

TestMarkdown-Analysis

2024-01-21

Software Requirements:

- R Installation
- RStudio **for** IDE
- LaTeX Installation **for** rendering RMarkdown to **PDF** (this file)
- GitHub Account **for** Repository/Data access

Setting up the Environment:

Required R Packages:

```
install.packages("rmarkdown")
install.packages("devtools")

install.packages("tidyverse")
install.packages("metafor")
install.packages("meta")

install.packages("tidyr")

install.packages("weightr")
```

Loading first Packages:

```
library(rmarkdown)

library(tidyverse)
```

```
## -- Attaching core tidyverse packages ----- tidyverse 2.0.0 --
## v dplyr      1.1.4      v readr      2.1.5
## v forcats    1.0.0      v stringr   1.5.1
## v ggplot2    3.4.4      v tibble    3.2.1
## v lubridate  1.9.3      v tidyr     1.3.0
## v purrr      1.0.2
## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()     masks stats::lag()
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors
library(metafor)

## Loading required package: Matrix
##
## Attaching package: 'Matrix'
```

```
##
## The following objects are masked from 'package:tidyr':
##
##   expand, pack, unpack
##
## Loading required package: metadat
## Loading required package: numDeriv
##
## Loading the 'metafor' package (version 4.4-0). For an
## introduction to the package please type: help(metafor)
```

```
library(meta)
```

```
## Loading 'meta' package (version 7.0-0).
## Type 'help(meta)' for a brief overview.
## Readers of 'Meta-Analysis with R (Use R!)' should install
## older version of 'meta' package: https://tinyurl.com/dt4y5drs
```

```
library(dmetar)
```

```
## Extensive documentation for the dmetar package can be found at:
## www.bookdown.org/MathiasHarrer/Doing\_Meta\_Analysis\_in\_R/
```

```
library(dplyr)
library(tidyr)
```

```
library(stringr)
library(readr)
```

Installing further R Packages:

```
devtools::install_github("MathiasHarrer/dmetar")
```

Loading remaining Packages:

```
library(dmetar)
```

Cloning Repository from Git-Hub (Fetching Data):

```
usethis::create_from_github(
  "https://github.com/VJMeyer/HPVPre_Repo.git",
  destdir = "~/path/to/where/you/want/the/local/repo/"
)
```

Set Working-Directory:

```
setwd("~/path/to/where/you/want/the/local/repo/")
```

Set Private Working-Directory:

Confirm Working-Directory:

Load Data:

```
library(tidyverse)

any_type <- read_csv("Anytype_OLDI.csv")

## Rows: 87 Columns: 24
## -- Column specification -----
## Delimiter: ","
## chr (19): study_id, author_year, title, study_design, world_region, world_su...
## dbl (5): ending_year, num_older_wom, num_hpv_pos, num_hpv_neg, any_prev
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.

hr_type <- read_csv("HR_OLDI.csv")

## Rows: 127 Columns: 24
## -- Column specification -----
## Delimiter: ","
## chr (19): study_id, author_year, title, study_design, world_region, world_su...
## dbl (5): ending_year, hr_hpv_nr, num_older_wom, num_hr_hpv_pos, hr_prev
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.

gtype <- read_csv("gtype.csv")

## Rows: 239 Columns: 22
## -- Column specification -----
## Delimiter: ","
## chr (16): study_id, author_year, title, study_design, world_region, world_su...
## dbl (6): ending_year, num_older_wom, num_hpv_pos, num_hr_hpv_pos, num_type,...
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

Quantitative Analysis

Data Cleaning

Ensure there are no MISSING values in the important columns of ANYTYPE Data:

```
library(tidyverse)

class(any_type)

## [1] "spec_tbl_df" "tbl_df"      "tbl"         "data.frame"

head(any_type)

## # A tibble: 6 x 24
```

```
##   study_id author_year          title    study_design ending_year world_region
##   <chr>    <chr>              <chr>    <chr>          <dbl> <chr>
## 1 10      Tsedenbal et al., 2018 "Human ~ cross-secti~    2017 Asia
## 2 20G     Çolakoğlu et al., 2017 "Human ~ retrospecti~    2015 Asia
## 3 30      Demirci et al., 2019  "Human ~ cross-secti~    2017 Asia
## 4 40G     Dutta et al., 2012    "Preval~ cross-secti~    2010 Asia
## 5 50H     Herrero et al., 2000  "Popula~ prospective     1994 Americas
## 6 60HG     Jin et al., 2019     "The pr~ retrospecti~    2018 Asia
## # i 18 more variables: world_subregion <chr>, country <chr>, city_state <chr>,
## #   focus <chr>, overall_cytology <chr>, pap_method <chr>,
## #   recruitment_setting <chr>, hpv_types_reported <chr>,
## #   hpv_types_tested <chr>, hpv_cat <chr>, hpv_test <chr>, test_details <chr>,
## #   num_older_wom <dbl>, num_hpv_pos <dbl>, num_hpv_neg <dbl>, any_prev <dbl>,
## #   risk_of_bias <chr>, Notes <chr>
```

```
str(any_type)
```

```
## spc_tbl_ [87 x 24] (S3: spec_tbl_df/tbl_df/tbl/data.frame)
## $ study_id      : chr [1:87] "10" "20G" "30" "40G" ...
## $ author_year   : chr [1:87] "Tsedenbal et al., 2018" "Çolakoğlu et al., 2017" "Demirci et al.
## $ title         : chr [1:87] "Human papillomavirus genotyping among women with cervical abnorma
## $ study_design  : chr [1:87] "cross-sectional" "retrospective" "cross-sectional" "cross-section
## $ ending_year   : num [1:87] 2017 2015 2017 2010 1994 ...
## $ world_region  : chr [1:87] "Asia" "Asia" "Asia" "Asia" ...
## $ world_subregion : chr [1:87] "Central Asia" "Western Asia" "Western Asia" "Southern Asia" ...
## $ country       : chr [1:87] "Mongolia" "Turkiye" "Turkiye" "India" ...
## $ city_state    : chr [1:87] "Ulaanbaatar" "Adana" "Istanbul" "West Bengal" ...
## $ focus         : chr [1:87] "Both" "Both" "Both" "Both" ...
## $ overall_cytology : chr [1:87] "Predominantly normal" "Predominantly normal" "Predominantly norma
## $ pap_method     : chr [1:87] "conventional" "LBC" "LBC" "conventional" ...
## $ recruitment_setting: chr [1:87] "clinical setting" "screening" "clinical setting" "screening" ...
## $ hpv_types_reported : chr [1:87] "overall" "16, 18, overall" "overall" "16, 18, overall" ...
## $ hpv_types_tested  : chr [1:87] "6, 11, 16 18, 26, 31, 33, 35, 39, 40, 42, 45, 51, 52, 53, 54, 55
## $ hpv_cat         : chr [1:87] "II" "II" "II" "II" ...
## $ hpv_test        : chr [1:87] "LA" "LA" "LA" "MY09/11" ...
## $ test_details     : chr [1:87] "L1 consensus PCR with Line-blot assay, Roche Linear Array test"
## $ num_older_wom    : num [1:87] 25 52 282 114 417 ...
## $ num_hpv_pos      : num [1:87] 9 23 63 11 69 745 677 405 6 137 ...
## $ num_hpv_neg      : num [1:87] 16 29 219 103 348 ...
## $ any_prev         : num [1:87] 0.36 0.442 0.223 0.096 0.165 ...
## $ risk_of_bias     : chr [1:87] "low" "high" "low" "high" ...
## $ Notes            : chr [1:87] "just overall HPV positivity reported by age for 55+; HR-HPV+ and
## - attr(*, "spec")=
## .. cols(
## ..   study_id = col_character(),
## ..   author_year = col_character(),
## ..   title = col_character(),
## ..   study_design = col_character(),
## ..   ending_year = col_double(),
## ..   world_region = col_character(),
## ..   world_subregion = col_character(),
## ..   country = col_character(),
## ..   city_state = col_character(),
## ..   focus = col_character(),
## ..   overall_cytology = col_character(),
```

