "mitre", lineend = "butt",
    arrow = arrow(length = unit(1, "mm"), type= "closed")) +
  geom_segment(
    x=50, x=65, y=65, y=65,
    size=0.10, linejoin = "mitre", lineend = "butt",
    arrow = arrow(length = unit(1, "mm"), type= "closed")) +
  geom_segment(
    x=50, x=50, y=50, y=60.3,
    size=0.10, linejoin = "mitre", lineend = "butt",
    arrow = arrow(length = unit(1, "mm"), type= "closed")) +
  geom segment (
    x=50, x=50, y=30, y=30, y=30,
    size=0.10, linejoin = "mitre", lineend = "butt",
    arrow = arrow(length = unit(1, "mm"), type= "closed"))
p + theme_void()
```

