The belief in irrigation as essential for food and water security

R code

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Contents

```r
#   PRELIMINARY FUNCTIONS ##########################################################

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

# 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),
          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),
          strip.text.y = element_text(size = 7.4),
          legend.key.width = unit(0.4, "cm"),
          legend.key.height = unit(0.4, "cm"),
          legend.title = element_text(size = 7.8))
}
```

1 Network analysis

```r
# 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(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      Ukranian     1
##  9:  water    Portuguese     1
## 10:  water             T     2
## 11:   food          <NA>   204
## 12:   food             T   649
## 13:   food             F  2875
```

```
# 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:= grepl("^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    48
##  3: fao aquastat 2010  water    11
##  4: fao aquastat 2020  water     3
##  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    22
## 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     4
## 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
## 30: fao aquastat 2021   food     1
##              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
```

```
# CHECK NUMBER OF FAOSTAT CITES ###################################################

faostat.cites <- network.dt[citation %like% "faostat"] %>%
  .[, .N, .(citation, topic)]

faostat.cites
```

```
##                   citation  topic     N
##                     <char> <char> <int>
##  1: faostat online service  water     1
##  2:           faostat 2011  water     3
##  3:           faostat 2019  water     2
##  4:           faostat 2008  water     2
##  5:           faostat 2020  water     3
##  6:           faostat 2012  water     1
##  7:           faostat 2021  water     2
##  8:         faostat online  water     1
##  9:                faostat  water     3
```

```
## 10:              faostat   water     5
## 11:          faostat 2023  water     1
## 12:          faostat 2012   food     2
## 13:          faostat 2011   food     1
## 14:          faostat 2019   food     2
## 15:          faostat 2002   food     2
## 16:          faostat 2016   food     2
## 17:          faostat 2003   food     1
## 18:          faostat 1999   food     1
## 19:               faostat   food     1
```

```
oldest.faostat.cite <- min(as.integer(sub(".* (\\d{4})[a-z]?$", "\\1",
                                          faostat.cites$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
##    <char>       <int>
## 1:  water        3671
## 2:   food         902
```

```
# 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 <- grepl("^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]])]
}

# Remove the year from mentions to FAOSTAT -------------------------------------

for (col in c("citation", "author")) {
  matches <- grepl("^faostat\\s+\\d+$", network.dt[[col]], ignore.case = TRUE)
```

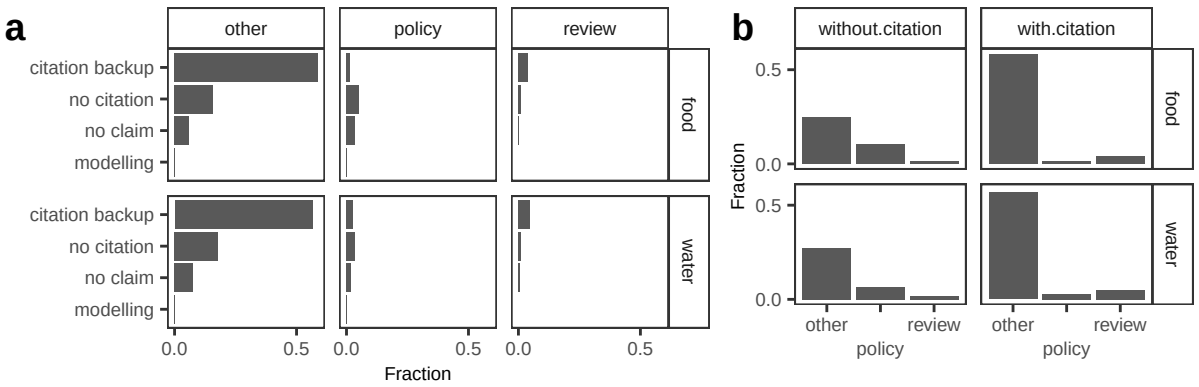
```
  network.dt[matches, (col) := gsub("\\d+", "", network.dt[[col]][matches], perl = TRUE)]
  network.dt[, (col) := trimws(network.dt[[col]])]
}

# 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"))
cols_to_change <- colnames(network.dt)
network.dt.claim[, (cols_to_change):= lapply(.SD, trimws), .SDcols = (cols_to_change)]
network.dt.claim[, (cols_to_change):= lapply(.SD, str_squish), .SDcols = (cols_to_change)]

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)]
network.dt[, (cols_to_change):= lapply(.SD, str_squish), .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   193        1037 0.186113790
##  2:   food citation backup   616        1037 0.594021215
##  3:   food        no claim    93        1037 0.089681774
```

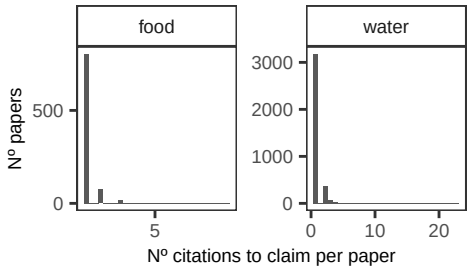
```
##  4:   food            <NA>    39        1037 0.037608486
##  5:   food       modelling     2        1037 0.001928640
##  6:  water citation backup  2751        4352 0.632123162
##  7:  water       modelling    20        4352 0.004595588
##  8:  water     no citation   972        4352 0.223345588
##  9:  water            <NA>   118        4352 0.027113971
## 10:  water        no claim   438        4352 0.100643382
```

```
# 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.claim <- plot_grid(a, b, ncol = 2, rel_widths = c(0.6, 0.4), labels = "auto")
plot.claim
```




```
# PLOT DISTRIBUTION OF CITATION SUPPORTING THE CLAIM ############################

plot.supporting.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)) +
  scale_y_continuous(breaks = breaks_pretty(n = 3)) +
  theme_AP() +
  labs(x = "Nº citations to claim per paper", y = "Nº papers")

plot.supporting.claim
```

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



1.1 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 -----------------------------------------------------------
```

```r
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"
```

```r
# Calculate network metrics ------------------------------------------------

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

```
## $food
## [1] 0.001132208
##
## $water
## [1] 0.0003275087
```

```r
# 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] 0.9235973
##
## $water
## [1] 0.8738732
```

```r
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     32          0           0       NaN 0.02976888
## 2:          fao 2002     18          0           0       NaN 0.01585667
## 3: morris et al 2003     16          0           0       NaN 0.01139905
##
## $water
##                  node degree degree.out betweenness closeness    pagerank
##                <char>  <num>      <num>       <num>     <num>       <num>
## 1:       fao aquastat    177          0      0.0000       NaN 0.059811249
## 2: siebert et al 2010     67          3    367.8333     0.125 0.008126115
## 3:           fao 2011     66          1    111.5000     1.000 0.014411345
```

```
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 0.0007651654
## 2:    pei et al 2017      1          6           4 0.20000000 0.0008952435
## 3: kadigi et al 2004      0          6           0 0.10000000 0.0007651654
##
## $water
##                node degree degree.out betweenness  closeness     pagerank
##              <char>  <num>      <num>       <num>      <num>        <num>
```

```
## 1:        wada 2015      0         23           0 0.02702703 0.0001778072
## 2: wada et al 2014a      1          9          10 0.09090909 0.0002080344
## 3: zarei et al 2021      0          9           0 0.06666667 0.0001778072
```

```
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: 0.004017118
## 2: 0.008412674
## 3: 0.006649393
##
## $water
##                     node degree degree.out betweenness  closeness    pagerank
##                   <char>  <num>      <num>       <num>      <num>       <num>
## 1:    siebert et al 2010     67          3    367.8333 0.12500000 0.008126115
## 2:             doll 2009     12          1    200.0000 0.33333333 0.004997032
## 3: boretti and rosa 2019     12          5    193.5000 0.03703704 0.001635011
```

```
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 0.0007651654
## 2:   du preez et al 2018      0          1           0         1 0.0007651654
## 3:      meier et al 2018      3          1           3         1 0.0023911418
##
## $water
##                     node degree degree.out betweenness closeness     pagerank
##                   <char>  <num>      <num>       <num>     <num>        <num>
## 1: sharma and irmak 2012      0          1           0         1 0.0001778072
## 2:       world bank 2007      5          1          46         1 0.0053126548
## 3:   brajovic et al 2015      0          1           0         1 0.0001778072
```

1.2 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, classificatio
                                 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]
}
```

```r
# 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])
}
```

```r
# EXPORT NODES AND EDGES ##########################################################

for (i in topics) {

  nodes <- graph.final[[i]] %>%
    activate(nodes) %>%
    data.frame() %>%
    data.table()

  edges <- graph.final[[i]] %>%
    activate(edges) %>%
    data.frame() %>%
    data.table()

  write.xlsx(nodes, paste(i, ".nodes.xlsx", sep = ""))
  write.xlsx(edges, paste(i, ".edges.xlsx", sep = ""))

}
```

```
# NUMBER OF NODES ##############################################################

lapply(graph.final, function(graph) V(graph))
```

```
## $food
## + 764/764 vertices, named, from ab93adb:
##   [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
## + 2926/2926 vertices, named, from df7a482:
##    [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 khalid awan 2022
##    [9] dunkelman et al 2017
##   [10] nordin et al 2013
## + ... omitted several vertices
```

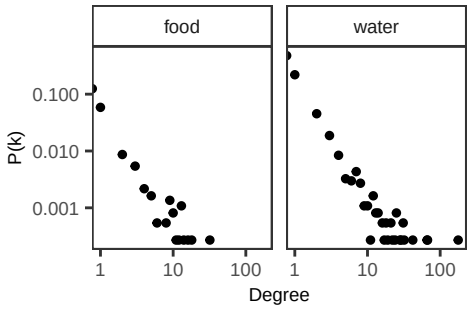
```
# NUMBER OF EDGES ##############################################################

lapply(graph.final, function(graph) ecount(graph))
```

```
## $food
## [1] 660
##
## $water
## [1] 2803
```

```
# SCALE-FREE PLOT ##############################################################

# Prepare data -----------------------------------------------------------------

dt.food <- graph.final[[1]] %>%
  activate(nodes) %>%
  data.frame() %>%
```

```
  data.table() %>%
  .[, topic:= "food"]

dt.water <- graph.final[[2]] %>%
  activate(nodes) %>%
  data.frame() %>%
  data.table() %>%
  .[, topic:= "water"]

tmp <- rbind(dt.food, dt.water)

# Calculate the degree distribution ------------------------------------------

degree_distribution <- tmp[, .(P_k = .N / nrow(tmp)), .(degree, topic)]

plot.degree.distribution <- degree_distribution %>%
  ggplot(., aes(degree, P_k)) +
  geom_point(size = 1) +
  scale_y_log10() +
  scale_x_log10() +
  facet_wrap(~topic) +
  labs(x = "Degree", y = "P(k)") +
  theme_AP()

plot.degree.distribution
```

```
## Warning in scale_x_log10(): log-10 transformation introduced infinite values.
```

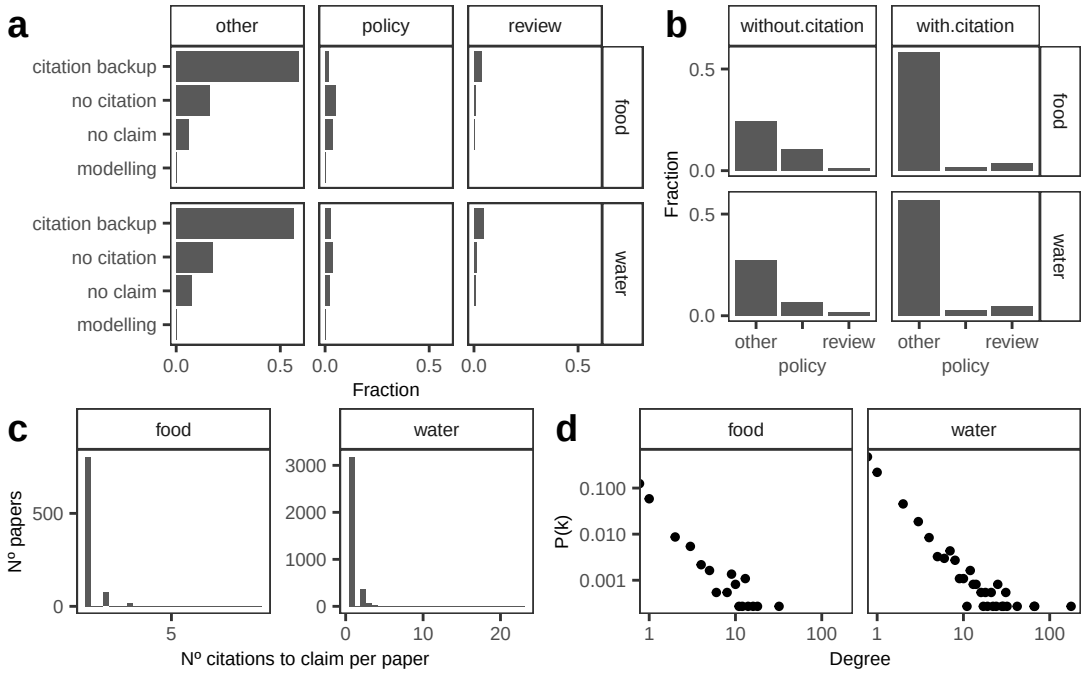



```
# MERGE DESCRIPTIVE PLOTS ###################################################

bottom <- plot_grid(plot.supporting.claim, plot.degree.distribution, ncol = 2,
                    labels = c("c", "d"))
```

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

```
## Warning in scale_x_log10(): log-10 transformation introduced infinite values.
```

```
plot_grid(plot.claim, bottom, ncol = 1, rel_heights = c(0.6, 0.4))
```




```
# CALCULATE ALL POSSIBLE PATHS ###################################################

# Define function ------------------------------------------------------------

count_paths <- function(g) {

  # Extract the top 5 nodes with highest betweenness ---------------------------

  top_nodes <- g %>%
    activate(nodes) %>%
    top_n(5, betweenness) %>%
    pull(name)

  # Initialize counts ----------------------------------------------------------

  total_paths_count <- 0
  top_nodes_paths_count <- 0

  g <- as.igraph(g)

  results <- foreach(i = V(g),
                     .combine = "c",
                     .packages = "igraph") %:%

    foreach(j = V(g),
            .combine = "c") %dopar% {
```

```
            total_paths_pair <- 0
            top_nodes_paths_pair <- 0

            if (i != j) {

              # Calculate all possible paths --------------------------------

              paths <- all_simple_paths(g, from = i, to = j)
              total_paths_pair <- length(paths)

              # Check how many paths pass through the top betweenness nodes --

              for (path in paths) {

                if (any(names(path) %in% top_nodes)) {
                  top_nodes_paths_pair <- top_nodes_paths_pair + 1

                }
              }
            }

            # Return the count of all paths and paths through top nodes ------

            return(c(total_paths_pair, top_nodes_paths_pair))
          }

  # Aggregate results ---------------------------------------------------------

  total_paths_count <- sum(results[seq(1, length(results), by = 2)])
  top_nodes_paths_count <- sum(results[seq(2, length(results), by = 2)])

  return(c(total_paths_count, top_nodes_paths_count))

}

# Define parallel computing -----------------------------------------------

cl <- makeCluster(floor(detectCores() * 0.75))
registerDoParallel(cl)

# Run the function --------------------------------------------------------

results.counts <- lapply(graph.final, function(graph)
  count_paths(graph))

# Stop the cluster --------------------------------------------------------
```

```r
stopCluster(cl)
```

```r
# SHOW TOTAL NUMBER OF PATHS AND PROPORTION OF PATHS PASSING
# THROUGH THE FIVE NODES WITH THE HIGHEST BETWEENNESS ##########################

results.counts
```

```
## $food
## [1] 823 104
##
## $water
## [1] 5286 1083
```

```r
lapply(results.counts, function(x) x[[2]] / x[[1]])
```

```
## $food
## [1] 0.126367
##
## $water
## [1] 0.2048808
```

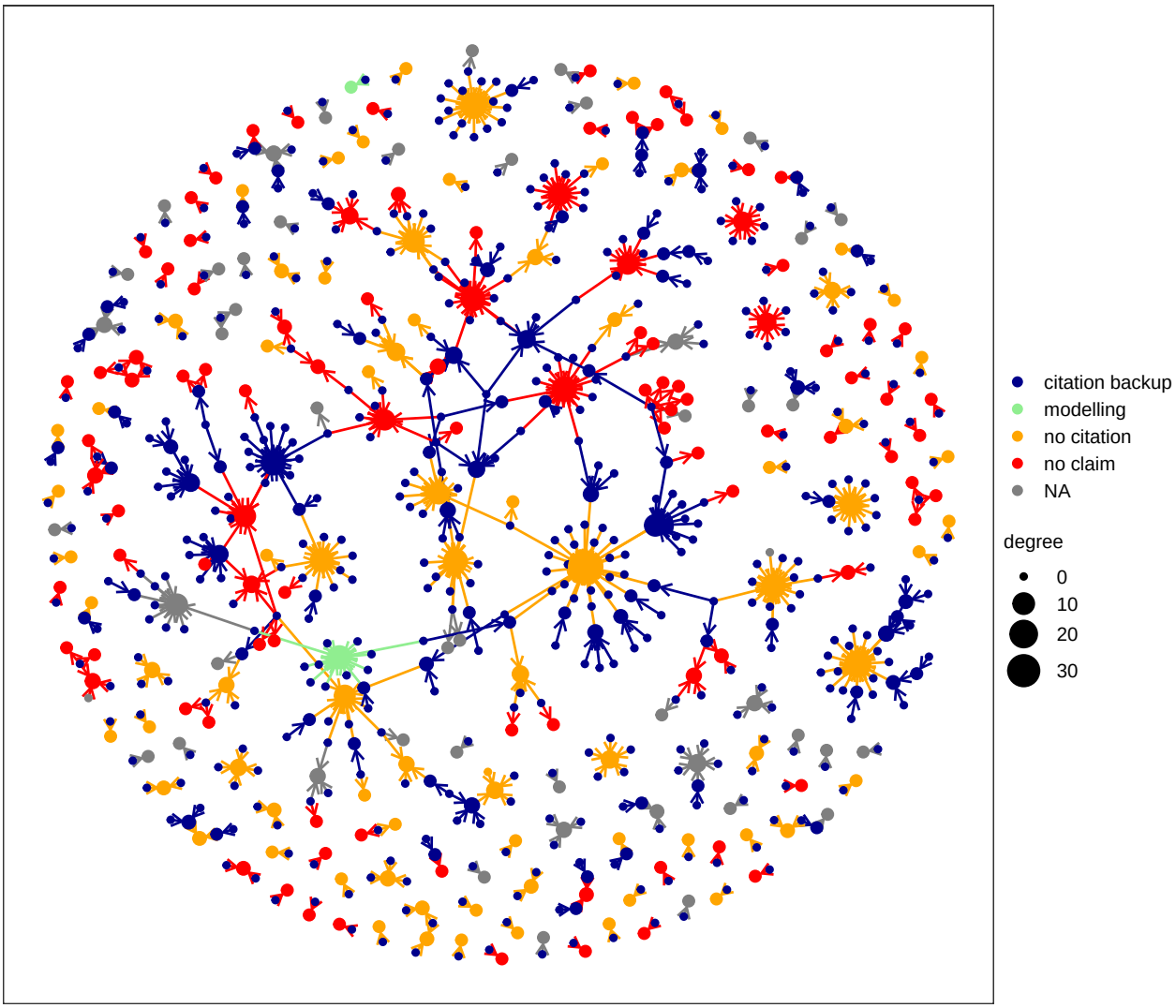
```r
# PLOT NETWORK ###################################################################

seed <- 1234
selected_colors <- c("darkblue", "lightgreen", "orange", "red", "grey")

# by nature of claim ------------------------------------------------------------

# Label the nodes with highest degree -------------------------------------------

p1 <- p2 <- p3 <- p4 <- p5 <- list()