```
## .. pap_method = col_character(),
## .. recruitment_setting = col_character(),
## .. hpv_types_reported = col_character(),
## .. hpv_types_tested = col_character(),
## .. hpv_cat = col_character(),
## .. hpv_test = col_character(),
## .. test_details = col_character(),
## .. num_older_wom = col_double(),
## .. num_hpv_pos = col_double(),
## .. num_hpv_neg = col_double(),
## .. any_prev = col_double(),
## .. risk_of_bias = col_character(),
## .. Notes = col_character()
## .. )
## - attr(*, "problems")=<externalptr>
```

```
summary(any_type)
```

```
##      study_id      author_year      title      study_design
## Length:87      Length:87      Length:87      Length:87
## Class :character Class :character Class :character Class :character
## Mode  :character Mode  :character Mode  :character Mode  :character
##
##
##
##      ending_year  world_region  world_subregion  country
## Min.   :1989      Length:87      Length:87      Length:87
## 1st Qu.:2006      Class :character Class :character Class :character
## Median :2010      Mode  :character Mode  :character Mode  :character
## Mean   :2009
## 3rd Qu.:2014
## Max.   :2019
## NA's   :4
##      city_state      focus      overall_cytology  pap_method
## Length:87      Length:87      Length:87      Length:87
## Class :character Class :character Class :character Class :character
## Mode  :character Mode  :character Mode  :character Mode  :character
##
##
##
##      recruitment_setting hpv_types_reported hpv_types_tested  hpv_cat
## Length:87      Length:87      Length:87      Length:87
## Class :character Class :character Class :character Class :character
## Mode  :character Mode  :character Mode  :character Mode  :character
##
##
##
##      hpv_test      test_details      num_older_wom      num_hpv_pos
## Length:87      Length:87      Min.   :    6.0      Min.   :    0.0
## Class :character Class :character      1st Qu.:   82.0      1st Qu.:   13.0
## Mode  :character Mode  :character      Median :  293.0      Median :   29.0
##                               Mean   : 1133.6      Mean   :  188.6
```

```
##              3rd Qu.: 697.5   3rd Qu.: 126.5
##              Max.    :18910.0   Max.    :6199.0
##              NA's    :4         NA's    :4
## num_hpv_neg    any_prev    risk_of_bias    Notes
## Min.      :    5   Min.      :0.0000   Length:87   Length:87
## 1st Qu.:   63   1st Qu.:0.0815   Class :character   Class :character
## Median :  225   Median :0.1480   Mode  :character   Mode  :character
## Mean      :  945   Mean      :0.1787
## 3rd Qu.:  569   3rd Qu.:0.2450
## Max.      :13973   Max.      :0.6670
## NA's      :4
```

```
view(any_type)
```

Filter rows where num_older_wom is NA and select study_id

```
na_in_num_older_wom <- any_type %>%
  filter(is.na(num_older_wom)) %>%
  select(study_id)
```

Filter rows where num_hpv_pos is NA and select study_id

```
na_in_num_hpv_pos <- any_type %>%
  filter(is.na(num_hpv_pos)) %>%
  select(study_id)
```

Filter rows where num_hpv_neg is NA and select study_id

```
na_in_num_hpv_neg <- any_type %>%
  filter(is.na(num_hpv_neg)) %>%
  select(study_id)
```

View the results

```
na_in_num_older_wom
```

```
## # A tibble: 4 x 1
##   study_id
##   <chr>
## 1 260GP
## 2 430P
## 3 560HGP
## 4 660HGP
```

```
na_in_num_hpv_pos
```

```
## # A tibble: 4 x 1
##   study_id
##   <chr>
## 1 260GP
## 2 430P
## 3 560HGP
## 4 660HGP
```

```
na_in_num_hpv_neg
```

```
## # A tibble: 4 x 1
##   study_id
##   <chr>
## 1 260GP
## 2 430P
## 3 560HGP
## 4 660HGP
```

there was missing data in one row (630) of num_hpv_neg which was corrected

Filter out rows where the identifier ends with 'P'

```
any_type_filtered <- any_type %>%
  filter(!str_detect(study_id, "P$"))
```

```
summary(any_type_filtered)
```

```
##   study_id          author_year          title          study_design
## Length:83          Length:83          Length:83          Length:83
## Class :character    Class :character    Class :character    Class :character
## Mode  :character    Mode  :character    Mode  :character    Mode  :character
##
##
##
##   ending_year    world_region    world_subregion    country
## Min.   :1989    Length:83          Length:83          Length:83
## 1st Qu.:2006    Class :character    Class :character    Class :character
## Median :2010    Mode  :character    Mode  :character    Mode  :character
## Mean   :2009
## 3rd Qu.:2014
## Max.   :2019
## NA's   :4
##   city_state          focus          overall_cytology    pap_method
## Length:83          Length:83          Length:83          Length:83
## Class :character    Class :character    Class :character    Class :character
## Mode  :character    Mode  :character    Mode  :character    Mode  :character
##
##
##
##   recruitment_setting hpv_types_reported hpv_types_tested    hpv_cat
## Length:83          Length:83          Length:83          Length:83
## Class :character    Class :character    Class :character    Class :character
## Mode  :character    Mode  :character    Mode  :character    Mode  :character
##
##
##
##   hpv_test          test_details          num_older_wom          num_hpv_pos
## Length:83          Length:83          Min.   :    6.0          Min.   :    0.0
## Class :character    Class :character    1st Qu.:   82.0          1st Qu.:   13.0
## Mode  :character    Mode  :character    Median :  293.0          Median :   29.0
```

```
##                               Mean   : 1133.6   Mean   : 188.6
##                               3rd Qu.:  697.5   3rd Qu.: 126.5
##                               Max.    :18910.0   Max.    :6199.0
##
##   num_hpv_neg    any_prev    risk_of_bias    Notes
##   Min.      :    5   Min.      :0.0000   Length:83   Length:83
##   1st Qu.:   63   1st Qu.:0.0790   Class :character   Class :character
##   Median :  225   Median :0.1490   Mode  :character   Mode  :character
##   Mean    :  945   Mean    :0.1812
##   3rd Qu.:  569   3rd Qu.:0.2470
##   Max.    :13973   Max.    :0.6670
##
```

