

Irrigation's real impact on global water and food security

R code

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Contents

1	Retrieve all corpus	6
1.1	Abstract corpus	6
1.2	Policy corpus	6
1.3	Full text corpus	7
2	Split full text corpus for analysis	8
3	Network analysis	9
3.1	Network metrics	15
3.2	Network plots	18
3.3	Uncertainties turned into facts	30
4	Proportion of paths ending up in no claim, no citation or modelling nodes	35
4.1	Network through time	37
5	Analysis of paths	56
5.1	“no claim” or “no citation” paths	56
5.2	Calculation of amplification	139
6	Study of Aquastat values	142
7	Session information	152

```

# PRELIMINARY FUNCTIONS #####
sensobol::load_packages(c("openxlsx", "data.table", "tidyverse", "bibliometrix",
                         "igraph", "ggraph", "cowplot", "tidygraph", "benchmarkme",
                         "parallel", "wesanderson", "scales", "countrycode"))

# Create custom theme
theme_AP <- function() {
  theme_bw() +
    theme(panel.grid.major = element_blank(),
          panel.grid.minor = element_blank(),
          legend.background = element_rect(fill = "transparent",
                                             color = NA),
          legend.key = element_rect(fill = "transparent",
                                     color = NA),
          strip.background = element_rect(fill = "white"),
          legend.margin = margin(0.5, 0.1, 0.1, 0.1),
          legend.box.margin = margin(0.2,-4,-7,-7),
          plot.margin = margin(3, 4, 0, 4),
          legend.text = element_text(size = 8),
          axis.title = element_text(size = 10),
          legend.key.width = unit(0.4, "cm"),
          legend.key.height = unit(0.4, "cm"),
          legend.title = element_text(size = 9))
}

```

```

# CREATION OF VECTORS WITH NAMES #####
database <- c("wos", "scopus", "dimensions")
topic <- c("water", "food")

# Create all possible combinations
combinations <- expand.grid(database = database, topic = topic)

# Combine the vectors with an underscore
file.name <- paste(combinations$database, "dt", combinations$topic, sep = "_")

# READ IN THE DATA #####
# Loop to create the file names -----
for (i in 1:length(file.name)) {

  database.type <- str_extract(file.name, "^(wos|scopus|dimensions)")

  if(isTRUE(database.type[i] == "wos")) {

    file.name[i] <- paste(file.name[i], "bib", sep = ".")
  } else {

    file.name[i] <- paste(file.name[i], "csv", sep = ".")
  }
}

# vector with new column names -----
new_colnames <- c("doi", "authors", "year", "title", "journal", "abstract", "database")
to_lower <- c("authors", "title", "journal", "abstract")

# Loop to read in the datasets -----
out <- list()

for (i in 1:length(file.name)) {

  database.type <- str_extract(file.name[i], "^(wos|scopus|dimensions)")

  if(isTRUE(database.type == "wos")) {

    out[[i]] <- convert2df(file = file.name[i],
      dbsource = "wos",

```

```

        format = "bibtex") %>%
  data.table() %>%
  .[, .(DI, AU, PY, TI, SO, AB)] %>%
  .[, database:= "wos"]

} else if (isTRUE(database.type == "dimensions")) {

  out[[i]] <- fread(file.name[i], skip = 1) %>%
  .[, .(DOI, Authors, PubYear, Title, `Source title`, Abstract)] %>%
  .[, database:= "dimensions"]

} else if(isTRUE(database.type == "scopus")) {

  out[[i]] <- fread(file.name[i]) %>%
  .[, .(DOI, Authors, Year, Title, `Source title`, Abstract)] %>%
  .[, database:= "scopus"]
}

setnames(out[[i]], colnames(out[[i]]), new_colnames) %>%
  .[, (to_lower):= lapply(.SD, tolower), .SDcols = (to_lower)] %>%
  .[, abstract:= sub("references.*", "", abstract)]

}

##  

## Converting your wos collection into a bibliographic dataframe  

##  

##  

## Warning:  

## In your file, some mandatory metadata are missing. Bibliometrix functions may not work prop  

##  

## Please, take a look at the vignettes:  

## - 'Data Importing and Converting' (https://www.bibliometrix.org/vignettes/Data-Importing-and-Converting)  

## - 'A brief introduction to bibliometrix' (https://www.bibliometrix.org/vignettes/Introduction-to-Bibliometrix)  

##  

##  

## Missing fields: C1 CR  

## Done!  

##  

##  

## Converting your wos collection into a bibliographic dataframe  

##  

##  

## Warning:  

## In your file, some mandatory metadata are missing. Bibliometrix functions may not work prop  

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```

```

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## - 'A brief introduction to bibliometrix' (https://www.bibliometrix.org/vignettes/Introduction-to-bibliometrix)
##
##
## Missing fields: C1 CR
## Done!

names(out) <- combinations$topic

# CLEAN THE DATASETS #####
# Arrange ----

dt <- rbindlist(out, idcol = "topic")

tmp <- split(dt, list(dt$topic, dt$database))

cols_to_merge_by <- c("doi", "year", "title", "journal", "abstract")

dt.water <- merge(merge(tmp$water.dimensions, tmp$water.scopus, by = cols_to_merge_by,
                        all = TRUE), tmp$water.wos, by = cols_to_merge_by,
                        all = TRUE)

dt.food <- merge(merge(tmp$food.dimensions, tmp$food.scopus, by = cols_to_merge_by,
                        all = TRUE), tmp$food.wos, by = cols_to_merge_by,
                        all = TRUE)

# Filter out duplicated studies by doi ----

tmp.list <- list(dt.water, dt.food)
duplicated.dois <- final.dt <- list()

for (i in 1:length(tmp.list)) {

  duplicated.dois[[i]] <- duplicated(tmp.list[[i]]$doi, incomparables = NA, na.rm = TRUE)
  final.dt[[i]] <- tmp.list[[i]][!duplicated.dois[[i]]][, location.belief.system := "abstract"]

}

names(final.dt) <- topic

# Check if there is any duplicated doi ----

any(duplicated(final.dt$food$doi, na.rm = TRUE, incomparables = NA))

## [1] FALSE

# Export to xlsx ----

```

```

for (i in names(final.dt)) {

  write.xlsx(final.dt[[i]][, .(doi, year, title, abstract, location.belief.system)],
            paste("final.dt", names(final.dt[i]), "xlsx", sep = "."))
}

```

1 Retrieve all corpus

1.1 Abstract corpus

```

final.dt.water.screened <- data.table(read.xlsx("final.dt.water_screened.xlsx"))
final.dt.food.screened <- data.table(read.xlsx("final.dt.food_screened.xlsx"))
screened.dt <- list(final.dt.water.screened, final.dt.food.screened)
names(screened.dt) <- c("water", "food")

lapply(screened.dt, function(x) x[, .N, screening])

## $water
##   screening      N
##       <char> <int>
## 1:      F    168
## 2:      T    163
##
## $food
##   screening      N
##       <char> <int>
## 1:      F    465
## 2:      T     39

# Export for close-reading only the references that do include
# the belief system in the abstract -----

```

```

for (i in names(screened.dt)) {

  screened.dt[[i]][screening == "T"] %>%
    unique(., by = "title") %>%
    .[, .(doi, title, year)] %>%
    write.xlsx(., paste("abstract.corpus", i, "xlsx", sep = "."))
}

}

```

1.2 Policy corpus

```

# LOAD IN DIMENSIONS DATASETS (POLICY TEXT) #####
# Function to load and preprocess data -----

```

```

load_and_preprocess_data <- function(file_path, topic) {
  fread(file_path, skip = 1)[, topic := topic]
}

colnames.full.text <- c("doi", "year", "title", "journal", "topic")
keywords <- c("water", "irrigat")

# Load data ----

dt.policy.water <- load_and_preprocess_data("dimensions_dt_policy.csv", "water")
dt.policy.food <- load_and_preprocess_data("dimensions_dt_policy_food.csv", "food")

dimensions.full.text.policy <- rbind(dt.policy.food, dt.policy.water) %>%
  .[, .(`Policy document ID`, PubYear, Title, `Publishing Organization`,
         `Sustainable Development Goals`, `Source Linkout`, topic)]

dimensions.full.text.policy[, .N, topic]

##      topic      N
##      <char> <int>
## 1:   food 10573
## 2:   water 3455

# Create a logical condition for pattern matching using grep
pattern_condition_policy <- sapply(keywords, function(keyword)
  grep1(keyword, dimensions.full.text.policy$Title, ignore.case = TRUE))

# Combine conditions with OR using rowSums
matching.rows.policy <- dimensions.full.text.policy[rowSums(pattern_condition_policy) > 0]

matching.rows.policy[, .N, topic]

##      topic      N
##      <char> <int>
## 1:   food    750
## 2:   water   450

# Export ----

for (i in c("water", "food")) {

  matching.rows.policy[topic == i] %>%
    write.xlsx(paste("policy.corpus", i, "xlsx", sep = "."))
}

```

1.3 Full text corpus

```
# LOAD IN DIMENSIONS DATASET (FULL TEXT) #####
full.text.corpus.water <- fread("full.text.corpus.water.csv")
```

2 Split full text corpus for analysis

```
# SPLIT THE DATASET INTO N FOR RESEARCH #####
# Function to split dataset in n chunks -----
split_dt_fun <- function(dt, num_parts) {

  split_dt <- list()

  # Calculate the number of rows in each part
  rows_per_part <- nrow(dt) %/% num_parts

  # Split the data.table into roughly equal parts
  for (i in 1:num_parts) {

    start_row <- (i - 1) * rows_per_part + 1
    end_row <- i * rows_per_part

    if (i == num_parts) {

      end_row <- nrow(dt)
    }
    split_dt[[i]] <- dt[start_row:end_row, ]
  }

  return(split_dt)
}

# Create the datasets for close reading -----

times.nanxin <- 2
times.arnald <- 1
nanxin <- paste(rep("nanxin", times.nanxin), 1:times.nanxin, sep = "")
arnald <- paste(rep("arnald", times.arnald), 1:times.arnald, sep = "")
names_surveyors <- c(arnald, nanxin, "seth", paste("student", 1:4, sep = ""))
n.surveyors <- length(names_surveyors)

survey.dt.split <- split_dt_fun(dt = full.text.corpus.water, num_parts = n.surveyors)
names(survey.dt.split) <- names_surveyors
```

```

# Export -----
for (i in 1:length(survey.dt.split)) {

  write.xlsx(survey.dt.split[[i]],
             file = paste0(names(survey.dt.split)[i], ".dt", ".xlsx"))

}

```

3 Network analysis

```

# CREATE VECTORS TO READ IN AND CLEAN THE DATASETS #####
tmp <- list()
names.files <- c("WORK", "NETWORK")
topics <- c("water", "food")
corpus <- c("abstract.corpus", "policy.corpus", "full.text.corpus")
cols_of_interest <- c("title", "author", "claim", "citation",
                      "document.type", "nature.claim")

# Paste all possible combinations of names -----
combs <- expand.grid(corpus = corpus, topics = topics, approach = names.files)
all.files <- paste(paste(combs$corpus, combs$topics, sep = "."),
                   combs$approach, sep = ".xlsx", sep = ".") 

# READ IN DATASETS AND TURN TO LOWERCAPS #####
tmp <- list()

for (i in 1:length(all.files)) {

  tmp[[i]] <- data.table(read.xlsx(all.files[i]))

  if (!str_detect(all.files[i], "NETWORK")) {

    tmp[[i]][, title:= tolower(title)]

  } else {

    tmp[[i]][, (cols_of_interest):= lapply(.SD, tolower), .SDcols = (cols_of_interest)]
  }
}

names(tmp) <- all.files

```

```

sub(".*\\.(^[^.]+)_.*", "\\1", all.files)

## [1] "water" "water" "water" "food" "food" "food" "water" "water" "water"
## [10] "food" "food" "food"
# CLEAN AND MERGE DATASETS #####
# Work datasets ----

dataset.works <- all.files[str_detect(all.files, "_WORK")]
dataset.works.topics <- sub(".*\\.(^[^.]+)_.*", "\\1", dataset.works)

tmp.works <- tmp[dataset.works]
names(tmp.works) <- dataset.works.topics
lapply(tmp.works, function(dt) dt[, .(doi, title, claim.in.text)]) %>%
  rbindlist(., idcol = "topic") %>%
  .[, .N, .(topic, claim.in.text)]

##      topic claim.in.text     N
##      <char>      <char> <int>
## 1: water             F 1377
## 2: water            <NA> 159
## 3: water             T 2674
## 4: water    Paywalled    9
## 5: water      Russian    1
## 6: water      French    1
## 7: water      Indian    1
## 8: water    Ukrainian    1
## 9: water    Portuguese    1
## 10: water             T    2
## 11: food            <NA> 294
## 12: food             T 627
## 13: food             F 2809

# Network datasets ----

dataset.networks <- all.files[str_detect(all.files, "NETWORK")]
dataset.networks.topics <- sub(".*\\.(^[^.]+)_.*", "\\1", dataset.networks)

tmp2 <- tmp[dataset.networks]
names(tmp2) <- dataset.networks.topics

network.dt <- rbindlist(tmp2, idcol = "topic") %>%
  .[, policy:= grep("policy", doi)] %>%
  .[, document.type:= trimws(document.type)] %>%
  .[, document.type:= tolower(document.type)]

# Retrieve year ----

```

```

network.dt[, year:= as.integer(sub(".* (\d{4})[a-z]?$", "\1", author))]

## Warning in eval(jsub, SDenv, parent.frame()): NAs introduced by coercion
# move policy to author ----

network.dt[, author:= ifelse(policy == TRUE, doi, author)]

# CHECK NUMBER OF FAO AQUASTAT CITES #####
aquastat.cites <- network.dt[citation %like% "fao aquastat"] %>%
  .[, .N, .(citation, topic)]

aquastat.cites

##          citation topic   N
##          <char> <char> <int>
## 1: fao aquastat 2006  water   31
## 2:      fao aquastat  water   46
## 3: fao aquastat 2010  water   11
## 4: fao aquastat 2020  water    4
## 5: fao aquastat 2011  water    3
## 6: fao aquastat 2012  water    9
## 7: fao aquastat 2021  water    4
## 8: fao aquastat 2017  water    2
## 9: fao aquastat 2015  water    9
## 10: fao aquastat 2019  water    4
## 11: fao aquastat 2016  water   23
## 12: fao aquastat 2014  water    5
## 13: fao aquastat 2023  water    4
## 14: fao aquastat 2018  water    5
## 15: fao aquastat 2004  water    6
## 16: fao aquastat 2005  water    3
## 17: fao aquastat 2003  water    2
## 18: fao aquastat 2013  water    5
## 19: fao aquastat 2008  water    1
## 20: fao aquastat 2022  water    1
## 21:      fao aquastat  food     8
## 22: fao aquastat 2014  food     2
## 23: fao aquastat 2012  food     9
## 24: fao aquastat 2019  food     1
## 25: fao aquastat 2016  food     6
## 26: fao aquastat 2018  food     1
## 27: fao aquastat 2020  food     1
## 28: fao aquastat 2015  food     1
## 29: fao aquastat 2022  food     2
##          citation topic   N

```

```

oldest.aquastat.cite <- min(as.integer(sub(".* (\d{4})[a-z]?$", "\1",
                                         aquastat.cites$citation)),
                                na.rm = TRUE)

## Warning: NAs introduced by coercion
# WRITE LOOKUP TABLE TO CHECK ALREADY RETRIEVED STUDIES #####
#####

lookup.dt <- network.dt[, .(doi, title, author, topic)] %>%
  .[order(title)] %>%
  unique()

lookup.dt[, .(number.rows = nrow(.SD)), topic]

##      topic number.rows
## 1: water        3738
## 2: food         892

# Export lookup tables -----
write.xlsx(lookup.dt, "lookup.dt.xlsx")
write.xlsx(lookup.dt[topic == "water"], "lookup.water.dt.xlsx")
write.xlsx(lookup.dt[topic == "food"], "lookup.food.dt.xlsx")

# Remove the year from mentions to FAO Aquastat -----
pattern <- "\b(?:19|20)\d{2}\b" # Matches years between 1900 and 2099

for (col in c("citation", "author")) {
  matches <- grep("^fao aquastat\\s+\\d+$", network.dt[[col]], ignore.case = TRUE)
  network.dt[matches, (col) := gsub("\\d+", "", network.dt[[col]][matches], perl = TRUE)]
  network.dt[, (col) := trimws(network.dt[[col]])]
}

# Rename columns -----
setnames(network.dt, c("author", "citation"), c("from", "to"))

# Rename category -----
network.dt[, category:= ifelse(!classification == "F", "Uncertain", "Fact")]

# Create copy and remove duplicated -----
network.dt.claim <- copy(network.dt)
network.dt.claim <- unique(network.dt.claim,
                             by = c("from", "to", "document.type", "nature.claim"))

```

```

fwrite(network.dt.claim, "network.dt.claim.csv")

# Convert all to lower caps -----
network.dt <- network.dt[, .(from, to, year, document.type, nature.claim,
                           classification, category, topic)]
cols_to_change <- colnames(network.dt)
network.dt[, (cols_to_change) := lapply(.SD, trimws), .SDcols = (cols_to_change)]

# PLOT DESCRIPTIVE STATISTICS #####
total.rows <- network.dt[, .(number.rows = nrow(.SD)), topic]

# Check proportion of studies by nature of claim -----
network.dt.claim[, .N, .(nature.claim, topic)] %>%
  merge(., total.rows, by = "topic") %>%
  .[, fraction:= N / number.rows] %>%
  print()

## Key: <topic>
##      topic    nature.claim      N number.rows      fraction
##      <char>          <char> <int>      <int>          <num>
##  1: food      no citation   182      1025 0.1775609756
##  2: food      citation backup  595      1025 0.5804878049
##  3: food      no claim     88      1025 0.0858536585
##  4: food            <NA>     41      1025 0.0400000000
##  5: food      modelling      1      1025 0.0009756098
##  6: food      citation backup   3      1025 0.0029268293
##  7: food      no claim      1      1025 0.0009756098
##  8: food      no citation     1      1025 0.0009756098
##  9: water      citation backup 2537     4436 0.5719116321
## 10: water      modelling      24     4436 0.0054102795
## 11: water      no citation    942     4436 0.2123534716
## 12: water            <NA>    130     4436 0.0293056808
## 13: water      no claim     402     4436 0.0906221821
## 14: water      citation backup  220     4436 0.0495942290
## 15: water      no claim      35     4436 0.0078899910
## 16: water      no citation    38     4436 0.0085662759
## 17: water      no claim      1     4436 0.0002254283

# Count document type by nature of claim -----
a <- network.dt[, .N, .(nature.claim, document.type, topic)] %>%
  merge(., total.rows, by = "topic") %>%
  .[, proportion:= N / number.rows] %>%
  na.omit() %>%
  ggplot(., aes(reorder(nature.claim, proportion), proportion)) +

```

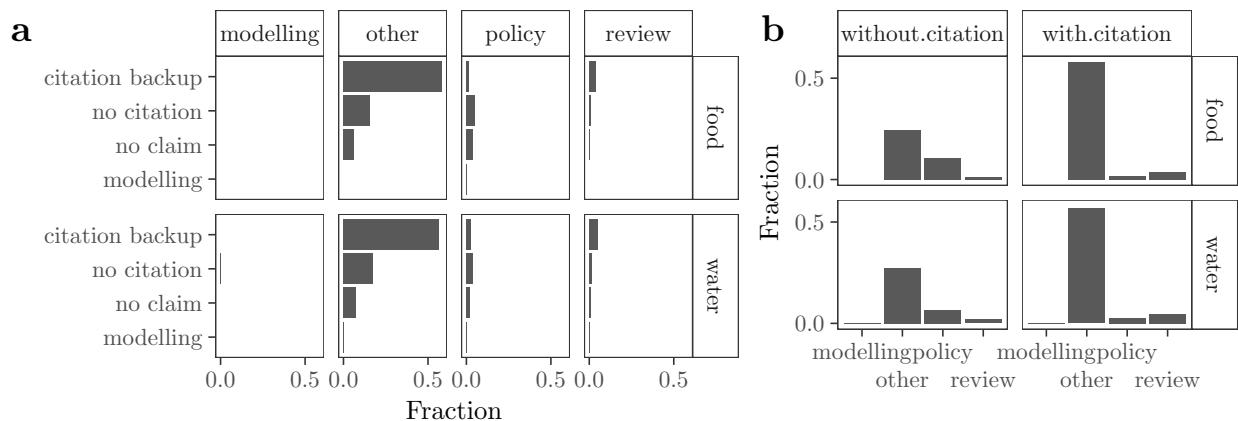
```

coord_flip() +
geom_bar(stat = "identity") +
facet_grid(topic~document.type) +
scale_y_continuous(breaks = breaks_pretty(n = 2)) +
labs(x = "", y = "Fraction") +
theme_AP()

# Count how many documents make the claim and cite / do not cite,
# by document.type -----
b <- network.dt[, .(without.citation = sum(is.na(to)),
                     with.citation = .N - sum(is.na(to))), .(document.type, topic)] %>%
  melt(., measure.vars = c("without.citation", "with.citation")) %>%
  merge(., total.rows, by = "topic") %>%
  .[, proportion:= value / number.rows] %>%
  ggplot(., aes(document.type, proportion)) +
  geom_bar(stat = "identity") +
  scale_y_continuous(breaks = breaks_pretty(n = 2)) +
  scale_x_discrete(guide = guide_axis(n.dodge = 2)) +
  labs(x = "", y = "Fraction") +
  facet_grid(topic~variable) +
  theme_AP()

# merge -----
plot_grid(a, b, ncol = 2, rel_widths = c(0.6, 0.4), labels = "auto")

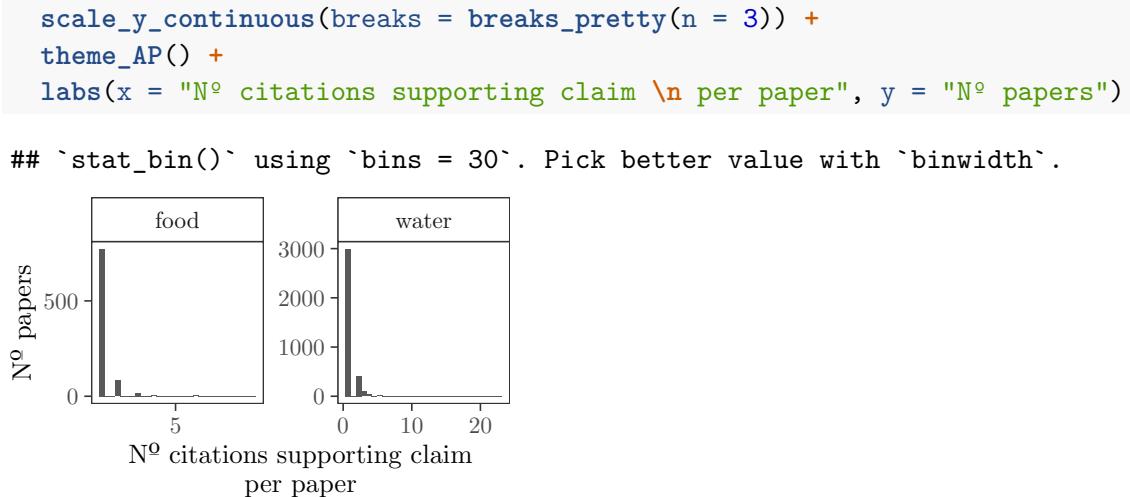
```



```

# PLOT DISTRIBUTION OF CITATION SUPPORTING THE CLAIM #####
network.dt[, .N, .(from, topic)] %>%
  .[order(-N)] %>%
  ggplot(., aes(N)) +
  geom_histogram() +
  facet_wrap(~topic, scale = "free") +
  scale_x_continuous(breaks = breaks_pretty(n = 3)) +

```



3.1 Network metrics