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

  set.seed(seed)

  p1[[i]] <- ggraph(graph.final[[i]], layout = "igraph", algorithm = "nicely") +
    geom_edge_link(arrow = 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
```

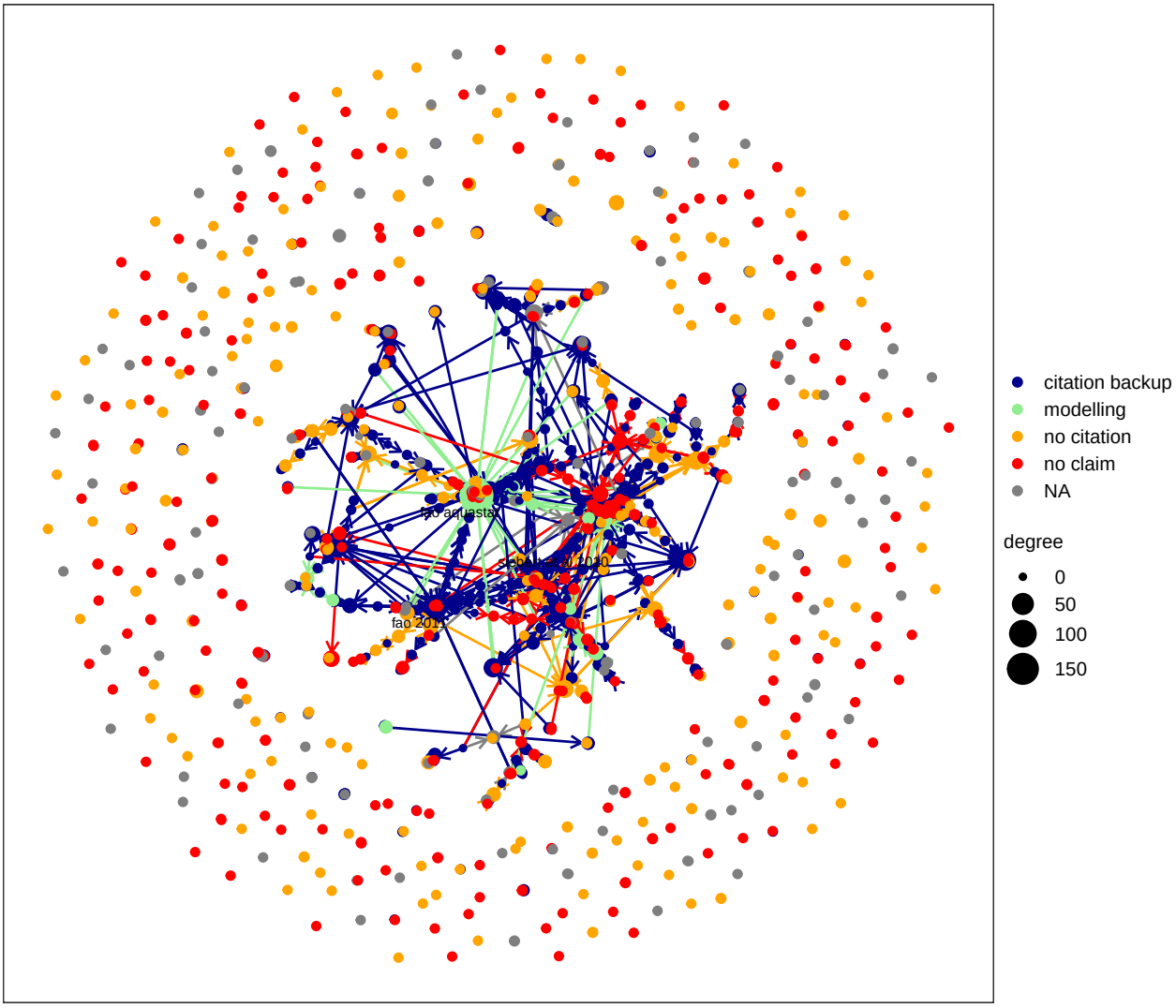
```
## Warning: Using the `size` aesthetic in this geom was deprecated in ggplot2 3.4.0.
## i Please use `linewidth` in the `default_aes` field and elsewhere instead.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.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

```
## Warning: Removed 764 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).
```



```
##
## $water
```

```
## Warning: Removed 2923 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).
```

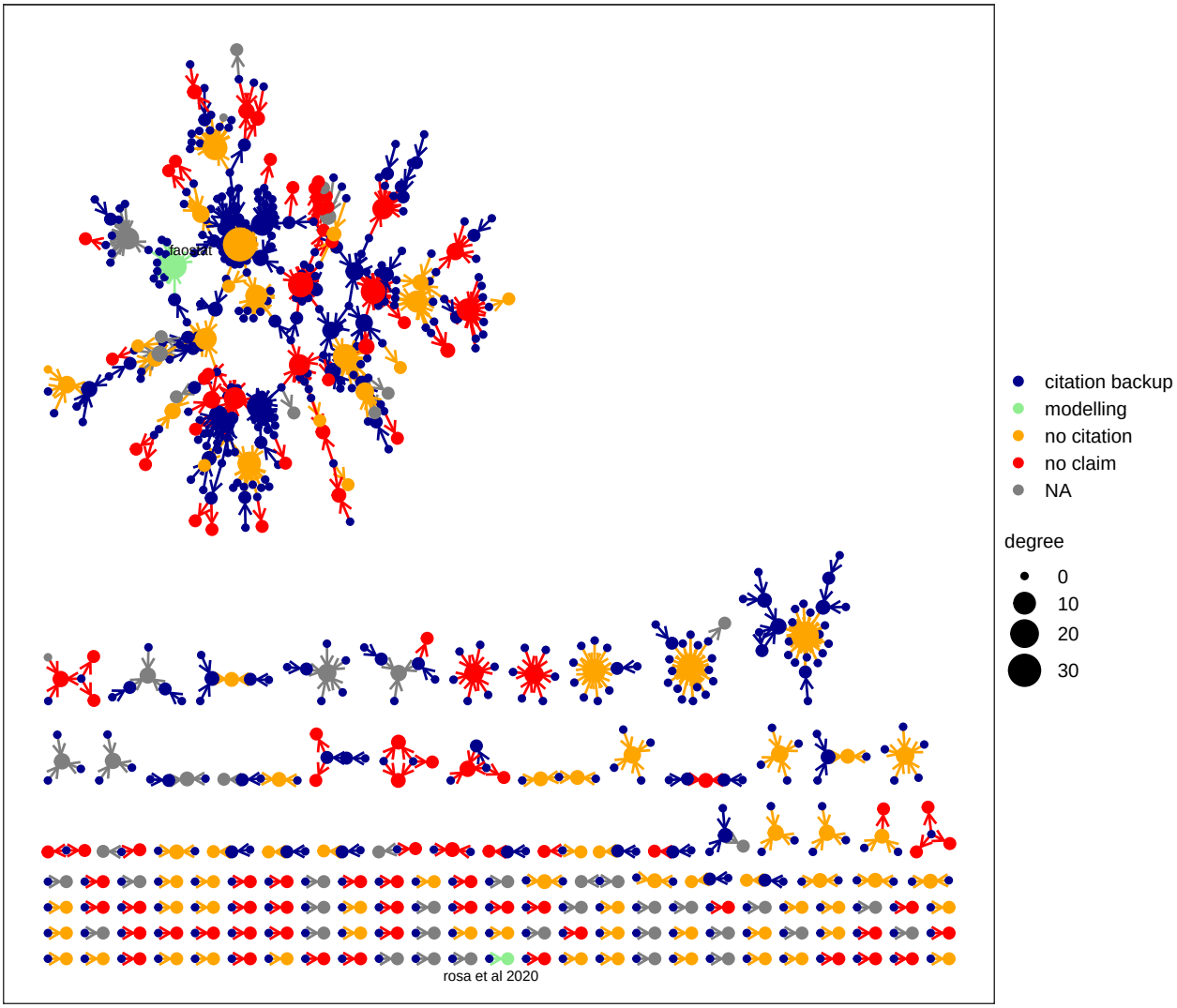



```
for(i in names(graph.final)) {

  set.seed(seed)

  p5[[i]] <- ggraph(graph.final[[i]], layout = "stress") +
    geom_edge_link(arrow = 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(nature.claim == "modelling", name, NA)),
                   repel = TRUE, size = 2.2) +
```

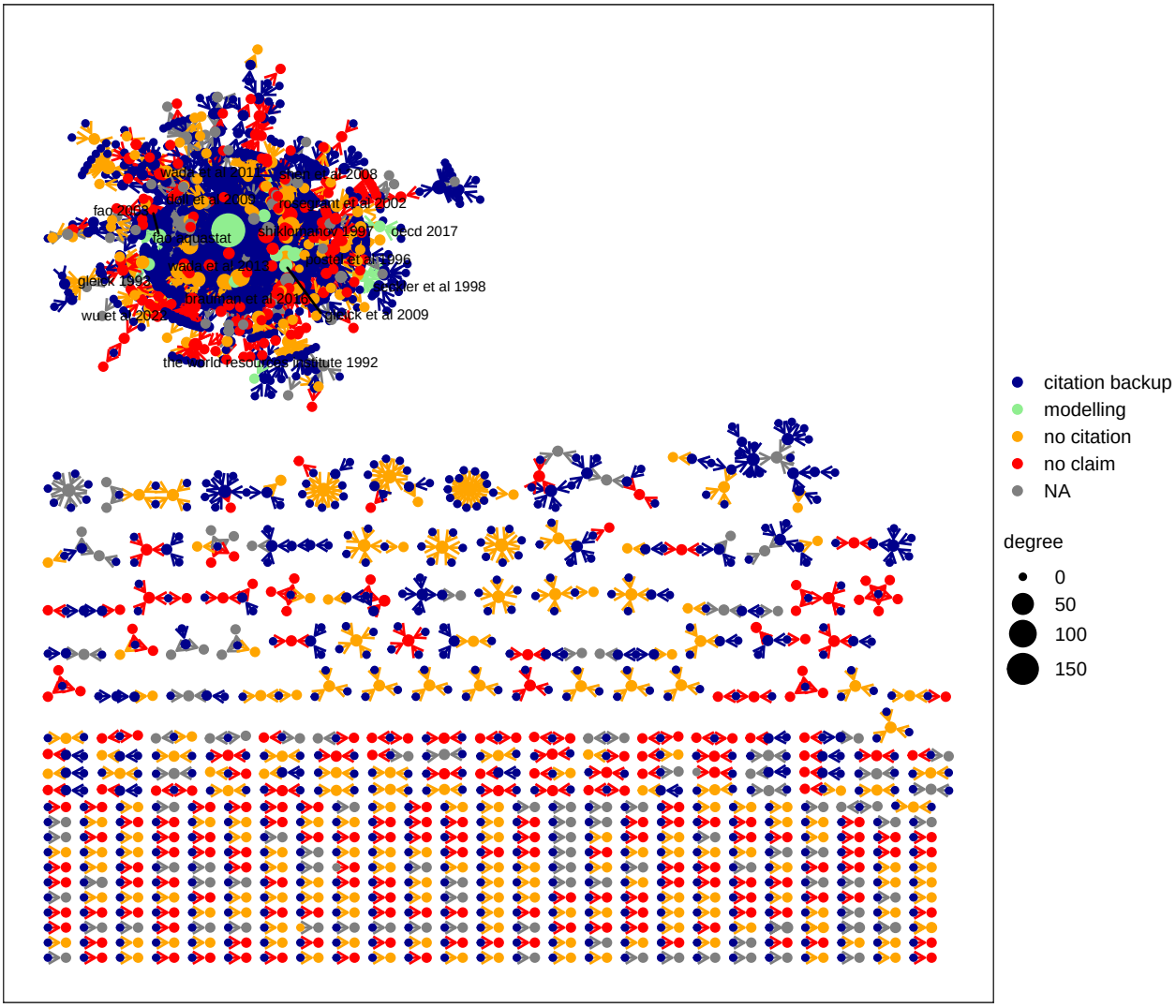
```
    labs(x = "", y = "") +
    scale_color_manual(name = "",
                       values = selected_colors) +
    theme_AP() +
    theme(axis.text.x = element_blank(),
          axis.ticks.x = element_blank(),
          axis.text.y = element_blank(),
          axis.ticks.y = element_blank(),
          legend.position = "right")
}

p5
```

```
## $food
```

```
## Warning: Removed 762 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).
```



```
##
## $water

## Warning: Removed 2910 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).
```

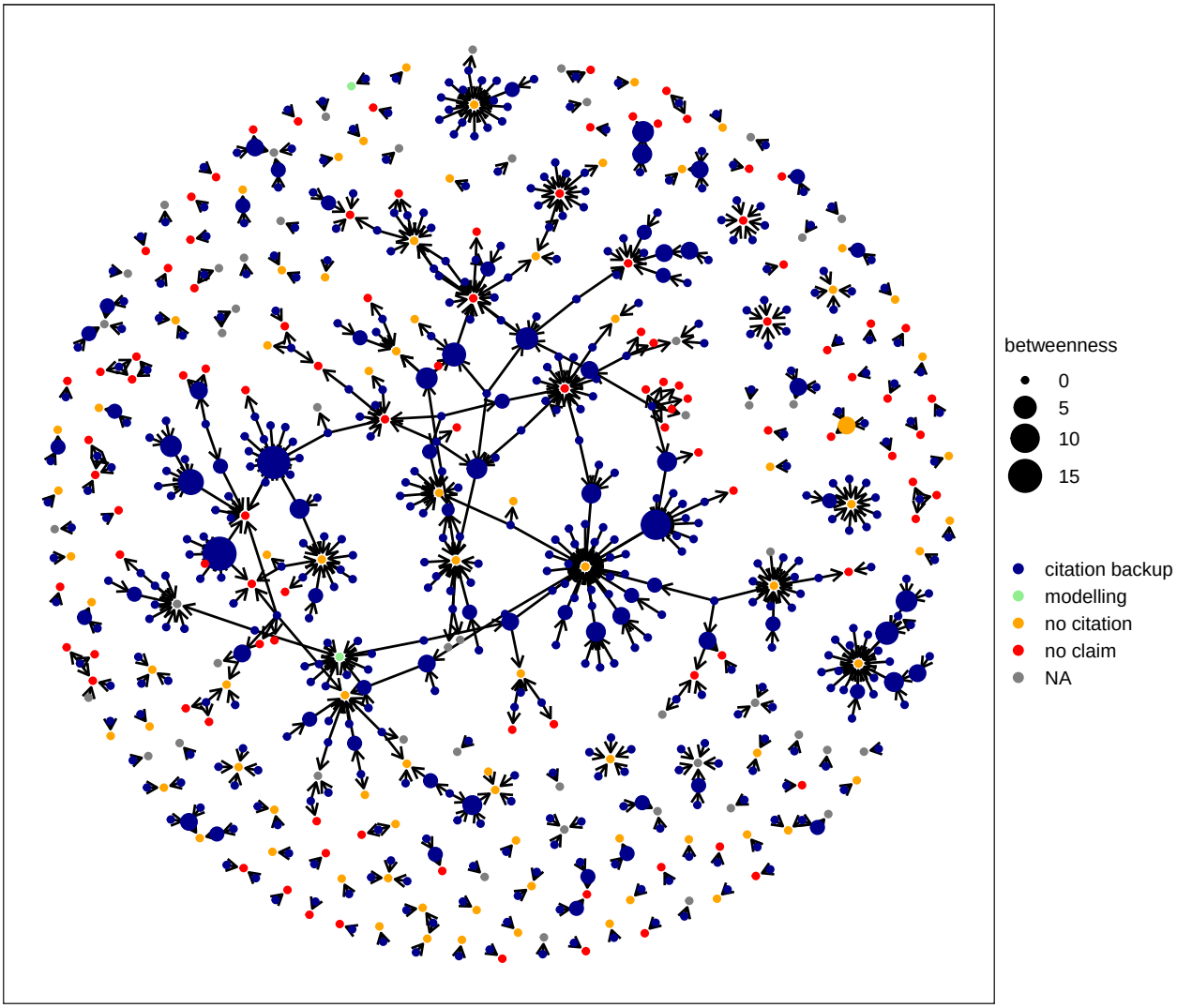



```
# Label the nodes with highest betweenness ----------------------------------

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

  set.seed(seed)

  p2[[i]] <- ggraph(graph.final[[i]], layout = "igraph", algorithm = "nicely") +
    geom_edge_link(arrow = 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
```

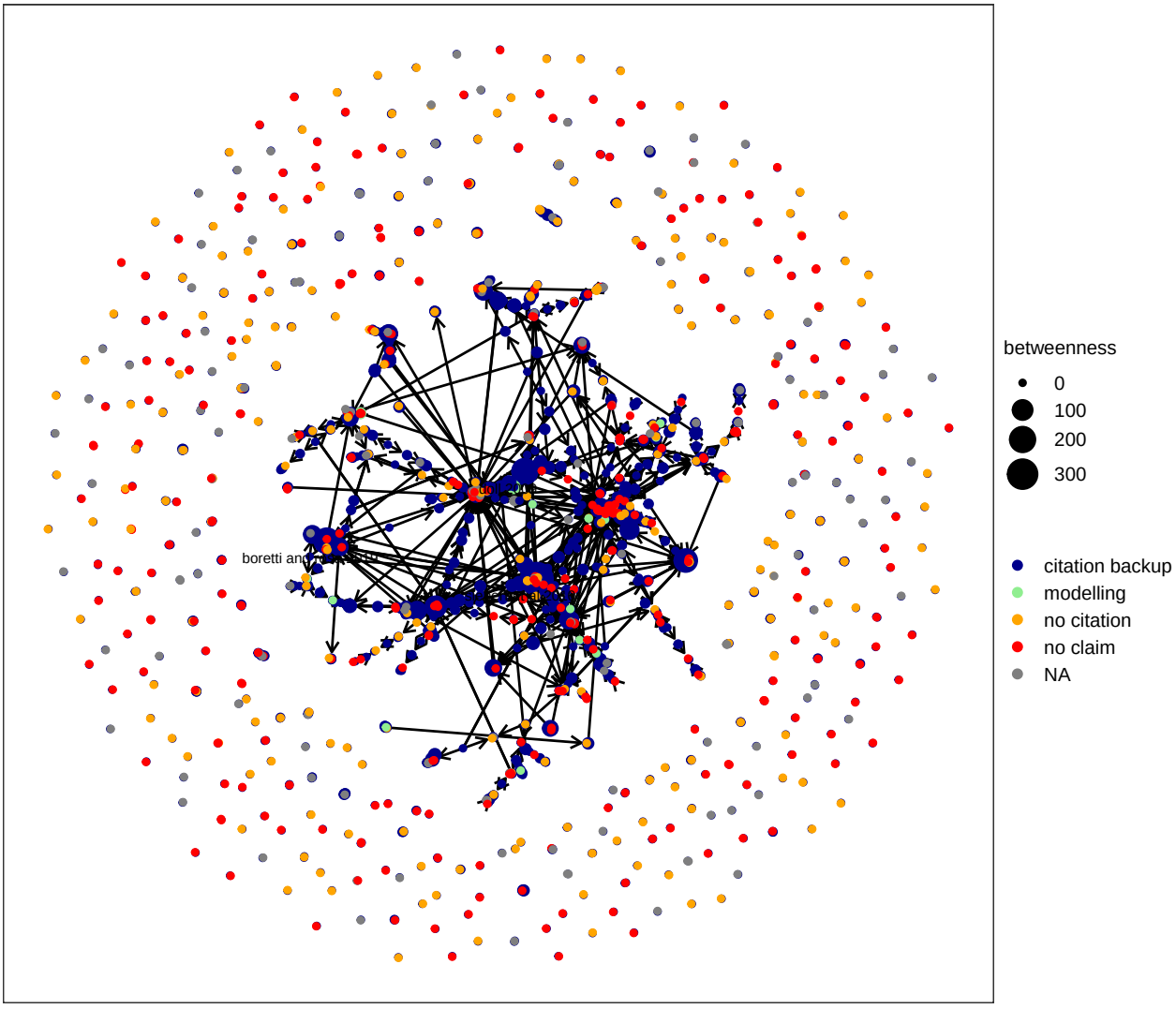
```
## $food
```

```
## Warning: Removed 764 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).
```




```
##
## $water
```

```
## Warning: Removed 2923 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).
```

