## Glacier Lake Outburst Floods: meta-analysis to pool mortality incidence rates

Periklis Charalampous, Institute of Health and Society, UCLouvain, Belgium

## Main meta-analysis

```
dta_1 <- metarate(Death, PTAR, data = dta_sorted, studlab = Country, method = "GLMM")
dta_1
# Forest plot for main meta-analysis
png("forest_plot_main_final.png", width = 700, height = 800)
forest(dta_1, fixed = FALSE, random = TRUE)
periodmeta<- metarate(Death,</pre>
                      PTAR,
                      data = dta_sorted,
                      studlab = Country,
                      method = "GLMM",
                      tau.common = FALSE,
                      hakn= TRUE,
                      method.tau="ML")
periodmeta
forest(periodmeta,
       sortvar = Country,
       col.square = "gray",
       col.square.lines = "gray",
       col.diamond.random = "black",
       col.diamond.lines.random = "black",
       allstudies = TRUE,
       comb.fixed= FALSE,
       comb.random = TRUE,
       col.label.left="red";
       col.label.right="blue",
       hetstat=FALSE,
       test.overall.random = TRUE,
       digits.mean=2,
       digits.sd=2,
       digits.weight = 0,
       weight.study = "random",
       test.effect.subgroup.random = TRUE,
       leftcols=c("studlab", "Year", "Death", "PTAR"),
       leftlabs = c("Country", "Year", "Death", "PTAR"),
       overall = TRUE,
       print.byvar = FALSE,
       col.by="navy",
```

```
addrow.subgroups=TRUE,
    addrow.overall=TRUE,
    addrow=TRUE,
    label.test.effect.subgroup.random="Subgroup effect",
    test.subgroup.random = TRUE)
dev.off()

# Plot results: main meta-analysis
```

## Sub-analysis\_1

```
# Sort data
dta$Region<-dta$Region
region1meta<- metarate(Death,</pre>
                      PTAR,
                      data = dta,
                      studlab = Country,
                      method = "GLMM",
                      byvar = Region,
                      tau.common = FALSE,
                      hakn= TRUE,
                      method.tau="ML")
dta_sorted <- dta %>%
  arrange(Region, Country, Year)
png("forest_plot_sub_analysis.png", width = 700, height = 950)
forest(region1meta,
       sortvar = Country,
       col.square = "gray",
       col.square.lines = "gray",
       col.diamond.random = "black",
       col.diamond.lines.random = "black",
       allstudies = TRUE,
       comb.fixed= FALSE,
       comb.random = TRUE,
       col.label.left="red";
       col.label.right="blue",
      hetstat=FALSE,
       test.overall.random = TRUE,
       digits.mean=2,
       digits.sd=2,
       digits.weight = 0,
       weight.study = "random",
       test.effect.subgroup.random = TRUE,
       leftcols=c("studlab", "Year", "Death", "PTAR"),
       leftlabs = c("Country", "Year", "Death", "PTAR"),
       overall = TRUE,
       print.byvar = FALSE,
       col.by="navy",
       addrow.subgroups=TRUE,
       addrow.overall=TRUE,
```

```
addrow=TRUE,
    label.test.effect.subgroup.random="Subgroup effect",
    test.subgroup.random = TRUE)
dev.off()

# Plot results: sub-analysis_1
```

## Sub-analysis\_2

```
# Sort data
dta$Period <- cut(dta$Year,
                  breaks = c(-Inf, 1900, 2000, Inf),
                  labels = c("Before 1900", "Between 1900 and 1999", "After 2000"))
dta_sorted <- dta %>%
  arrange(Country, Year)
periodmeta_2<- metarate(Death,</pre>
                       PTAR,
                       data = dta,
                       studlab = Country,
                       method = "GLMM",
                       byvar = Period,
                       tau.common = FALSE,
                       hakn= TRUE,
                       method.tau="ML")
# metarate
png("forest_plot_main_sub-analysis_2.png", width = 700, height = 950)
forest(periodmeta_2,
       sortvar = Country,
       col.square = "gray",
       col.square.lines = "gray",
       col.diamond.random = "black",
       col.diamond.lines.random = "black",
       allstudies = TRUE,
       comb.fixed = FALSE,
       comb.random = TRUE,
       col.label.left = "red",
       col.label.right = "blue",
       hetstat = TRUE,
       test.overall.random = TRUE,
       digits.mean = 2,
       digits.sd = 2,
       digits.weight = 0,
       weight.study = "random",
       test.effect.subgroup.random = TRUE,
       leftcols = c("studlab", "Year", "Death", "PTAR"),
       leftlabs = c("Country", "Year", "Death", "PTAR"),
       overall = TRUE,
       print.byvar = FALSE,
       col.by = "navy",
       addrow.subgroups = TRUE,
```

```
addrow.overall = TRUE,
    addrow = TRUE,
    label.test.effect.subgroup.random = "Subgroup effect",
    test.subgroup.random = TRUE)

dev.off()

## pdf
## 2

# Plot results: sub-analysis_2
```