```

# CALCULATE NETWORK METRICS #####
# only complete cases ----

network.dt.complete <- network.dt[complete.cases(network.dt$to), ]
split.networks <- split(network.dt.complete, network.dt.complete$topic)

# Export-----
write.xlsx(network.dt.complete, "network.dt.complete.xlsx")

# Transform to graph ----

citation_graph <- lapply(split.networks, function(dt)
  graph_from_data_frame(d = dt, directed = TRUE))

## Warning in graph_from_data_frame(d = dt, directed = TRUE): In `d` `NA` elements
## were replaced with string "NA"

## Warning in graph_from_data_frame(d = dt, directed = TRUE): In `d` `NA` elements
## were replaced with string "NA"

# Calculate network metrics ----

lapply(citation_graph, function(x) edge_density(x))

## $food
## [1] 0.001158407
##
## $water
## [1] 0.0003483051

```

```

# Modularity:
# - c.1: Strong community structure, where nodes within groups are highly connected.
# - c. -1: Opposite of community structure, where nodes between groups are more connected.
# - c. 0: Indicates absence of community structure or anti-community structure in the network.
wtc <- lapply(citation_graph, function(x) cluster_walktrap(x))
lapply(wtc, function(x) modularity(x))

## $food
## [1] 0.9276213
##
## $water
## [1] 0.8541407

network_metrics <- lapply(citation_graph, function(x)
  data.table(node = V(x)$name,

    # Degree of a node: The number of connections or
    # edges linked to that node.
    # It represents how well-connected or central a
    # node is within the graph.
    degree = degree(x, mode = "in"),

    degree.out = degree(x, mode = "out"),

    # Betweenness centrality of a node: Measures the
    # extent to which a node lies on the shortest
    # paths between all pairs of other nodes in the graph.
    # Nodes with high betweenness centrality act as
    # bridges or intermediaries, facilitating
    # communication and information flow between other nodes.
    betweenness = betweenness(x),

    # Closeness centrality of a node: Measures how
    # close a node is to all other nodes in the graph,
    # taking into account the length of the shortest paths.
    # Nodes with high closeness centrality are able to
    # efficiently communicate or interact with other
    # nodes in the graph.
    closeness = closeness(x),
    pagerank = page_rank(x)$vector
  )
)

# Define the max number of rows
max.number <- 3

degree.nodes <- lapply(network_metrics, function(dt) dt[order(-degree)] [1:max.number])
degree.nodes.out <- lapply(network_metrics, function(dt) dt[order(-degree.out)] [1:max.number])
betweenness.nodes <- lapply(network_metrics, function(dt) dt[order(-betweenness)] [1:max.number])

```

```

pagerank.nodes <- lapply(network_metrics, function(dt) dt[order(-closeness)][1:max.number])

degree.nodes

## $food
##           node degree degree.out betweenness closeness    pagerank
##           <char>  <num>      <num>      <num>      <num>      <num>
## 1:     fao aquastat     31         0         0       NaN 0.02986764
## 2:     fao 2002       17         0         0       NaN 0.01616455
## 3: morris et al 2003     16         0         0       NaN 0.01169232
##
## $water
##           node degree degree.out betweenness closeness    pagerank
##           <char>  <num>      <num>      <num>      <num>      <num>
## 1:     fao aquastat    178         0     0.0000       NaN 0.055896532
## 2: siebert et al 2010     70         3   220.0833 0.3333333 0.008107633
## 3:     fao 2011       66         1   81.5000 1.0000000 0.010989269

degree.nodes.out

## $food
##           node degree degree.out betweenness closeness    pagerank
##           <char>  <num>      <num>      <num>      <num>      <num>
## 1: taguta et al 2022     0         9         0 0.04761905 0.0007848513
## 2:     guo et al 2023     0         6         0 0.05882353 0.0007848513
## 3:     pei et al 2017     1         6         4 0.20000000 0.0008960386
##
## $water
##           node degree degree.out betweenness closeness    pagerank
##           <char>  <num>      <num>      <num>      <num>      <num>
## 1:     wada 2015       0        23         0 0.02702703 0.0001847862
## 2: wada et al 2016     1        17        13 0.04347826 0.0002371423
## 3: zhang et al 2022     0        12         0 0.04000000 0.0001847862

betweenness.nodes

## $food
##           node degree degree.out betweenness closeness
##           <char>  <num>      <num>      <num>      <num>
## 1: vorosmarty and sahagian 2000     5         3       15 0.3333333
## 2:     siebert et al 2005     13         2       14 1.0000000
## 3:     united nations 2009     10         2       11 1.0000000

##     pagerank
##           <num>
## 1: 0.004120469
## 2: 0.008629113
## 3: 0.006820467
##
## $water

```

```

##          node degree degree.out betweenness closeness      pagerank
##          <char>  <num>     <num>      <num>    <num>      <num>
## 1: siebert et al 2010      70         3    220.0833 0.33333333 0.008107633
## 2: boretti and rosa 2019     12         5    195.0000 0.03703704 0.001659919
## 3: molden et al 2007      44         1    145.0000 0.33333333 0.008437017
pagerank.nodes

## $food
##          node degree degree.out betweenness closeness      pagerank
##          <char>  <num>     <num>      <num>    <num>      <num>
## 1: okorogbona et.al 2018      0         1         0      1 0.0007848513
## 2: du preez et al 2018       0         1         0      1 0.0007848513
## 3: meier et al 2018        3         1         3      1 0.0024526603
##
## $water
##          node degree degree.out betweenness closeness      pagerank
##          <char>  <num>     <num>      <num>    <num>      <num>
## 1: sharma and irmak 2012      0         1         0      1 0.0001847862
## 2: world bank 2007        5         1        48      1 0.0053763930
## 3: brajovic et al 2015       0         1         0      1 0.0001847862

```

3.2 Network plots

```

# ADD FEATURES TO NODES #####
# Retrieve a vector with the node names -----
graph <- lapply(split.networks, function(nt)
  tidygraph::as_tbl_graph(nt, directed = TRUE))

## Warning in graph_from_data_frame(x, directed = directed): In `d` `NA` elements
## were replaced with string "NA"

## Warning in graph_from_data_frame(x, directed = directed): In `d` `NA` elements
## were replaced with string "NA"

vec.names <- lapply(graph, function(graph)
  graph %>%
    activate(nodes) %>%
    pull() %>%
    data.table(name = .))

# Merge with info from the network.dt -----
tmp.network <- split(network.dt, network.dt$topic)

vec.nature.claim <- list()

```

```

for(i in names(tmp.network)) {

  vec.nature.claim[[i]] <- merge(merge(vec.names[[i]], unique(tmp.network[[i]])[, .(from, year,
    by.x = "name", by.y = "from", all.x = TRUE),
    unique(tmp.network[[i]])[, .(from, document.type, classification,
    by.x = "name", by.y = "from", all.x = TRUE)
  }
}

# Merge with the correct order -----
order_indices <- final.vec.nature.claim <- final.vec.document.type <-
final.vec.year <- final.vec.classification <- final.vec.category <- list()

for (i in names(vec.names)) {

  order_indices[[i]] <- match(vec.names[[i]]$name, vec.nature.claim[[i]]$name)
  final.vec.nature.claim[[i]] <- vec.nature.claim[[i]][order_indices[[i]], ] %>%
    .[, nature.claim]
  final.vec.document.type[[i]] <- vec.nature.claim[[i]][order_indices[[i]], ] %>%
    .[, document.type]
  final.vec.year[[i]] <- vec.nature.claim[[i]][order_indices[[i]], ] %>%
    .[, year] %>%
    as.numeric()
  final.vec.classification[[i]] <- vec.nature.claim[[i]][order_indices[[i]], ] %>%
    .[, classification]
  final.vec.category[[i]] <- vec.nature.claim[[i]][order_indices[[i]], ] %>%
    .[, category]
}

# Attach to the graph -----
graph.final <- list()

for (i in names(graph)) {

  graph.final[[i]] <- graph[[i]] %>%
    activate(nodes) %>%
    mutate(nature.claim = final.vec.nature.claim[[i]],
      document.type = final.vec.document.type[[i]],
      year = final.vec.year[[i]],
      degree = network_metrics[[i]]$degree,
      classification = final.vec.classification[[i]],
      category = final.vec.category[[i]],
      degree.out = network_metrics[[i]]$degree.out,
      betweenness = network_metrics[[i]]$betweenness,
      pagerank = network_metrics[[i]]$pagerank)
}

```

```

}

for (i in names(graph.final)) {

  graph.final[[i]] <- graph.final[[i]] %>%
    activate(edges) %>%
    mutate(edge_color = .N()$nature.claim[to])
}

# NUMBER OF NODES #####
lapply(graph.final, function(graph) V(graph))

## $food
## + 749/749 vertices, named, from c13a091:
## [1] okorogbona et.al 2018
## [2] du preez et al 2018
## [3] niu et al 2023
## [4] meier et al 2018
## [5] lobell et al 2006
## [6] rosa 2022
## [7] rolle et al 2021
## [8] mitchell et al 2018
## [9] wang et al 2012
## [10] hanjra and qureshi 2010
## + ... omitted several vertices
##
## $water
## + 2860/2860 vertices, named, from 804d173:
## [1] sharma and irmak 2012
## [2] doreau et al 2012
## [3] world water assessment programme 2009
## [4] world bank 2007
## [5] brajovic et al 2015
## [6] rivers et al 2015
## [7] kijne 2005
## [8] hafeez and khald awan 2022
## [9] dunkelman et al 2017
## [10] nordin et al 2013
## + ... omitted several vertices
#
# NUMBER OF EDGES #####
lapply(graph.final, function(graph) ecount(graph))

## $food
## [1] 649
##

```

```

## $water
## [1] 2848
# PROPORTION OF ALL PATHS THAT PASS THROUGH FIVE HIGHEST BETWEENNESS NODES #####
lapply(graph.final, function(graph) {

  bc <- betweenness(graph)
  nodes_of_interest <- sort(bc, decreasing = TRUE)[1:5]
  total_paths <- choose(vcount(graph), 2) # Total number of paths
  total_paths
  sum(nodes_of_interest) / total_paths

})

## $food
## [1] 0.0001892006
##
## $water
## [1] 0.0001760685
# PROPORTION OF LINKS CONNECTED TO THE 5 NODES WITH HIGHEST DEGREE #####
lapply(graph.final, function(graph) {

  dg <- degree(graph)
  nodes_of_interest_degree <- sort(dg, decreasing = TRUE)[1:5]
  total_edges <- ecount(graph) # Total number of edges
  sum(nodes_of_interest_degree) / total_edges

})

## $food
## [1] 0.1417565
##
## $water
## [1] 0.1390449
# PLOT NETWORK #####
seed <- 1234
selected_colors <- c("darkblue", "lightgreen", "orange", "red", "grey")

# by nature of claim -----
# Label the nodes with highest degree -----

p1 <- p2 <- p3 <- p4 <- list()

for(i in names(graph.final)) {

```

```

set.seed(seed)

p1[[i]] <- ggraph(graph.final[[i]], layout = "igraph", algorithm = "nicely") +
  geom_edge_link(arrows = arrow(length = unit(1.8, 'mm')),
                 end_cap = circle(1, "mm"),
                 aes(color = edge_color)) +
  scale_edge_color_manual(values = selected_colors, guide = "none") +
  geom_node_point(aes(color = nature.claim, size = degree)) +
  geom_node_text(aes(label = ifelse(degree >= min(degree.nodes[[i]]$degree), name, NA)),
                 repel = TRUE, size = 2.2) +
  labs(x = "", y = "") +
  scale_color_manual(name = "",
                     values = selected_colors) +
  theme_AP() +
  theme(axis.text.x = element_blank(),
        axis.ticks.x = element_blank(),
        axis.text.y = element_blank(),
        axis.ticks.y = element_blank(),
        legend.position = "right")
}

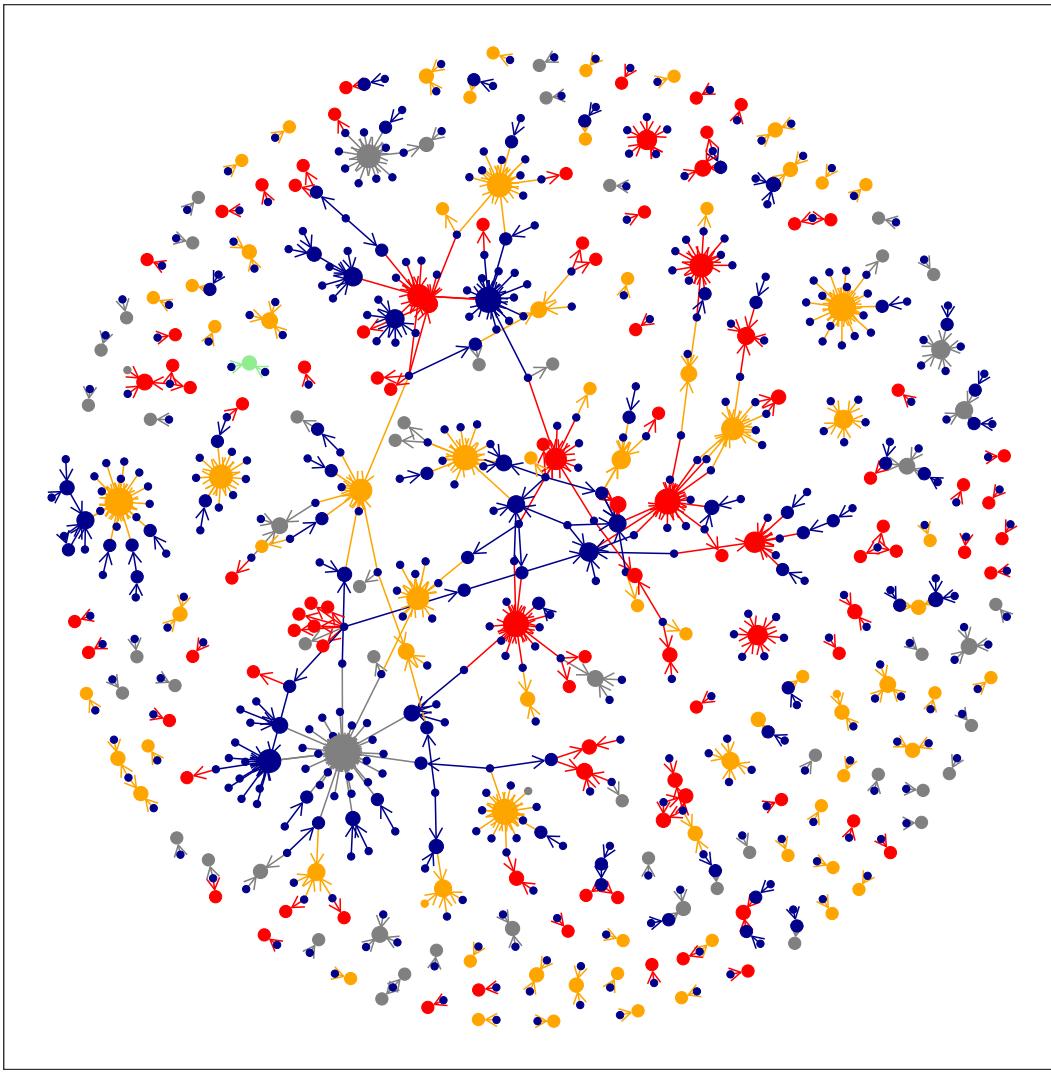
p1

## $food

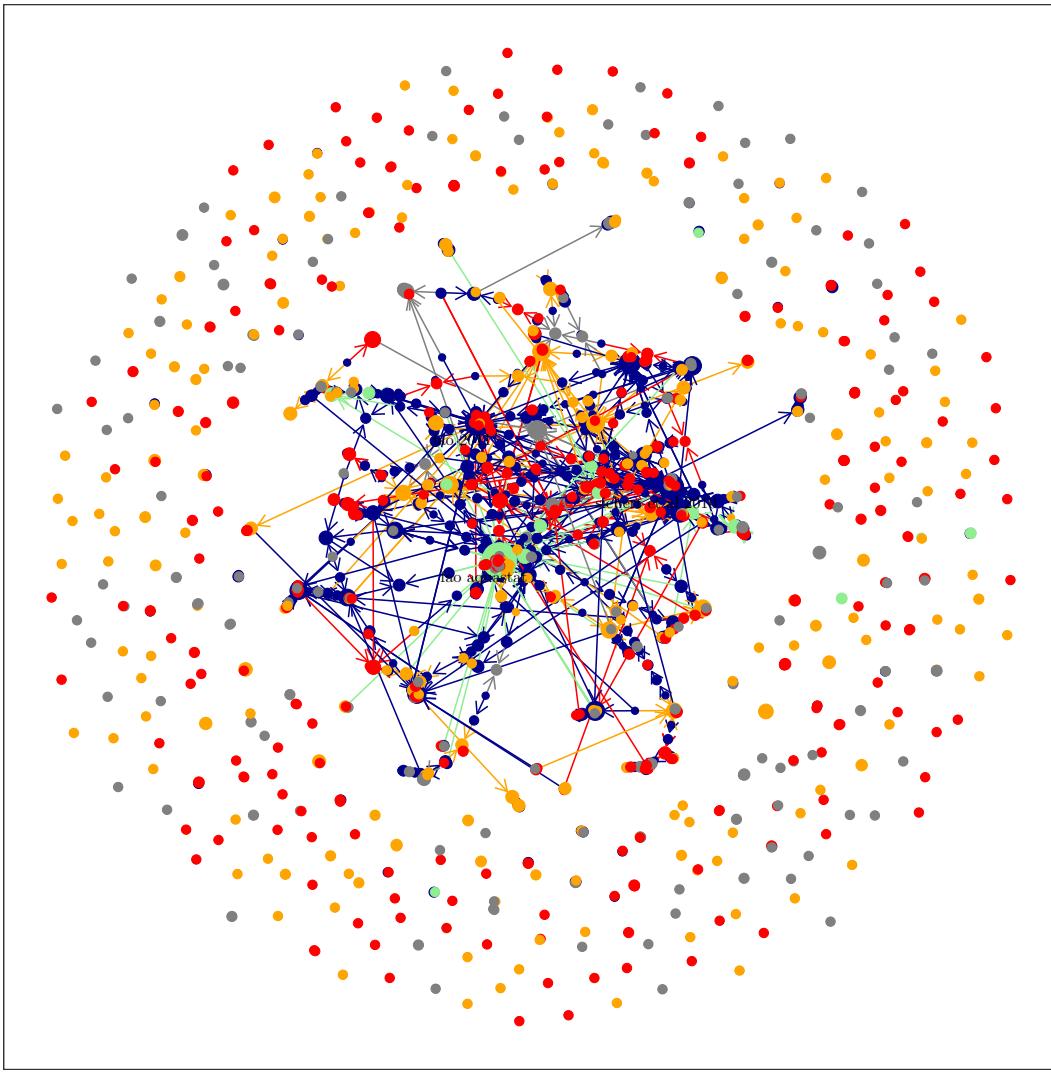
## Warning: Using the `size` aesthetic in this geom was deprecated in ggplot2 3.4.0.
## i Please use `linewidth` in the `default_aes` field and elsewhere instead.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.

## Warning: Removed 749 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).

```



```
##  
## $water  
  
## Warning: Removed 2857 rows containing missing values or values outside the scale range  
## (`geom_text_repel()`).
```



```
# Label the nodes with highest betweenness -----
for (i in names(graph.final)) {

  set.seed(seed)

  p2[[i]] <- ggraph(graph.final[[i]], layout = "igraph", algorithm = "nicely") +
    geom_edge_link(arrows = arrow(length = unit(1.8, 'mm')),
                  end_cap = circle(1, "mm")) +
    geom_node_point(aes(color = nature.claim, size = betweenness)) +
    geom_node_text(aes(label = ifelse(betweenness >= min(betweenness.nodes[[i]]$betweenness),
                                name, NA)),
                  repel = TRUE, size = 2.2) +
    labs(x = "", y = "") +
    scale_color_manual(name = "",
                      values = selected_colors) +
    theme_AP()
```