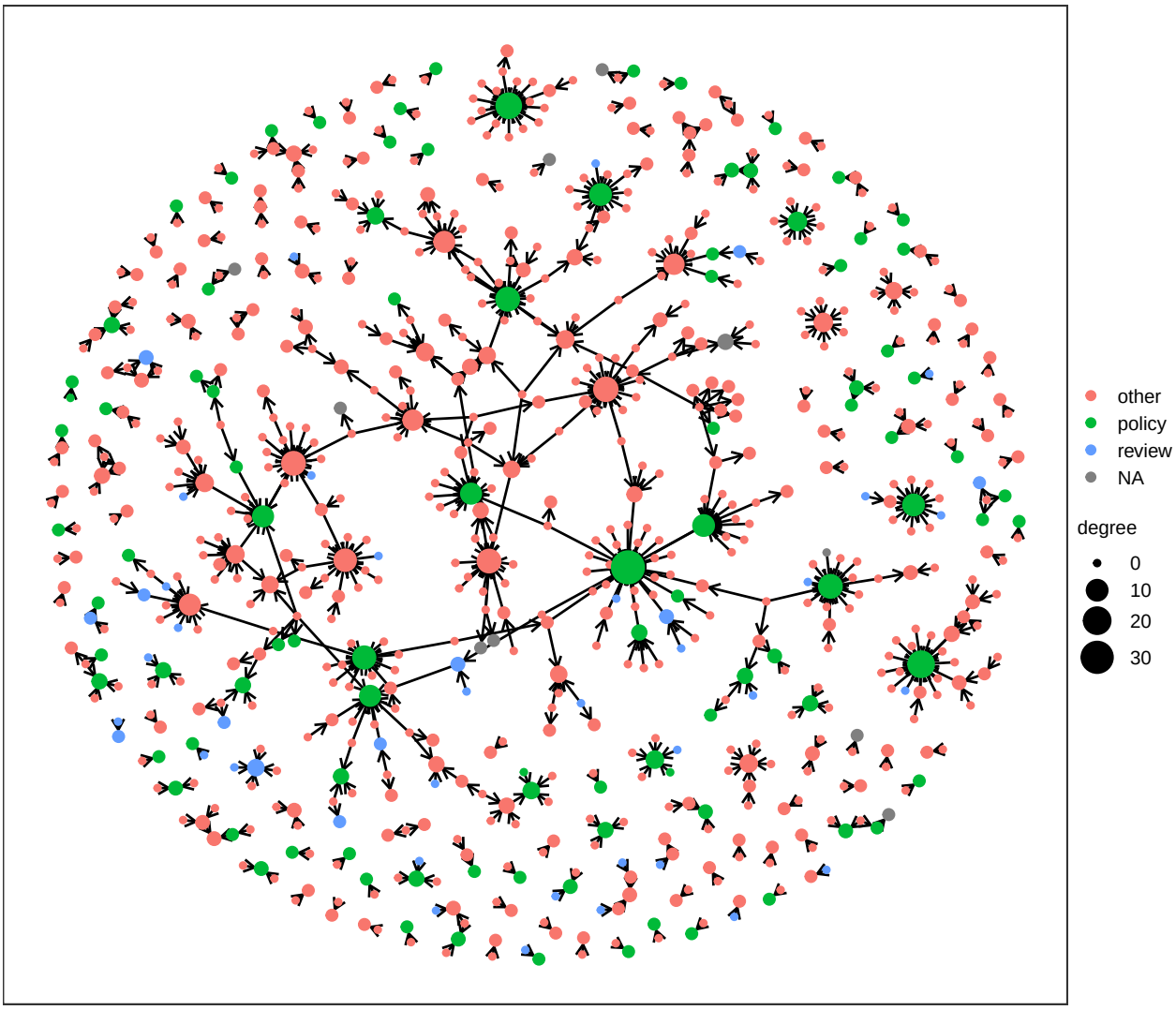



```
# by document.type-----------------------------------------------------------

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

  set.seed(seed)

  p3[[i]] <- ggraph(graph.final[[i]], layout = "igraph", algorithm = "nicely") +
    geom_edge_link(arrow = 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
```

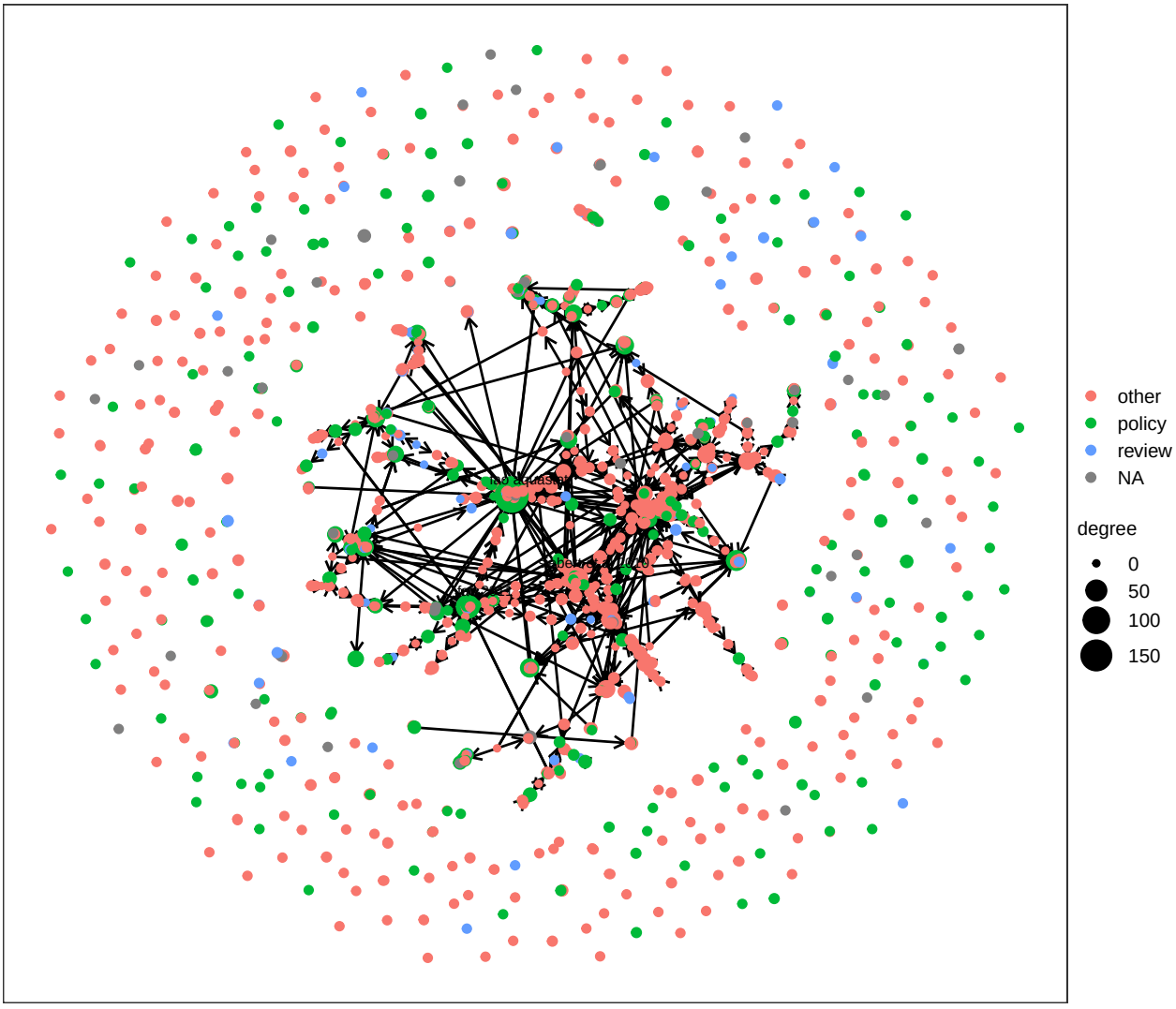
```
## $food
```

```
## Warning: Removed 764 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).
```




```
##
## $water
```

```
## Warning: Removed 2923 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).
```

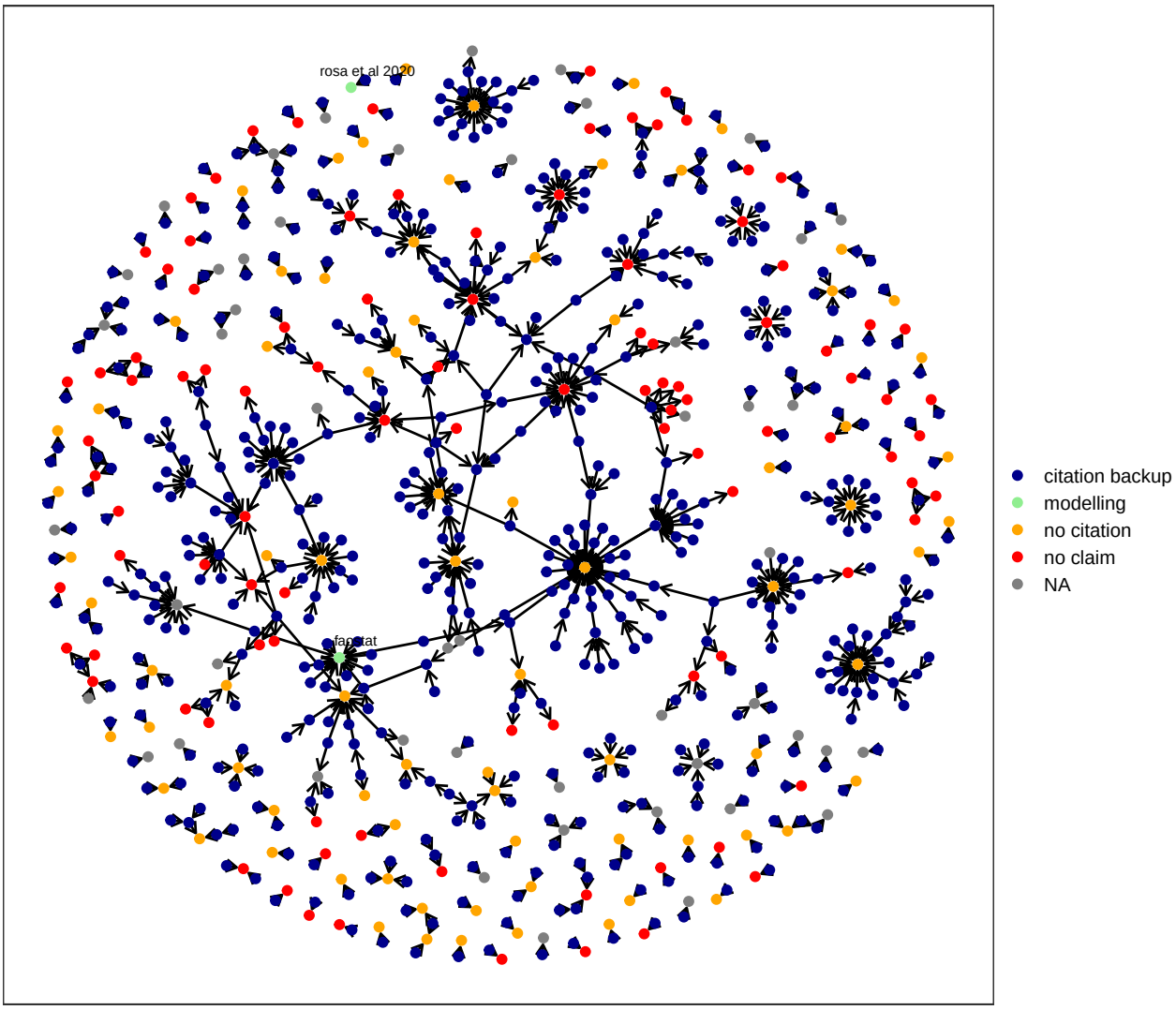



```
# Label nodes that are modelling exercises -----------------------------------

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

  set.seed(seed)

  p4[[i]] <- ggraph(graph.final[[i]], layout = "igraph", algorithm = "nicely") +
    geom_edge_link(arrow = 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
```

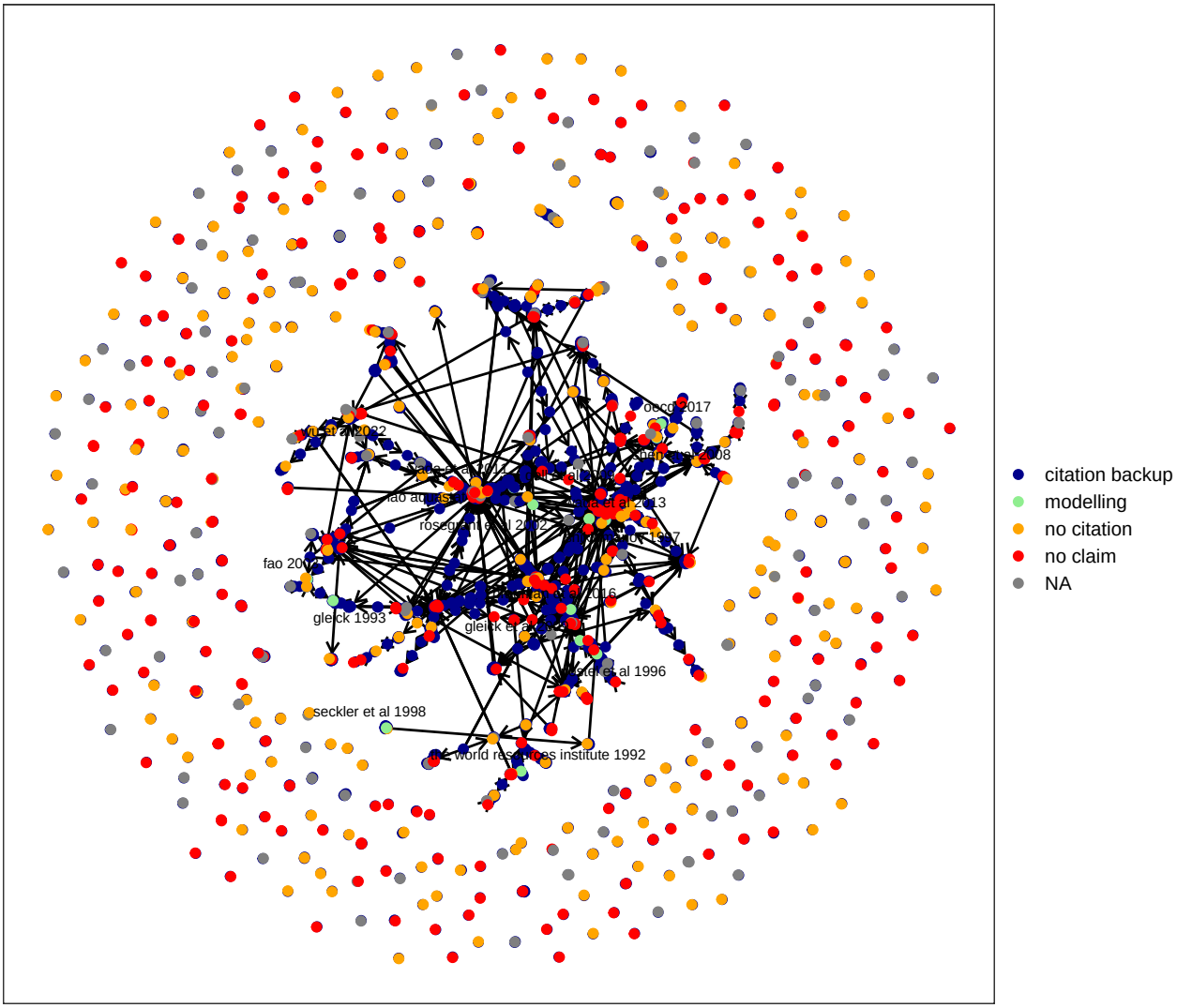
```
## $food
```

```
## Warning: Removed 762 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).
```




```
##
## $water
```

```
## Warning: Removed 2910 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).
```




```
# PLOT EVOLUTION NATURE CLAIM THROUGH TIME ######################################

out <- list()

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

    selected_colors <- c("darkblue", "lightgreen", "orange", "red", "grey")

  out[[i]] <- graph.final[[i]] %>%
    activate(nodes) %>%
    data.frame() %>%
    data.table() %>%
    .[, .N, .(year, nature.claim)] %>%
    ggplot(., aes(year, N, fill = nature.claim)) +
    scale_fill_manual(values = selected_colors, name = "") +
    geom_area() +
    scale_x_continuous(breaks = breaks_pretty(n = 3)) +
```

```
    theme_AP() +
    ggtitle(names(graph.final[i])) +
    theme(legend.position = "none",
          plot.title = element_text(size = 8))

}

legend <- get_legend(out[[2]] + theme(legend.position = "right"))
```

```
## Warning: Removed 4 rows containing non-finite outside the scale range
## (`stat_align()`).
```

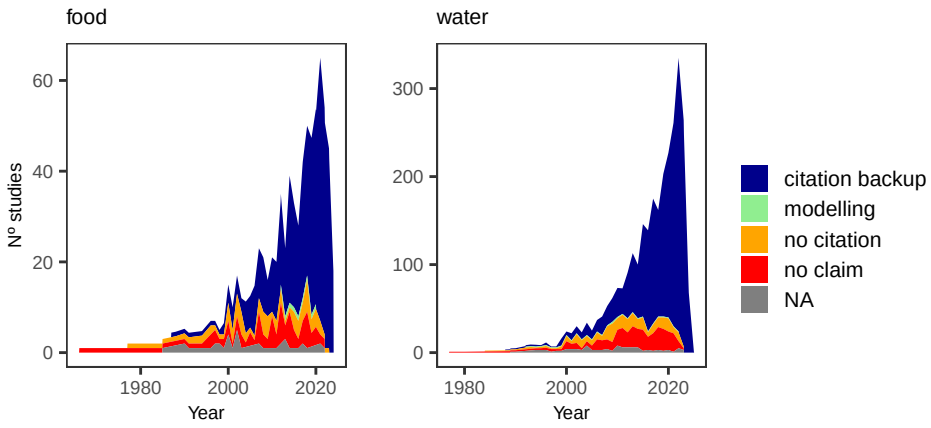
```
## Warning in get_plot_component(plot, "guide-box"): Multiple components found;
## returning the first one. To return all, use `return_all = TRUE`.
```

```
bottom <- plot_grid(out[[1]] + labs(x = "Year", y = "Nº studies"),
                    out[[2]] + labs(x = "Year", y = ""))
```

```
## Warning: Removed 3 rows containing non-finite outside the scale range
## (`stat_align()`).
```

```
## Warning: Removed 4 rows containing non-finite outside the scale range
## (`stat_align()`).
```

```
plot.network.claims <- plot_grid(bottom, legend, rel_widths = c(0.75, 0.25),
                                 ncol = 2)
plot.network.claims
```



1.3 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 %>%
```

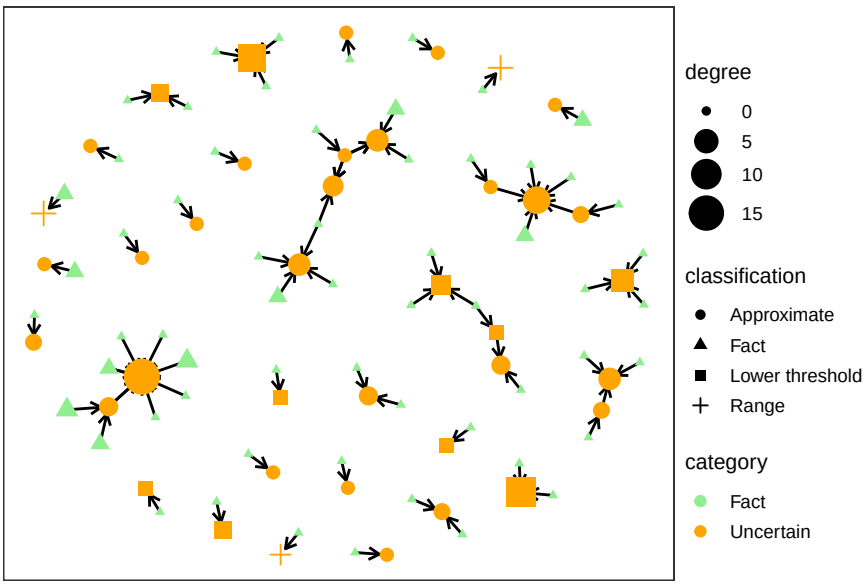
```
    activate(nodes) %>%
    pull(name)