```
nrow(any_type_filtered)
```

```
## [1] 83
```

Extract and view unique study ids in `hr_type_filtered` to make sure it is correct

```
unique_study_ids_any <- any_type_filtered %>%
  select(study_id) %>%
  distinct()

print(unique_study_ids_any, n = 83)
```

```
## # A tibble: 83 x 1
##   study_id
##   <chr>
## 1 10
## 2 20G
## 3 30
## 4 40G
## 5 50H
## 6 60HG
## 7 70
## 8 80
## 9 90
## 10 100HG
## 11 110
## 12 130
## 13 140
## 14 150
## 15 160HG
## 16 170
## 17 180HG
## 18 190H
## 19 200H
## 20 210H
## 21 220
## 22 230
## 23 240H
## 24 250H
## 25 270H
## 26 280H
## 27 290
```


28 300G
29 310G
30 320H
31 330H
32 340HG
33 350
34 360
35 370H
36 380H
37 390G
38 400HG
39 410HG
40 440
41 450HG
42 460H
43 470HG
44 480H
45 490HG
46 500H
47 510HG
48 520HG
49 530H
50 540H
51 570HG
52 580HG
53 590HG
54 600HG
55 610H
56 620H
57 630
58 640H
59 650
60 670HG
61 680HG
62 690
63 700H
64 710
65 720H
66 730H
67 740H
68 750H
69 760
70 770H
71 780G
72 790
73 800
74 810H
75 820H
76 830HG
77 840H
78 850HG
79 860H
80 870H
81 880H

```

## 82 890
## 83 900H

### Ensure there are no MISSING values in the columns of HR TYPE where there should be data
class(hr_type)

## [1] "spec_tbl_df" "tbl_df"      "tbl"          "data.frame"

head(hr_type)

## # A tibble: 6 x 24
##   study_id author_year      title      study_design ending_year world_region
##   <chr>      <chr>          <chr>      <chr>          <dbl> <chr>
## 1 1H        Abulizi et al., 2021 "At what~ cross-secti~      2014 Asia
## 2 2H        Bae et al., 2009    "Natural~ prospective      2004 Asia
## 3 3H        Clarke et al, 2021  "Age-spe~ prospective      2018 Americas
## 4 4HG       Yoshida et al., 2007 "Quantit~ cross-secti~      2004 Asia
## 5 5H        Dalstein., 2009    "HPV Per~ prospective      2002 Europe
## 6 6H        Ernstson et al., 2019 "Detecti~ cross-secti~      2017 Europe
## # i 18 more variables: world_subregion <chr>, country <chr>, city_state <chr>,
## #   focus <chr>, overall_cytology <chr>, pap_method <chr>,
## #   recruitment_setting <chr>, hpv_types_reported <chr>,
## #   hpv_types_tested <chr>, hr_hpv_nr <dbl>, hr_hpv_cat <chr>, hpv_test <chr>,
## #   test_details <chr>, num_older_wom <dbl>, num_hr_hpv_pos <dbl>,
## #   hr_prev <dbl>, risk_of_bias <chr>, Comments <chr>

str(hr_type)

## spc_tbl_ [127 x 24] (S3: spec_tbl_df/tbl_df/tbl/data.frame)
## $ study_id      : chr [1:127] "1H" "2H" "3H" "4HG" ...
## $ author_year   : chr [1:127] "Abulizi et al., 2021" "Bae et al., 2009" "Clarke et al, 2021" ...
## $ title         : chr [1:127] "At what age should the Uyghur minority initiate cervical cancer ...
## $ study_design  : chr [1:127] "cross-sectional" "prospective" "prospective" "cross-sectional" ...
## $ ending_year   : num [1:127] 2014 2004 2018 2004 2002 ...
## $ world_region  : chr [1:127] "Asia" "Asia" "Americas" "Asia" ...
## $ world_subregion : chr [1:127] "Eastern Asia" "Eastern Asia" "Northern America" "Eastern Asia" ...
## $ country       : chr [1:127] "China" "South Korea" "USA" "Japan" ...
## $ city_state    : chr [1:127] "South Xinjiang" "Goyang" "Mississippi" "Gunma" ...
## $ focus         : chr [1:127] "Both" "Both" "Both" "Both" ...
## $ overall_cytology : chr [1:127] "Predominantly normal" "Predominantly normal" "Predominantly normal" ...
## $ pap_method    : chr [1:127] "LBC" "conventional" "LBC" "LBC" ...
## $ recruitment_setting: chr [1:127] "clinical setting" "screening" "screening" "clinical setting" ...
## $ hpv_types_reported : chr [1:127] "HR-HPV" "HR-HPV" "HR-HPV" "HR-HPV" ...
## $ hpv_types_tested  : chr [1:127] "16, 18, 31, 33, 35, 39, 45, 51, 52, 56, 58, 59, 66, 68" "16,18,31,33,35,39,45,51,52,56,58,59,66,68" ...
## $ hr_hpv_nr       : num [1:127] 14 13 14 7 14 14 13 12 13 17 ...
## $ hr_hpv_cat      : chr [1:127] "III" "III" "III" "II" ...
## $ hpv_test        : chr [1:127] "other PCR" "HC2" "Multiple\n" "PCR E6/E7" ...
## $ test_details    : chr [1:127] "careHPVTM\ntest (Qiagen Inc.)" "Full HPV genome detection by HC2" ...
## $ num_older_wom   : num [1:127] 1614 1815 1118 148 77 ...
## $ num_hr_hpv_pos  : num [1:127] 215 100 185 30 13 27 79 43 8 650 ...
## $ hr_prev         : num [1:127] 0.133 0.055 0.165 0.203 0.169 0.062 0.142 0.041 0.018 0.351 ...
## $ risk_of_bias    : chr [1:127] "low" "low" "low" "high" ...
## $ Comments       : chr [1:127] "Used plot digitizer on Fig. 2" "Age related data only available" ...
## - attr(*, "spec")=
## .. cols(
## ..   study_id = col_character(),

```

```
## .. author_year = col_character(),
## .. title = col_character(),
## .. study_design = col_character(),
## .. ending_year = col_double(),
## .. world_region = col_character(),
## .. world_subregion = col_character(),
## .. country = col_character(),
## .. city_state = col_character(),
## .. focus = col_character(),
## .. overall_cytology = col_character(),
## .. pap_method = col_character(),
## .. recruitment_setting = col_character(),
## .. hpv_types_reported = col_character(),
## .. hpv_types_tested = col_character(),
## .. hr_hpv_nr = col_double(),
## .. hr_hpv_cat = col_character(),
## .. hpv_test = col_character(),
## .. test_details = col_character(),
## .. num_older_wom = col_double(),
## .. num_hr_hpv_pos = col_double(),
## .. hr_prev = col_double(),
## .. risk_of_bias = col_character(),
## .. Comments = col_character()
## .. )
## - attr(*, "problems")=<externalptr>
```