```

    theme(axis.text.x = element_blank(),
          axis.ticks.x = element_blank(),
          axis.text.y = element_blank(),
          axis.ticks.y = element_blank(),
          legend.position = "right")
}

p2

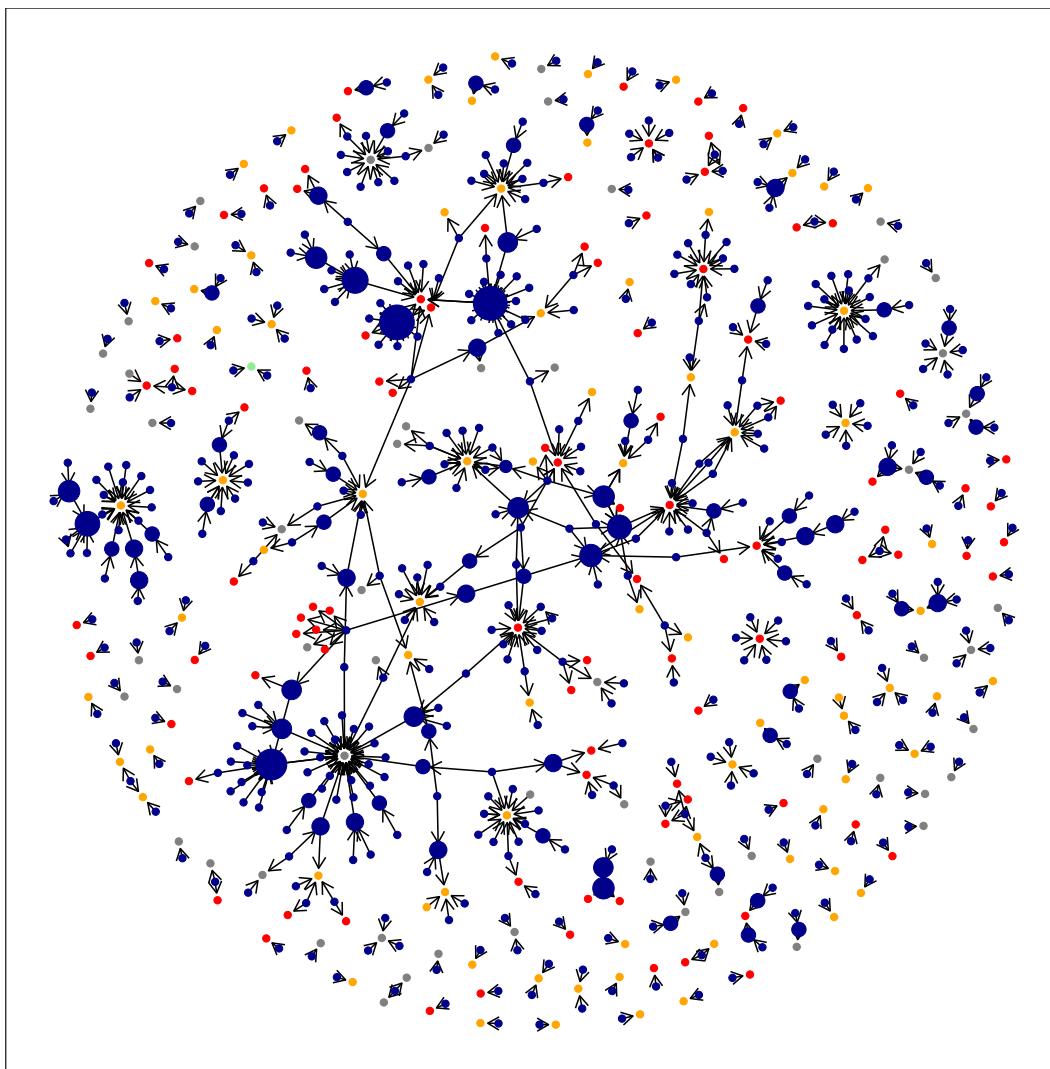
```

\$food

```

## Warning: Removed 749 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).

```



##

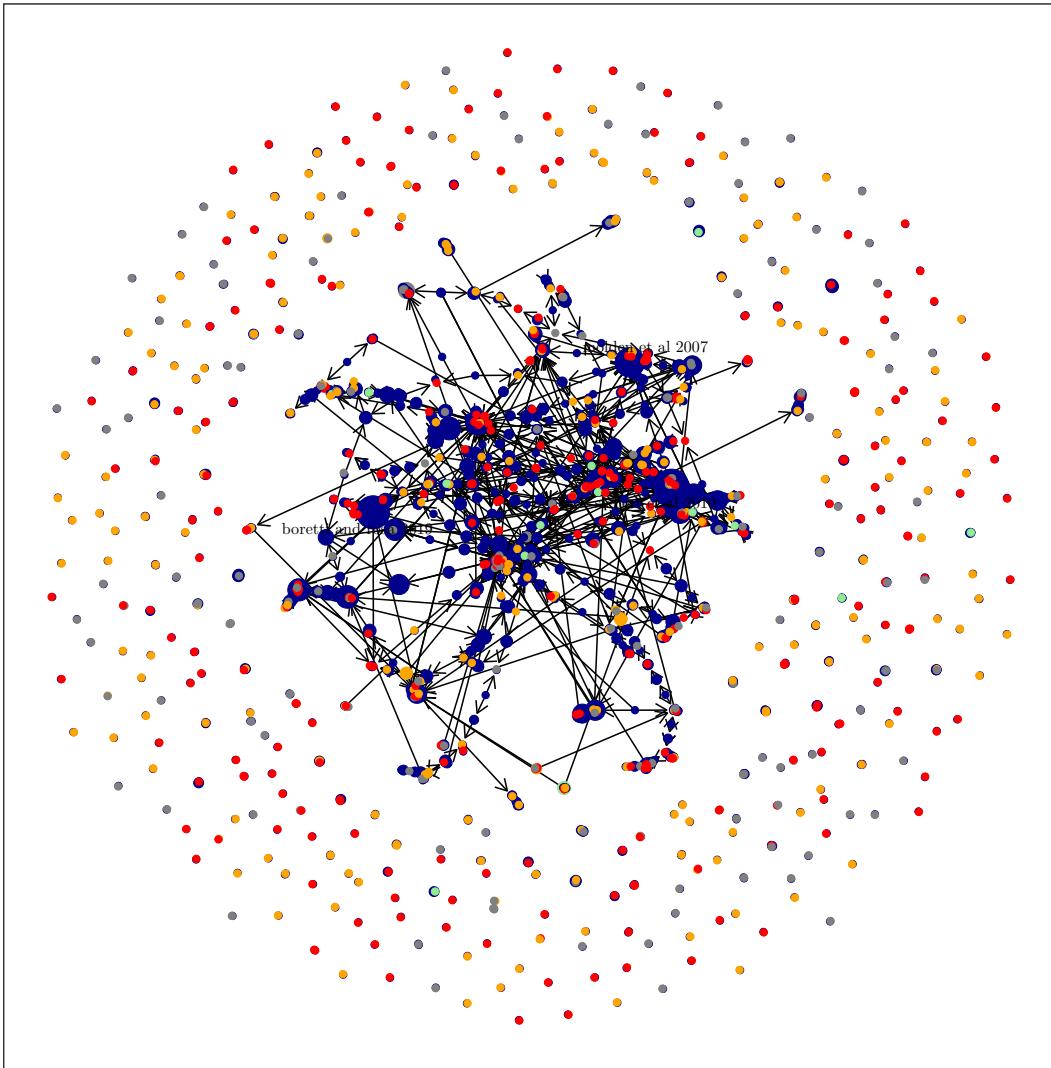
\$water

```

## Warning: Removed 2857 rows containing missing values or values outside the scale range

```

```
## (`geom_text_repel()`).
```



```
# by document.type-----  
  
for (i in names(graph.final)) {  
  
  set.seed(seed)  
  
  p3[[i]] <- ggraph(graph.final[[i]], layout = "igraph", algorithm = "nicely") +  
    geom_edge_link(arrows = arrow(length = unit(1.8, 'mm')),  
                  end_cap = circle(1, "mm")) +  
    geom_node_point(aes(color = document.type, size = degree)) +  
    geom_node_text(aes(label = ifelse(degree >= min(degree.nodes[[i]]$degree), name, NA)),  
                  repel = TRUE, size = 2.2) +  
    labs(x = "", y = "") +  
    scale_color_discrete(name = "") +  
    theme_AP() +  
    theme(axis.text.x = element_blank(),
```

```

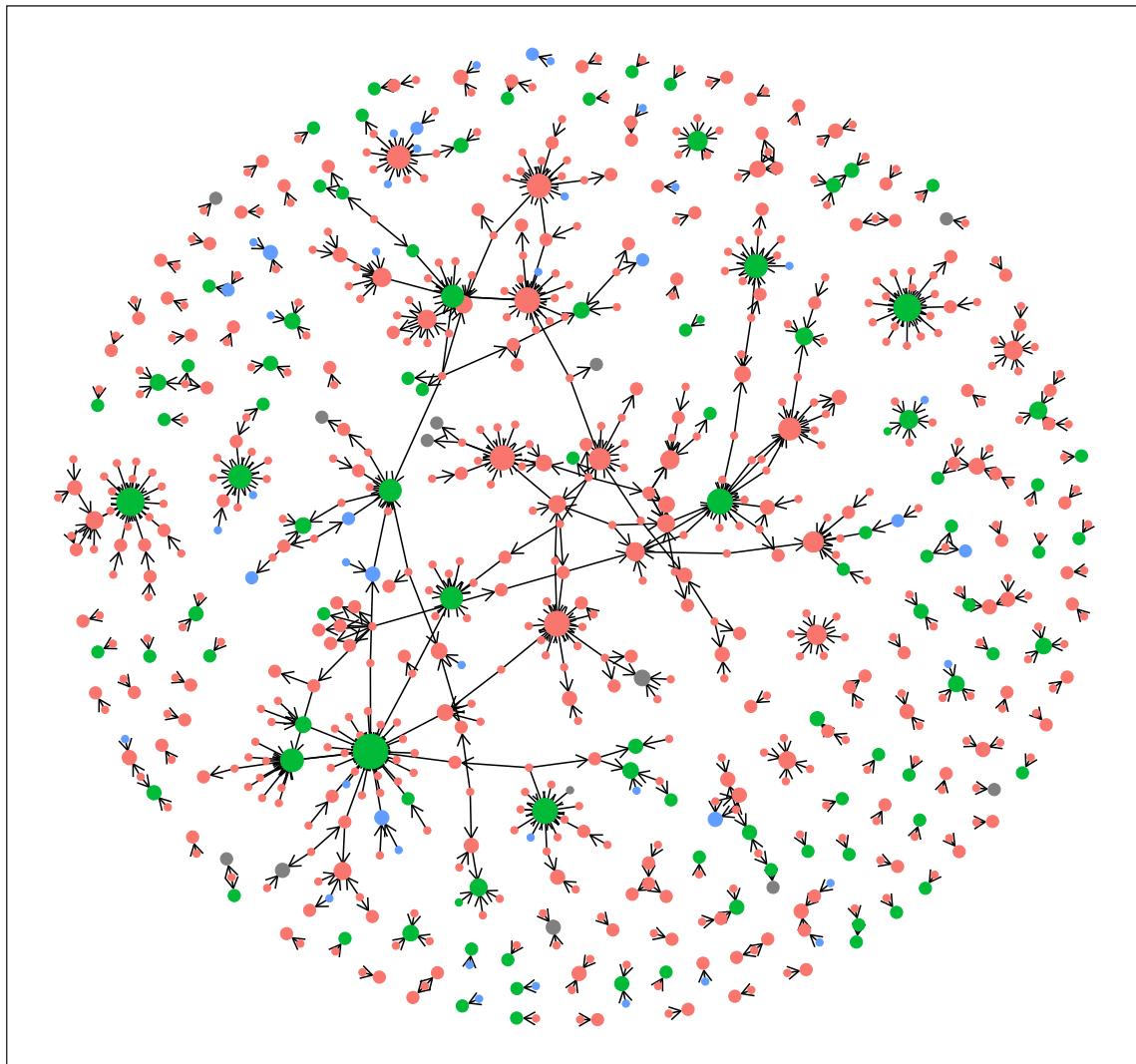
        axis.ticks.x = element_blank(),
        axis.text.y = element_blank(),
        axis.ticks.y = element_blank(),
        legend.position = "right")
}

p3

## $food

## Warning: Removed 749 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).

```

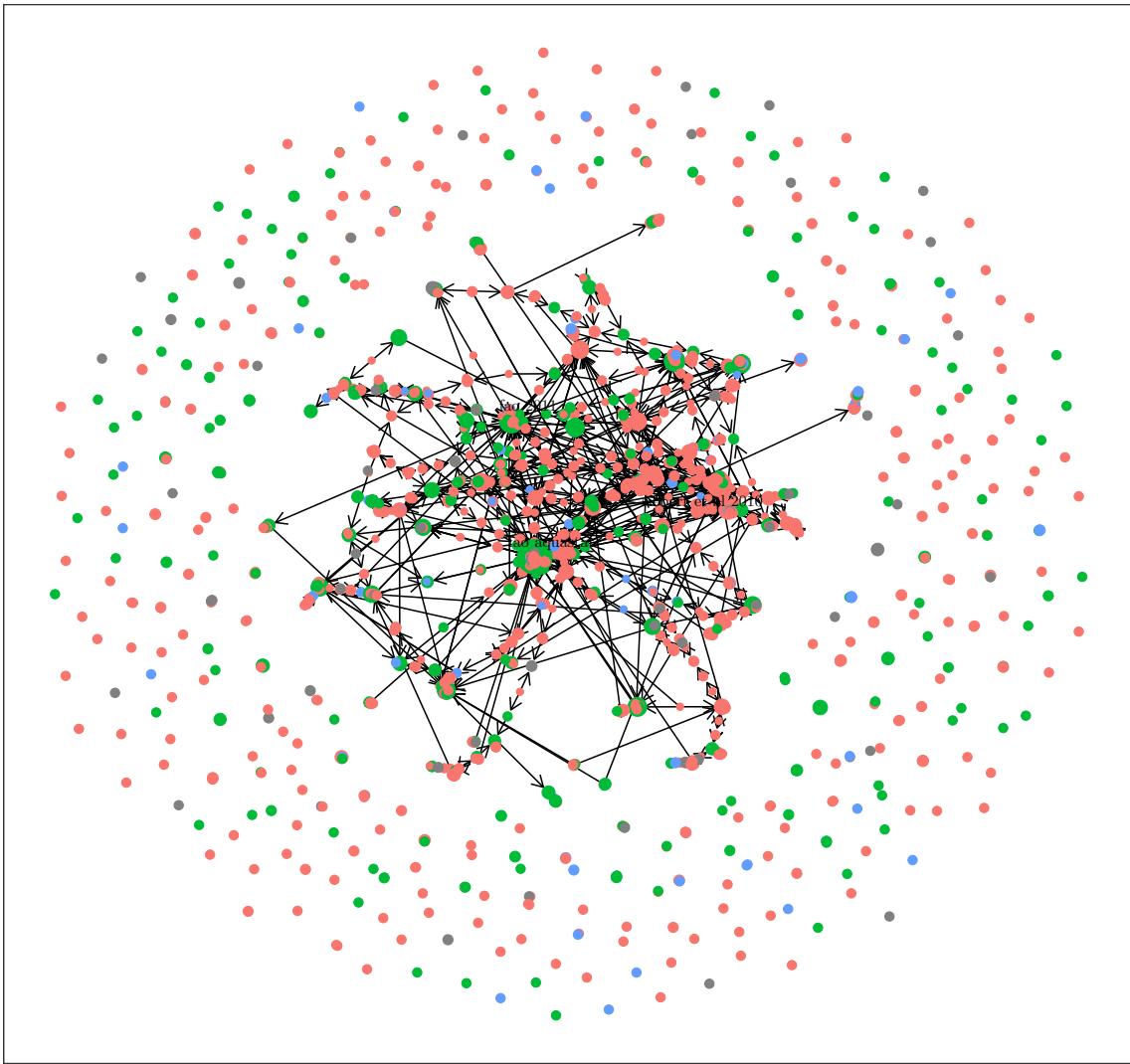


```

## 
## $water

## Warning: Removed 2857 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).

```



```
# Label nodes that are modelling exercises ----

for (i in names(graph.final)) {

  set.seed(seed)

  p4[[i]] <- ggraph(graph.final[[i]], layout = "igraph", algorithm = "nicely") +
    geom_edge_link(arrows = arrow(length = unit(1.8, 'mm')),
                  end_cap = circle(1, "mm")) +
    geom_node_point(aes(color = nature.claim)) +
    geom_node_text(aes(label = ifelse(nature.claim == "modelling", name, NA)),
                  repel = TRUE, size = 2.2) +
    labs(x = "", y = "") +
    scale_color_manual(name = "",
                      values = selected_colors) +
    theme_AP() +
    theme(axis.text.x = element_blank(),
```

```

        axis.ticks.x = element_blank(),
        axis.text.y = element_blank(),
        axis.ticks.y = element_blank(),
        legend.position = "right")
}

```

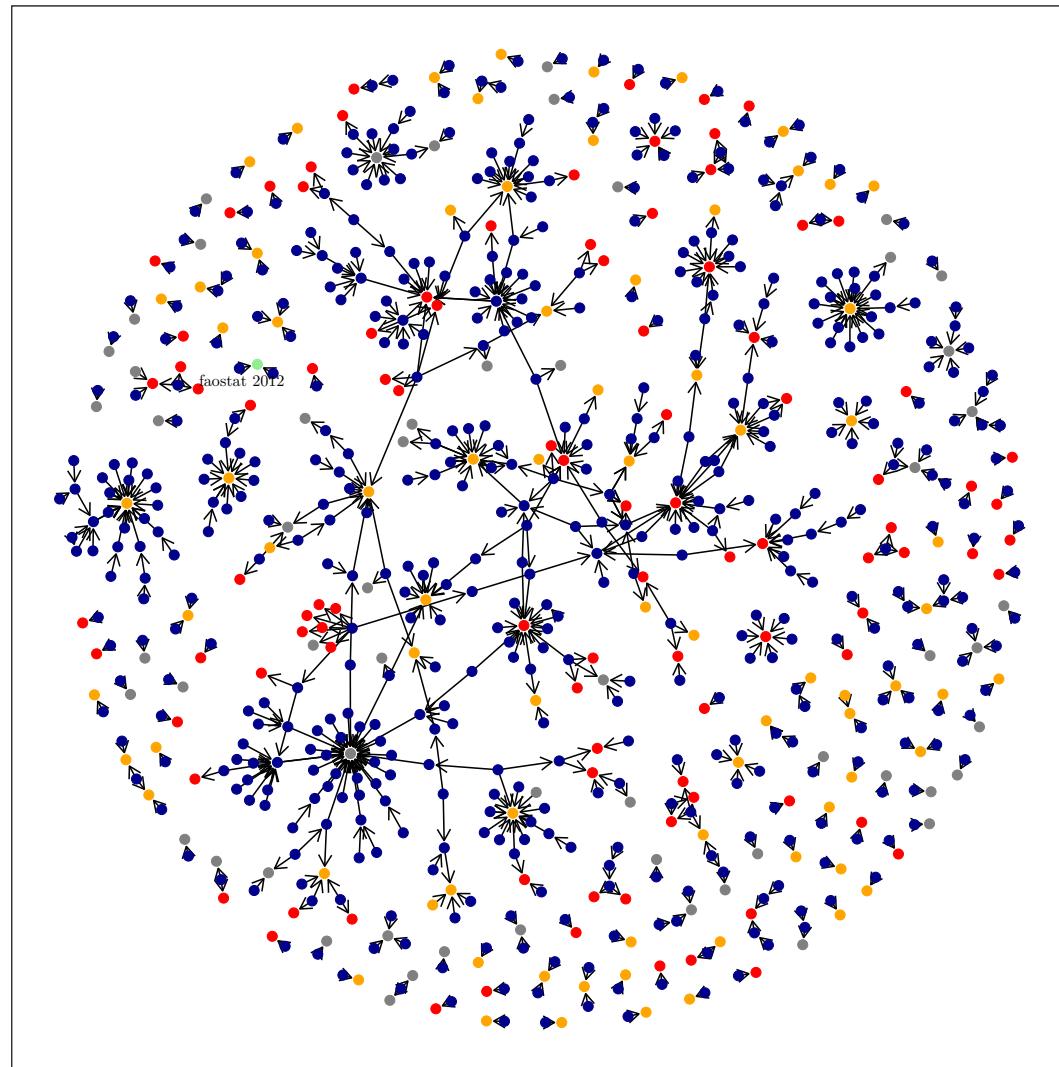
p4

\$food

```

## Warning: Removed 748 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).

```



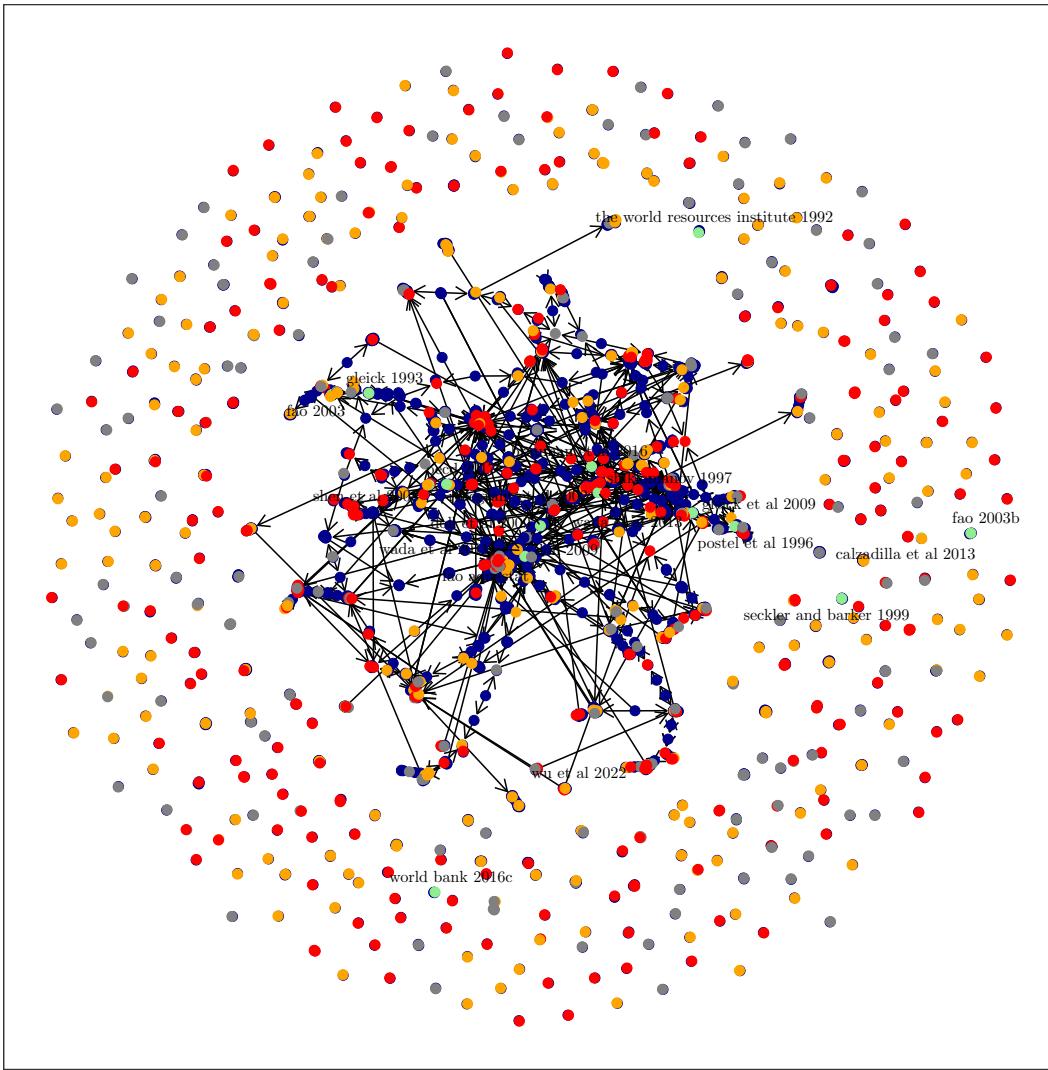
##

\$water

```

## Warning: Removed 2840 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).

```



3.3 Uncertainties turned into facts

```
# COUNT PROPORTION OF NODES THAT STATE AS FACT A CLAIM UTTERED AS UNCERTAIN #####
uncertainty_plot_fun <- function(graph) {
  # Extract name of all studies -----
  all.names <- graph %>%
    activate(nodes) %>%
    pull(name)
  # Extract name of studies stating claim as fact -----
  f.names <- graph %>%
    activate(nodes) %>%
    data.frame() %>%
    filter(name %in% all.names)
```

```

filter(classification == "F") %>%
pull(name)

# Add names to edges -----
add.names.edges <- graph %>%
  activate(edges) %>%
  mutate(from.name = all.names[from],
         to.name = all.names[to])

# Calculate, for each study stating claim as fact, the studies it cites -----
out.classes <- lapply(f.names, function(x) {

  out_nodes <- add.names.edges %>%
    activate(edges) %>%
    filter(from.name == x) %>%
    pull(to.name)

})

# unlist names of studies cited by studies uttering claim as fact -----
di <- sort(unlist(out.classes))

# Extract only those that do not state claim as fact -----
nodes.no.fact <- graph %>%
  activate(nodes) %>%
  data.frame() %>%
  data.table() %>%
  .[name %in% di] %>%
  .[!classification == "F"] %>%
  .$name

name.edges <- add.names.edges %>%
  activate(edges) %>%
  data.frame() %>%
  filter(from.name %in% f.names & to.name %in% nodes.no.fact) %>%
  .[, c("from.name", "to.name")] %>%
  c() %>%
  unlist() %>%
  unique()

output <- add.names.edges %>%
  activate(nodes) %>%
  filter(name %in% name.edges) %>%
  activate(edges) %>%

```

```

    filter(from.name %in% name.edges & to.name %in% name.edges)

  return(output)
}

# PLOT GRAPH UNCERTAINTIES TURNED INTO FACTS #####
#####

out <- lapply(graph.final, function(x) uncertainty_plot_fun(x))

p7 <- list()

for (i in names(out)) {

  set.seed(seed)