# Extract name of studies stating claim as fact -------------------------------

  f.names <- graph %>%
    activate(nodes) %>%
    data.frame() %>%
    filter(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(1.6, '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 t
    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",
          legend.text = element_text(size = 7.2))
}

p7
```

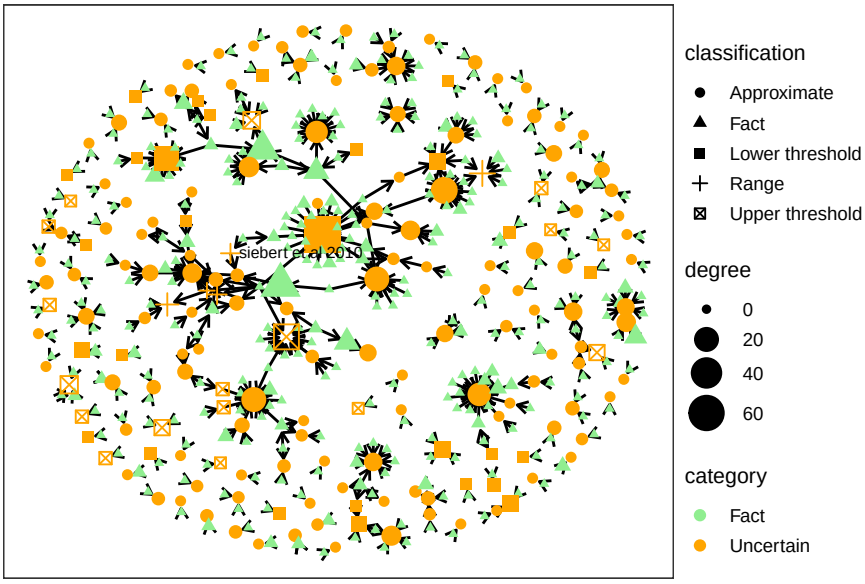
```
## $food
```

```
## Warning: Removed 99 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).
```




```
##
## $water
```

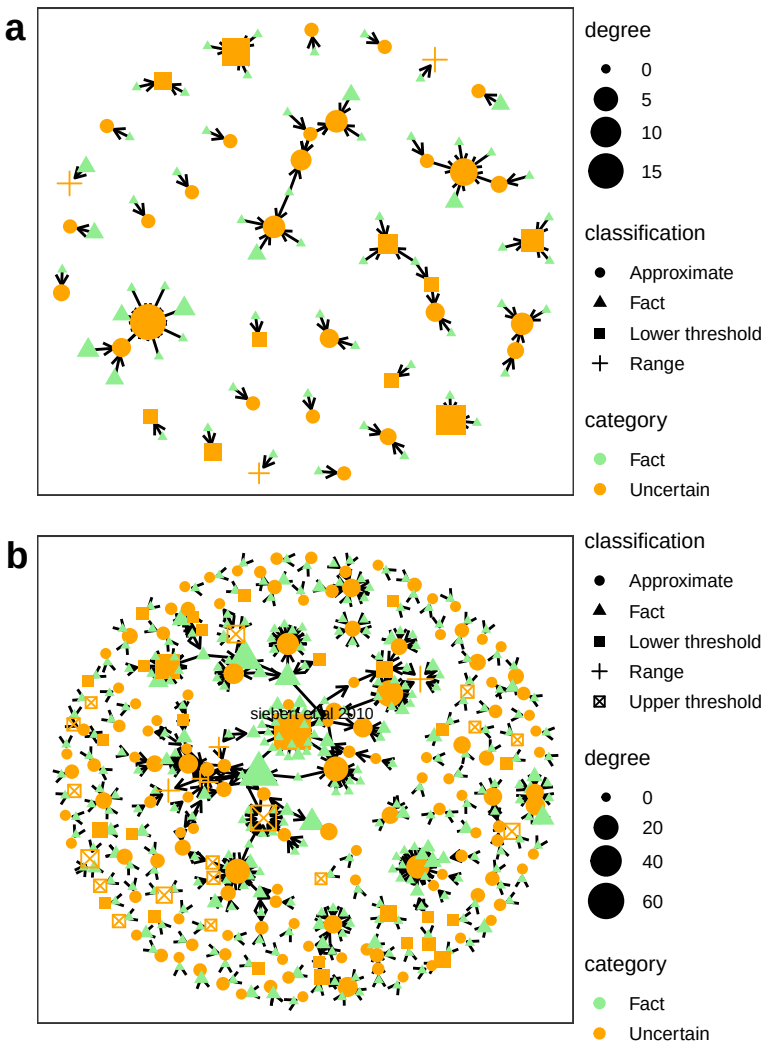
```
## Warning: Removed 496 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).
```




```
# MERGE PLOTS ######################################################################

plot_grid(p7[[1]], p7[[2]], ncol = 1, labels = "auto")
```

```
## Warning: Removed 99 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).
```

```
## Warning: Removed 496 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 -------------------------------------------------------------

  igraph_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] 0.08837971
## [1] 0.08708273
```

2 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:   0.4622222 0.3940741 0.02074074 0.122963
##
## $water
##    no citation no claim modelling        NA
##          <num>    <num>     <num>     <num>
## 1:   0.3169629 0.271166 0.2931606 0.1187105
```

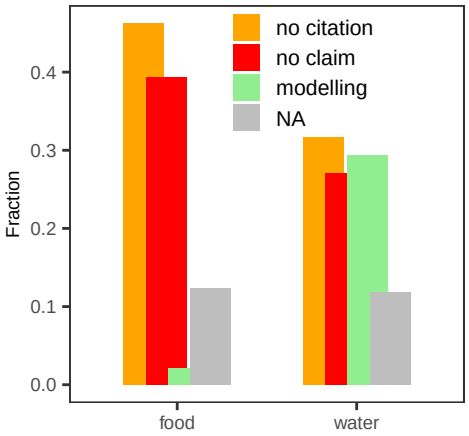
```
# SUM PROPORTION NO CLAIM AND NO CITATION ######################################

lapply(out, function(x) x[, `no citation` + `no claim`])
```

```
## $food
## [1] 0.8562963
##
## $water
## [1] 0.588129
```

```
# PLOT PROPORTION OF PATHS ENDING IN MODELLING, NO CLAIM AND NO CITATION #######

rbindlist(out, idcol = "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))
```

```
## 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.
```



2.1 Network through time

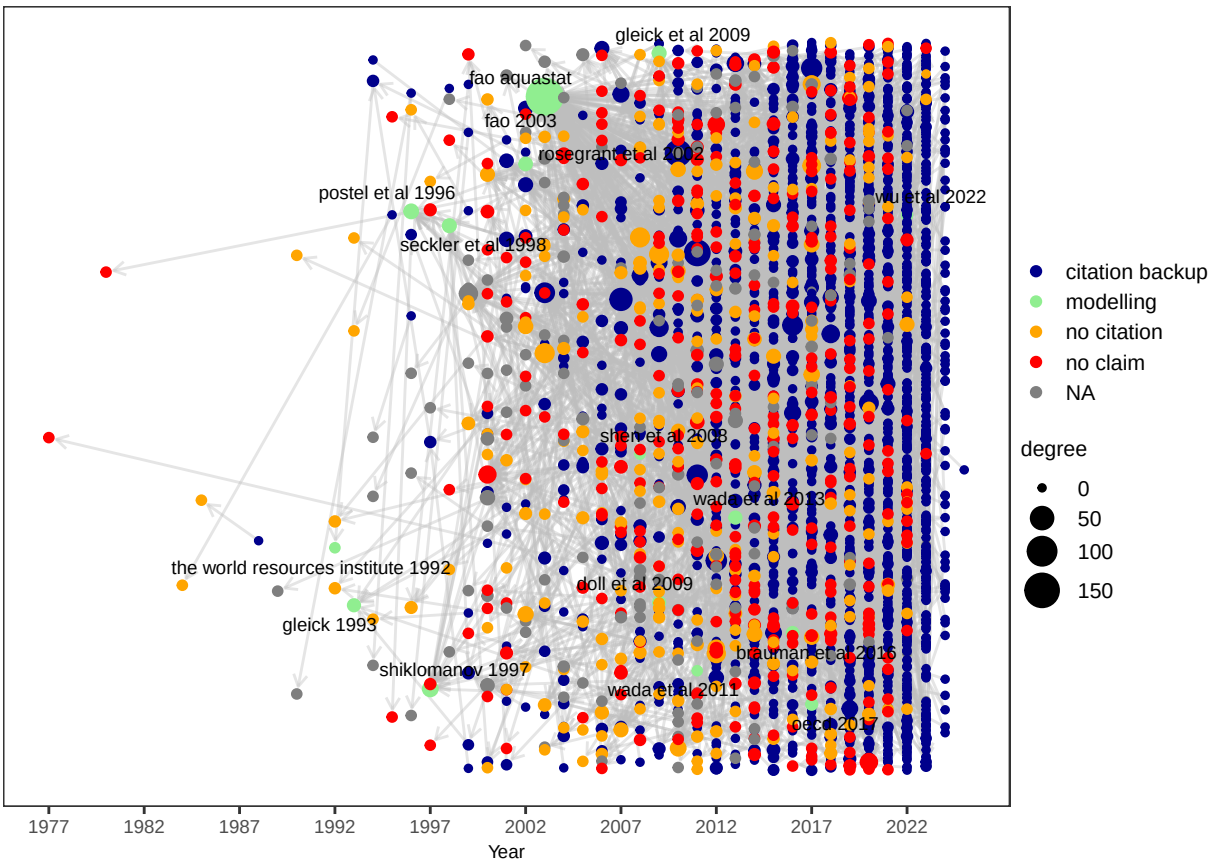
```
# PLOT NETWORK THROUGH TIME ###################################

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", .)

    location_faostat <- graph.final[[i]] %>%
    activate(nodes) %>%
    data.frame() %>%
    pull(name) %>%
    grep("faostat", .)

  # Extract vector with years ------------------------------------------------

  v_years <- graph.final[[i]] %>%
  activate(nodes) %>%
  data.frame() %>%
  pull(year)
```

```r
  # Substitute fao aquastat/faostat without year with the oldest citations -----

  v_years[location_aquastat] <- oldest.aquastat.cite
  v_years[location_faostat] <- oldest.faostat.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
```

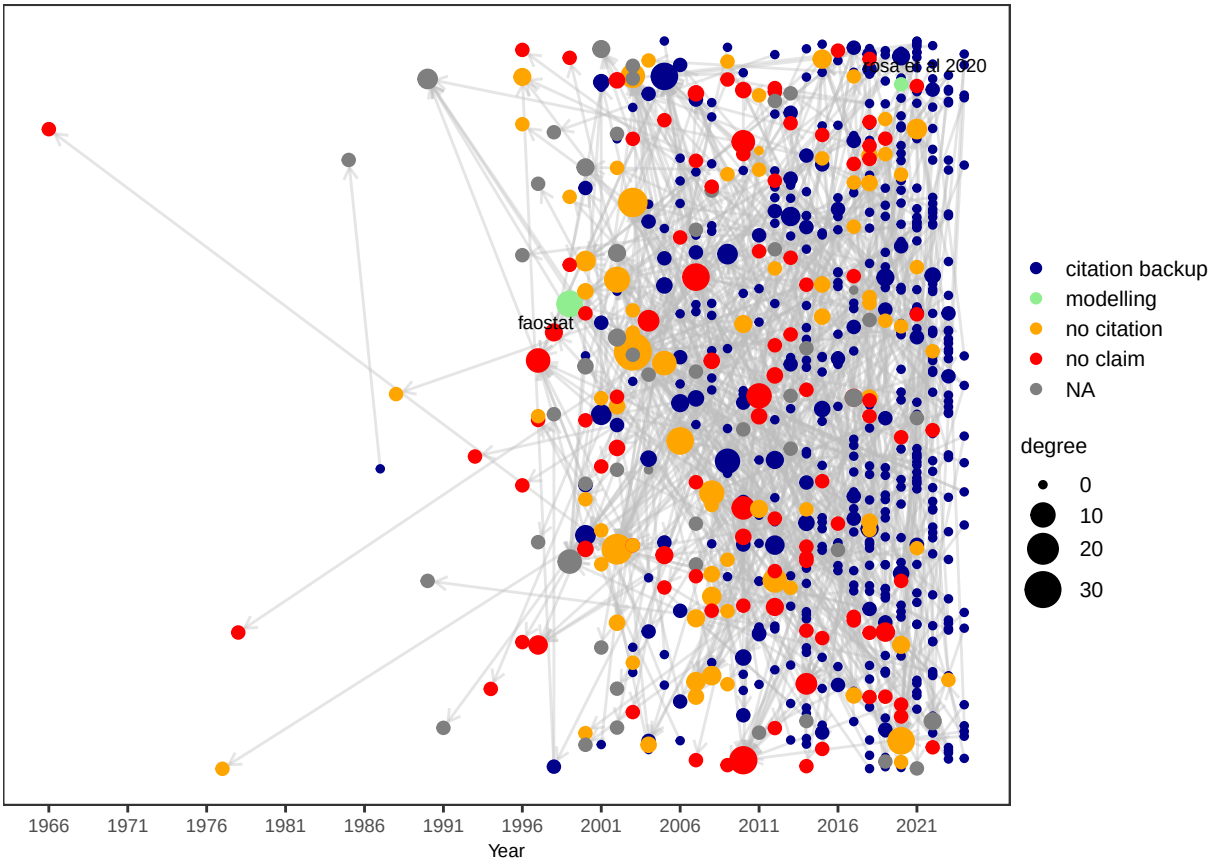
```
## $water
```

```
## Warning: Removed 2910 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).
```




```
##
## $food
```

```
## Warning: Removed 762 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).
```



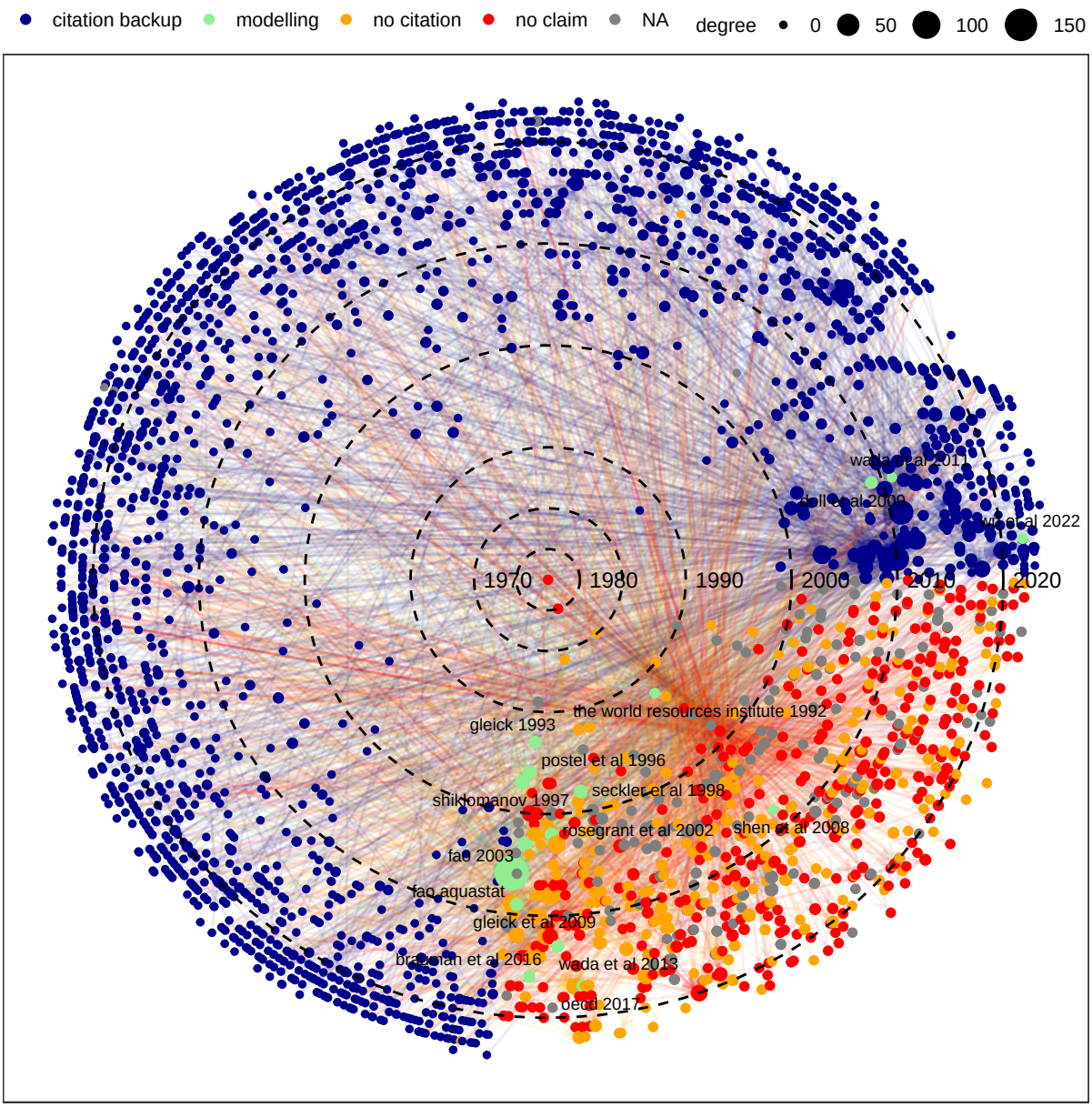

```
# ANOTHER VISUALIZATION FOR YEARS BASED ON POLAR COORDINATES ####################

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)
```

```r
  )

# 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 -------------------------------------------------------------------

# Set seed -------------------------------

set.seed(seed)

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
```

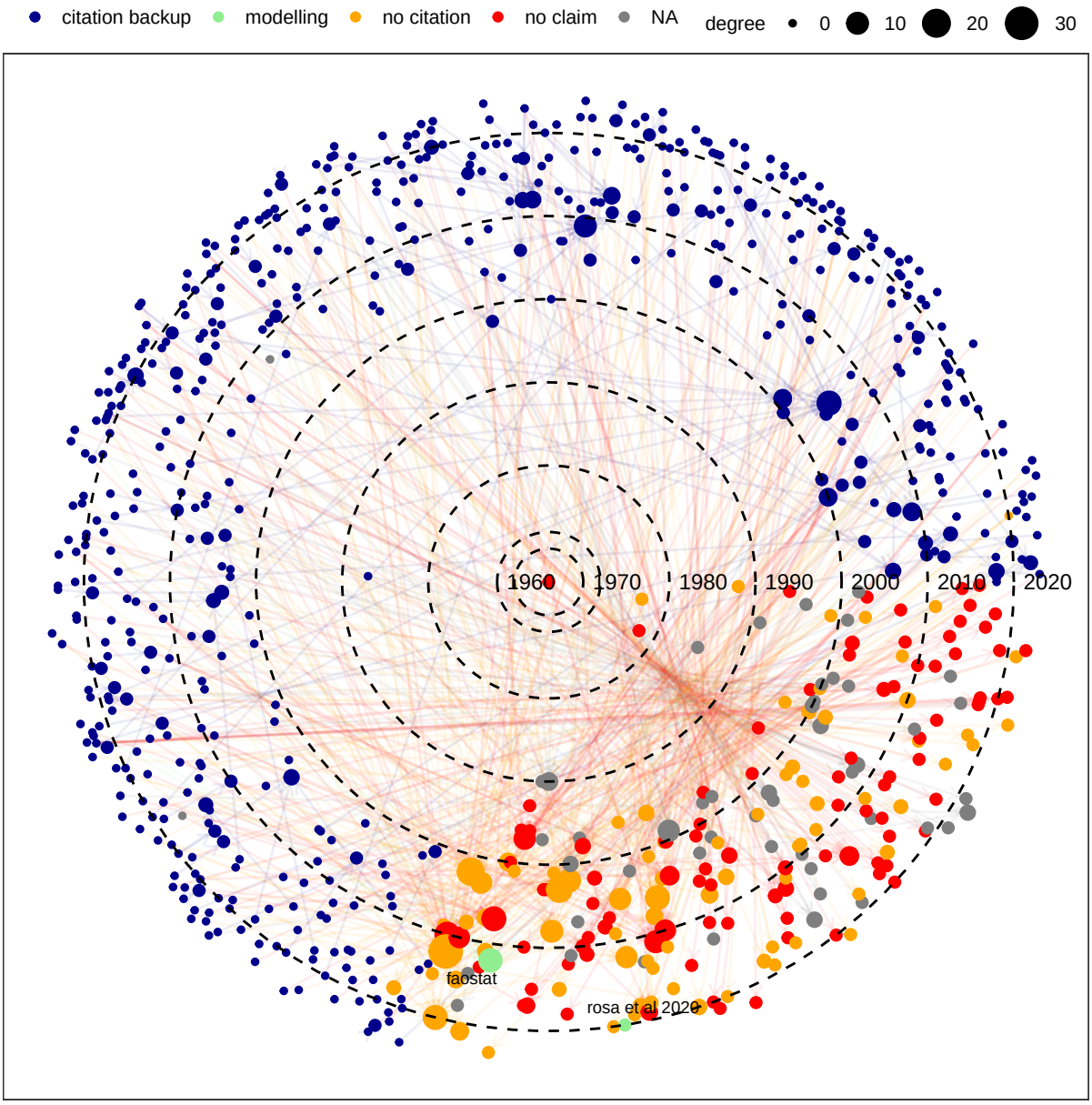
```
## $water
```

```
## Warning: Removed 2910 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).
```




```
##
## $food
```

```
## Warning: Removed 762 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).
```




```
# 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(arrow = 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)
```