```
summary(hr_type)
```

```
##   study_id      author_year      title      study_design
## Length:127      Length:127      Length:127      Length:127
## Class :character Class :character Class :character Class :character
## Mode  :character Mode  :character Mode  :character Mode  :character
##
##
##
##   ending_year  world_region      world_subregion      country
## Min.   :1994   Length:127      Length:127      Length:127
## 1st Qu.:2006   Class :character Class :character Class :character
## Median :2011   Mode  :character Mode  :character Mode  :character
## Mean   :2010
## 3rd Qu.:2015
## Max.   :2019
## NA's   :6
##   city_state      focus      overall_cytology      pap_method
## Length:127      Length:127      Length:127      Length:127
## Class :character Class :character Class :character Class :character
## Mode  :character Mode  :character Mode  :character Mode  :character
##
##
##
##   recruitment_setting hpv_types_reported hpv_types_tested      hr_hpv_nr
## Length:127      Length:127      Length:127      Min.   : 2.00
## Class :character Class :character Class :character      1st Qu.:13.00
```

```
## Mode :character      Mode :character      Mode :character      Median :14.00
##                                                                Mean :14.16
##                                                                3rd Qu.:15.00
##                                                                Max. :23.00
##
## hr_hpv_cat           hpv_test           test_details           num_older_wom
## Length:127           Length:127           Length:127           Min. : 12
## Class :character      Class :character      Class :character      1st Qu.: 187
## Mode :character      Mode :character      Mode :character      Median : 454
##                                                                Mean : 5027
##                                                                3rd Qu.: 1138
##                                                                Max. :299259
##                                                                NA's :14
## num_hr_hpv_pos       hr_prev           risk_of_bias           Comments
## Min. : 1.0           Min. :0.0160          Length:127           Length:127
## 1st Qu.: 16.0         1st Qu.:0.0530         Class :character      Class :character
## Median : 40.0         Median :0.0960         Mode :character      Mode :character
## Mean : 287.3          Mean :0.1214
## 3rd Qu.: 117.2        3rd Qu.:0.1530
## Max. :12014.0         Max. :0.6120
## NA's :15             NA's :1
```

```
view(hr_type)
nrow(hr_type)
```

```
## [1] 127
```

Filter rows where num_older_wom is NA and select study_id

```
na_in_num_older_wom_hr <- hr_type %>%
  filter(is.na(num_older_wom)) %>%
  select(study_id)
```

Filter rows where num_hr_hpv_pos is NA and select study_id

```
na_in_num_hr_hpv_pos <- hr_type %>%
  filter(is.na(num_hr_hpv_pos)) %>%
  select(study_id)
```

Filter rows where hr_prev is NA and select study_id

```
na_in_hr_prev <- hr_type %>%
  filter(is.na(hr_prev)) %>%
  select(study_id)
```

View the results

```
na_in_num_older_wom_hr
```

```
## # A tibble: 14 x 1
##   study_id
##   <chr>
## 1 14HP
## 2 16HP
```

```
## 3 28HP
## 4 38HP
## 5 41HGP
## 6 42HGP
## 7 46HGP
## 8 560HGP
## 9 51HP
## 10 660HGP
## 11 60HP
## 12 63HGP
## 13 70HGP
## 14 72HP
```

```
na_in_num_hr_hpv_pos
```

```
## # A tibble: 15 x 1
##   study_id
##   <chr>
## 1 14HP
## 2 16HP
## 3 23HG
## 4 28HP
## 5 38HP
## 6 41HGP
## 7 42HGP
## 8 46HGP
## 9 560HGP
## 10 51HP
## 11 660HGP
## 12 60HP
## 13 63HGP
## 14 70HGP
## 15 72HP
```

```
na_in_hr_prev
```

```
## # A tibble: 1 x 1
##   study_id
##   <chr>
## 1 23HG
```

we must exclude study id 23HG from the HR analysis because it has crude numbers for all gtypes but not for HR type Filter out rows where the identifier ends with 'P' or is '23HG'

```
hr_type_filtered <- hr_type %>%
  filter(!str_detect(study_id, "P$"), study_id != "23HG")
```

```
summary(hr_type_filtered)
```

```
##   study_id      author_year      title      study_design
## Length:112      Length:112      Length:112      Length:112
## Class :character Class :character Class :character Class :character
## Mode  :character Mode  :character Mode  :character Mode  :character
##
##
##
```

```
##
##   ending_year   world_region   world_subregion   country
##   Min.   :1994   Length:112       Length:112       Length:112
##   1st Qu.:2006   Class :character   Class :character   Class :character
##   Median :2011   Mode  :character   Mode  :character   Mode  :character
##   Mean   :2010
##   3rd Qu.:2015
##   Max.   :2019
##   NA's   :6
##   city_state      focus        overall_cytology   pap_method
##   Length:112      Length:112       Length:112       Length:112
##   Class :character Class :character   Class :character   Class :character
##   Mode  :character Mode  :character   Mode  :character   Mode  :character
##
##
##
##   recruitment_setting hpv_types_reported hpv_types_tested   hr_hpv_nr
##   Length:112          Length:112       Length:112       Min.   : 2.00
##   Class :character    Class :character   Class :character   1st Qu.:13.00
##   Mode  :character    Mode  :character   Mode  :character   Median :14.00
##                                     Mean   :14.09
##                                     3rd Qu.:15.00
##                                     Max.   :23.00
##
##   hr_hpv_cat      hpv_test      test_details      num_older_wom
##   Length:112      Length:112       Length:112       Min.   : 12
##   Class :character Class :character   Class :character   1st Qu.: 185
##   Mode  :character Mode  :character   Mode  :character   Median : 446
##                                     Mean   : 5066
##                                     3rd Qu.: 1169
##                                     Max.   :299259
##
##   num_hr_hpv_pos   hr_prev      risk_of_bias      Comments
##   Min.   : 1.0     Min.   :0.0160     Length:112       Length:112
##   1st Qu.: 16.0    1st Qu.:0.0530     Class :character   Class :character
##   Median : 40.0    Median :0.0960     Mode  :character   Mode  :character
##   Mean   : 287.3    Mean   :0.1226
##   3rd Qu.: 117.2    3rd Qu.:0.1510
##   Max.   :12014.0   Max.   :0.6120
##
```

```
nrow(hr_type_filtered)
```

```
## [1] 112
```

Extract and view unique study ids in hr_type_filtered to make sure it is correct