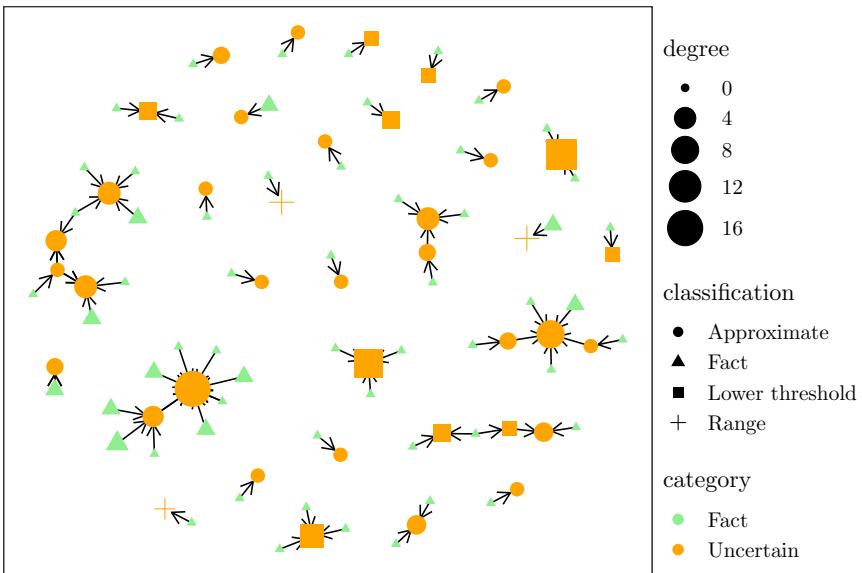
  p7[[i]] <- ggraph(out[[i]], layout = "igraph", algorithm = "nicely") +
    geom_edge_link(arrow = arrow(length = unit(1.8, 'mm')),
                   end_cap = circle(1, "mm")) +
    geom_node_point(aes(color = category, size = degree, shape = classification)) +
    scale_color_manual(values = c("lightgreen", "orange")) +
    scale_shape_discrete(labels = c("Approximate", "Fact", "Lower threshold", "Range", "Upper " +
      geom_node_text(aes(label = ifelse(degree >= min(degree.nodes[[i]]$degree), name, NA)),
                     repel = TRUE, size = 2.2) +
    labs(x = "", y = "") +
    theme_AP() +
    theme(axis.text.x = element_blank(),
          axis.ticks.x = element_blank(),
          axis.text.y = element_blank(),
          axis.ticks.y = element_blank(),
          legend.position = "right")
}

p7

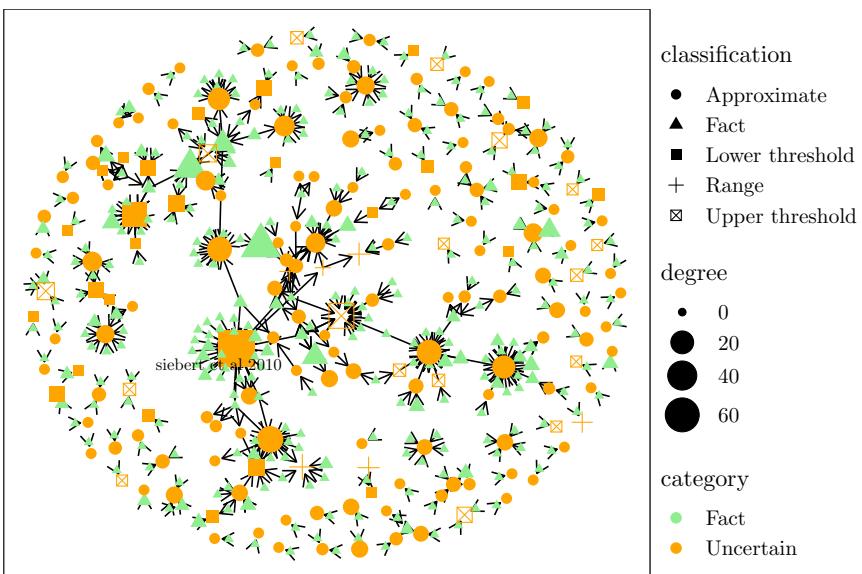
## $food

## Warning: Removed 98 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).

```



```
##  
## $water  
  
## Warning: Removed 477 rows containing missing values or values outside the scale range  
## (`geom_text_repel()`).
```



```
# FUNCTION TO CALCULATE ALL PATHS BETWEEN PAIRS OF NODES #####  
  
calculate_paths <- function(graph) {  
  
  # Convert to igraph -----  
  
  graph_graph <- as.igraph(graph)  
  
  # Get all unique pairs of nodes -----
```

```

node_pairs <- expand.grid(from = V(igraph_graph), to = V(igraph_graph))
node_pairs <- node_pairs[node_pairs$from != node_pairs$to, ]

# Function to calculate all simple paths between a pair of nodes-----

calculate_paths <- function(from, to) {
  paths <- all_simple_paths(igraph_graph, from = from, to = to)
  lapply(paths, names)
}

# Apply the function to all node pairs and unnest the results-----

all_paths <- node_pairs %>%
  rowwise() %>%
  mutate(paths = list(calculate_paths(from, to))) %>%
  unnest(cols = c(paths))

out <- sum(sapply(all_paths$paths, function(x) length(x)))

return(out)
}

# CALCULATE ALL PATHS / PATHS TURNING HYPOTHESIS INTO FACTS #####
all.paths <- hypothesis.into.facts.paths <- list()

for (i in names(graph.final)) {

  all.paths[[i]] <- calculate_paths(graph.final[[i]])
  hypothesis.into.facts.paths[[i]] <- uncertainty_plot_fun(graph.final[[i]]) %>%
    calculate_paths()

}

# Print results: proportion of paths turning uncertainties into facts ----

for (i in names(all.paths)) {
  print(hypothesis.into.facts.paths[[i]] / all.paths[[i]])
}

## [1] 0.09101061
## [1] 0.09258984

```

4 Proportion of paths ending up in no claim, no citation or modelling nodes

```
# DEFINE FUNCTION #####
proportion_paths <- function(graph) {

  # Turn into data.frame -----
  end_nodes <- graph %>%
    activate(nodes) %>%
    filter(degree.out == 0) %>%
    data.frame()

  end_node_indices <- end_nodes$name

  # Loop to store all paths to all end-nodes -----
  all_paths <- list()

  for (v in igraph::V(as.igraph(graph))) {

    paths_from_v <- igraph::all_simple_paths(as.igraph(graph),
                                              from = v,
                                              to = end_node_indices)

    if (length(paths_from_v) > 0) {

      all_paths <- c(all_paths, paths_from_v)
    }
  }

  # Extract the label of the last node in each path -----
  end_labels <- sapply(all_paths, function(path) {

    last_node <- tail(path, 1)
    last_node_name <- V(as.igraph(graph))[last_node]$name

    graph %>%
      activate(nodes) %>%
      filter(name == last_node_name) %>%
      pull(nature.claim)
  })
}

# Proportion of paths ending in "no citation", "no claim" and "modelling" ----
no_citation_paths <- sum(end_labels == "no citation", na.rm = TRUE)
```

```

no_claim_paths <- sum(end_labels == "no claim", na.rm = TRUE)
modelling_paths <- sum(end_labels == "modelling", na.rm = TRUE)
na_paths <- sum(is.na(end_labels))
total_paths <- length(end_labels)

proportion_no_citation <- no_citation_paths / total_paths
proportion_no_claim <- no_claim_paths / total_paths
proportion_modelling <- modelling_paths / total_paths
proportion_na <- na_paths / total_paths

# Wrap up for output -----
output <- data.table("no citation" = proportion_no_citation,
                      "no claim" = proportion_no_claim,
                      "modelling" = proportion_modelling,
                      "NA" = proportion_na)
return(output)
}

# RUN FUNCTION #####
out <- lapply(graph.final, function(graph) proportion_paths(graph))
out

## $food
##   no citation  no claim  modelling      NA
##       <num>      <num>      <num>      <num>
## 1:  0.3848485 0.3909091 0.003030303 0.2212121
##
## $water
##   no citation  no claim modelling      NA
##       <num>      <num>      <num>      <num>
## 1:  0.2678784 0.2818832 0.3107867 0.1394517

# PLOT PROPORTION OF PATHS ENDING IN MODELLING, NO CLAIM AND NO CITATION #####
rbindlist(out, idcol = "belief") %>%
  .[, belief:= ifelse(belief == "food", "40\\% (food belief)", "70\\% (water belief)")] %>%
  melt(., measure.vars = colnames(.)[-1]) %>%
  ggplot(., aes(belief, value, fill = variable)) +
  geom_bar(stat = "identity",
            position = position_dodge(0.5)) +
  labs(x = "", y = "Fraction") +
  scale_fill_manual(values = c("orange", "red", "lightgreen", "grey"),
                    name = "") +
  theme_AP() +

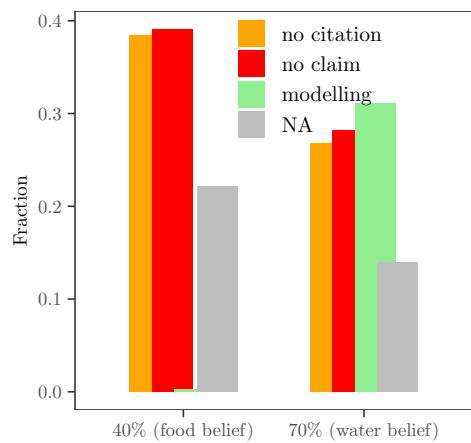
```

```

theme(legend.position = c(0.6, 0.9),
      axis.text.x = element_text(size = 7),
      axis.text.y = element_text(size = 7),
      axis.title.x = element_text(size = 7.3),
      axis.title.y = element_text(size = 7.3),
      strip.text.x = element_text(size = 7.4))

## Warning: A numeric `legend.position` argument in `theme()` was deprecated in ggplot2
## 3.5.0.
## i Please use the `legend.position.inside` argument of `theme()` instead.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.

```



4.1 Network through time

```

# PLOT NETWORK THROUGH TIME #####
plot.years <- list()

for (i in c("water", "food")) {

  # Extract vector with names -----
  location_aquastat <- graph.final[[i]] %>%
    activate(nodes) %>%
    data.frame() %>%
    pull(name) %>%
    grep("aquastat", .)

  # Extract vector with years -----
  v_years <- graph.final[[i]] %>%
    activate(nodes) %>%

```

```

data.frame() %>%
pull(year)

# Substitute fao aquastat without year with the oldest aquastat citation ----

v_years[location_aquastat] <- oldest.aquastat.cite

# Find NA values ----

na_indices <- is.na(v_years)
sum(na_indices)

# Generate random values to replace NA ----

random_values <- sample(2000:2020, sum(na_indices), replace = TRUE)

# Replace NA with random values ----

v_years[na_indices] <- random_values

# Define the coordinates-----

y_positions <- runif(length(v_years), min = -3, max = 3) # Random y-axis position
layout <- cbind(v_years, y_positions) # Use actual years for x-axi
layout_matrix <- as.matrix(layout)
colnames(layout_matrix) <- c("x", "y")

# PLOT NETWORK THROUGH TIME #####
# Set seed ----

set.seed(seed)

# Plot ----

plot.years[[i]] <- ggraph(graph.final[[i]], layout = layout_matrix, algorithm = "nicely") +
  geom_edge_link(arrow = arrow(length = unit(1.8, "mm")),
                 end_cap = circle(1, "mm"),
                 color = "grey",
                 alpha = 0.4) +
  geom_node_point(aes(color = nature.claim, size = degree)) +
  geom_node_text(aes(label = ifelse(nature.claim == "modelling", name, NA)),
                repel = TRUE, size = 2.5) +
  scale_color_manual(name = "",
                     values = selected_colors) +
  scale_x_continuous(name = "Year",
                     limits = range(v_years),

```

```

        breaks = seq(min(v_years),
                      max(v_years), by = 5)) +
      labs(x = "Year", y = "") +
      theme_AP() +
      theme(axis.text.y = element_blank(),
            axis.ticks.y = element_blank())

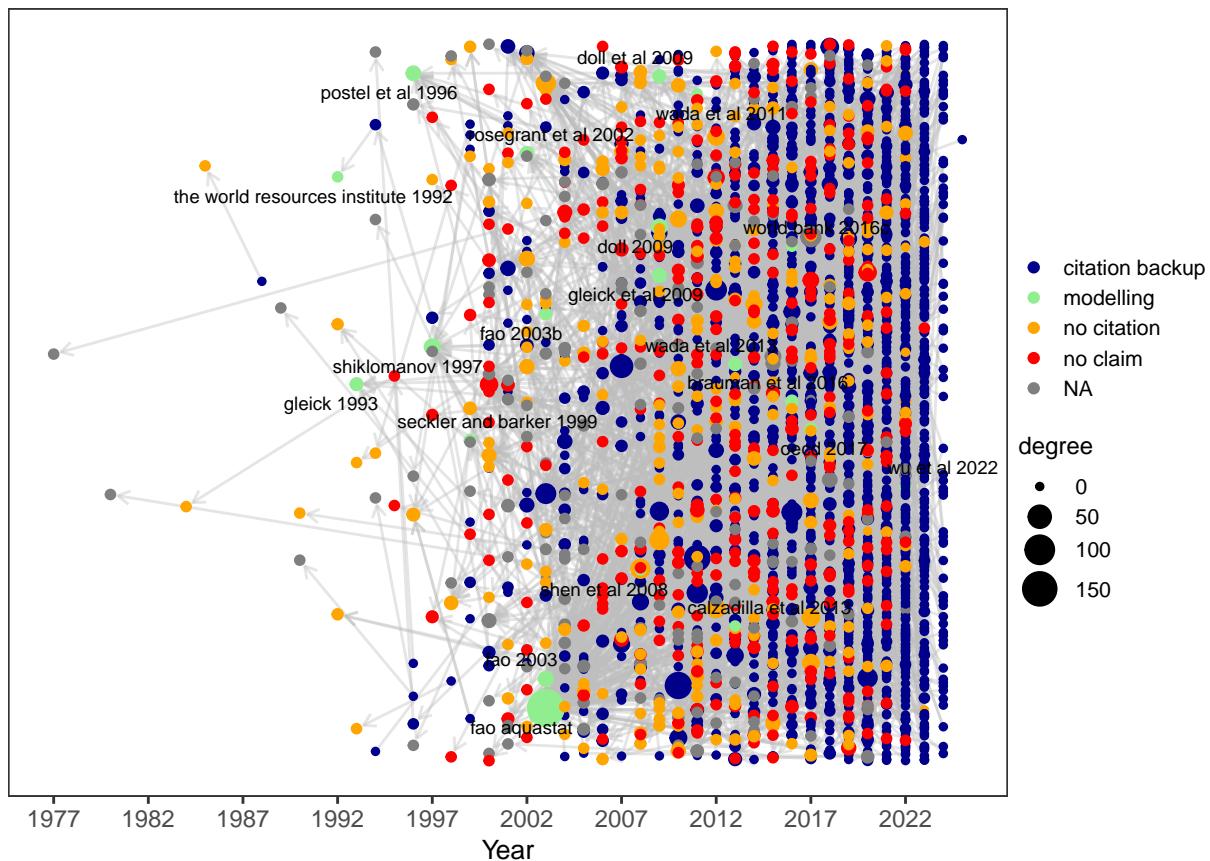
}

plot.years

## $water

## Warning: Removed 2840 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).

```



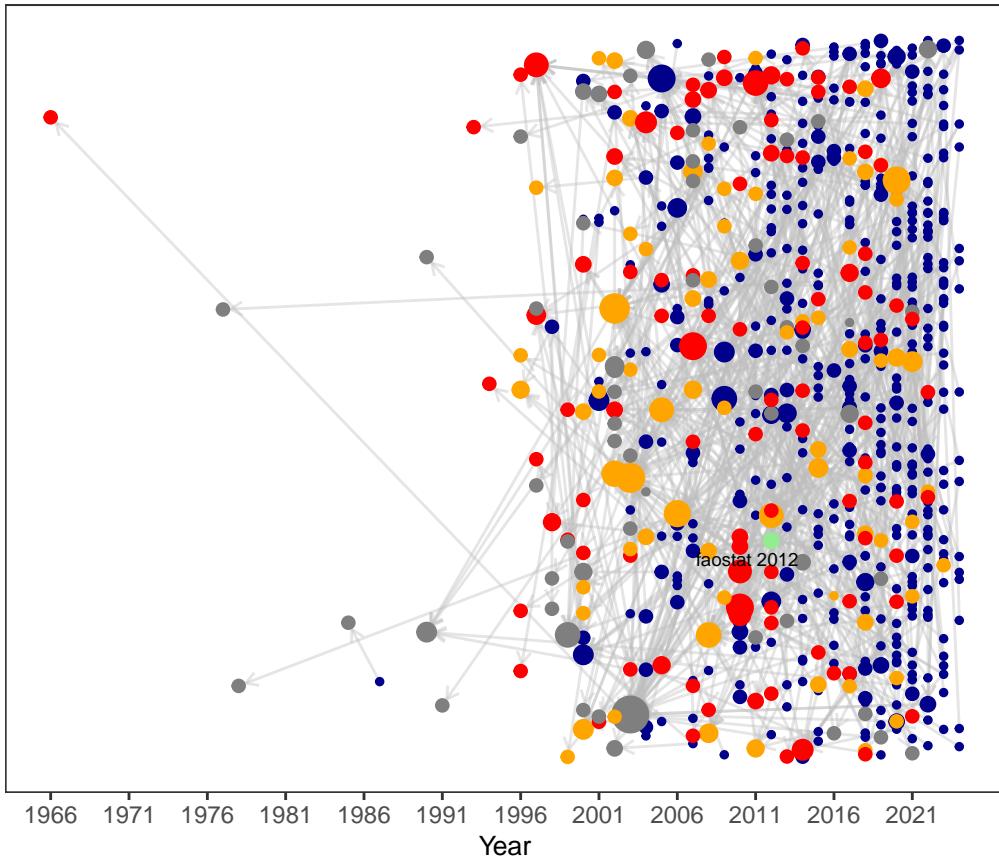
```

##

## $food

## Warning: Removed 748 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).

```



```
# ANOTHER VISUALIZATION FOR YEARS BASED ON POLAR COORDINATES #####
#####

plot.years <- list()

for (i in c("water", "food")) {

  # Replace NA values in year with random samples from 2000 to 2020 -----
  g <- graph.final[[i]] %>%
    activate(nodes) %>%
    mutate(year = ifelse(is.na(year), sample(2000:2020, replace = TRUE), year)) %>%
    mutate(
      year_normalized = (year - min(year)) / (2024 - min(year)), # Normalize relative to 2024
      radius = year_normalized
    )

  # Assign the calculated positions -----
  g <- g %>%
    mutate(
      angle = seq(0, 2 * pi, length.out = n() + 1)[1:n()],
      x = radius * cos(angle),
      y = radius * sin(angle)
    )
}
```

```

)

# Determine the range of years -----
min_year <- min(g %>% pull(year))

# Dynamically determine the start year for the concentric circles -----
start_year <- floor(min_year / 10) * 10 # Round down to the nearest decade
end_year <- 2024 # Explicitly set the end year to 2024
year_intervals <- seq(start_year, end_year, by = 10)

# Create concentric circles every ten years -----
circle_data <- lapply(year_intervals, function(yr) {
  r <- (yr - min_year) / (end_year - min_year)
  tibble(
    x = r * cos(seq(0, 2 * pi, length.out = 100)),
    y = r * sin(seq(0, 2 * pi, length.out = 100)),
    year = yr,
    label_x = r, # Label position on the x-axis (angle = 0)
    label_y = 0 # Label position on the y-axis (angle = 0)
  )
}) %>% bind_rows()

# Remove duplicate labels -----
label_data <- circle_data %>%
  distinct(year, .keep_all = TRUE) # Keep only unique year labels

# Plot -----
plot.years[[i]] <- ggraph(g, layout = "manual", x = x, y = y) +
  # Add concentric circles
  geom_edge_link(arrow = arrow(length = unit(1.8, "mm")),
                 end_cap = circle(1, "mm"),
                 alpha = 0.07,
                 aes(color = edge_color)) +
  scale_edge_color_manual(values = selected_colors, guide = "none") +
  geom_node_point(aes(color = nature.claim, size = degree)) +
  geom_node_text(aes(label = ifelse(nature.claim == "modelling", name, NA)),
                repel = TRUE, size = 2.5) +
  scale_color_manual(name = "",
                     values = selected_colors) +
  geom_path(data = circle_data, aes(x = x, y = y, group = factor(year)),
            color = "black", linetype = "dashed") +
  # Add year labels
  geom_text(data = label_data, aes(x = label_x, y = label_y, label = year),
            hjust = -0.2, vjust = 0.5, size = 3) +
  labs(x = "", y = "") +
  theme_AP()

```

```

    theme(axis.text.y = element_blank(),
          axis.ticks.y = element_blank(),
          axis.text.x = element_blank(),
          axis.ticks.x = element_blank(),
          legend.position = "top")
}