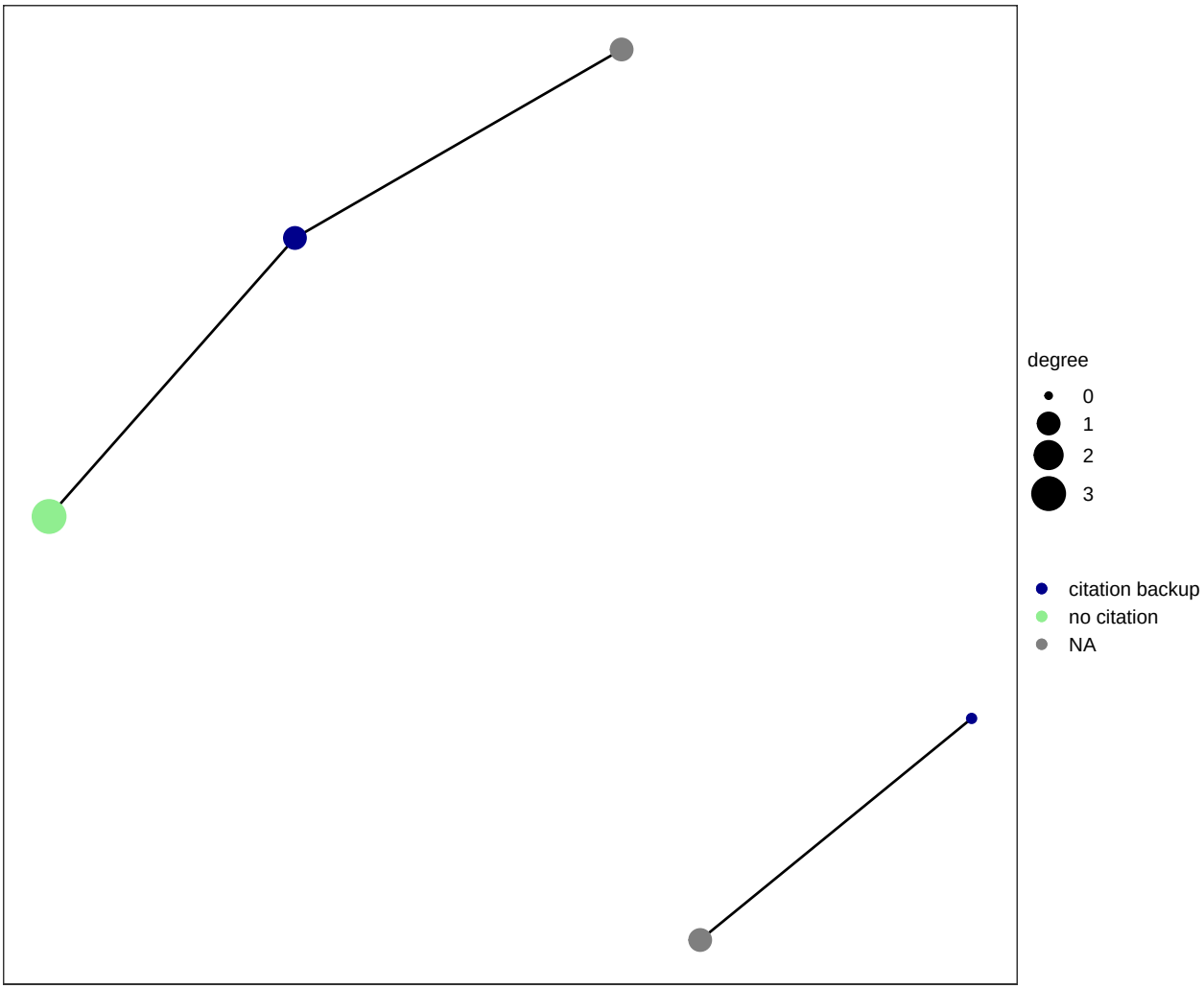
```
# RUN FUNCTION ######################################################################

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()`).
```

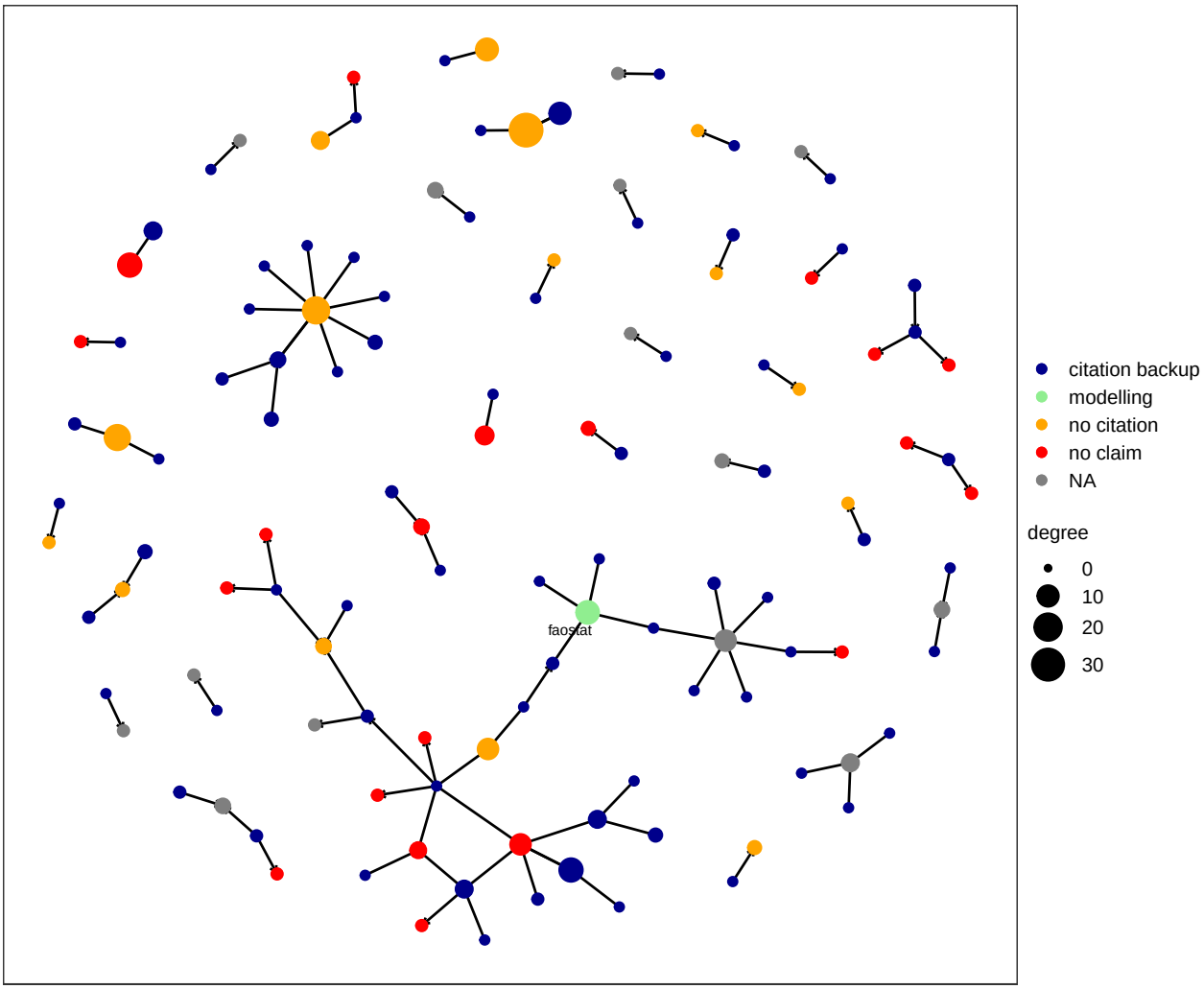
2000




```
##
## $food[[2]]
```

```
## Warning: Removed 123 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).
```

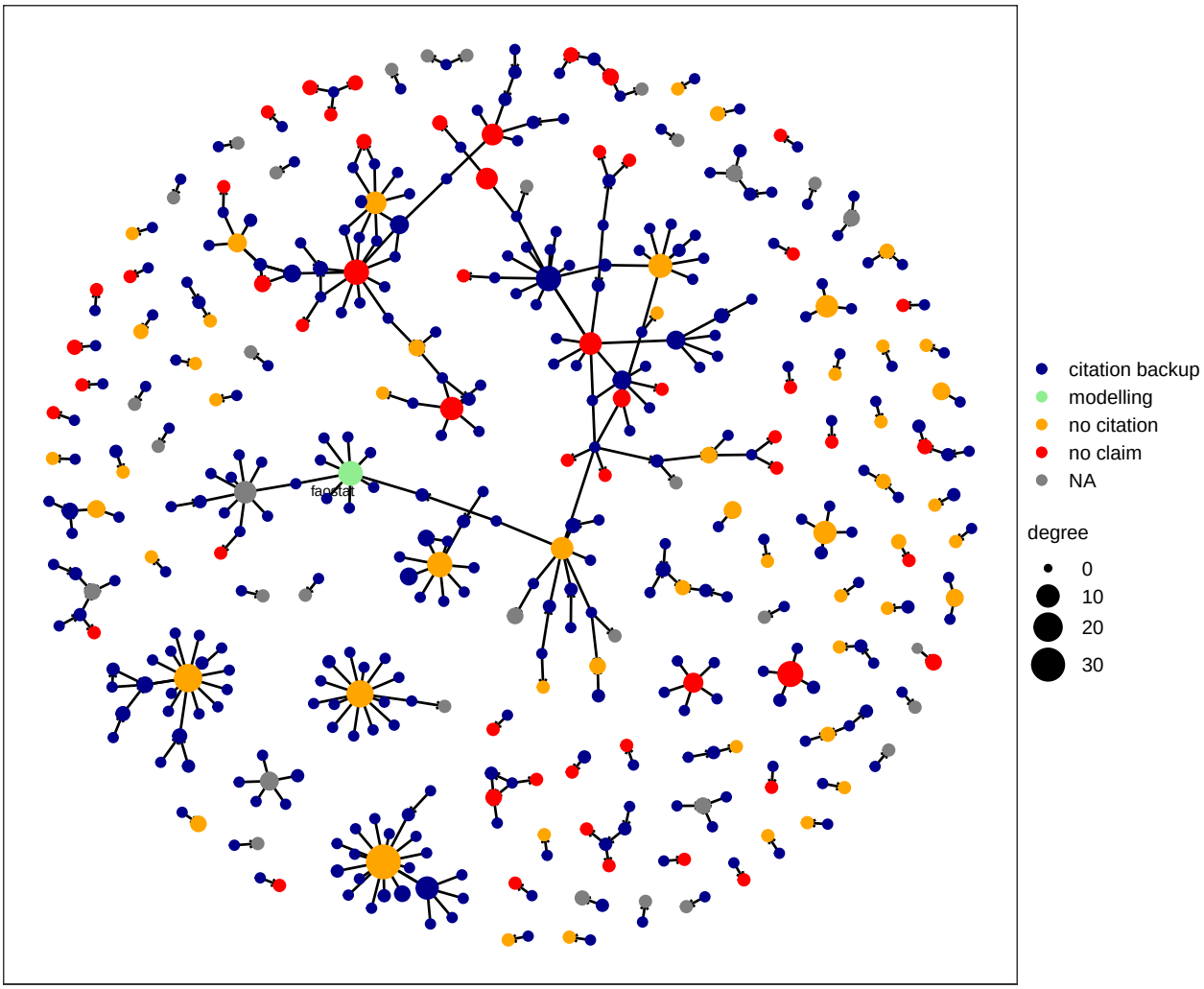
2010




```
##
## $food[[3]]
```

```
## Warning: Removed 449 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).
```

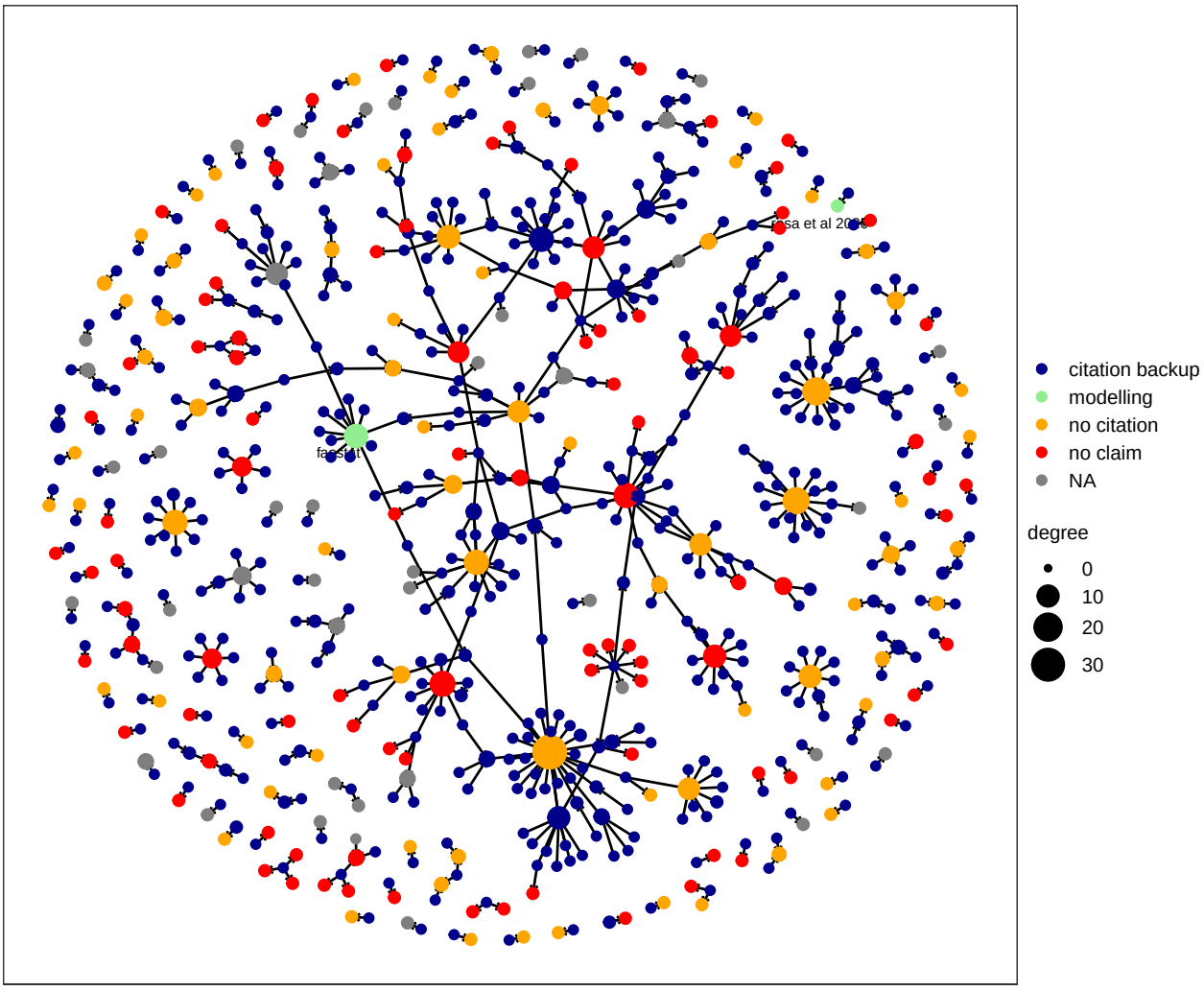
2020




```
##
## $food[[4]]
```

```
## Warning: Removed 724 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).
```

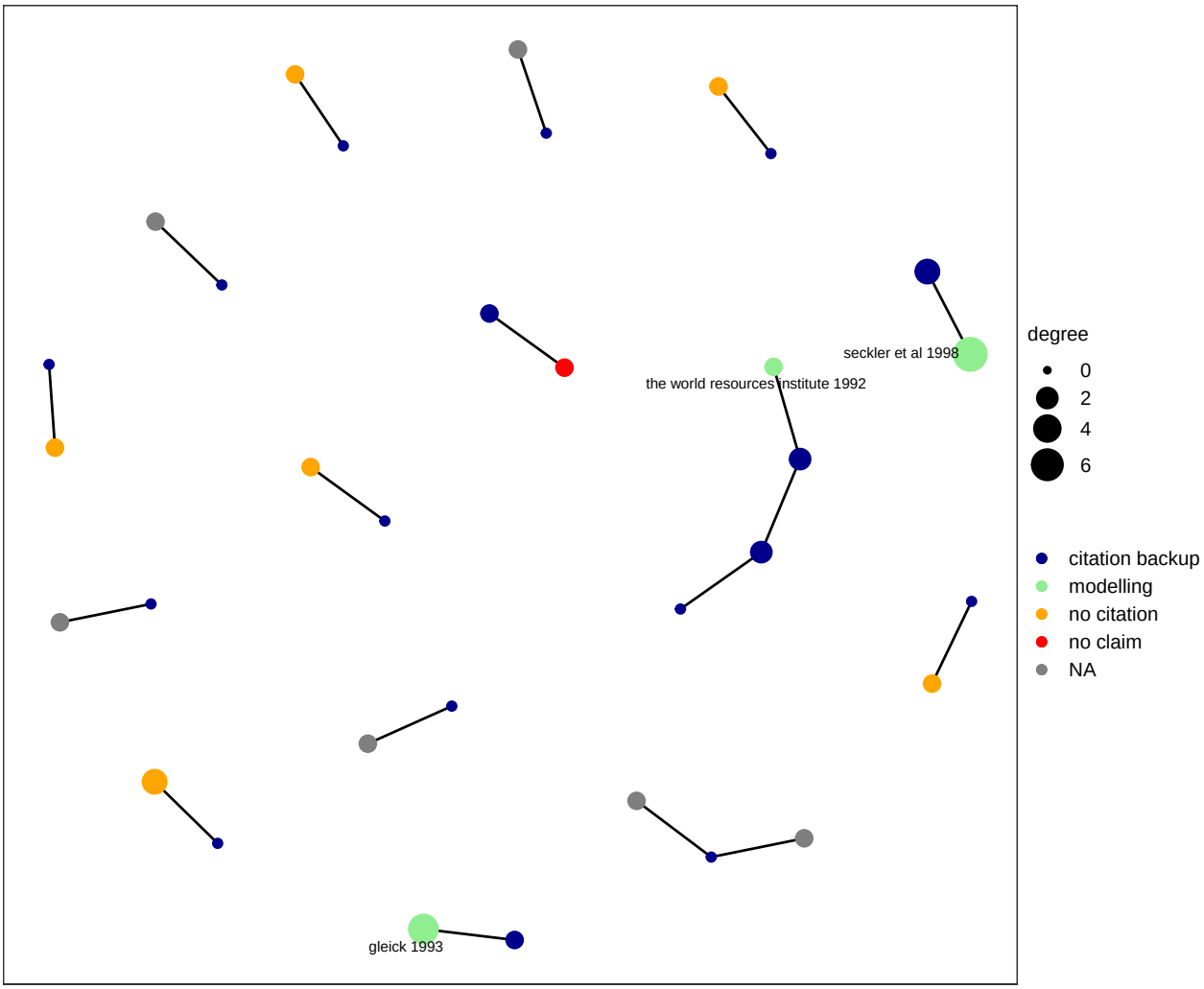
2024




```
##
##
## $water
## $water[[1]]
```

```
## Warning: Removed 30 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).
```