```
unique_study_ids_hr <- hr_type_filtered %>%
  select(study_id) %>%
  distinct()

print(unique_study_ids_hr, n = 112)
```

```
## # A tibble: 112 x 1
```

```

##      study_id
##      <chr>
##  1 1H
##  2 2H
##  3 3H
##  4 4HG
##  5 5H
##  6 6H
##  7 7H
##  8 8HG
##  9 50H
## 10 60HG
## 11 9H
## 12 10H
## 13 11H
## 14 12H
## 15 13H
## 16 15H
## 17 100HG
## 18 17HG
## 19 18H
## 20 19H
## 21 160HG
## 22 20H
## 23 21HG
## 24 22H
## 25 24HG
## 26 25HG
## 27 26H
## 28 27H
## 29 180HG
## 30 190H
## 31 200H
## 32 210H
## 33 240H
## 34 250H
## 35 29HG
## 36 30HG
## 37 31H
## 38 270H
## 39 280H
## 40 32H
## 41 33H
## 42 320H
## 43 34H
## 44 330H
## 45 340HG
## 46 35H
## 47 36H
## 48 37H
## 49 370H
## 50 380H
## 51 400HG
## 52 410HG

```

53 39H
54 40H
55 450HG
56 460H
57 470HG
58 43HG
59 480H
60 490HG
61 44H
62 500H
63 510HG
64 45H
65 520HG
66 47H
67 48HG
68 530H
69 540H
70 49H
71 570HG
72 50HG
73 580HG
74 52HG
75 590HG
76 600HG
77 610H
78 53HG
79 620H
80 54HG
81 55H
82 56H
83 640H
84 57H
85 58H
86 670HG
87 680HG
88 59H
89 700H
90 720H
91 730H
92 740H
93 750H
94 61H
95 62H
96 770H
97 64H
98 65HG
99 810H
100 820H
101 66H
102 830HG
103 67H
104 840H
105 850HG
106 860H


```
## 107 68H
## 108 870H
## 109 880H
## 110 69H
## 111 900H
## 112 71HG
```

Filter out rows where the identifier ends with 'P' for prevalence only for gtype_filtered

```
###trim whitespaces
```

```
gtype <- gtype %>%
  mutate(study_id = trimws(study_id))

gtype_filtered <- gtype %>%
  filter(!str_detect(study_id, "P$"))

class(gtype_filtered)
```

```
## [1] "tbl_df"      "tbl"        "data.frame"
```

```
head(gtype_filtered)
```

```
## # A tibble: 6 x 22
##   study_id author_year      title  study_design ending_year world_region
##   <chr>    <chr>          <chr>  <chr>          <dbl> <chr>
## 1 4HG      Yoshida et al., 2007 "Quant~ cross-secti~      2004 Asia
## 2 20G      Çolakoğlu et al., 2017 "Human~ cross-secti~      2015 Asia
## 3 40G      Dutta et al, 2012    "Preva~ cross-secti~      2010 Asia
## 4 40G      Dutta et al, 2012    "Preva~ cross-secti~      2010 Asia
## 5 8HG      Hermansson et al., 2018 "HPV p~ retrospecti~      2015 Europe
## 6 8HG      Hermansson et al., 2018 "HPV p~ retrospecti~      2015 Europe
## # i 16 more variables: world_subregion <chr>, country <chr>, city_state <chr>,
## #   focus <chr>, overall_cytology <chr>, pap_method <chr>,
## #   recruitment_setting <chr>, hpv_types_reported <chr>, hpv_test <chr>,
## #   num_older_wom <dbl>, num_hpv_pos <dbl>, num_hr_hpv_pos <dbl>,
## #   hpv_type <chr>, num_type <dbl>, type_prev <dbl>, notes <chr>
```

```
str(gtype_filtered)
```

```
## tibble [229 x 22] (S3: tbl_df/tbl/data.frame)
##  $ study_id      : chr [1:229] "4HG" "20G" "40G" "40G" ...
##  $ author_year   : chr [1:229] "Yoshida et al., 2007" "Çolakoğlu et al., 2017" "Dutta et al, 20
##  $ title         : chr [1:229] "Quantitative real-time polymerase chain reaction analysis of the
##  $ study_design  : chr [1:229] "cross-sectional" "cross-sectional" "cross-sectional" "cross-sect
##  $ ending_year   : num [1:229] 2004 2015 2010 2010 2015 ...
##  $ world_region  : chr [1:229] "Asia" "Asia" "Asia" "Asia" ...
##  $ world_subregion : chr [1:229] "Eastern Asia" "Western Asia" "Southern Asia" "Southern Asia" ..
##  $ country       : chr [1:229] "Japan" "Turkey" "India" "India" ...
##  $ city_state    : chr [1:229] "Gunma" "Adana" "West Bengal" "West Bengal" ...
##  $ focus         : chr [1:229] "Both" "Both" "Both" "Both" ...
##  $ overall_cytology : chr [1:229] "Predominantly normal" "Predominantly normal" "Predominantly normal"
##  $ pap_method     : chr [1:229] "LBC" "LBC" "Conventional" "Conventional" ...
##  $ recruitment_setting: chr [1:229] "clinical setting" "screening" "screening" "screening" ...
##  $ hpv_types_reported : chr [1:229] "HR-HPV, 16" "16, 18 overall" "16, 18, overall" "16, 18, overall"
##  $ hpv_test       : chr [1:229] "PCR E6/E7" "LA" "MY09/11" "MY09/11" ...
```

```
## $ num_older_wom      : num [1:229] 148 52 114 114 1051 ...
## $ num_hpv_pos        : num [1:229] NA 23 11 11 NA NA NA NA NA ...
## $ num_hr_hpv_pos     : num [1:229] 30 NA NA NA 43 43 43 43 43 ...
## $ hpv_type           : chr [1:229] "16" "16,18" "16" "18" ...
## $ num_type           : num [1:229] 3.6 7 1 1 12 5 6 9 3 4 ...
## $ type_prev          : num [1:229] 0.02432 0.13462 0.00877 0.00877 0.01142 ...
## $ notes              : chr [1:229] "numbers are not reported in table format but as figures therefor
```

```
summary(gtype_filtered)
```

```
##      study_id      author_year      title      study_design
## Length:229      Length:229      Length:229      Length:229
## Class :character Class :character Class :character Class :character
## Mode  :character Mode  :character Mode  :character Mode  :character
##
##
##
##      ending_year  world_region  world_subregion  country
## Min.   :1993      Length:229      Length:229      Length:229
## 1st Qu.:2005      Class :character Class :character Class :character
## Median :2011      Mode  :character Mode  :character Mode  :character
## Mean   :2010
## 3rd Qu.:2017
## Max.   :2019
## NA's   :4
##      city_state      focus      overall_cytology  pap_method
## Length:229      Length:229      Length:229      Length:229
## Class :character Class :character Class :character Class :character
## Mode  :character Mode  :character Mode  :character Mode  :character
##
##
##
##      recruitment_setting hpv_types_reported  hpv_test      num_older_wom
## Length:229      Length:229      Length:229      Min.   :    7
## Class :character Class :character Class :character 1st Qu.: 276
## Mode  :character Mode  :character Mode  :character Median : 1458
##                                     Mean   : 3406
##                                     3rd Qu.: 3859
##                                     Max.   :18910
##
##      num_hpv_pos  num_hr_hpv_pos  hpv_type      num_type
## Min.   :    2.0  Min.   :    4.0  Length:229      Min.   :    0.0
## 1st Qu.:   40.0  1st Qu.:   33.0  Class :character 1st Qu.:    4.0
## Median :  133.5  Median :  104.0  Mode  :character Median :   16.0
## Mean   :  850.6  Mean   :  363.2      Mean   :  107.6
## 3rd Qu.:  713.0  3rd Qu.:  405.0      3rd Qu.:   41.0
## Max.   :6199.0  Max.   :2836.0      Max.   :5054.5
## NA's   :    97  NA's   :   24
##      type_prev      notes
## Min.   :0.000000      Length:229
## 1st Qu.:0.004905      Class :character
## Median :0.012000      Mode  :character
## Mean   :0.032086
```