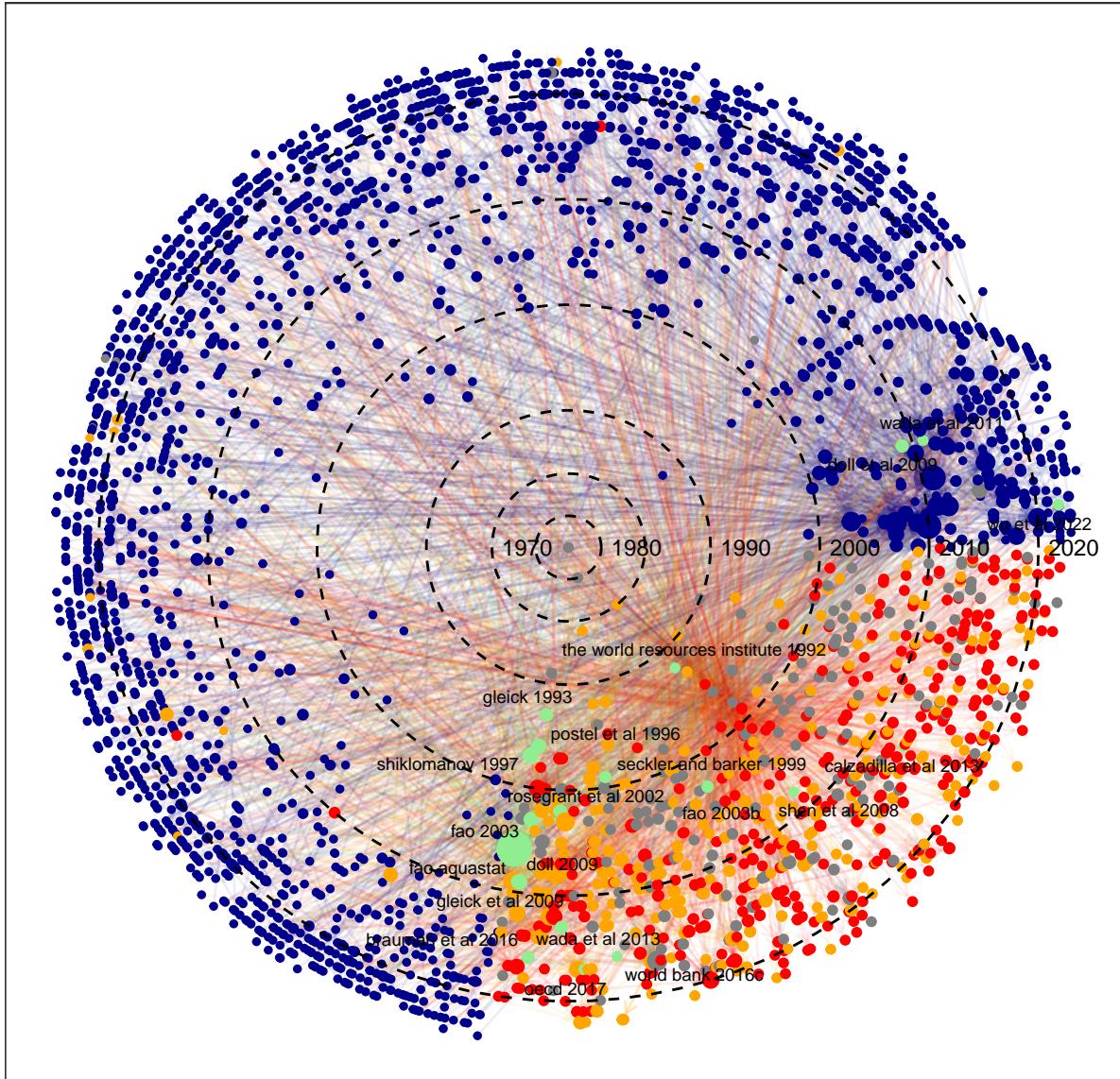
plot.years

## $water

## Warning: Removed 2840 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).

● citation backup ● modelling ● no citation ● no claim ● NA degree ● 0 ● 50 ● 100 ● 150

```



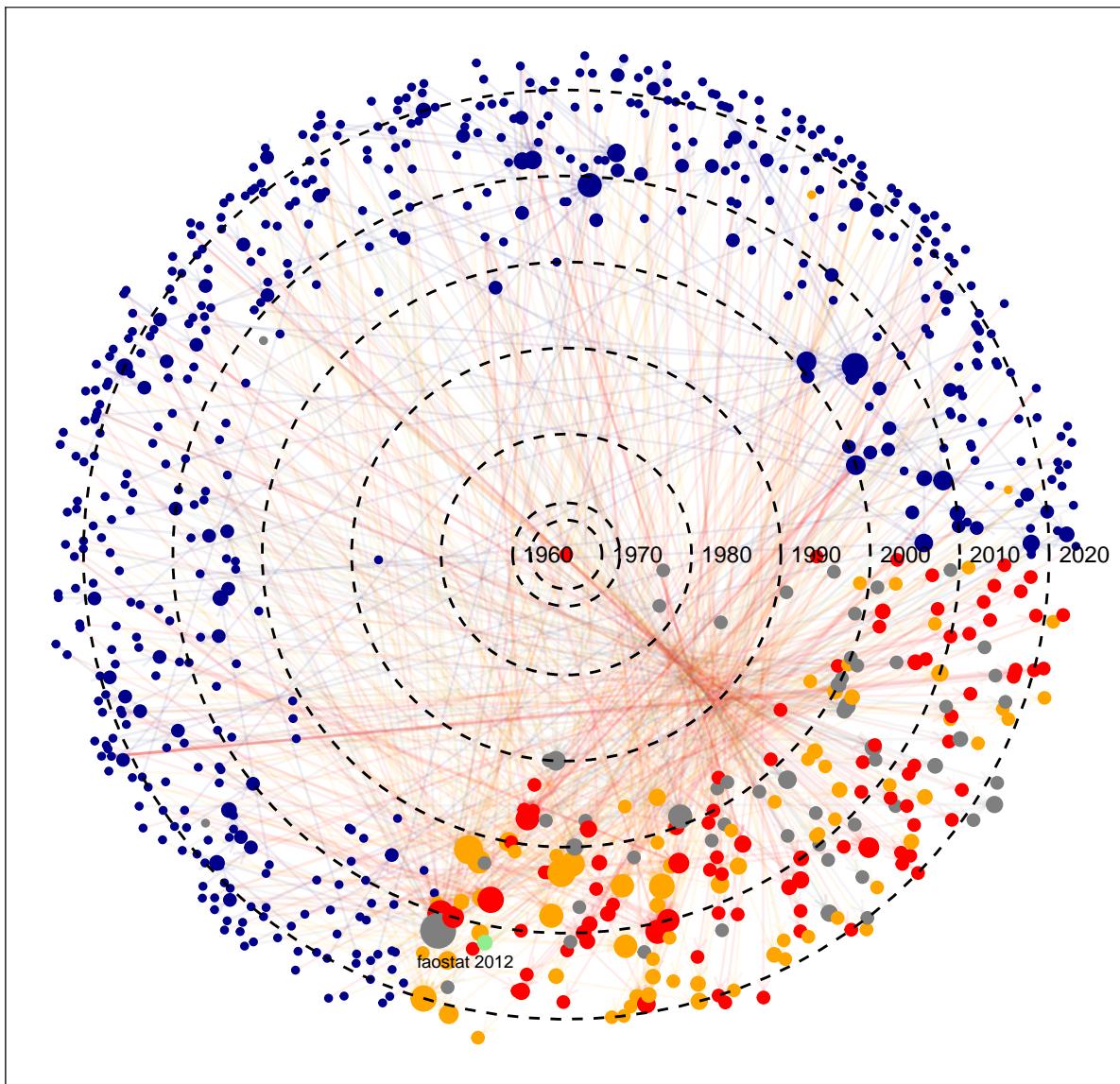
```

## 
## $food

## Warning: Removed 748 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).

● citation backup ● modelling ● no citation ● no claim ● NA degree ● 0 ● 10 ● 20 ● 30

```



```

# FUNCTION TO PLOT EVOLUTION OF NETWORK THROUGH TIME #####
network_through_time_fun <- function(graph, Year, seed) {

  # Extract all names -----
  all.names <- graph %>%
    activate(nodes) %>%
    pull(name)
}

```

```

# Add names to edges -----
add.names.edges <- graph %>%
  activate(edges) %>%
  mutate(from.name = all.names[from],
         to.name = all.names[to])

# Extract nodes by year -----
names.targeted <- add.names.edges %>%
  activate(edges) %>%
  filter(year < Year) %>%
  data.frame() %>%
  .[, c("from.name", "to.name")] %>%
  c() %>%
  unlist() %>%
  unique()

name.nodes <- add.names.edges %>%
  activate(nodes) %>%
  filter(name %in% names.targeted) %>%
  activate(edges) %>%
  filter(from.name %in% names.targeted & to.name %in% names.targeted)

set.seed(seed)

# Plot -----
out <- ggraph(name.nodes, layout = "igraph", algorithm = "nicely") +
  geom_edge_link(arrows = arrow(length = unit(1, 'mm')),
                 end_cap = circle(0.3, "mm")) +
  geom_node_point(aes(color = nature.claim, size = degree)) +
  geom_node_text(aes(label = ifelse(nature.claim == "modelling", name, NA)),
                 repel = TRUE, size = 2.2) +
  scale_color_manual(name = "",
                     values = selected_colors) +
  labs(x = "", y = "") +
  theme_AP() +
  theme(axis.text.x = element_blank(),
        axis.ticks.x = element_blank(),
        axis.text.y = element_blank(),
        axis.ticks.y = element_blank(),
        legend.position = "none")

return(out)
}

```

```

# DEFINE YEARS OF INTEREST #####
years.vector <- c(seq(2000, 2020, 10), 2024)

# RUN FUNCTION #####
plots.through.time <- list()

for (i in names(graph.final)) {

  plots.through.time[[i]] <- lapply(years.vector, function(year)
    network_through_time_fun(graph = graph.final[[i]], Year = year, seed = seed) +
    ggtitle(year))
}

da <- list()

for (i in names(plots.through.time)) {

  for (j in 1:length(plots.through.time[[i]])) {

    da[[i]][[j]] <- plots.through.time[[i]][[j]] +
      geom_node_point(aes(color = nature.claim)) +
      theme(axis.text.x = element_blank(),
            axis.ticks.x = element_blank(),
            axis.text.y = element_blank(),
            axis.ticks.y = element_blank(),
            legend.position = "right")
  }
}

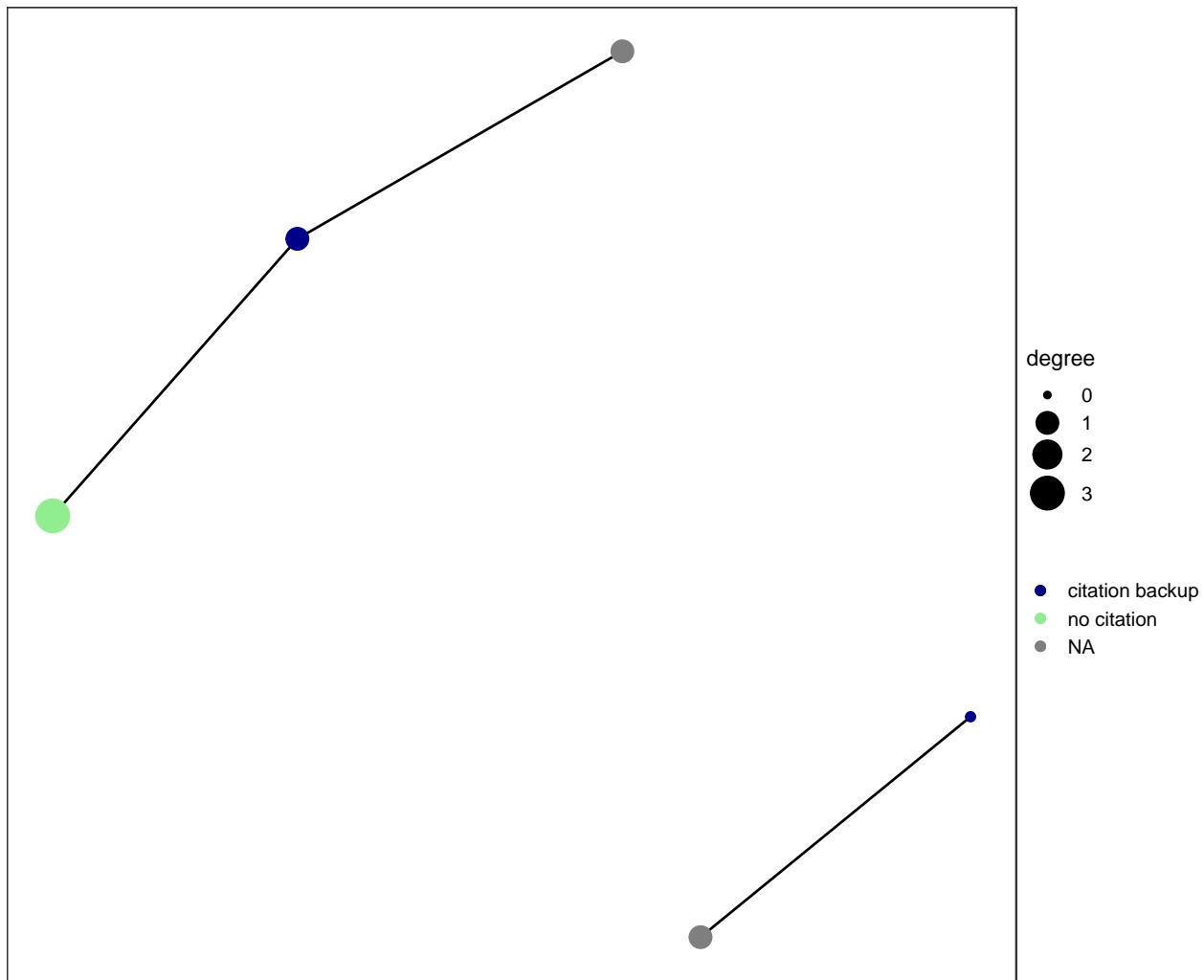
da

## $food
## $food[[1]]

## Warning: Removed 5 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).

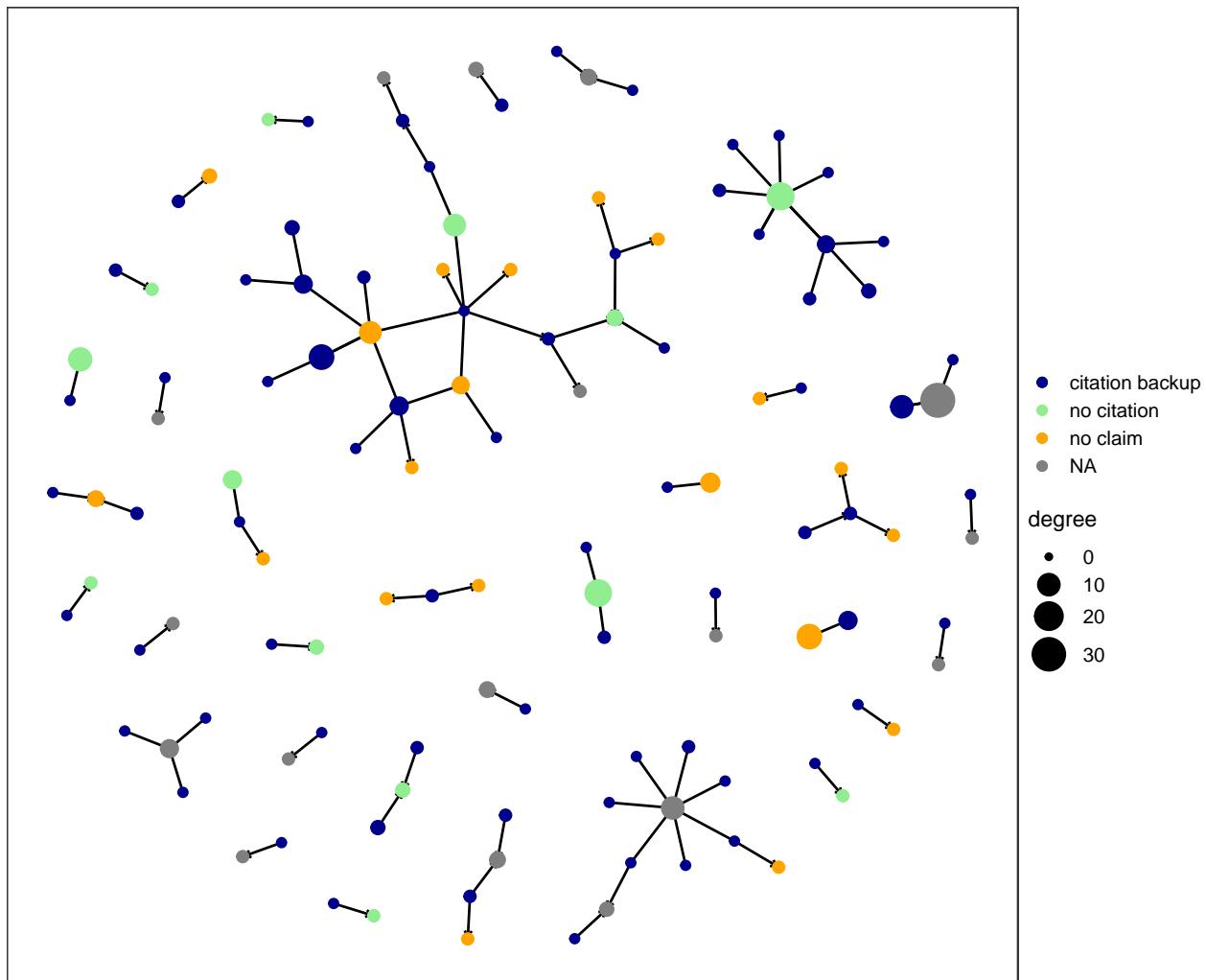
```

2000



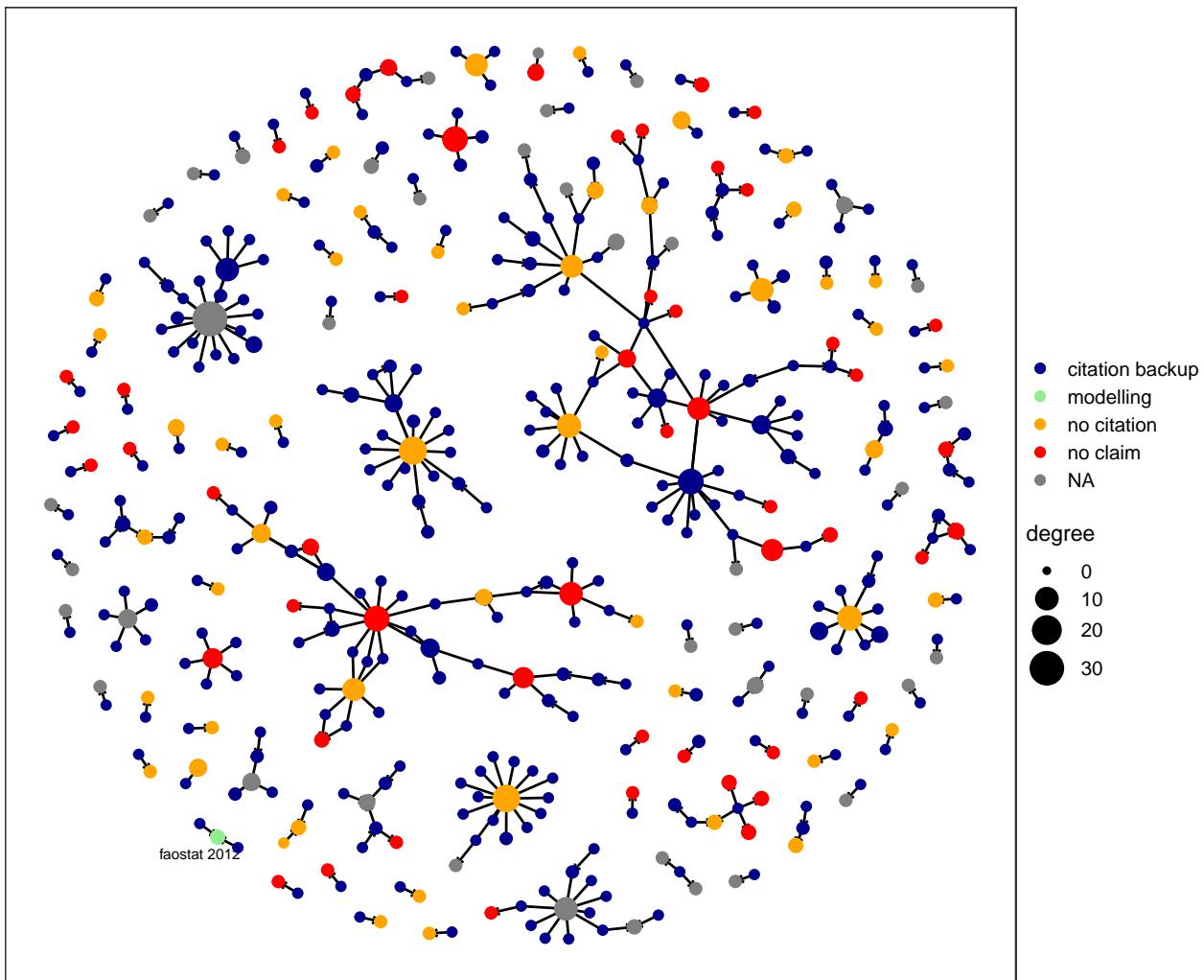
```
##  
## $food[[2]]  
## Warning: Removed 122 rows containing missing values or values outside the scale range  
## (`geom_text_repel()`).
```

2010



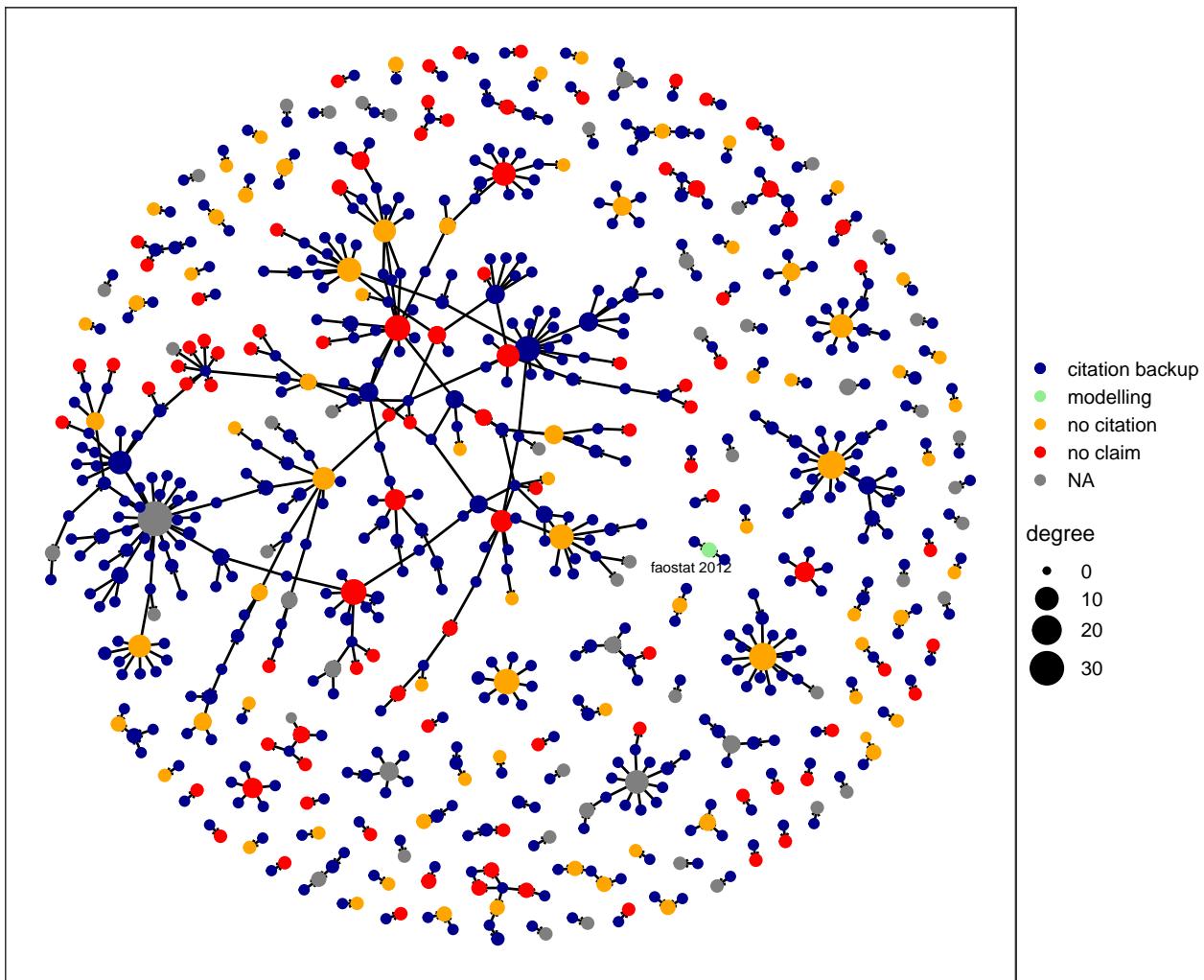
```
##  
## $food[[3]]  
  