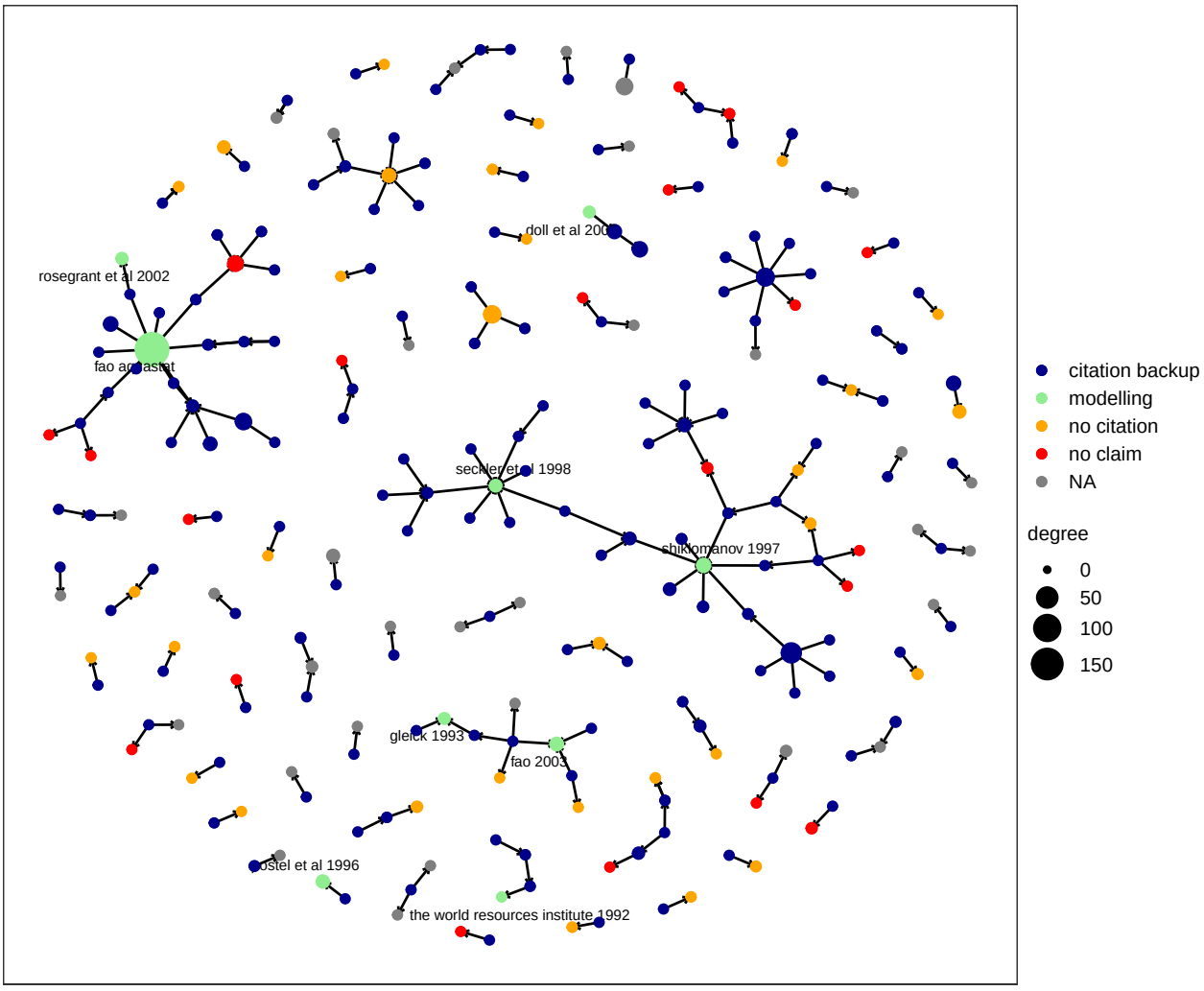
2000




```
##
## $water[[2]]
```

```
## Warning: Removed 237 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).
```

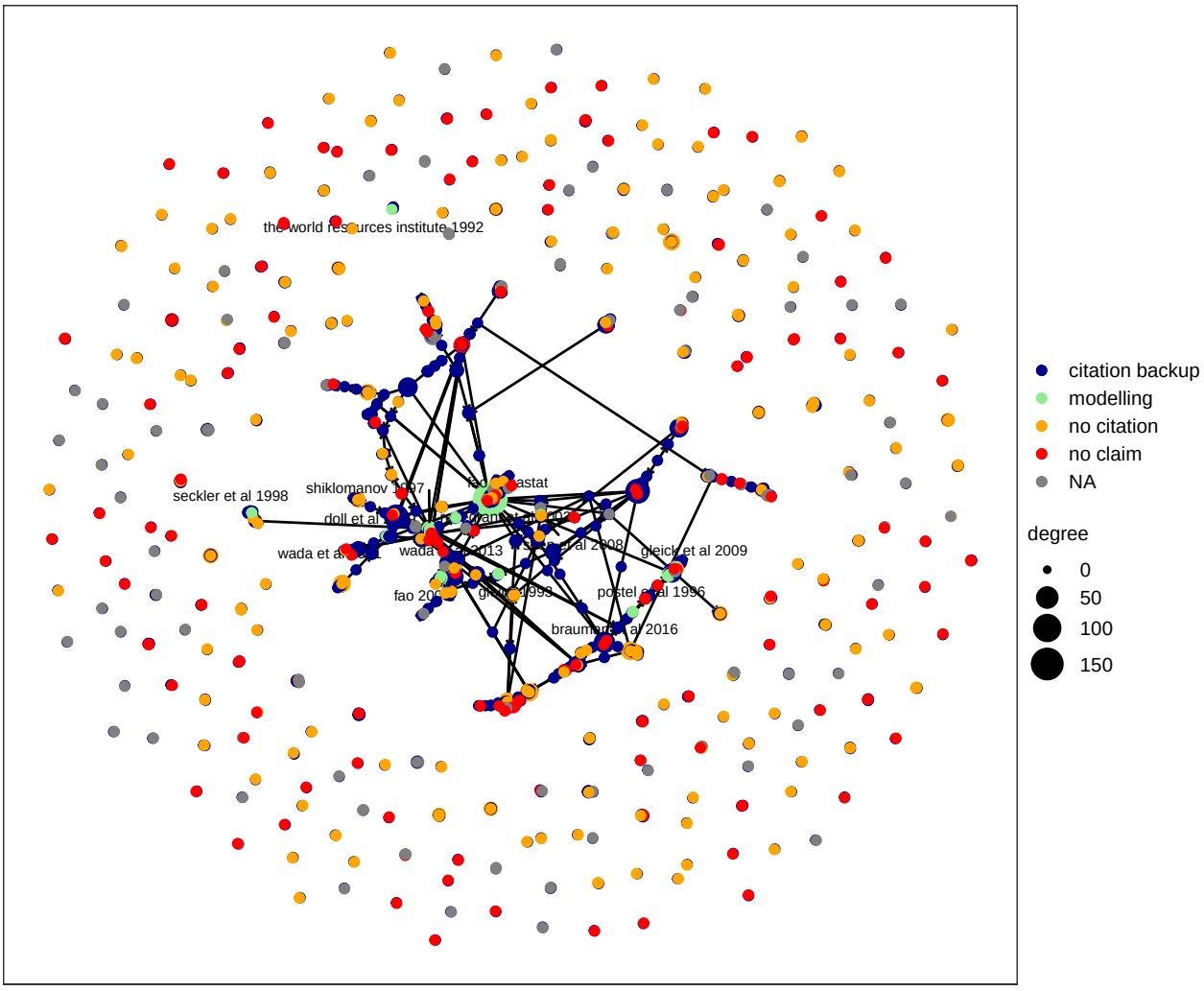
2010




```
##
## $water[[3]]
```

```
## Warning: Removed 1476 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).
```

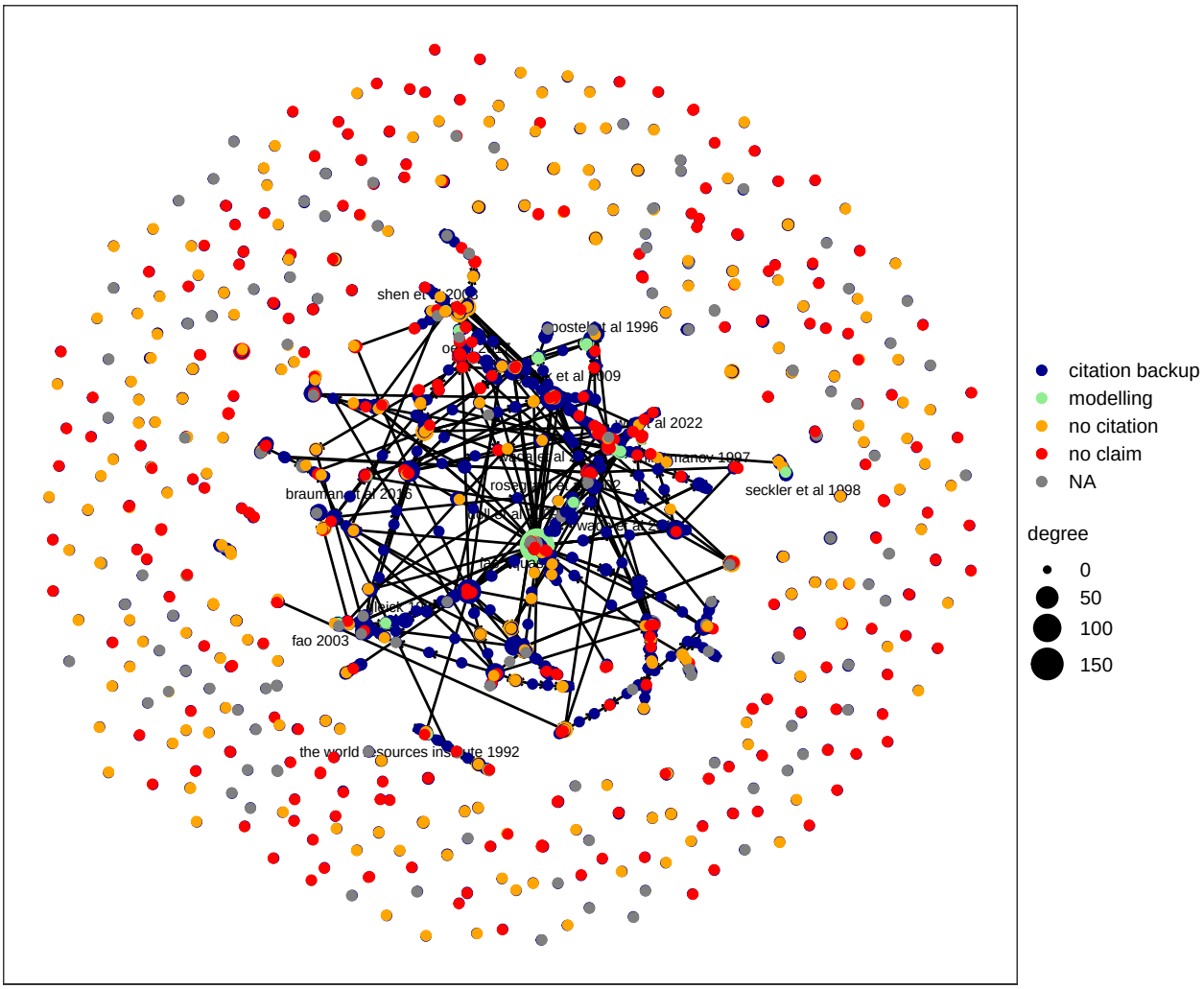
2020




```
##
## $water[[4]]
```

```
## Warning: Removed 2781 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 724 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 2781 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 123 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).
```

```
## Warning: Removed 449 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).
```

```
## Warning: Removed 724 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).
```

```
## Warning: Removed 30 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).
```

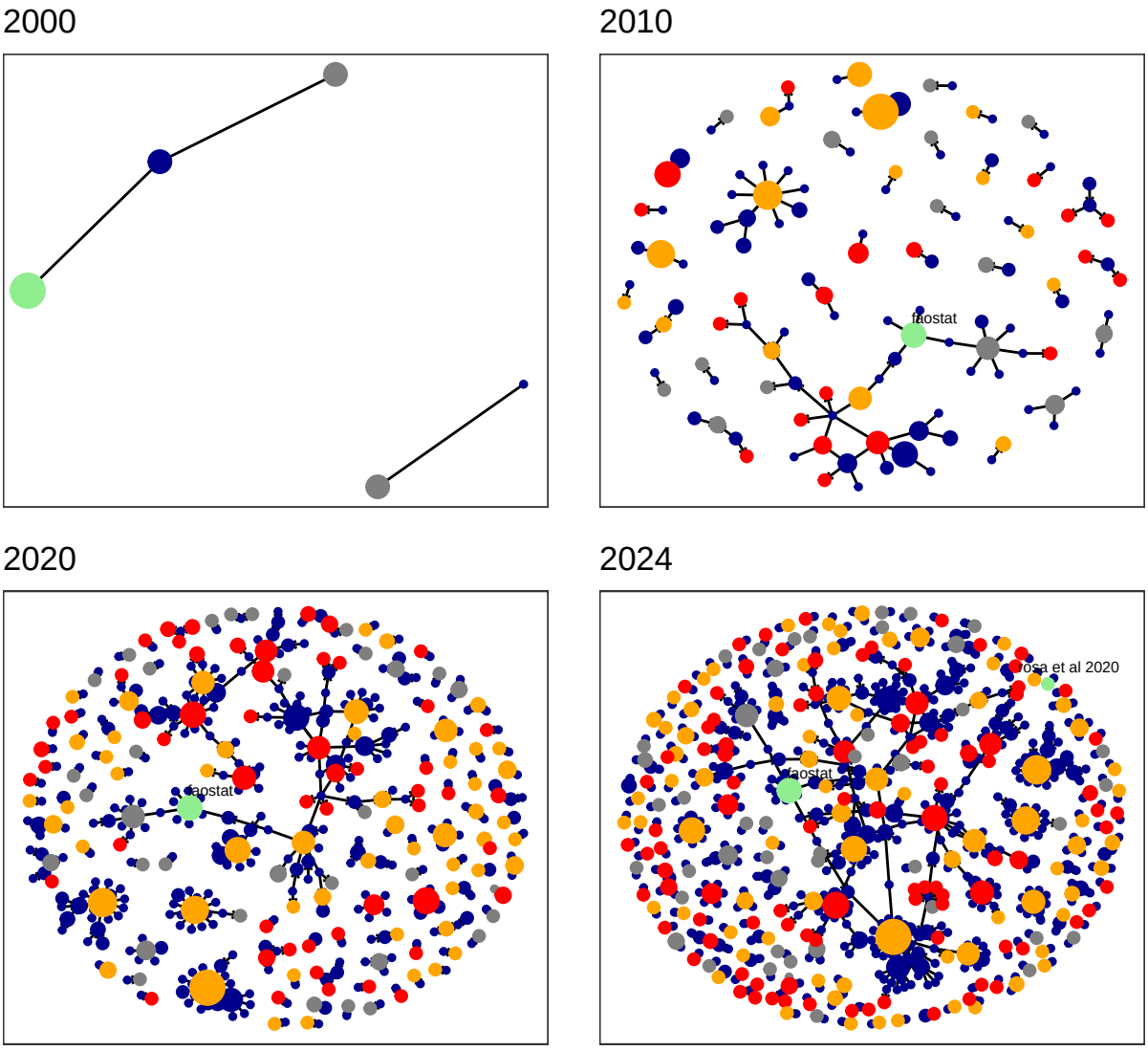
```
## Warning: Removed 237 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).
```

```
## Warning: Removed 1476 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).
```

```
## Warning: Removed 2781 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).
```

```
out.plot
```

```
## $food
```

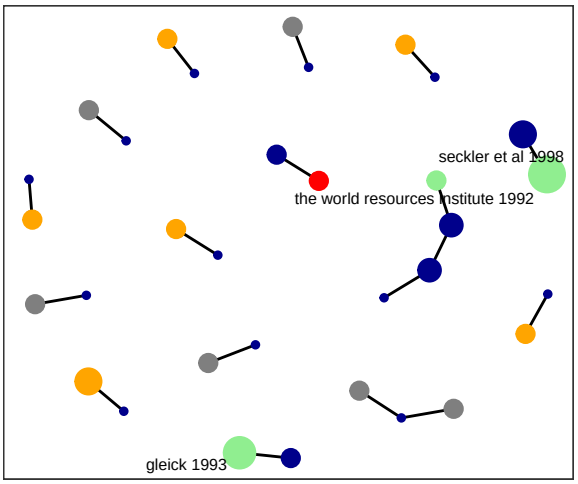



```
##
## $water
```

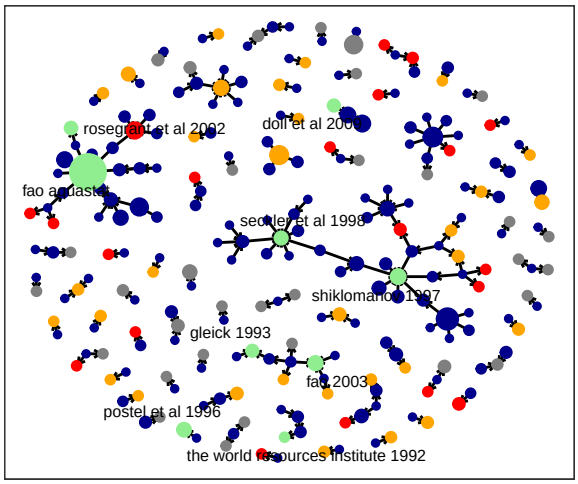
```
## Warning: ggrepel: 8 unlabeled data points (too many overlaps). Consider
## increasing max.overlaps
```

```
## Warning: ggrepel: 1 unlabeled data points (too many overlaps). Consider
## increasing max.overlaps
```

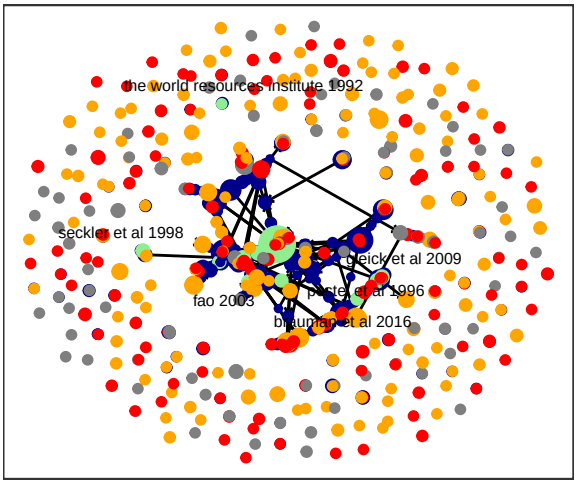
2000



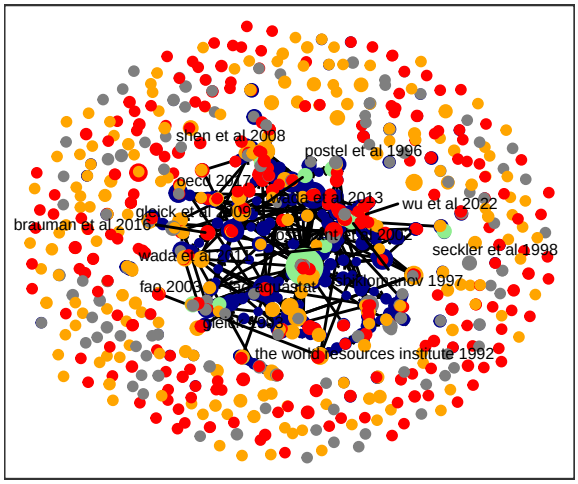
2010



2020



2024



3 Analysis of paths

3.1 "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")
}

# 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] 0.395288
##
## $food$`path ending in no claim or no citation`
## [1] 0.8376963
##
##
## $water
## $water$`path ending in no claim`
## [1] 0.3571429
##
## $water$`path ending in no claim or no citation`
## [1] 0.6842105
```

3.2 Calculation of amplification

```
# CALCULATE AMPLIFICATION FUNCTION ############################################

# Prepare data ------------------------------------------------------------

vec.topics <- c("food", "water")
```

```r
graph <- modelling.papers <- list()

for (i in 1:length(vec.topics)) {

  graph[[i]] <- network.dt.complete[topic == vec.topics[[i]]] %>%
    graph_from_data_frame(.)

  modelling.papers[[i]] <- network.dt.complete[topic == vec.topics[[i]] &
                                                 nature.claim == "modelling"] %>%
    .[, from] %>%
    unique()
}
```