```
## 3rd Qu.:0.034980
## Max. :0.413793
##
```

```
view(gtype_filtered)
```

```
summary(gtype_filtered)
```

```
##      study_id      author_year      title      study_design
## Length:229      Length:229      Length:229      Length:229
## Class :character Class :character Class :character Class :character
## Mode :character Mode :character Mode :character Mode :character
##
##
##
##      ending_year  world_region  world_subregion  country
## Min. :1993      Length:229      Length:229      Length:229
## 1st Qu.:2005     Class :character Class :character Class :character
## Median :2011     Mode :character Mode :character Mode :character
## Mean :2010
## 3rd Qu.:2017
## Max. :2019
## NA's :4
##      city_state      focus      overall_cytology  pap_method
## Length:229      Length:229      Length:229      Length:229
## Class :character Class :character Class :character Class :character
## Mode :character Mode :character Mode :character Mode :character
##
##
##
##      recruitment_setting hpv_types_reported  hpv_test      num_older_wom
## Length:229      Length:229      Length:229      Min. : 7
## Class :character Class :character Class :character 1st Qu.: 276
## Mode :character Mode :character Mode :character Median : 1458
##                                     Mean : 3406
##                                     3rd Qu.: 3859
##                                     Max. :18910
##
##      num_hpv_pos  num_hr_hpv_pos  hpv_type      num_type
## Min. : 2.0      Min. : 4.0      Length:229      Min. : 0.0
## 1st Qu.: 40.0    1st Qu.: 33.0      Class :character 1st Qu.: 4.0
## Median : 133.5    Median : 104.0      Mode :character Median : 16.0
## Mean : 850.6      Mean : 363.2                      Mean : 107.6
## 3rd Qu.: 713.0    3rd Qu.: 405.0                      3rd Qu.: 41.0
## Max. :6199.0      Max. :2836.0                      Max. :5054.5
## NA's :97          NA's :24
##      type_prev      notes
## Min. :0.000000      Length:229
## 1st Qu.:0.004905     Class :character
## Median :0.012000     Mode :character
## Mean :0.032086
## 3rd Qu.:0.034980
## Max. :0.413793
```

```
##
```

```
nrow(gtype_filtered)
```

```
## [1] 229
```

Extract and view unique study ids in gtype_filtered to make sure it is correct

```
unique_study_ids_gtype <- gtype_filtered %>%  
  select(study_id) %>%  
  distinct()
```

```
nrow(unique_study_ids_gtype)
```

```
## [1] 43
```

```
print(unique_study_ids_gtype, n = 43)
```

```
## # A tibble: 43 x 1
```

```
##   study_id
```

```
##   <chr>
```

```
## 1 4HG
```

```
## 2 20G
```

```
## 3 40G
```

```
## 4 8HG
```

```
## 5 60HG
```

```
## 6 100HG
```

```
## 7 71HG
```

```
## 8 17HG
```

```
## 9 160HG
```

```
## 10 24HG
```

```
## 11 25HG
```

```
## 12 180HG
```

```
## 13 29HG
```

```
## 14 30HG
```

```
## 15 300G
```

```
## 16 310G
```

```
## 17 340HG
```

```
## 18 390G
```

```
## 19 400HG
```

```
## 20 410HG
```

```
## 21 450HG
```

```
## 22 470HG
```

```
## 23 43HG
```

```
## 24 490HG
```

```
## 25 510HG
```

```
## 26 48HG
```

```
## 27 520HG
```

```
## 28 570HG
```

```
## 29 50HG
```

```
## 30 580HG
```

```
## 31 52HG
```

```
## 32 590HG
```

```
## 33 600HG
```

```
## 34 53HG
```

```
## 35 54HG
## 36 670HG
## 37 680HG
## 38 780G
## 39 65HG
## 40 830HG
## 41 850HG
## 42 21HG
## 43 23HG
```

```
#Data frames for quantitative analysis ----
# any hpv type analysis ---> any_type_filtered
#hr type analysis ---> hr_type_filtered
#type-specific analysis ---> gtype_filtered
```

Meta-analysis model for any_type_filtered —

```
summary(any_type_filtered) # there are zero event values in the num_hpv_pos
```

```
##      study_id      author_year      title      study_design
## Length:83      Length:83      Length:83      Length:83
## Class :character Class :character Class :character Class :character
## Mode  :character Mode  :character Mode  :character Mode  :character
##
##
##
##      ending_year  world_region  world_subregion  country
## Min.   :1989      Length:83      Length:83      Length:83
## 1st Qu.:2006      Class :character Class :character Class :character
## Median :2010      Mode  :character Mode  :character Mode  :character
## Mean   :2009
## 3rd Qu.:2014
## Max.   :2019
## NA's   :4
##      city_state      focus      overall_cytology  pap_method
## Length:83      Length:83      Length:83      Length:83
## Class :character Class :character Class :character Class :character
## Mode  :character Mode  :character Mode  :character Mode  :character
##
##
##
##      recruitment_setting hpv_types_reported hpv_types_tested  hpv_cat
## Length:83      Length:83      Length:83      Length:83
## Class :character Class :character Class :character Class :character
## Mode  :character Mode  :character Mode  :character Mode  :character
##
##
##
##      hpv_test      test_details      num_older_wom      num_hpv_pos
## Length:83      Length:83      Min.   :    6.0      Min.   :    0.0
## Class :character Class :character      1st Qu.:   82.0      1st Qu.:   13.0
```

```
## Mode :character Mode :character Median : 293.0 Median : 29.0
## Mean : 1133.6 Mean : 188.6
## 3rd Qu.: 697.5 3rd Qu.: 126.5
## Max. :18910.0 Max. :6199.0
##
## num_hpv_neg any_prev risk_of_bias Notes
## Min. : 5 Min. :0.0000 Length:83 Length:83
## 1st Qu.: 63 1st Qu.:0.0790 Class :character Class :character
## Median : 225 Median :0.1490 Mode :character Mode :character
## Mean : 945 Mean :0.1812
## 3rd Qu.: 569 3rd Qu.:0.2470
## Max. :13973 Max. :0.6670
##
```

Identifying zero-event cases

```
zero_event_cases <- any_type_filtered[any_type_filtered$num_hpv_pos == 0, ]
```

Counting the number of zero-event cases

```
num_zero_event_cases <- nrow(zero_event_cases)
```

Printing the number of zero-event cases

```
print(paste("Number of zero-event cases:", num_zero_event_cases))
```

```
## [1] "Number of zero-event cases: 3"
```

Printing the study IDs of zero-event cases