## Warning: Removed 444 rows containing missing values or values outside the scale range  
## (`geom_text_repel()`).
```

2020



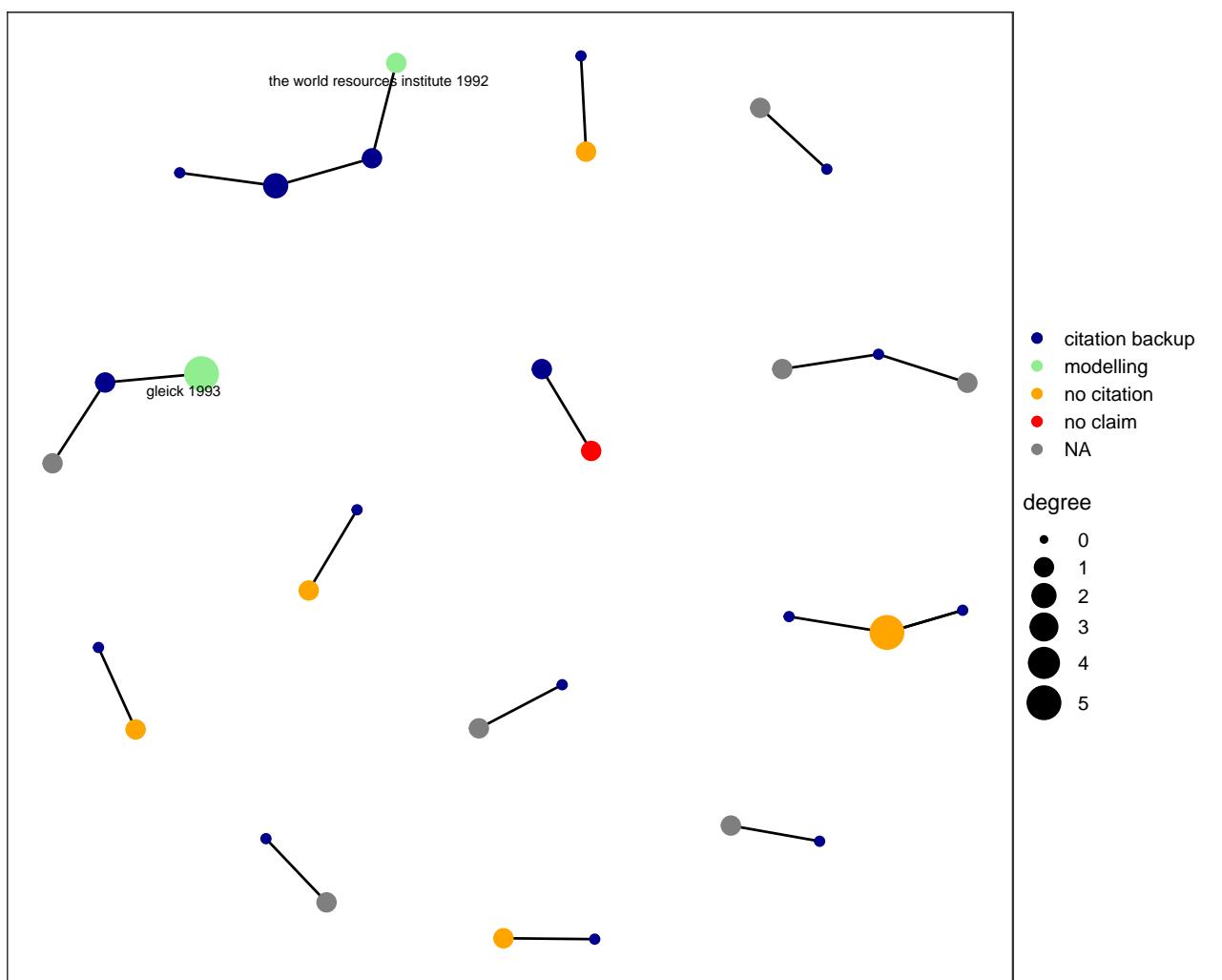
```
##  
## $food[[4]]  
  
## Warning: Removed 712 rows containing missing values or values outside the scale range  
## (`geom_text_repel()`).
```

2024



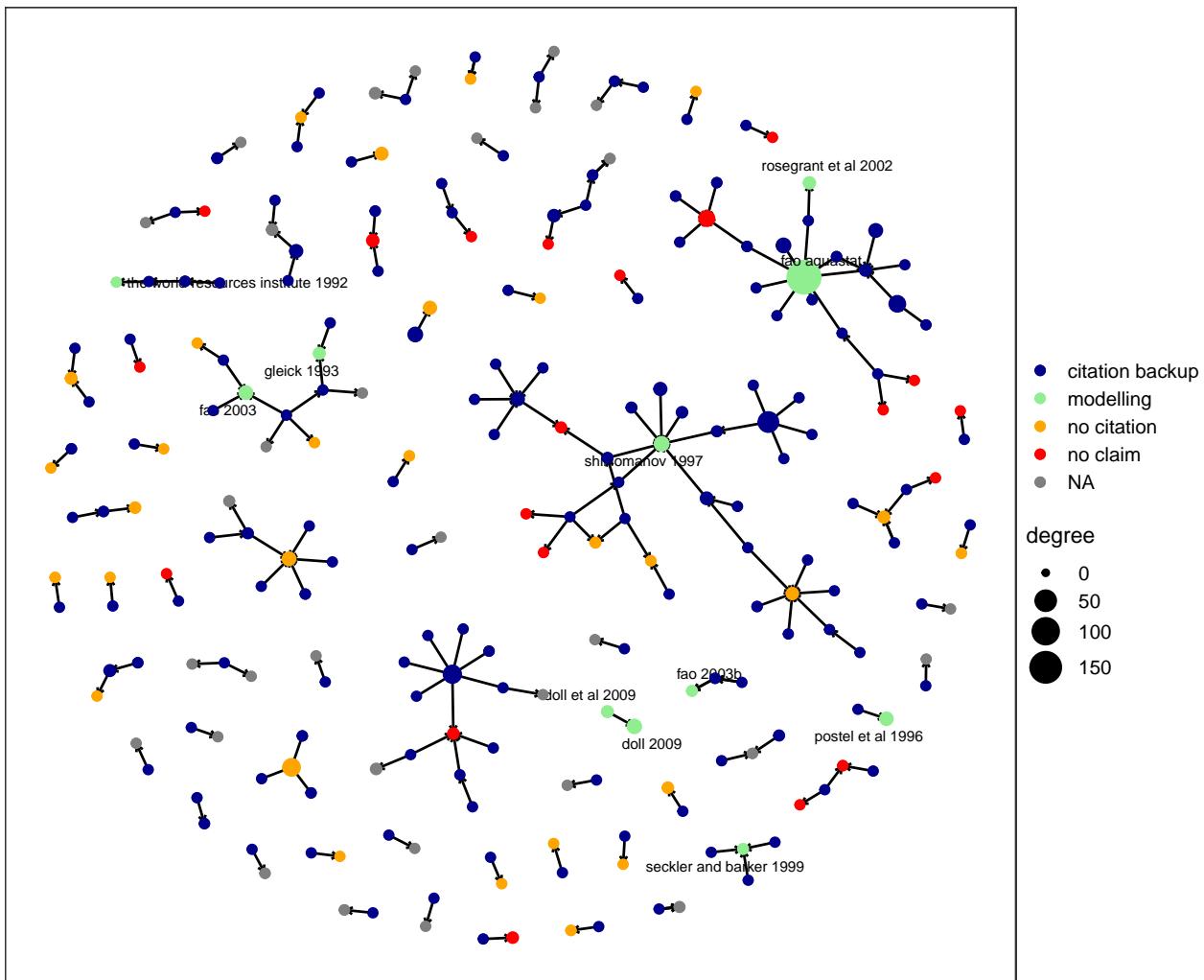
```
##  
##  
## $water  
## $water[[1]]  
  
## Warning: Removed 29 rows containing missing values or values outside the scale range  
## (`geom_text_repel()`).
```

2000



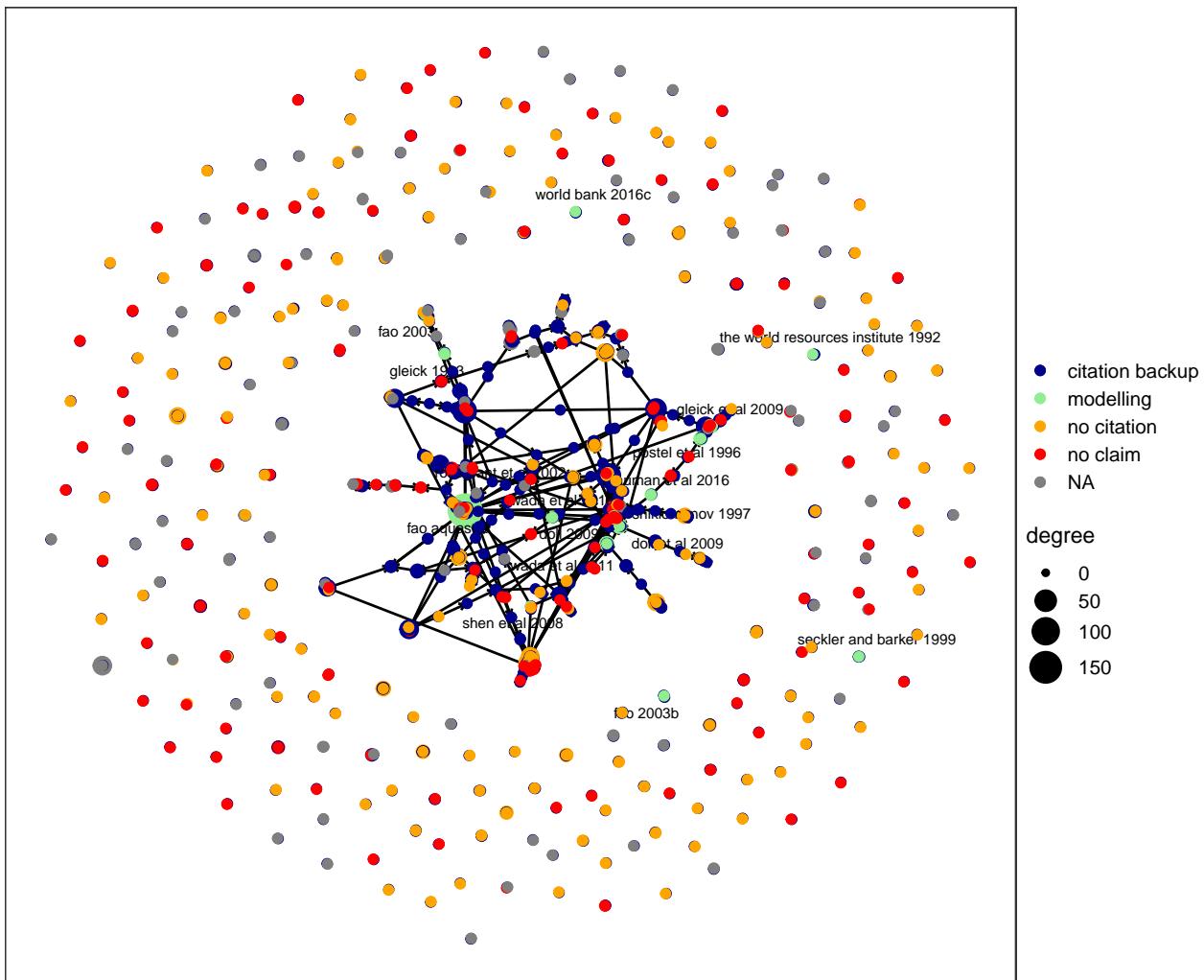
```
##  
## $water[[2]]  
  
## Warning: Removed 230 rows containing missing values or values outside the scale range  
## (`geom_text_repel()`).
```

2010



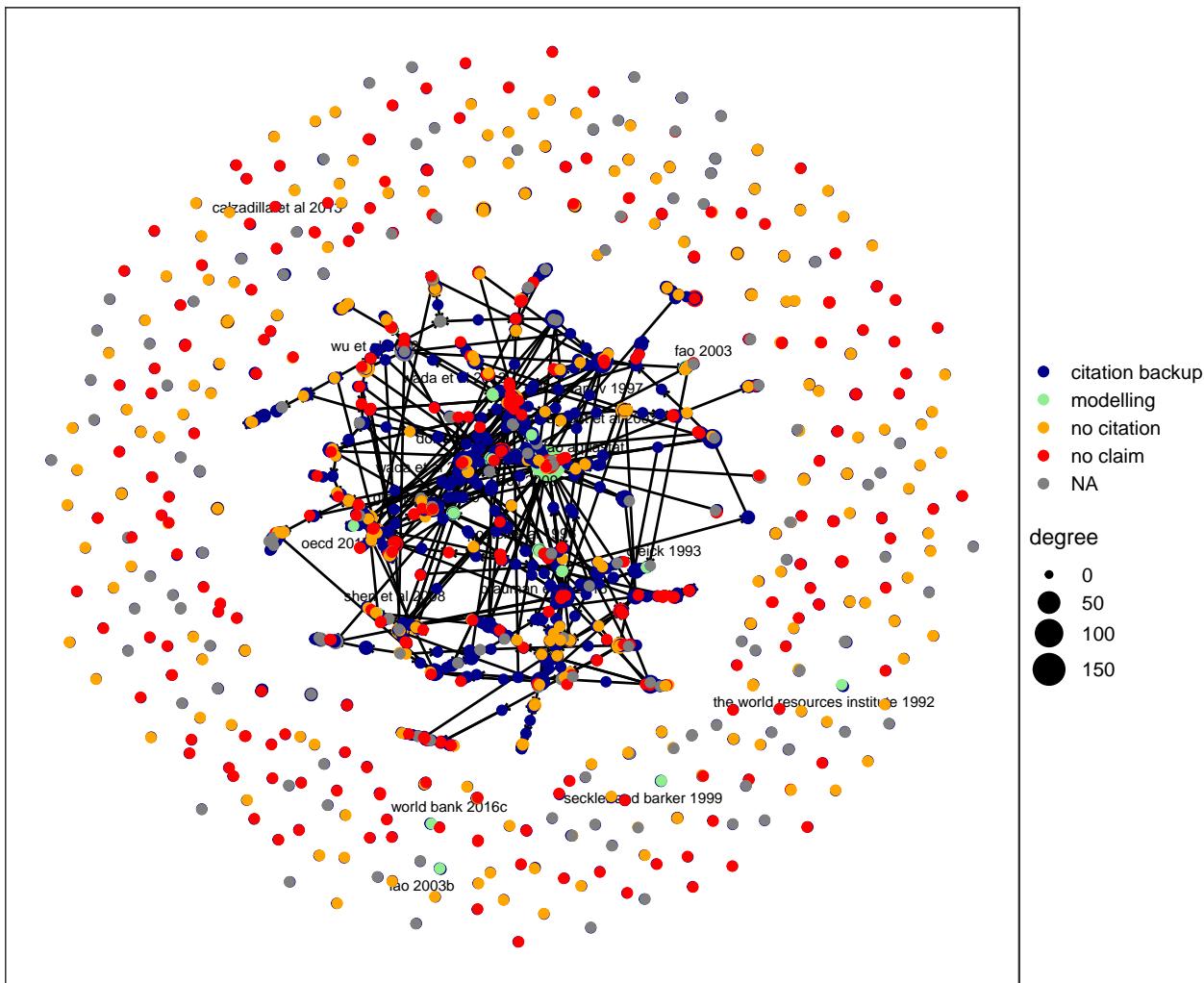
```
##  
## $water[[3]]  
  
## Warning: Removed 1463 rows containing missing values or values outside the scale range  
## (`geom_text_repel()`).
```

2020



```
##  
## $water[[4]]  
  
## Warning: Removed 2703 rows containing missing values or values outside the scale range  
## (`geom_text_repel()`).
```

2024



```
# PLOT #####
# Extract legend -----
legend.plot <- list()
for (i in names(plots.through.time)) {
  legend.plot[[i]] <- get_legend(plots.through.time[[i]][[length(plots.through.time[[i]])]] +
    theme(legend.position = "top"))
}
## Warning: Removed 712 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).
## Warning in get_plot_component(plot, "guide-box"): Multiple components found;
## returning the first one. To return all, use `return_all = TRUE` .
## Warning: Removed 2703 rows containing missing values or values outside the scale range
```

```

## (`geom_text_repel()`).

## Warning in get_plot_component(plot, "guide-box"): Multiple components found;
## returning the first one. To return all, use `return_all = TRUE`.

# Plot ----

bottom <- out.plot <- list()

for (i in names(plots.through.time)) {

  bottom[[i]] <- do.call(plot_grid, c(plots.through.time[[i]],
                                      nrow = floor(length(years.vector) / 2)))
  out.plot[[i]] <- plot_grid(legend.plot[[i]],
                            bottom[[i]], ncol = 1, rel_heights = c(0.1, 0.9))

}

## Warning: Removed 5 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).

## Warning: Removed 122 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).

## Warning: Removed 444 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).

## Warning: Removed 712 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).

## Warning: Removed 29 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).

## Warning: Removed 230 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).

## Warning: Removed 1463 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).

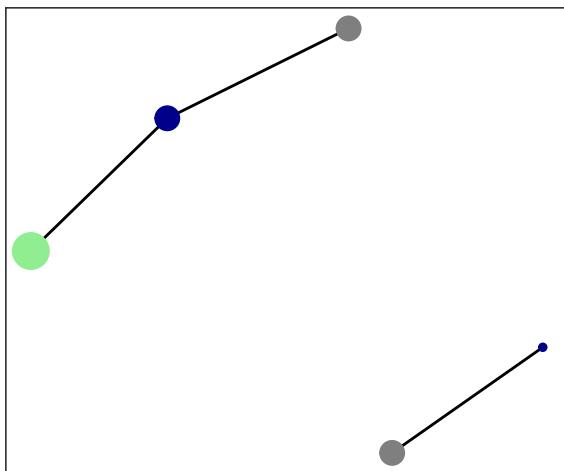
## Warning: Removed 2703 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).

out.plot

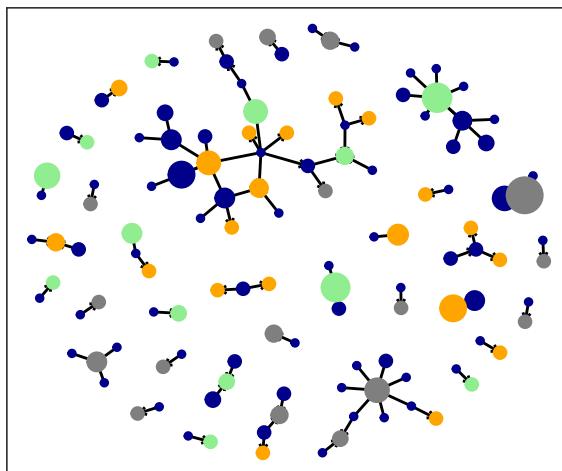
## $food

```

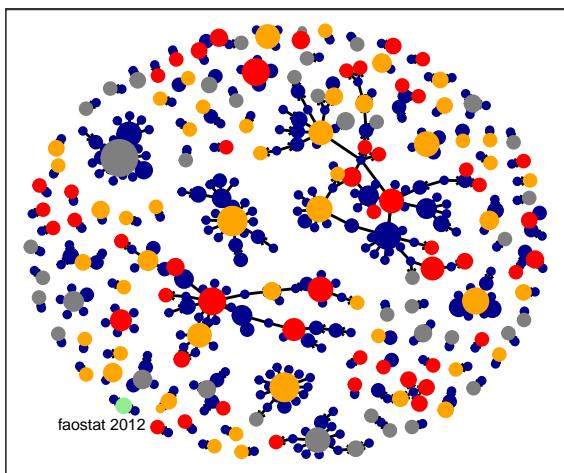
2000



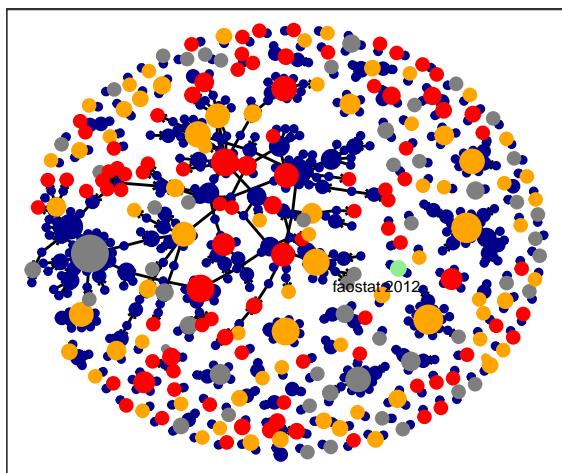
2010



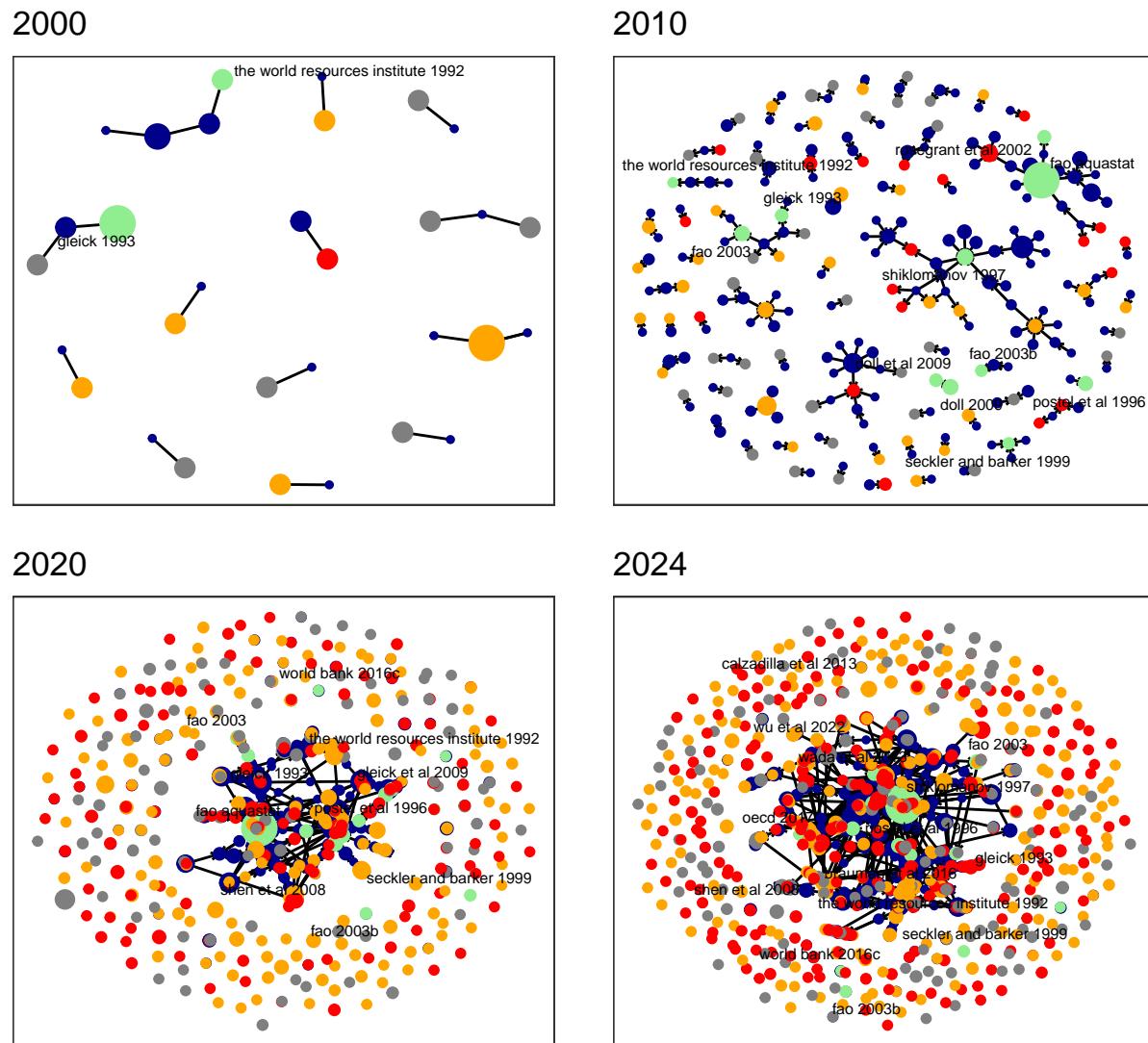
2020



2024