```
## Warning in graph_from_data_frame(.): In `d' `NA' elements were replaced with
## string "NA"

## Warning in graph_from_data_frame(.): In `d' `NA' elements were replaced with
## string "NA"
```

```r
names(graph) <- vec.topics
names(modelling.papers) <- vec.topics

# DEFINE AMPLIFICATION FUNCTIONS ################################################

# Citation amplification function ----------------------------------------------

citation_amplification_index <- function(graph, source_paper, modelling_papers) {

  # Get all simple paths from paper P ------------------------------------------

  all_paths <- all_simple_paths(graph, from = source_paper, mode = "out")

  # Filter out paths of length 1 that lead to modelling papers -----------------

  filtered_paths <- Filter(function(path) {

    if (length(path) > 2) {

      return(TRUE)

    } else {

      # If length is 2, check if terminal node is modelling paper --------------

      return(!(tail(path, n = 1) %in% modelling_papers))
    }
  }, all_paths)
```

```
  # Calculate the number of paths ------------------------------------------

  citation_amplification_index <- length(filtered_paths)

  return(citation_amplification_index)
}

# Function to apply previous function to all papers ----------------------------

calculate_all_cai <- function(graph, modelling_papers) {

  papers <- V(graph)$name

  # Initialize an empty data.table to store results ----------------------------

  result_dt <- data.table(
    paper = character(),
    cai = numeric()
  )

  # Iterate over each paper ----------------------------------------------------

  for (paper in papers) {

    cai <- citation_amplification_index(graph, paper, modelling_papers)
    result_dt <- rbind(result_dt, data.table(paper = paper, cai = cai))
  }

  return(result_dt)
}

# CALCULATE AMPLIFICATION INDEX ################################################

# 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)

out <- list()

for(i in names(modelling.papers)) {

  out[[i]] <- calculate_all_cai(graph[[i]], modelling.papers[[i]])
}

# ARRANGE DATA #################################################################

tmp <- rbindlist(out, idcol = "topic")
```

```r
# SUMMARY STATISTICS ##############################################################

tmp[, mean(cai), topic]
```

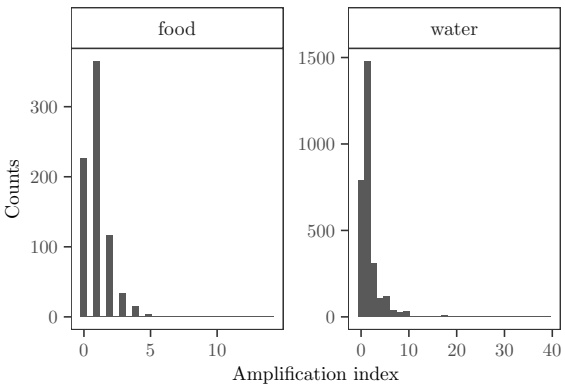
```
##     topic       V1
##    <char>    <num>
## 1:   food 1.077225
## 2:  water 1.806562
```

```r
# First 5 papers amplifying the most ------------------------------------------

tmp2 <- tmp[, .SD, topic] %>%
  .[order(-cai, topic)] %>%
  .[, head(.SD, 5), topic]

tmp2
```

```
##      topic               paper   cai
##     <char>              <char> <num>
##  1:  water           wada 2015    39
##  2:  water neysiani et al 2022    27
##  3:  water          habtu 2024    22
##  4:  water   abioye et al 2023    21
##  5:  water  derossi et al 2024    21
##  6:   food   taguta et al 2022    14
##  7:   food     guo et al 2023a    12
##  8:   food   kadigi et al 2004     8
##  9:   food   xie and lark 2021     7
## 10:   food      mao et al 2024     6
```

```r
# PLOT DISTRIBUTION OF AMPLIFICATION INDIXES ##################################

plot.amplification <- list()

# PLOT ########################################################################

plot.amplification <- ggplot(tmp, aes(cai)) +
  geom_histogram() +
  facet_wrap(~topic, scales = "free") +
  theme_AP() +
  labs(y = "Counts", x = "Amplification index")

plot.amplification
```

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



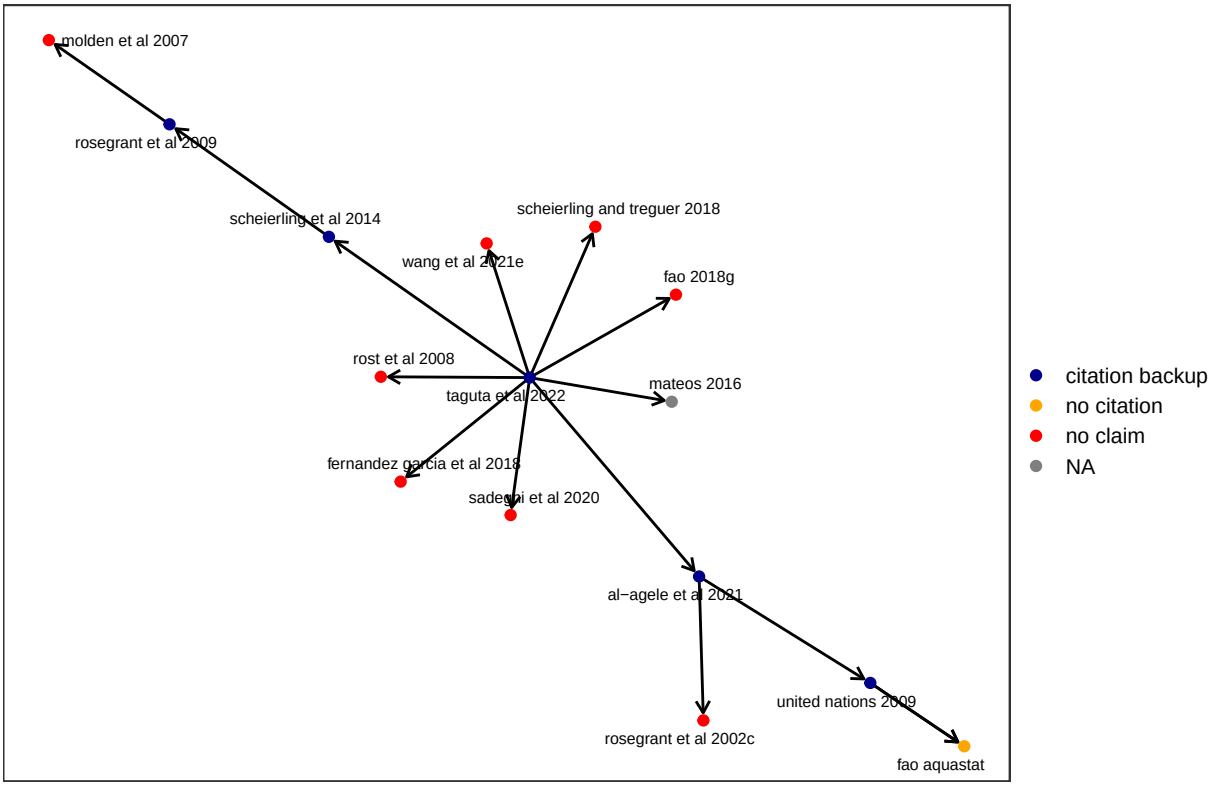

```
# PLOT THE NETWORK OF TOP AMPLIFYING PAPERS ###################################

# Define the starting nodes ---------------------------------------------------

vec.names.amplification <- tmp2[, slice_max(.SD, cai, n = 1), topic] %>%
  .[, paper]

# Reorder so the top node for food comes first --------------------------------

vec.names.amplification <- vec.names.amplification[order(vec.names.amplification)]

out <- list()

for (i in 1:length(vec.names.amplification)) {

  start_node <- vec.names.amplification[[i]]

  # Get all simple paths from the starting node to all reachable nodes
  paths <- all_simple_paths(graph[[i]], from = V(graph[[i]])[name == start_node])

  # Convert paths to a list of edge pairs for easy visualization
  edge_list <- lapply(paths, function(path) {
    edges <- as_edgelist(induced_subgraph(graph[[i]], path), names = TRUE)
    data.frame(from = edges[, 1], to = edges[, 2])
  })

  # Combine all path edges into a single data frame
  path_edges <- do.call(rbind, edge_list)

  #Get the unique nodes involved in the paths
  path_nodes <- unique(c(path_edges$from, path_edges$to))

  # Create the subgraph of all paths starting from the target node
  subgraph <- induced_subgraph(graph[[i]], vids = V(graph[[i]])[name %in% path_nodes])

  # Convert the subgraph to a tidygraph object
```

```r
subgraph_tbl <- as_tbl_graph(subgraph)

# Retrieve a vector with the node names ---------------------------------------

vec.names <- subgraph_tbl %>%
  activate(nodes) %>%
  pull() %>%
  data.table(name = .)

nature.claim.vec <- graph.final[[i]] %>%
  activate(nodes) %>%
  data.frame() %>%
  data.table() %>%
  .[name %in% vec.names$name] %>%
  .[, nature.claim]

subgraph_tbl <- subgraph_tbl %>%
  activate(nodes) %>%
  mutate(nature.claim = nature.claim.vec)

# Plot the subgraph with ggraph

if (i == 1) {

  selected_colors <- c("darkblue", "orange", "red")

} else {

selected_colors <- c("darkblue", "lightgreen", "orange", "red")

}

set.seed(123)

out[[i]] <- ggraph(subgraph_tbl, layout = "igraph", algorithm = "nicely") +
  geom_edge_link(arrow = arrow(length = unit(1.8, 'mm')),
                 end_cap = circle(1, "mm")) +
  geom_node_point(size = 1.5, aes(color = nature.claim)) +
  geom_node_text(aes(label = name), repel = TRUE, size = 2.2) +
  scale_color_manual(name = "",
                     values = selected_colors) +
  theme_AP() +
  labs(x = "", y = "") +
  theme(axis.text.x = element_blank(),
        axis.ticks.x = element_blank(),
        axis.text.y = element_blank(),
        axis.ticks.y = element_blank(),
```

```
          legend.position = "right") +
    ggtitle(paste("Paths Activated by", start_node))
}

out
```

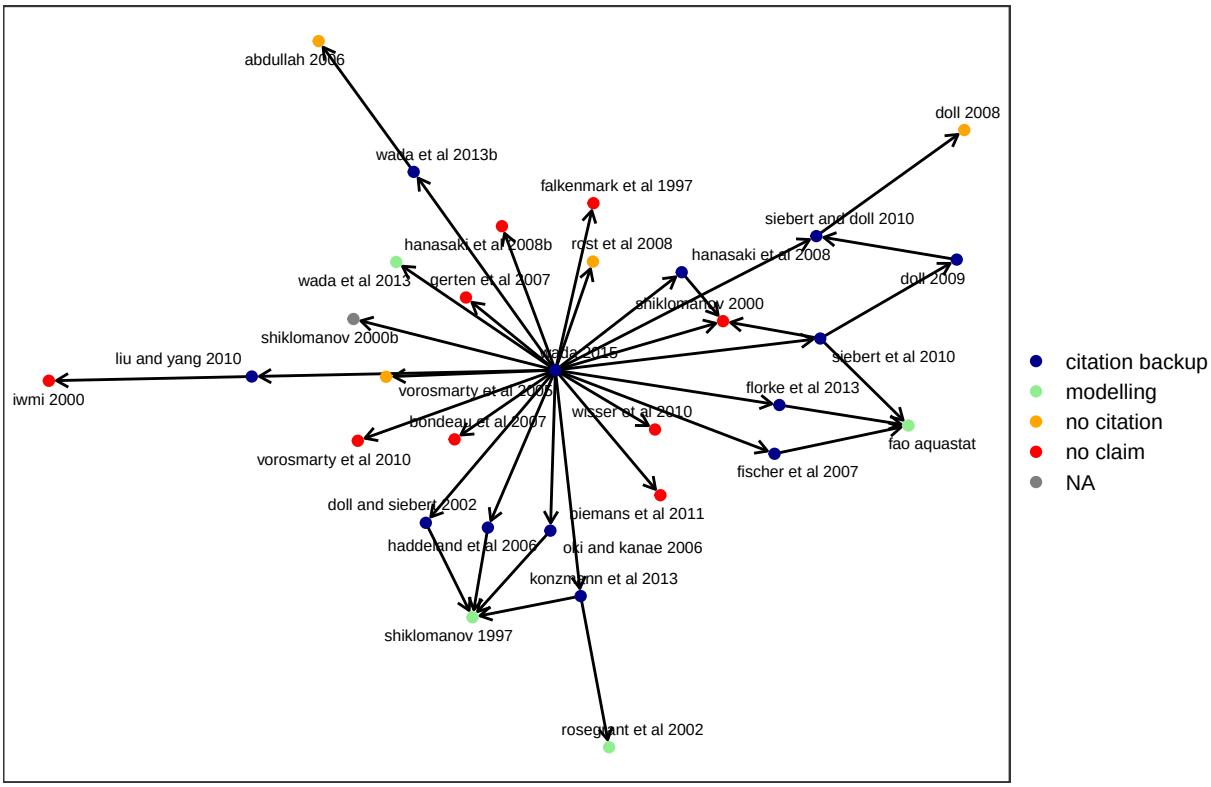
```
## [[1]]
```

```
## 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.
```




```
##
## [[2]]
```

Paths Activated by wada 2015



4 Both networks

4.1 Overlap between networks

```
# CHECK FULL NETWORK AND OVERLAP BETWEEN WATER AND FOOD NETWORK #################

# Prepare data ------------------------------------------------------------------

dd <- tidygraph::as_tbl_graph(network.dt.complete, directed = TRUE)
```

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

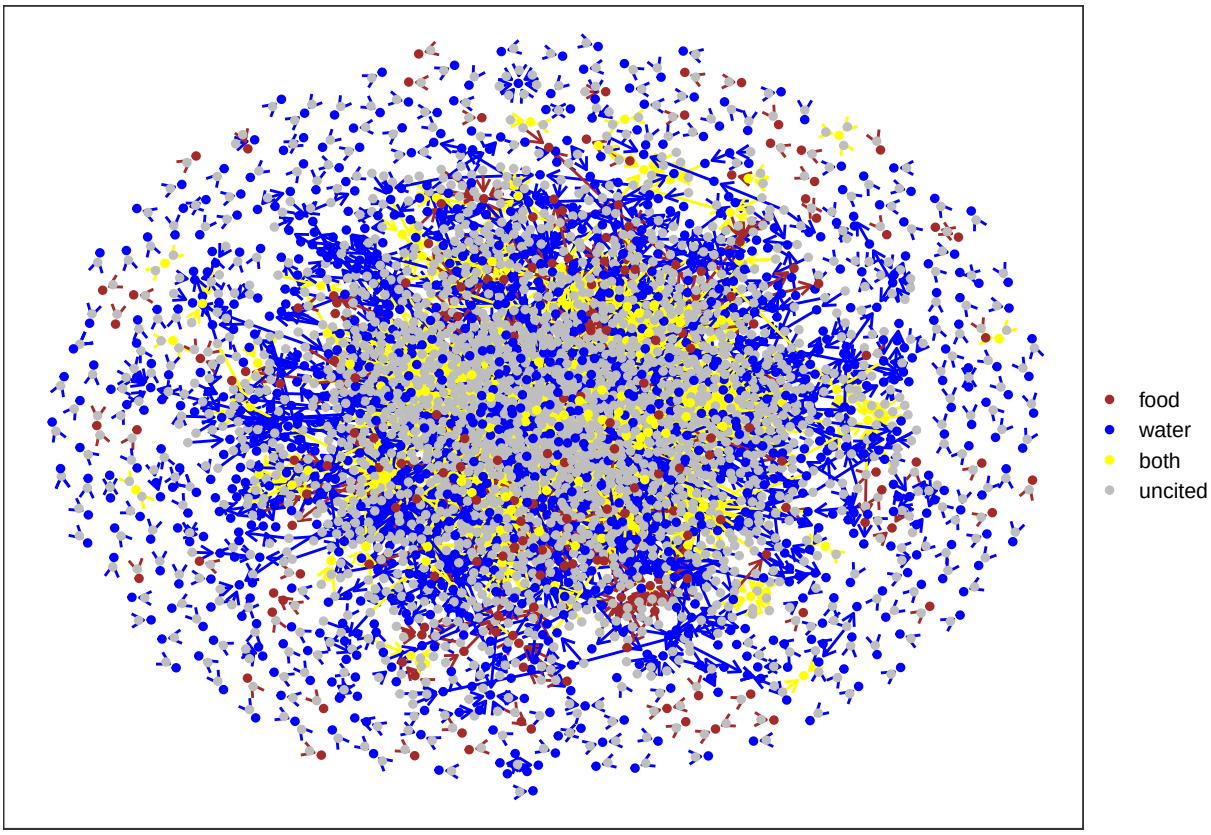
```
# Extract vector with names -----------------------------------------------------

all.names <- dd %>%
  activate(nodes) %>%
  pull(name)

# Retrieve names from water and food belief system ------------------------------

names.food <- network.dt.complete[topic == "food", to]
names.water <- network.dt.complete[topic == "water", to]
```

```r
# Define intersections and differences ----------------------------------------

names.only.food <- setdiff(names.food, names.water)
names.only.water <- setdiff(names.water, names.food)
names.both <- intersect(names.water, names.food)

# New column defining whether nodes are in water, food or in both networks -----

final.graph <- dd %>%
  activate(nodes) %>%
  mutate(topic.final = ifelse(name %in% names.only.food, "food",
                              ifelse(name %in% names.only.water, "water",
                                     ifelse(name %in% names.both, "both", "uncited"))),
         topic.final = factor(topic.final, levels = c("food", "water", "both", "uncited")))

final.graph <- final.graph %>%
  activate(edges) %>%
  mutate(edge_color = .N()$topic.final[to])

# SOME STATS ###################################################################

dt.nodes <- final.graph %>%
  activate(nodes) %>%
  data.frame() %>%
  data.table()

# Fraction of network overlap -------------------------------------------------

dt.nodes[, .N, topic.final] %>%
  .[, fraction:= N / nrow(dt.nodes)] %>%
  print
```

```
##    topic.final     N   fraction
##         <fctr> <int>      <num>
## 1:     uncited  2115 0.61074213
## 2:       water  1044 0.30147271
## 3:        both   125 0.03609587
## 4:        food   179 0.05168929
```

```r
# PLOT MERGED NETWORK ##########################################################

selected.colors <- c("brown", "blue", "yellow", "grey")

ggraph(final.graph, layout = "graphopt") +
  geom_edge_link(arrow = arrow(length = unit(1.8, 'mm')),
                 end_cap = circle(1, "mm"),
                 aes(color = edge_color)) +
  geom_node_point(aes(color = topic.final), size = 1) +
```

```
  scale_edge_color_manual(values = selected.colors, guide = "none") +
  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 = "right")
```



4.2 Shared network