```
if(num_zero_event_cases > 0) {
  print("Study IDs with zero-event cases:")
  print(zero_event_cases$author_year)
  print(zero_event_cases$study_id)
} else {
  print("There are no zero-event cases.")
}
```

```
## [1] "Study IDs with zero-event cases:"
## [1] "Becker et al., 1991" "Eren et al., 2010" "Rahmat et al., 2021"
## [1] "230" "440" "710"
```

Random effects MA, Freeman-Tukey double arcsine transformation, restricted maximum likelihood estimator, Knapp-Hartung adjustment

```
any_type_ma <- metaprop(event = num_hpv_pos,
  n = num_older_wom,
  studlab = author_year,
  data = any_type_filtered,
  sm = "PFT",
  method.tau = "REML",
  method.ci = "NAsm",### Specify the method for confidence intervals
  add = 0,
```

```

fixed = FALSE,
random = TRUE,
hahn = TRUE,
title = "Anytype HPV Prevalence in Women (50+) with Predominantly Normal Cytology"

summary(any_type_ma)

```

```

## Review:      Anytype HPV Prevalence in Women (50+) with Predominantly Normal ...
##

```

	proportion	95%-CI	%W(random)
## Tsedenbal et al., 2018	0.3600	[0.1812; 0.5598]	1.0
## Çolakoğlu et al., 2017	0.4423	[0.3091; 0.5797]	1.1
## Demirci et al., 2019	0.2234	[0.1766; 0.2740]	1.3
## Dutta et al., 2012	0.0965	[0.0482; 0.1583]	1.2
## Herrero et al., 2000	0.1655	[0.1313; 0.2027]	1.3
## Jin et al., 2019	0.4025	[0.3802; 0.4249]	1.3
## Li, P. et al., 2021	0.1880	[0.1754; 0.2009]	1.3
## Li, XF. et al., 2021	0.1235	[0.1125; 0.1350]	1.3
## Nuñez-Troconis et al., 2009	0.2400	[0.0895; 0.4295]	1.0
## Richter et al., 2013	0.4215	[0.3683; 0.4757]	1.3
## Souho et al., 2016	0.5167	[0.4533; 0.5798]	1.3
## Tezcan et al., 2014	0.2453	[0.1376; 0.3711]	1.1
## Donkoh et al., 2022	0.3662	[0.2574; 0.4821]	1.2
## Maehama et al., 2002	0.1050	[0.0933; 0.1173]	1.3
## Brotherton et al., 2015	0.1704	[0.1112; 0.2389]	1.2
## Ahmadi et al., 2020	0.1500	[0.0534; 0.2798]	1.1
## Andujar et al., 2020	0.0806	[0.0677; 0.0944]	1.3
## Ardhaoui et al., 2016	0.1702	[0.0743; 0.2927]	1.1
## Balanda et al., 2016	0.0774	[0.0515; 0.1079]	1.3
## Baloch et al., 2017	0.1667	[0.1017; 0.2434]	1.2
## Bansal et al., 2014	0.0718	[0.0473; 0.1009]	1.3
## Becker et al., 1991	0.0000	[0.0000; 0.0515]	1.0
## Bell et al., 2007	0.1667	[0.0396; 0.3464]	0.9
## Bi et al., 2015	0.2866	[0.2620; 0.3119]	1.3
## Castellsague et al., 2012	0.0705	[0.0486; 0.0960]	1.3
## Castellsague et al., 2001	0.2195	[0.1042; 0.3607]	1.1
## Castle et al., 2006	0.1222	[0.0968; 0.1501]	1.3
## Cathro et al., 2009	0.0682	[0.0089; 0.1656]	1.1
## Centurioni et al., 2005	0.1553	[0.1139; 0.2017]	1.3
## Chan et al., 2002	0.0298	[0.0112; 0.0560]	1.3
## Chansaeroj et al., 2010	0.0678	[0.0470; 0.0919]	1.3
## Chen et al., 2015	0.1473	[0.1227; 0.1736]	1.3
## Chong et al., 2010	0.3913	[0.1996; 0.6006]	0.9
## Coser et al., 2013	0.2449	[0.1643; 0.3354]	1.2
## Dai et al., 2006	0.1429	[0.0776; 0.2231]	1.2
## DeVuyst et al., 2003	0.2500	[0.0393; 0.5392]	0.7
## Debrah et al., 2021	0.2857	[0.0098; 0.6822]	0.6
## Demers et al., 2012	0.0939	[0.0580; 0.1371]	1.3
## Dufit et al., 2016	0.4396	[0.3387; 0.5429]	1.2
## Eren et al., 2010	0.0000	[0.0000; 0.2680]	0.5
## Foliaki et al., 2014	0.1857	[0.1022; 0.2863]	1.2
## Gravitt et al., 2013	0.1533	[0.1146; 0.1965]	1.3
## Hamlin-Douglas et al., 2008	0.1983	[0.1317; 0.2745]	1.2
## Hernandez-Rosas et al., 2021	0.0607	[0.0367; 0.0901]	1.3

```

## Herrero et al., 2005      0.2845 [0.2626; 0.3068]      1.3
## Hong et al., 2015       0.1415 [0.0976; 0.1919]      1.3
## Hooi et al., 2018       0.1705 [0.1302; 0.2149]      1.3
## Jiang et al., 2011      0.1479 [0.1256; 0.1717]      1.3
## Shen et al., 2021       0.1373 [0.0868; 0.1967]      1.2
## Xiao et al., 2016       0.3458 [0.3244; 0.3675]      1.3
## Klug et al., 2007       0.0254 [0.0184; 0.0333]      1.3
## Kobetz et al., 2012     0.1852 [0.0913; 0.3012]      1.1
## Lee et al., 2012        0.3278 [0.3211; 0.3345]      1.3
## Leinonen et al., 2013   0.0486 [0.0452; 0.0522]      1.3
## Levert et al., 2000     0.1485 [0.1223; 0.1769]      1.3
## Li et al., 2019         0.2857 [0.2537; 0.3188]      1.3
## Li et al., 2011         0.0625 [0.0331; 0.0999]      1.3
## Liu et al., 2014        0.2724 [0.2382; 0.3081]      1.3
## López Rivera et al., 2012 0.0927 [0.0595; 0.1323]      1.3
## Moore et al., 2009      0.1160 [0.0980; 0.1353]      1.3
## Mudderis et al., 2019   0.1781 [0.0978; 0.2751]      1.2
## Anh et al., 2003        0.0422 [0.0273; 0.0600]      1.3
## Pista et al., 2011      0.0566 [0.0364; 0.0808]      1.3
## Rahmat et al., 2021     0.0000 [0.0000; 0.1507]      0.7
## Schmitt et al., 2013    0.3367 [0.2721; 0.4046]      1.3
## Shakya et al., 2017     0.1293 [0.0890; 0.1758]      1.3
## Sukvirach et al., 2003  0.0447 [0.0300; 0.0620]      1.3
## Sun et al., 2014        0.4094 [0.3652; 0.4543]      1.3
## Tang et al., 2017       0.3341 [0.3166; 0.3518]      1.3
## Thomas et al., 2004     0.2491 [0.2012; 0.3004]      1.3
## Vu et al., 2013         0.0857 [0.0687; 0.1043]      1.3
## Wang et al., 2018       0.1885 [0.1758; 0.2014]      1.3
## Wei et al., 2014        0.0230 [0.0206; 0.0255]      1.3
## Wu et al., 2013         0.1156 [0.0915; 0.1422]      1.3
## Xue et al., 2015        0.1152 [0.0972; 0.1346]      1.3
## Yip et al., 2010        0.1275 [0.0965; 0.1621]      1.3
## Zhao et al., 2009       0.0489 [0.0326; 0.0682]      1.3
## Zhu et al., 2021        0.2349 [0.2051; 0.2660]      1.3
## Zoa Assoumou et al., 2016 0.6667 [0.5159; 0.8024]      1.1
## Giorgi Rossi et al., 2010 0.0465 [0.0299; 0.0665]      1.3
## Giuliano et al., 2005   0.0604 [0.0270; 0.1051]      1.2
## Giuliano et al., 2001   0.0441 [0.0056; 0.1088]      1.2
## Jin et al., 2010        0.0905 [0.0574; 0.1301]      1.3
##
## Number of studies: k = 83
## Number of observations: o = 94086
## Number of events: e = 15654
##
##              proportion      95%-CI
## Random effects model    0.1603 [0.1338; 0.1887]
##
## Quantifying heterogeneity:
## tau^2 = 0.0255 [0.0187; 0.0369]; tau = 0.1596 [0.1369; 0.1922]
## I^2 = 99.4% [99.3%; 99.4%]; H = 12.41 [11.99; 12.83]
##
## Test of heterogeneity:
##      Q d.f. p-value
## 12620.36  82      0

```