```
##  
## $water  
  
## Warning: ggrepel: 7 unlabeled data points (too many overlaps). Consider  
## increasing max.overlaps  
  
## Warning: ggrepel: 6 unlabeled data points (too many overlaps). Consider  
## increasing max.overlaps
```



5 Analysis of paths

5.1 “no claim” or “no citation” paths

```
# COUNT THE NUMBER OF NODES WITH PATHS ULTIMATELY LEADING TO NODES
# THAT DO NOT MAKE THE CITATION #####
# Function: loop through each node that do not make the claim to find all nodes
# connected to it -----
nodes_to_no_claim_node_fun <- function(g, terminal_nodes) {

  if (!is.igraph(g)) {
    g <- as.igraph(g)
  }
}
```

```

all_predecessors <- vector("list", length(terminal_nodes))

for (i in seq_along(terminal_nodes)) {

  terminal_node <- terminal_nodes[i]
  predecessors <- subcomponent(g, terminal_node, mode = "in")
  all_predecessors[[i]] <- predecessors
}

unique_predecessors <- unique(names(unlist(all_predecessors)))

return(unique_predecessors)
}

# CALCULATE

# Extract name of all nodes -----
all_nodes <- lapply(graph.final, function(graph)
  graph %>%
    activate(nodes) %>%
    pull(name))

# Extract name of nodes that do not make the claim -----

no.claim_nodes <- lapply(graph.final, function(graph)
  graph %>%
    activate(nodes) %>%
    filter(degree.out == 0 & nature.claim == "no claim") %>%
    pull(., "name"))

# Extract name of nodes that do not make the claim and those that make
# the claim but do not cite anybody -----

no.claim.and.no.citation.nodes <- lapply(graph.final, function(graph)
  graph %>%
    activate(nodes) %>%
    filter(degree.out == 0 & nature.claim == "no claim" | nature.claim == "no citation" ) %>%
    pull(., "name"))

# Run the function -----

tmp <- list()

for(i in names(graph.final)) {

  tmp[[i]] <- lapply(list(no.claim_nodes[[i]],

```

```

            no.claim.and.no.citation.nodes[[i]]), function(x)
  sort(nodes_to_no_claim_node_fun(graph.final[[i]], terminal_nodes = x)))
}

## Warning: `is.igraph()` was deprecated in igraph 2.0.0.
## i Please use `is_igraph()` instead.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.

for(i in names(graph.final)) {
  names(tmp[[i]]) <- c("path ending in no claim",
                      "path ending in no claim or no citation")
}

tmp

## $food
## $food$path ending in no claim
## [1] "abafe et al 2022"
## [2] "abd-elghany et al 2021"
## [3] "abdelmoneim et al 2023"
## [4] "ahmad et al 2018"
## [5] "ahmad et al 2022"
## [6] "al tenaiji et al 2019"
## [7] "al-agele et al 2021"
## [8] "alexandratos and bruinsma 2012"
## [9] "anderson et al 2012"
## [10] "appiah and asomani-boateng 2018"
## [11] "aseyehhegn et al 2012"
## [12] "attia et al 2022"
## [13] "avellan and gremillion 2019"
## [14] "barbier 2016"
## [15] "barbosa et al 2022"
## [16] "bastiaanssen et al 2000"
## [17] "bastiaanssen et al 2007"
## [18] "bazzi et al 2020"
## [19] "bekchanov et al 2015"
## [20] "bennett et al 2015"
## [21] "bindraban 2012"
## [22] "blanco et al 2019"
## [23] "bovolo et al 2009"
## [24] "cai and rosegrant 2002"
## [25] "camacho et al 2021"
## [26] "cecilia et al 2022"
## [27] "cervera-gasco et al 2020"
## [28] "cervera-gasco et al 2021"
## [29] "chateau et al 2014"

```

```
## [30] "chen et al 2017"
## [31] "chen et al 2018"
## [32] "chowdhury et al 2022"
## [33] "clay 2004"
## [34] "cotera et al 2023"
## [35] "cruse et al 2016"
## [36] "dalin et al 2017"
## [37] "das et al 2018"
## [38] "de vrese et al 2016"
## [39] "defries 2008"
## [40] "dinar et al 2019"
## [41] "dong et al 2023"
## [42] "dos santos et al 2016"
## [43] "drastig et al 2016"
## [44] "du et al 2015"
## [45] "elbakidze and cobourn 2014"
## [46] "emami and koch 2018"
## [47] "ertas et al 2021"
## [48] "es'haghi et al 2022"
## [49] "falkenmark 2013"
## [50] "famiglietti et al 2011"
## [51] "fao 1999d"
## [52] "fao 2002e"
## [53] "fao 2008b"
## [54] "fao 2011"
## [55] "fao 2012"
## [56] "fao 2012f"
## [57] "fao 2012g"
## [58] "fao 2012i"
## [59] "fao 2014c"
## [60] "fao 2015d"
## [61] "fao 2016e"
## [62] "fao 2017c"
## [63] "fao 2018g"
## [64] "fao 2019"
## [65] "fao 2019d"
## [66] "faostat 2006"
## [67] "farrag et al 2015"
## [68] "fereres and connor 2004"
## [69] "fereres and soriano 2006"
## [70] "fernandez garcia et al 2018"
## [71] "finkenbiner et al 2019"
## [72] "flemer and champ 2006"
## [73] "foley et al 1996"
## [74] "foley et al 2011"
## [75] "gebul 2021"
## [76] "gerber et al 2013"
## [77] "gheewala et al 2014"
```

```

## [78] "gibson et al 2017"
## [79] "gibson et al 2018"
## [80] "gleick 1993"
## [81] "godfray et al 2010"
## [82] "goel et al 2007"
## [83] "grados et al 2022"
## [84] "grassini et al 2011"
## [85] "guimberteau et al 2011"
## [86] "guo et al 2023"
## [87] "hamdani et al 2023"
## [88] "hammond and dubé 2012"
## [89] "hando 2022"
## [90] "hanjra and qureshi 2010"
## [91] "hardie 2020"
## [92] "harmel et al 2020"
## [93] "hassan et al 2022"
## [94] "hubert et al 2010"
## [95] "huffaker 2008"
## [96] "hussain et al 2010"
## [97] "jain et al 2021"
## [98] "jambo et al 2021"
## [99] "jenkins et al 2021"
## [100] "johansson 2000"
## [101] "johnson et al 2001"
## [102] "jury and vaux jr 2005"
## [103] "kadigi et al 2004"
## [104] "karimzadeh et al 2024"
## [105] "kataoka et al 2017"
## [106] "knapp and schwabe 2008"
## [107] "koch et al 2020"
## [108] "konikow 2015"
## [109] "kundzewicz et al 2007"
## [110] "lado et al 2024"
## [111] "lawston et al 2017"
## [112] "lele et al 2013"
## [113] "leng et al 2016"
## [114] "leng et al 2017"
## [115] "li et al 2021f"
## [116] "li et al 2023f"
## [117] "liagre et al 2015"
## [118] "lin et al 2024"
## [119] "lipan et al 2019"
## [120] "liu et al 2018"
## [121] "liu et al 2022"
## [122] "liu et al 2023 b"
## [123] "ma et al 2021"
## [124] "machibya and mdemu 2005"
## [125] "madramootoo and fyles 2012"

```

```
## [126] "magidi et al 2021"
## [127] "mahapatra et al 2020"
## [128] "mao et al 2003"
## [129] "mao et al 2024"
## [130] "maponya et al 2015"
## [131] "martins et al 2023"
## [132] "mathur and achutarao 2019"
## [133] "mazengo et al 2022"
## [134] "mccabe and wolock 2007"
## [135] "mcdermid et al 2023"
## [136] "mebrahtu et al 2018"
## [137] "mehta et al 2024"
## [138] "millenium ecosystem assessment 2005"
## [139] "mitchell et al 2018"
## [140] "molden 2007"
## [141] "molden and de fraiture 2010"
## [142] "molden et al 2007"
## [143] "molden et al 2007b"
## [144] "molden et al 2010"
## [145] "moyo et al 2020"
## [146] "mueller et al 2012"
## [147] "mukherji et al 2009"
## [148] "muratoglu et al 2023"
## [149] "mutambara 2016"
## [150] "ngouajio et al 2008"
## [151] "nikolaou et al 2020"
## [152] "ning et al 2023"
## [153] "niu et al 2022"
## [154] "niu et al 2023"
## [155] "norton et al 2021"
## [156] "obembe et al 2023"
## [157] "oecd 2012b"
## [158] "oecd and fao 2020"
## [159] "onishi et al 2019"
## [160] "owens et al 2022"
## [161] "ozdogan 2011"
## [162] "panettieri et al 2013"
## [163] "papdopoulos et al 2005"
## [164] "pawlak and kołodziejczak 2020"
## [165] "pei et al 2017"
## [166] "peña-guerrero et al 2020"
## [167] "perry and steduto 2017"
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## [1692] "united nations 2014"
## [1693] "united nations 2018c"
## [1694] "united nations 2020b"
## [1695] "united nations 2020c"
## [1696] "united nations 2021"
## [1697] "united nations 2022"
## [1698] "united nations 2023"
## [1699] "united nations department of economic and social affairs, 2014"
## [1700] "united nations environment programme 2019"
## [1701] "united nations nd"
## [1702] "untari et al 2021"
## [1703] "usda 2019"
## [1704] "vaddula and singh 2023"
## [1705] "valipour 2013"
## [1706] "valipour 2014"
## [1707] "valmassoi et al 2020"
## [1708] "van der ploeg et al 2008"
## [1709] "van helden 2011"
## [1710] "van tol de castro et al 2022"
## [1711] "van winterfeldt 2013"
## [1712] "vapnek et al 2009"
## [1713] "varis et al 2017"
## [1714] "varma et al 2021"
## [1715] "vashisht et al 2020"
## [1716] "vatanpour et al 2021"
## [1717] "vaverka et al 2021"
## [1718] "velarde-guillen et al 2022"

```

```
## [1719] "velasco-munoz et al 2018"
## [1720] "velasco-munoz et al 2019"
## [1721] "velez sanchez et al 2023"
## [1722] "velis et al 2017"
## [1723] "velpuri et al 2009"
## [1724] "vera-puerto et al 2022"
## [1725] "verdegem et al 2006"
## [1726] "vereeken et al 2009"
## [1727] "vereeken et al 2019"
## [1728] "vermeulen et al 2012"
## [1729] "viala 2007"
## [1730] "viala 2008"
## [1731] "vigneswaran et al 2021"
## [1732] "villar-navascues et al 2020"
## [1733] "vineesha and singh 2008"
## [1734] "vivirola et al 2003"
## [1735] "vizinho et al 2021"
## [1736] "vlek et al 2017"
## [1737] "voit et al 2023"
## [1738] "von braun 2008"
## [1739] "vorosmarty et al 2000"
## [1740] "vorosmarty et al 2005"
## [1741] "vorosmarty et al 2010"
## [1742] "waaswa et al 2022"
## [1743] "wada 2015"
## [1744] "wada and bierkens 2014"
## [1745] "wada et al 2013b"
## [1746] "wada et al 2014"
## [1747] "wada et al 2016"
## [1748] "wada et al 2016b"
## [1749] "wajima 2018"
## [1750] "wallace 2000"
## [1751] "wallace et al 2003"
## [1752] "wallingford 1997"
## [1753] "walter et al 2017"
## [1754] "wan et al 2018"
## [1755] "wang 2022"
## [1756] "wang and dickinson 2012"
## [1757] "wang et al 2014"
## [1758] "wang et al 2016"
## [1759] "wang et al 2017b"
## [1760] "wang et al 2018"
## [1761] "wang et al 2018b"
## [1762] "wang et al 2019"
## [1763] "wang et al 2020"
## [1764] "wang et al 2021 a"
## [1765] "wang et al 2022a"
## [1766] "wang et al 2022b"
```

```
## [1767] "wang et al 2022c"
## [1768] "wang et al 2022e"
## [1769] "wang et al 2022f"
## [1770] "wang et al 2022g"
## [1771] "wang et al 2022h"
## [1772] "wang et al 2023"
## [1773] "wang et al 2023 b"
## [1774] "wang et al 2023c"
## [1775] "wang et al 2024"
## [1776] "wanyama et al 2023"
## [1777] "wardiman and yonariza 2023"
## [1778] "watto and mugera 2015"
## [1779] "wbcisd 2009"
## [1780] "weatherhead and howden 2009"
## [1781] "weaver 2015"
## [1782] "weerakoon et al 2021"
## [1783] "wef 2020"
## [1784] "wei et al 2023"
## [1785] "weiss and slobodian 2014"
## [1786] "wen et al 2022"
## [1787] "whitmee et al 2015"
## [1788] "who 2014"
## [1789] "wicaksono et al 2019"
## [1790] "wichaidist et al 2023"
## [1791] "widiasri et al 2021"
## [1792] "wiquesiri et al 2020"
## [1793] "willett et al 2019"
## [1794] "williams et al 2017"
## [1795] "wilson 2013"
## [1796] "wilson et al 2019"
## [1797] "winpenny et al 2010"
## [1798] "wirth et al 2021"
## [1799] "wisser et al 2008"
## [1800] "wisser et al 2010"
## [1801] "wmo 1997"
## [1802] "wokem and lawson-jack 2015"
## [1803] "wong et al 2021"
## [1804] "wood et al 2000"
## [1805] "world bank 1992"
## [1806] "world bank 2001"
## [1807] "world bank 2017"
## [1808] "world bank 2020"
## [1809] "world bank 2021"
## [1810] "world bank 2022"
## [1811] "world economic forum 2010"
## [1812] "world economic forum 2011"
## [1813] "world economic forum 2014"
## [1814] "world resources institute 2001"
```

```
## [1815] "world resources institute 2010"
## [1816] "world resources institute 2020"
## [1817] "world watch institute 2004"
## [1818] "world water assessment programme 2003"
## [1819] "world water assessment programme 2006"
## [1820] "world water assessment programme 2012b"
## [1821] "world water vision"
## [1822] "worldometers 2019"
## [1823] "wri 1994"
## [1824] "wri 1996"
## [1825] "wri 2000"
## [1826] "wri 2016"
## [1827] "wu and zheng 2023"
## [1828] "wu et al 2018"
## [1829] "wu et al 2019"
## [1830] "wu et al 2020"
## [1831] "wu et al 2022"
## [1832] "wu et al 2022c"
## [1833] "wu et al 2023"
## [1834] "wu et al 2024"
## [1835] "wwf 2006"
## [1836] "wwf 2019"
## [1837] "xia et al 2022"
## [1838] "xiang et al 2020"
## [1839] "xiao et al 2005"
## [1840] "xiao et al 2024"
## [1841] "xiaogang et al 2020"
## [1842] "xie and lark 2021"
## [1843] "xie et al 2014"
## [1844] "xinchun et al 2017"
## [1845] "xing yuan et al 2024"
## [1846] "xiu et al 2022"
## [1847] "xiu et al 2022b"
## [1848] "xu et al 2020"
## [1849] "xu et al 2022"
## [1850] "xu et al 2023"
## [1851] "xue et al 2016"
## [1852] "xue et al 2017"
## [1853] "xue et al 2018"
## [1854] "yan et al 2022"
## [1855] "yan et al 2023"
## [1856] "yanes et al 2020"
## [1857] "yang et al 2003"
## [1858] "yang et al 2006"
## [1859] "yang et al 2015"
## [1860] "yang et al 2016"
## [1861] "yang et al 2021"
## [1862] "yang et al 2022"
```

```
## [1863] "yang et al 2023"
## [1864] "yannopoulos et al 2015"
## [1865] "yao et al 2022"
## [1866] "yasin et al 2022"
## [1867] "ye et al 2023"
## [1868] "yetik and sen 2023"
## [1869] "yigezu et al 2021"
## [1870] "yilmaz 2023"
## [1871] "yilmazkuday et al 2021"
## [1872] "yin et al 2022"
## [1873] "yip et al 2024"
## [1874] "yoshida et al 2013"
## [1875] "younes et al 2024"
## [1876] "young et al 2019"
## [1877] "yu 2014"
## [1878] "yu and songhao 2020"
## [1879] "yu et al 2015"
## [1880] "yu et al 2017"
## [1881] "yu et al 2019"
## [1882] "yu et al 2020"
## [1883] "yu et al 2021"
## [1884] "yu et al 2022"
## [1885] "yuli et al 2018"
## [1886] "zarei and mahmoudi 2020"
## [1887] "zarei and moghimi 2019a"
## [1888] "zarei and moghimi 2019b"
## [1889] "zarei et al 2021"
## [1890] "zeman et al 2006"
## [1891] "zeng and cai 2014"
## [1892] "zeng et al 2022"
## [1893] "zeraatkar et al 2016"
## [1894] "zhang 2011"
## [1895] "zhang 2013"
## [1896] "zhang and guo 2017"
## [1897] "zhang and guo 2018"
## [1898] "zhang et al 2015"
## [1899] "zhang et al 2015b"
## [1900] "zhang et al 2017"
## [1901] "zhang et al 2018b"
## [1902] "zhang et al 2019b"
## [1903] "zhang et al 2019c"
## [1904] "zhang et al 2021"
## [1905] "zhang et al 2021c"
## [1906] "zhang et al 2021f"
## [1907] "zhang et al 2022"
## [1908] "zhang et al 2022b"
## [1909] "zhang et al 2022c"
## [1910] "zhang et al 2022d"
```

```

## [1911] "zhang et al 2023"
## [1912] "zhao et al 2021"
## [1913] "zhao et al 2022"
## [1914] "zheng et al 2020"
## [1915] "zhi et al 2022"
## [1916] "zhou et al 2015"
## [1917] "zhou et al 2021"
## [1918] "zhou et al 2022"
## [1919] "zhu et al 2018"
## [1920] "zhu et al 2022"
## [1921] "zhu et al 2023"
## [1922] "zhuang et al 2023"
## [1923] "zhuo et al 2022"
## [1924] "zhupley et al 2021"
## [1925] "zia et al 2021"
## [1926] "zisopoulou et al 2022"
## [1927] "zong et al 2023"
## [1928] "zou and he 2016"
## [1929] "zou et al 2013"
## [1930] "zucchinelli et al 2021"

# Calculate proportions -----
out <- list()

for(i in names(tmp)) {
  out[[i]] <- lapply(tmp[[i]], function(x) length(x) / length(all_nodes[[i]]))
}

out

## $food
## $food$path ending in no claim
## [1] 0.388518
##
## $food$path ending in no claim or no citation
## [1] 0.7690254
##
## 
## $water
## $water$path ending in no claim
## [1] 0.3622378
##
## $water$path ending in no claim or no citation
## [1] 0.6748252

```

5.2 Calculation of amplification

```
# CREATE FUNCTION TO CHECK AMPLIFICATION #####
```

amplification measure for paper P : defined as the number of
citation-paths originating at P and terminating at all other papers,
except for paths of length 1 flowing directly to modelling papers.

```
amplification_fun <- function(graph) {  
  
  # Convert tbl_graph to igraph object -----  
  
  ig <- as.igraph(graph)  
  nature_claims <- V(ig)$nature.claim  
  
  # initialize counter to store results for each paper -----  
  
  results <- numeric(vcount(ig))  
  
  # Loop over each paper -----  
  
  for (P in V(ig)) {  
  
    # Initialize counter for valid paths  
    path_count <- 0  
  
    # Traverse through all nodes and count paths avoiding direct "modelling"  
    for (target in V(ig)) {  
  
      if (P != target) {  
  
        all_paths <- all_simple_paths(ig, from = P, to = target, mode = "out")  
  
        # Filter out paths of length 1 that end in a "modelling" node  
        valid_paths <- Filter(function(path) {  
          !(length(path) == 2 && nature_claims[path[2]] == "modelling")  
        }, all_paths)  
  
        path_count <- path_count + length(valid_paths)  
      }  
    }  
  
    results[P] <- path_count  
  }  
  
  return(results)  
}
```

```

# RUN AMPLIFICATION FUNCTION #####
amplification.indices <- lapply(graph.final, function(graph)
  amplification_fun(graph))

# Calculate average amplification index of the networks -----
# (e.g., the number paths initiated by the average paper
# leading to studies that do # not flow directly to "primary" data)
lapply(amplification.indices, function(x) mean(x))

## $food
## [1] 0.9212283
##
## $water
## [1] 1.582867

# PLOT DISTRIBUTION OF AMPLIFICATION INDEXES #####
plot.amplification <- list()

for (i in names(amplification.indices)) {

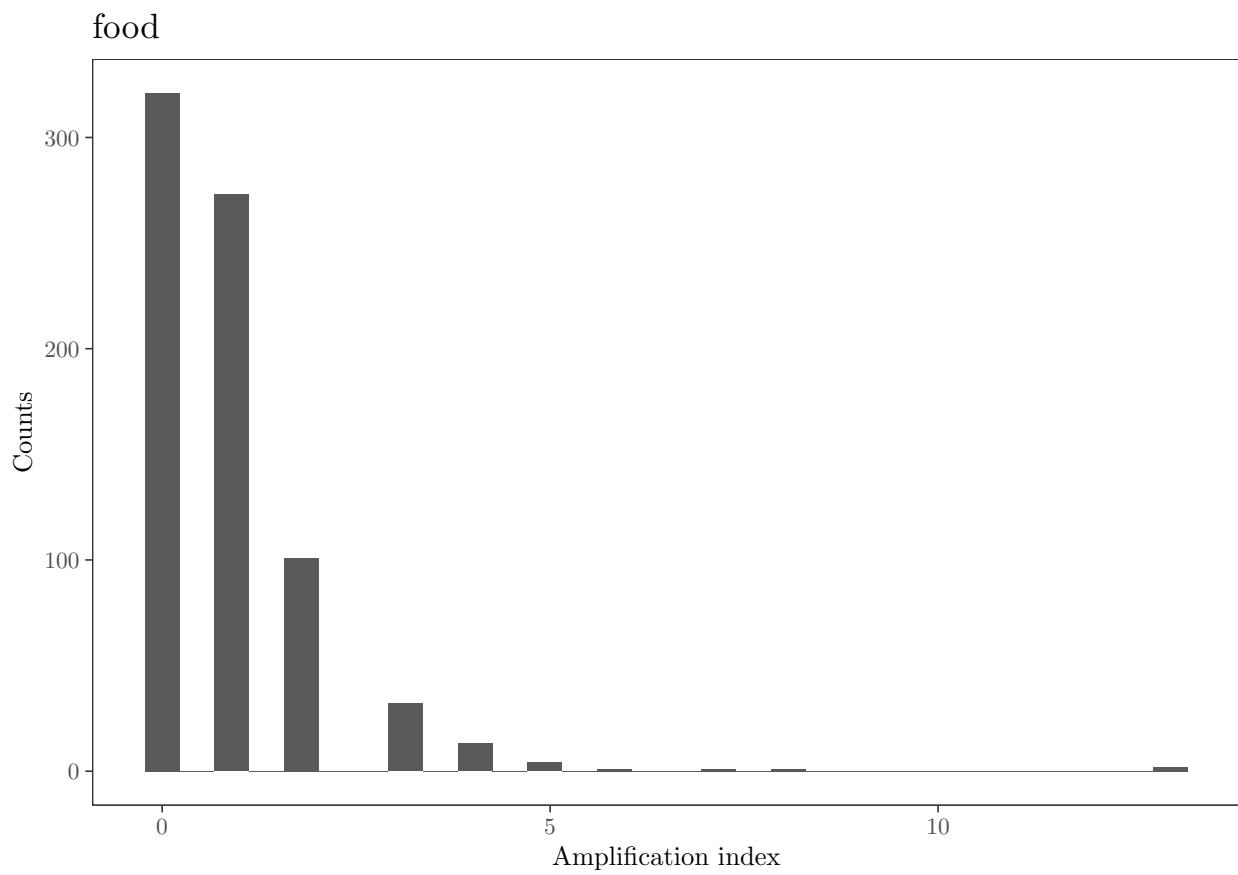
  plot.amplification[[i]] <- amplification.indices[[i]] %>%
    data.frame("index" = .) %>%
    ggplot(., aes(index)) +
    geom_histogram() +
    theme_AP() +
    labs(y = "Counts", x = "Amplification index") +
    ggtitle(names(amplification.indices[i]))