```
##
## Details on meta-analytical method:
## - Inverse variance method
## - Restricted maximum-likelihood estimator for tau^2
## - Q-Profile method for confidence interval of tau^2 and tau
## - Hartung-Knapp adjustment for random effects model (df = 82)
## - Freeman-Tukey double arcsine transformation
## - Normal approximation confidence interval for individual studies
```

ANYTYPE FOREST PLOT —

Create a forest plot based on the meta-analysis results

```
pdf("forestplot.pdf", width=10, height=20) # Width and height in inches, adjust as needed
```

```
forest(any_type_ma,
  common = TRUE,
  print.tau2 = TRUE,
  print.Q = TRUE,
  print.pval.Q = TRUE,
  print.I2 = TRUE,
  rightcols = FALSE,
  pooled.totals = TRUE,
  weight.study = "random",
  leftcols = c("studlab", "num_hpv_pos", "num_older_wom", "effect", "ci"),
  leftlabs = c("Study", "HPV+ Cases", "Total", "Prevalence", "95% C.I."),
  xlab = "Pooled Prevalence Rate",
  smlab = "",
  xlim = c(0,1),
  pscale = 1,
  squaresize = 0.5,
  fs.hetstat = 10,
  digits = 2,
  col.square = "navy",
  col.square.lines = "navy",
  col.diamond = "maroon",
  col.diamond.lines = "maroon")
```

```
## Warning in grid.Call(C_textBounds, as.graphicsAnnot(x$label), x$x, x$y, :
## conversion failure on 'Çolakoğlu et al., 2017' in 'mbcsToSbcs': dot substituted
## for <c4>
```

```
## Warning in grid.Call(C_textBounds, as.graphicsAnnot(x$label), x$x, x$y, :
## conversion failure on 'Çolakoğlu et al., 2017' in 'mbcsToSbcs': dot substituted
## for <9f>
```

```
## Warning in grid.Call.graphics(C_text, as.graphicsAnnot(x$label), x$x, x$y, :
## conversion failure on 'Çolakoğlu et al., 2017' in 'mbcsToSbcs': dot substituted
## for <c4>
```

```
## Warning in grid.Call.graphics(C_text, as.graphicsAnnot(x$label), x$x, x$y, :
## conversion failure on 'Çolakoğlu et al., 2017' in 'mbcsToSbcs': dot substituted
## for <9f>
```

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

```

## conversion failure on 'Çolakoğlu et al., 2017' in 'mbcsToSbcs': dot substituted
## for <c4>

## Warning in grid.Call.graphics(C_text, as.graphicsAnnot(x$label), x$x, x$y, :
## conversion failure on 'Çolakoğlu et al., 2017' in 'mbcsToSbcs': dot substituted
## for <9f>

dev.off()

## pdf
## 2

pdf("forestplot2.pdf", width=10, height=20) # Width and height in inches, adjust as needed

forest(any_type_ma,
  common = TRUE,
  print.tau2 = TRUE,
  print.Q = TRUE,
  print.pval.Q = TRUE,
  print.I2 = TRUE,
  rightcols = FALSE,
  pooled.totals = TRUE,
  weight.study = "random",
  xlab = "Pooled Prevalence Rate",
  leftcols = c("studlab", "num_hpv_pos", "n", "effect", "ci"),
  leftlabs = c("Study", "HPV+ Cases", "Total", "Prevalence", "95% C.I."),
  smlab = "",
  xlim = c(0,1),
  pscale = 1,
  squaresize = 0.5,
  fs.hetstat = 10,
  digits = 2,
  col.square = "navy",
  col.square.lines = "navy",
  col.diamond = "maroon",
  col.diamond.lines = "maroon"
)

## Warning in grid.Call(C_textBounds, as.graphicsAnnot(x$label), x$x, x$y, :
## conversion failure on 'Çolakoğlu et al., 2017' in 'mbcsToSbcs': dot substituted
## for <c4>

## Warning in grid.Call(C_textBounds, as.graphicsAnnot(x$label), x$x, x$y, :
## conversion failure on 'Çolakoğlu et al., 2017' in 'mbcsToSbcs': dot substituted
## for <9f>

## Warning in grid.Call.graphics(C_text, as.graphicsAnnot(x$label), x$x, x$y, :
## conversion failure on 'Çolakoğlu et al., 2017' in 'mbcsToSbcs': dot substituted
## for <c4>

## Warning in grid.Call.graphics(C_text, as.graphicsAnnot(x$label), x$x, x$y, :
## conversion failure on 'Çolakoğlu et al., 2017' in 'mbcsToSbcs': dot substituted
## for <9f>

## Warning in grid.Call.graphics(C_text, as.graphicsAnnot(x$label), x$x, x$y, :
## conversion failure on 'Çolakoğlu et al., 2017' in 'mbcsToSbcs': dot substituted
## for <c4>

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

```

```
## conversion failure on 'Çolakoğlu et al., 2017' in 'mbcsToSbcs': dot substituted  
## for <9f>
```

```
dev.off()
```

```
## pdf  
## 2
```

Show Forest Plot

```
system2('open', args = 'forestplot2.pdf', wait = FALSE)
```

Funnel Plot

```
funnel(any_type_ma, main="Funnel Plot for Meta-Analysis", xlim=c(0, 1))
```