}

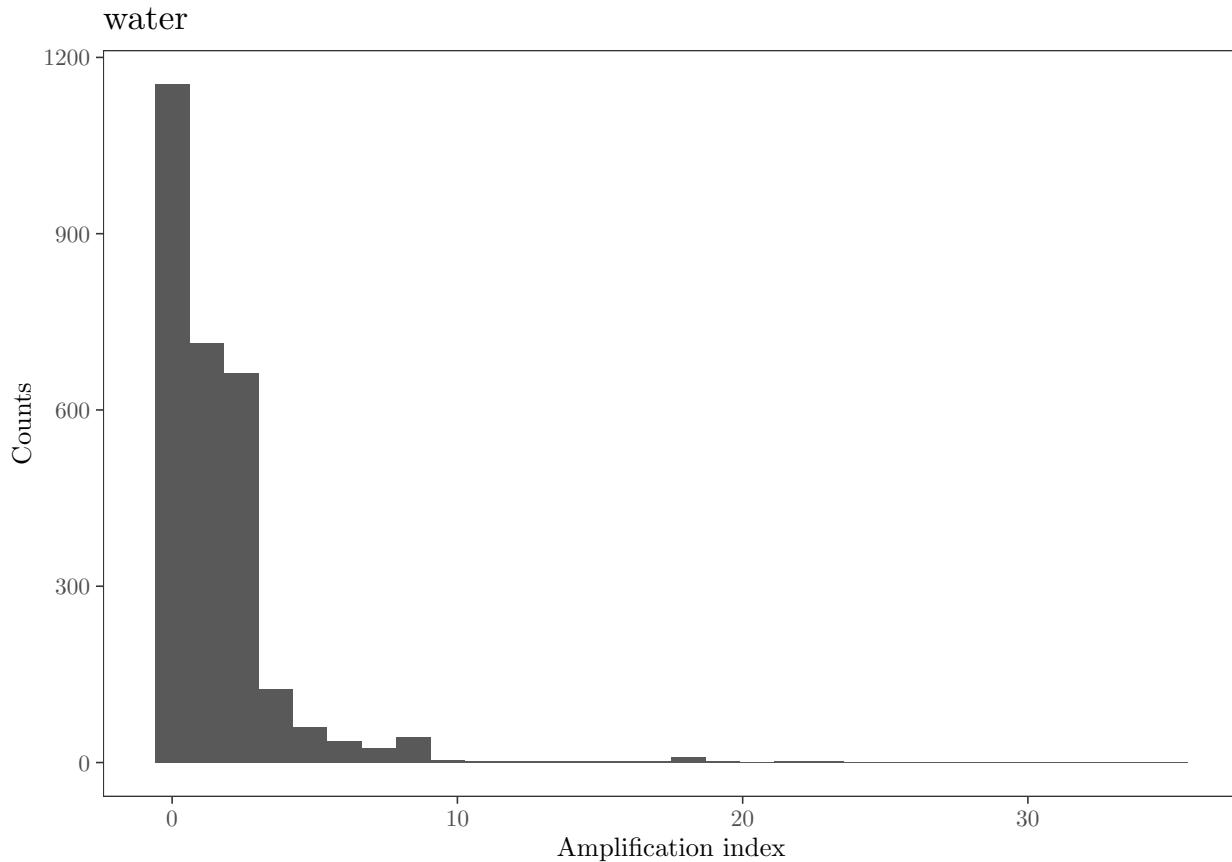
plot.amplification

## $food
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.

```



```
##  
## $water  
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



6 Study of Aquastat values

```
# STUDY OF AQUASTAT PERCENTAGES #####
# Read in aquastat dataset -----
aquastat.dt <- read.xlsx("aquastat_dt.xlsx") %>%
  data.table() %>%
  .[Year == 2020] %>%
  setnames(., c("Value", "Area"), c("percentage", "country")) %>%
  .[, .(country, percentage)] %>%
  .[, data:= "aquastat 2020"] %>%
  .[, country:= countrycode(country, origin = "country.name", destination = "country.name")]

## Warning: Some values were not matched unambiguously: Australia and New Zealand
## Warning: Some strings were matched more than once, and therefore set to <NA> in the result:
aquastat.dt[, continent:= countrycode(country, origin = "country.name", destination = "continent")]

# Read in world resources institute dataset -----

wri <- fread("world_resources_institut_guide_to_the_global_environment_1994.csv") %>%
```

```

. [order(country)] %>%
. [, data:= "wri 1994"] %>%
. [, country:= countrycode(country, origin = "country.name", destination = "country.name")]

## Warning: Some values were not matched unambiguously: , Cote d'lvoire
wri[, continent:= countrycode(country, origin = "country.name", destination = "continent")]

## Warning: Some values were not matched unambiguously: Czechoslovakia, Yugoslavia
# Compare distributions ----

dt.comparison <- rbind(aquastat.dt, wri) %>%
  .[, data:= factor(data, levels = c("wri 1994", "aquastat 2020"))]

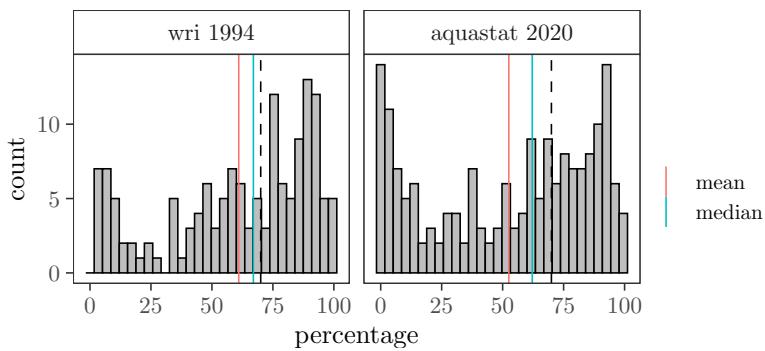
dt.stats.comparison <- dt.comparison[, .(mean = mean(percentage, na.rm = TRUE),
                                         median = median(percentage, na.rm = TRUE)), data] %>%
  melt(., measure.vars = c("mean", "median"))

ggplot(dt.comparison, aes(percentage)) +
  geom_histogram(color = "black", fill = "grey") +
  facet_wrap(~data) +
  geom_vline(data = dt.stats.comparison, aes(xintercept = value, color = variable)) +
  scale_color_discrete(name = "") +
  geom_vline(xintercept = 70, lty = 2) +
  theme_AP()

## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.

## Warning: Removed 1 rows containing non-finite values (`stat_bin()`).

```



```
# At the country level -----
```

```

tmp <- aquastat.dt[wri, on = c("country", "continent")] %>%
  .[, .(country, continent, percentage, i.percentage)] %>%
  setnames(., c("percentage", "i.percentage"), c("aquastat 2020", "wri 1994")) %>%
  melt(., measure.vars = c("aquastat 2020", "wri 1994")) %>%
  .[, country:= ifelse(country == "Trinidad & Tobago", "Trinidad and Tobago", country)] %>%
  na.omit() %>%

```

```

split(., .$continent)

## Warning in melt.data.table(., measure.vars = c("aquastat 2020", "wri 1994")):
## 'measure.vars' [aquastat 2020, wri 1994] are not all of the same type. By order
## of hierarchy, the molten data value column will be of type 'double'. All
## measure variables not of type 'double' will be coerced too. Check DETAILS in
## ?melt.data.table for more on coercion.

out <- list()

for(i in names(tmp)) {

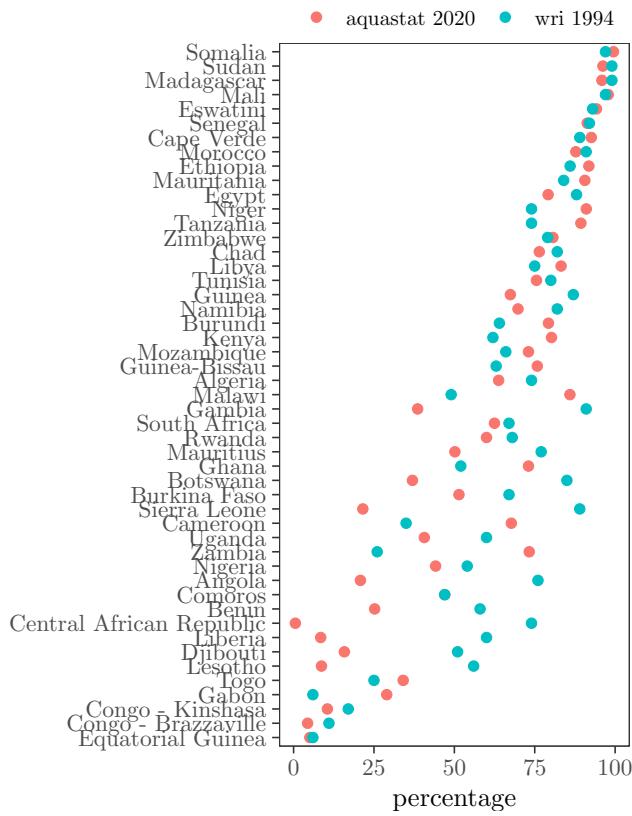
  out[[i]] <- ggplot(tmp[[i]], aes(reorder(country, value),
                                    value, color = variable)) +
    coord_flip() +
    scale_color_discrete(name = "") +
    geom_point() +
    theme_AP() +
    theme(legend.position = "top") +
    labs(x = "", y = "percentage") +
    ggtitle(names(tmp[i]))
}

out

## $Africa

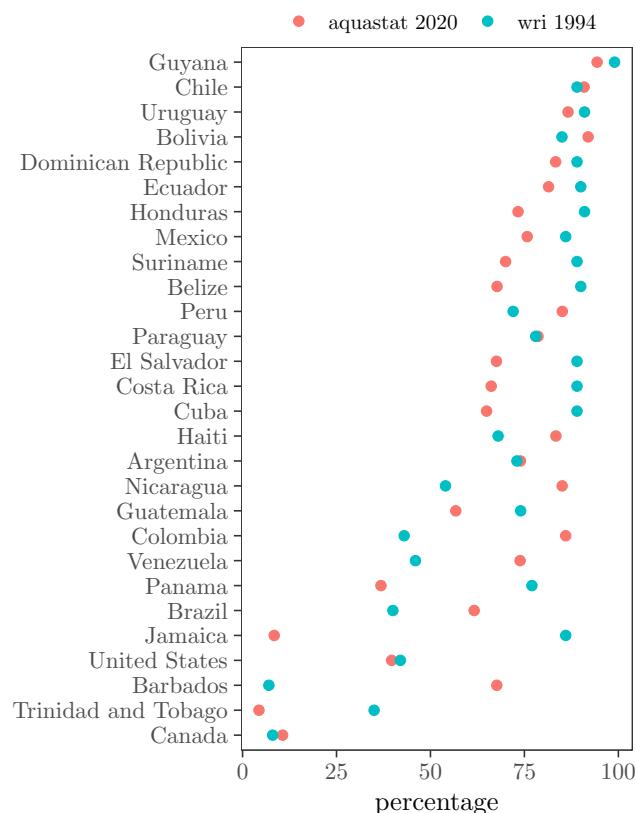
```

Africa



```
##  
## $Americas
```

Americas



```
##  
## $Asia
```

Asia



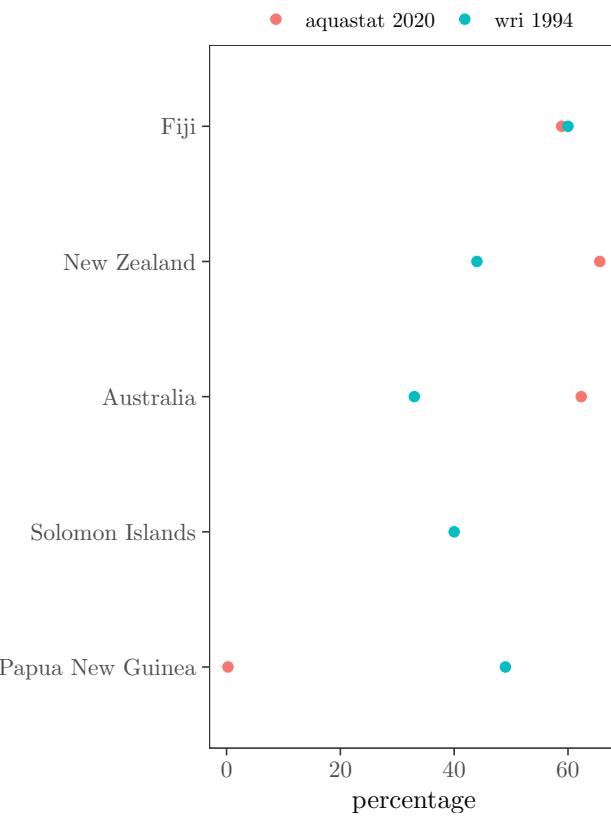
```
##  
## $Europe
```

Europe



```
##  
## $Oceania
```

Oceania



```

# AQUASTAT ALL YEARS #####
# Read in dataset -----
aquastat <- read.xlsx("AQUASTAT_Dissemination_System.xlsx") %>%
  data.table() %>%
  .[, Country:= countrycode(Area, origin = "country.name", destination = "country.name")] %>%
  .[!is.na(Country)] %>%
  .[, .(Country, Year, Variable, Value, Unit, Symbol)]

name.variables <- unique(aquastat$Variable)

aquastat.aww <- aquastat[Variable == name.variables[3]]
aquastat.aww.stats <- aquastat.aww[, .(mean = mean(Value, na.rm = TRUE),
                                         median = median(Value, na.rm = TRUE)), Year] %>%
  melt(., measure.vars = c("mean", "median"))

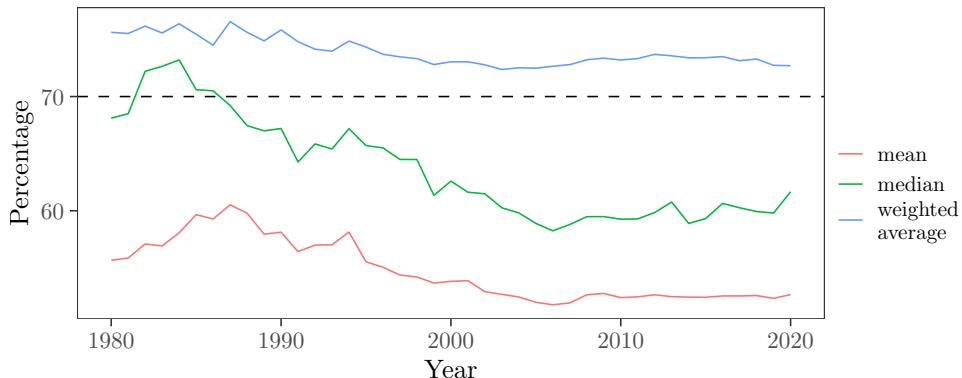
# Weighted average -----
aquastat.aww[, weights:= Value / sum(Value), Year]
weighted.average.dt <- aquastat.aww[, .(value = sum(Value * weights)), Year] %>%
  .[, variable:= "weighted \n average"]

```

```
# Plot ---

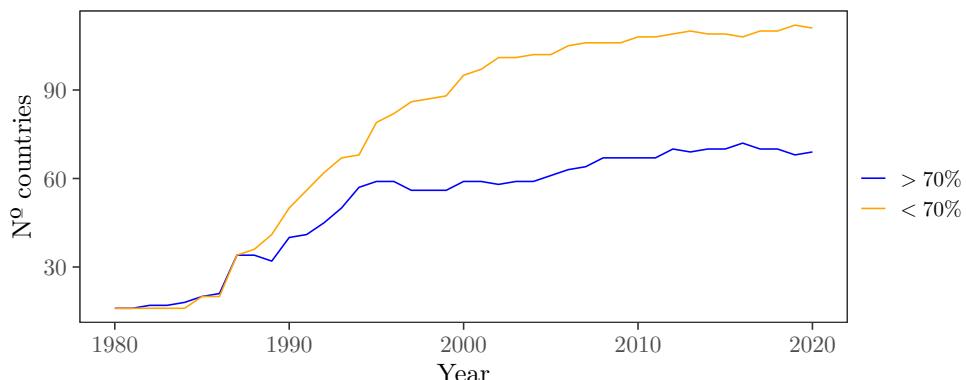
a <- aquastat.aww.stats %>%
  rbind(weighted.average.dt) %>%
  ggplot(., aes(Year, value, group = variable, color = variable)) +
  geom_line() +
  scale_color_discrete(name = "") +
  geom_hline(yintercept = 70, lty = 2) +
  theme_AP() +
  labs(x = "Year", y = "Percentage")
```

a

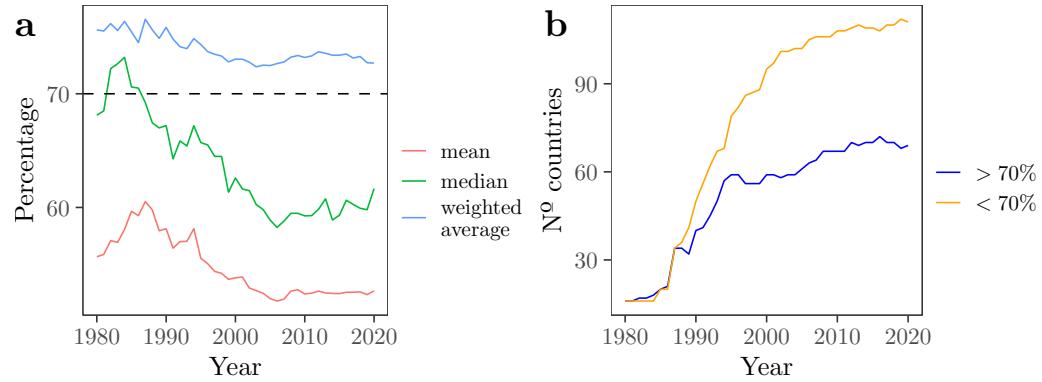


```
b <- aquastat.aww[, .(above.70 = sum(Value > 70),
                     below.70 = sum(Value < 70)), Year] %>%
  melt(., measure.vars = c("above.70", "below.70")) %>%
  ggplot(., aes(Year, value, color = variable)) +
  geom_line() +
  theme_AP() +
  scale_color_manual(name = "", labels = c("$>70$\n%", "$<70$\n%"),
                     values = c("blue", "orange")) +
  labs(x = "Year", y = "Nº countries")
```

b



```
plot_grid(a, b, ncol = 2, labels = "auto")
```



7 Session information

```
# SESSION INFORMATION #####
sessionInfo()

## R version 4.3.3 (2024-02-29)
## Platform: aarch64-apple-darwin20 (64-bit)
## Running under: macOS Sonoma 14.2.1
##
## Matrix products: default
## BLAS:    /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/lib/libRblas.0.dylib
## LAPACK:  /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/lib/libRlapack.dylib;
##
## locale:
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
## 
## time zone: Europe/London
## tzcode source: internal
##
## attached base packages:
## [1] parallel stats      graphics grDevices utils      datasets methods
## [8] base
##
## other attached packages:
## [1] scales_1.3.0      wesanderson_0.3.6  benchmarkme_1.0.8  tidygraph_1.3.0
## [5] cowplot_1.1.1     ggraph_2.1.0       igraph_1.6.0      bibliometrix_4.0.1
## [9] lubridate_1.9.2  forcats_1.0.0     stringr_1.5.1     dplyr_1.1.4
## [13] purrr_1.0.2      readr_2.1.4       tidyverse_2.0.0    tibble_3.2.1
## [17] ggplot2_3.4.4    tidyverse_2.0.0    data.table_1.14.99 openxlsx_4.2.5.2
##
## loaded via a namespace (and not attached):
## [1] Rdpack_2.6          gridExtra_2.3      readxl_1.4.2
## [4] rlang_1.1.3         magrittr_2.0.3     tidytext_0.4.1
## [7] compiler_4.3.3      vctrs_0.6.5        crayon_1.5.2
## [10] pkgconfig_2.0.3     fastmap_1.1.1     ellipsis_0.3.2
## [13] labeling_0.4.3     utf8_1.2.4        promises_1.2.0.1
## [16] rmarkdown_2.21      tzdb_0.3.0        tinytex_0.45
## [19] bit_4.0.5          xfun_0.39         jsonlite_1.8.4
## [22] flashClust_1.01-2  highr_0.10        SnowballC_0.7.1
## [25] later_1.3.0        tweenr_2.0.2      cluster_2.1.6
## [28] R6_2.5.1           stringi_1.8.3     RColorBrewer_1.1-3
## [31] cellranger_1.1.0   estimability_1.4.1 iterators_1.0.14
## [34] Rcpp_1.0.12         knitr_1.42        filehash_2.4-5
## [37] httpuv_1.6.9       rentrez_1.2.3     Matrix_1.6-5
## [40] timechange_0.2.0   tidyselect_1.2.0   viridis_0.6.4
## [43] rstudioapi_0.15.0 stringdist_0.9.10  pubmedR_0.0.3
## [46] yaml_2.3.7         codetools_0.2-19  doParallel_1.0.17
```

```

## [49] lattice_0.22-5          plyr_1.8.8           shiny_1.7.4
## [52] withr_3.0.0             benchmarkmeData_1.0.4 coda_0.19-4
## [55] evaluate_0.20          polyclip_1.10-6       zip_2.3.0
## [58] pillar_1.9.0            janeaustenr_1.0.0      foreach_1.5.2
## [61] DT_0.27                 plotly_4.10.1        generics_0.1.3
## [64] vroom_1.6.1             hms_1.1.3            munsell_0.5.0
## [67] sensobol_1.1.4          xtable_1.8-4        leaps_3.1
## [70] glue_1.7.0              tikzDevice_0.12.4     emmeans_1.8.5
## [73] scatterplot3d_0.3-43    lazyeval_0.2.2       tools_4.3.3
## [76] tokenizers_0.3.0         mvtnorm_1.1-3       graphlayouts_1.0.2
## [79] XML_3.99-0.14           grid_4.3.3          rbibutils_2.2.16
## [82] rscopus_0.6.6            colorspace_2.1-0     dimensionsR_0.0.3
## [85] ggforce_0.4.1            bibliometrixData_0.3.0 cli_3.6.2
## [88] fansi_1.0.6              viridisLite_0.4.2     gtable_0.3.4
## [91] digest_0.6.34            ggrepel_0.9.5        FactoMineR_2.8
## [94] htmlwidgets_1.6.2          farver_2.1.1        htmltools_0.5.5
## [97] factoextra_1.0.7         lifecycle_1.0.4      httr_1.4.5
## [100] multcompView_0.1-9      mime_0.12           bit64_4.0.5
## [103] MASS_7.3-60.0.1

## Return the machine CPU
cat("Machine:      "); print(get_cpu()$model_name)

## Machine:
## [1] "Apple M1 Max"

## Return number of true cores
cat("Num cores:   "); print(detectCores(logical = FALSE))

## Num cores:
## [1] 10

## Return number of threads
cat("Num threads: "); print(detectCores(logical = FALSE))

## Num threads:
## [1] 10

```