```
# PLOT ONLY THE NETWORK OF NODES BEING CITED FOR BOTH BELIEFS ##################

# Prepare data ----------------------------------------------------------------

intersect.network <- network.dt.complete[to %in% names.both] %>%
  tidygraph::as_tbl_graph(., directed = TRUE)
```

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

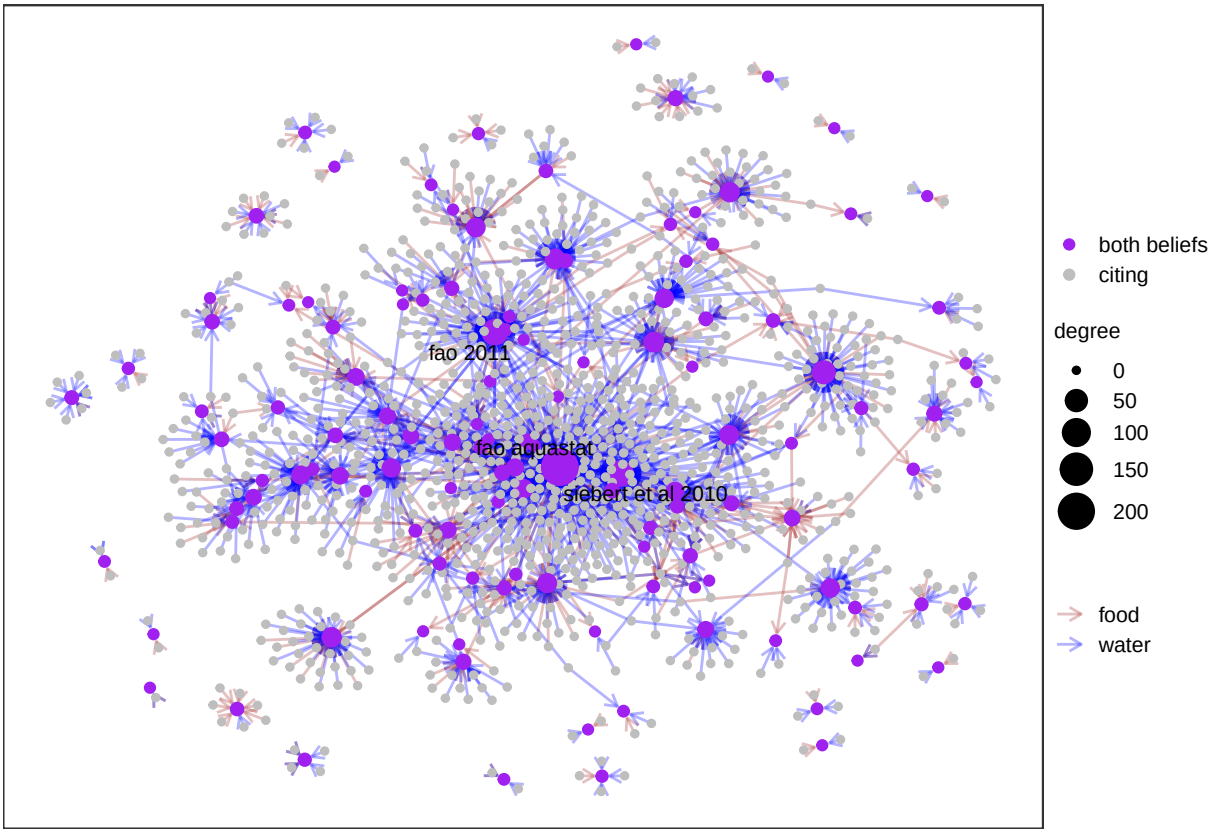
```
intersect.graph <- network.dt.complete[to %in% names.both] %>%
  graph_from_data_frame(d = ., directed = TRUE)
```

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

```
# Calculate metrics ------------------------------------------------------------

intersect.metrics <- data.table(node = V(intersect.graph)$name,
                                degree = degree(intersect.graph, mode = "in"),
                                degree.out = degree(intersect.graph, mode = "out"),
                                betweenness = betweenness(intersect.graph),
                                closeness = closeness(intersect.graph),
                                pagerank = page_rank(intersect.graph)$vector)

degree.nodes <- intersect.metrics[order(-degree)][1:3]
degree.out.nodes <- intersect.metrics[order(-degree.out)][1:3]
betweenness.nodes <- intersect.metrics[order(-betweenness)][1:3]

# Retrieve a vector with the node names ----------------------------------------

vec.names <- intersect.network %>%
  activate(nodes) %>%
  pull() %>%
  data.table(name = .)

order <- match(vec.names$name, intersect.metrics$node)
tmp <- intersect.metrics[order]

intersect.graph.final <- intersect.network %>%
  activate(nodes) %>%
  mutate(degree = tmp$degree,
         degree.out = tmp$degree.out,
         betweenness = tmp$betweenness)

intersect.graph.final <- intersect.graph.final %>%
  activate(nodes) %>%
  mutate(topic = ifelse(name %in% names.both, "both beliefs", "citing"))

# PLOT ###########################################################################

set.seed(12)

ggraph(intersect.graph.final, layout = "graphopt") +
  geom_edge_link(arrow = arrow(length = unit(1.8, 'mm')),
                 end_cap = circle(1, "mm"),
                 aes(color = topic),
                 alpha = 0.3) +
```

```
  geom_node_point(aes(color = topic, size = degree)) +
  geom_node_text(aes(label = ifelse(degree >= min(degree.nodes$degree),
                                    name, NA)),
                 repel = TRUE,
                 size = 2.7) +
  scale_edge_color_manual(values = c("brown", "blue"),
                          name = "") +
  scale_color_manual(name = "",
                     values = c("purple", "grey")) +
  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")
```

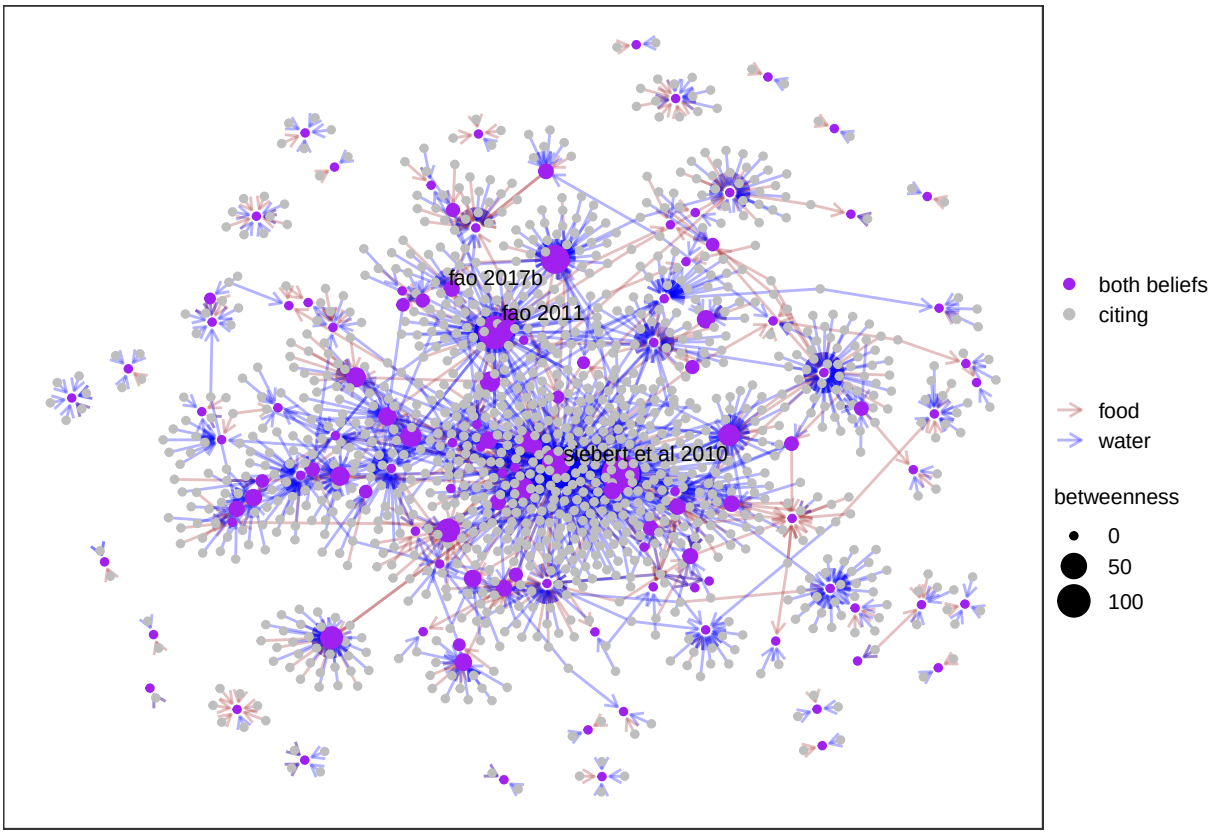
```
## Warning: Removed 1281 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).
```




```
set.seed(12)

ggraph(intersect.graph.final, layout = "graphopt") +
  geom_edge_link(arrow = arrow(length = unit(1.8, 'mm')),
```

```
                end_cap = circle(1, "mm"),
                aes(color = topic),
                alpha = 0.3) +
  geom_node_point(aes(color = topic, size = betweenness)) +
  geom_node_text(aes(label = ifelse(betweenness >= min(betweenness.nodes$betweenness),
                                    name, NA)),
                repel = TRUE,
                size = 2.7) +
  scale_edge_color_manual(values = c("brown", "blue"),
                          name = "") +
  scale_color_manual(name = "",
                     values = c("purple", "grey")) +
  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")
```

```
## Warning: Removed 1281 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).
```



5 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 = "continer

# 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
```

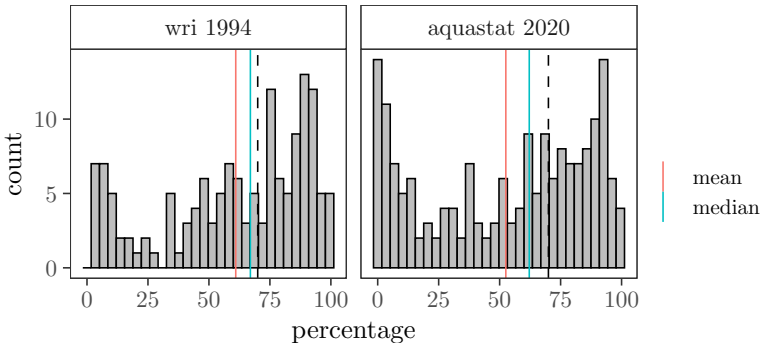
```
wri[, continent:= countrycode(country, origin = "country.name", destination = "continent")]
```

```
## 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 row containing non-finite outside the scale range
## (`stat_bin()`).
```

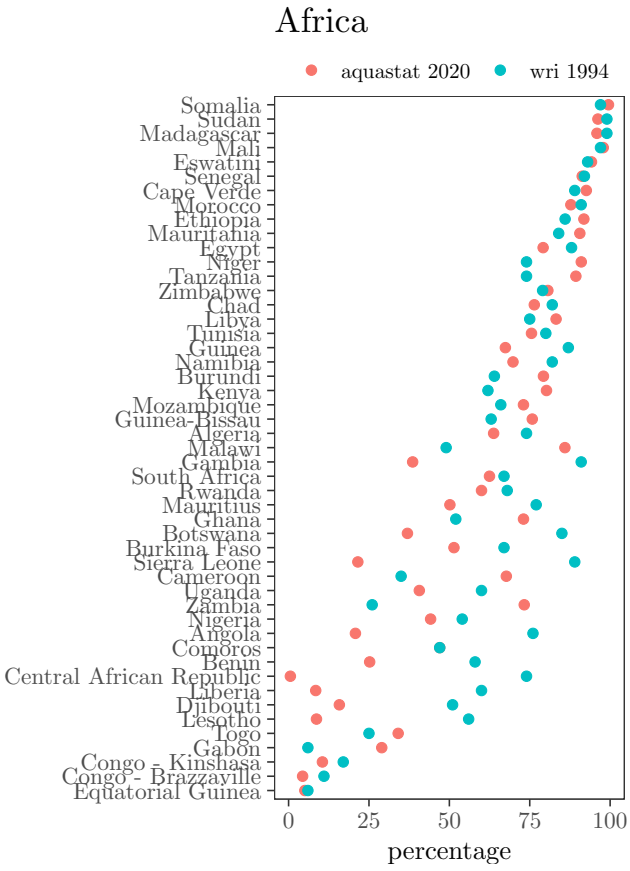



```
# At the country level ------------------------------------------------------

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)
```

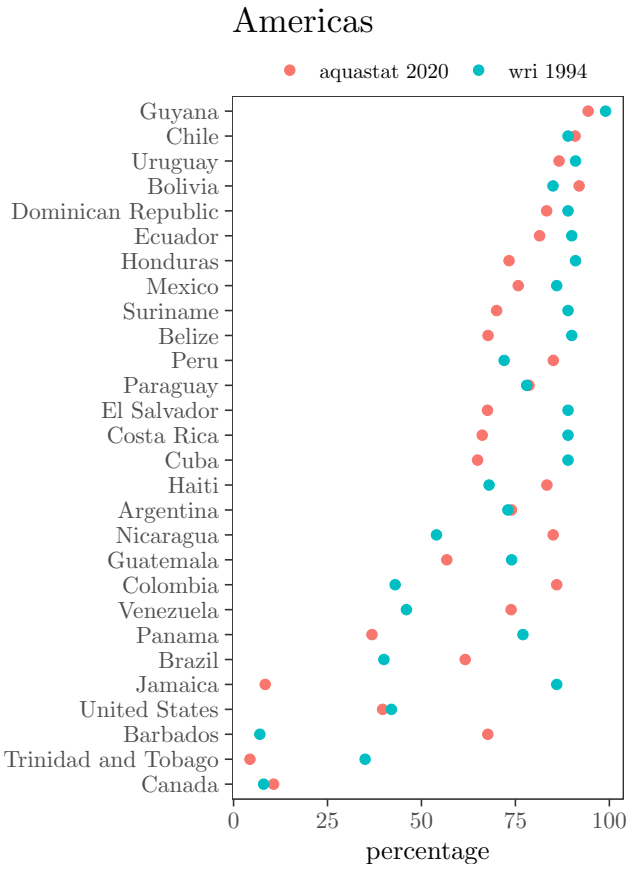
```
## Warning in melt.data.table(., measure.vars = c("aquastat 2020", "wri 1994")):
## 'measure.vars' [aquastat 2020, wri 1994] are not all of the same type. By order
## of hierarchy, the molten data value column will be of type 'double'. All
## measure variables not of type 'double' will be coerced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

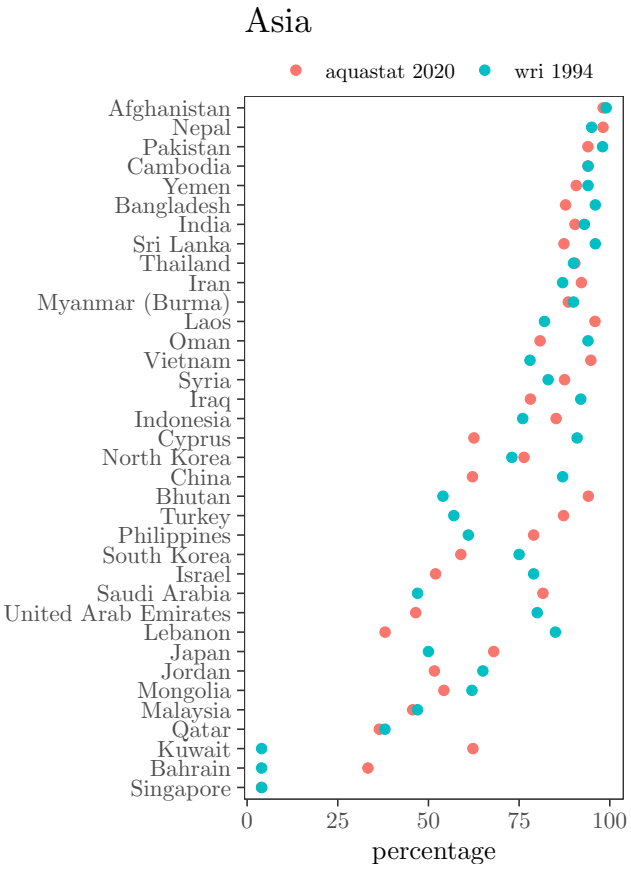
```
## $Africa
```


Africa
aquastat 2020
wri 1994
Somalia
Sudan
Madagascar
Mali
Eswatini
Senegal
Cape Verde
Morocco
Ethiopia
Mauritania
Egypt
Niger
Tanzania
Zimbabwe
Chad
Libya
Tunisia
Guinea
Namibia
Burundi
Kenya
Mozambique
Guinea-Bissau
Algeria
Malawi
Gambia
South Africa
Rwanda
Mauritius
Ghana
Botswana
Burkina Faso
Sierra Leone
Cameroon
Uganda
Zambia
Nigeria
Angola
Comoros
Benin
Central African Republic
Liberia
Djibouti
Lesotho
Togo
Gabon
Congo - Kinshasa
Congo - Brazzaville
Equatorial Guinea
0
25
50
75
100
percentage

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


Americas
aquastat 2020
wri 1994
Guyana
Chile
Uruguay
Bolivia
Dominican Republic
Ecuador
Honduras
Mexico
Suriname
Belize
Peru
Paraguay
El Salvador
Costa Rica
Cuba
Haiti
Argentina
Nicaragua
Guatemala
Colombia
Venezuela
Panama
Brazil
Jamaica
United States
Barbados
Trinidad and Tobago
Canada
0
25
50
75
100
percentage

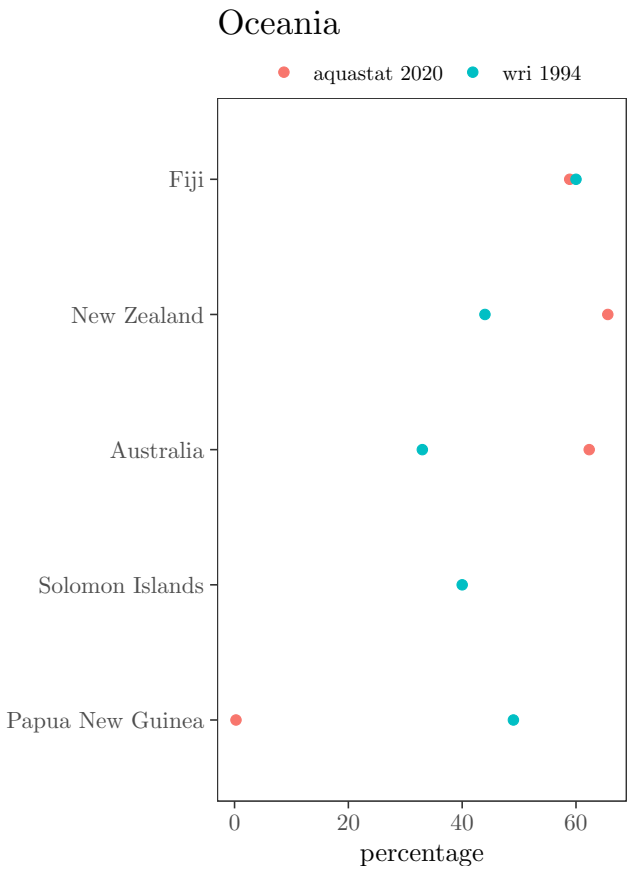
```
##
## $Asia
```


Asia
aquastat 2020
wri 1994
Afghanistan
Nepal
Pakistan
Cambodia
Yemen
Bangladesh
India
Sri Lanka
Thailand
Iran
Myanmar (Burma)
Laos
Oman
Vietnam
Syria
Iraq
Indonesia
Cyprus
North Korea
China
Bhutan
Turkey
Philippines
South Korea
Israel
Saudi Arabia
United Arab Emirates
Lebanon
Japan
Jordan
Mongolia
Malaysia
Qatar
Kuwait
Bahrain
Singapore
0
25
50
75
100
percentage

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


Europe
aquastat 2020
wri 1994
Albania
Greece
Spain
Italy
Portugal
Denmark
Romania
Bulgaria
Malta
Hungary
Norway
Poland
Netherlands
Finland
France
Germany
United Kingdom
Sweden
Switzerland
Luxembourg
Ireland
Austria
Iceland
Belgium
0
20
40
60
80
percentage

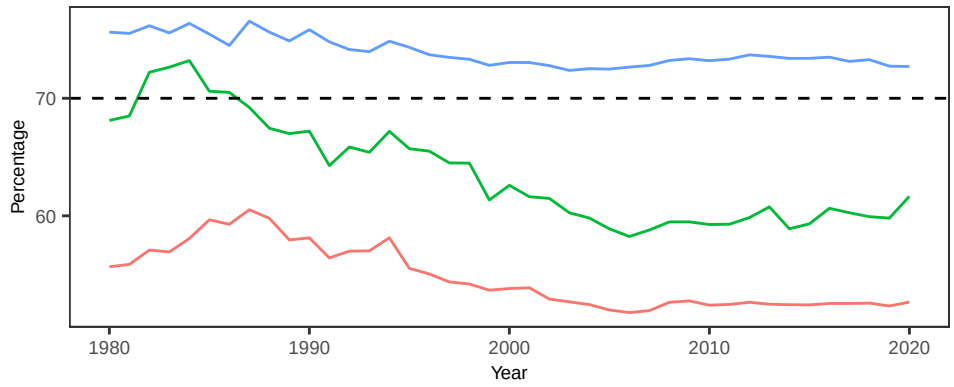
```
##
## $Oceania
```




```
# AQUASTAT ALL YEARS ##############################################################

# DATA FOR THE WATER BELIEF ########################################################

# Read in dataset ----------------------------------------------------------

aquastat.aww <- fread("aquastat.fraction.agriculture.withdrawals.csv")
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() +
```

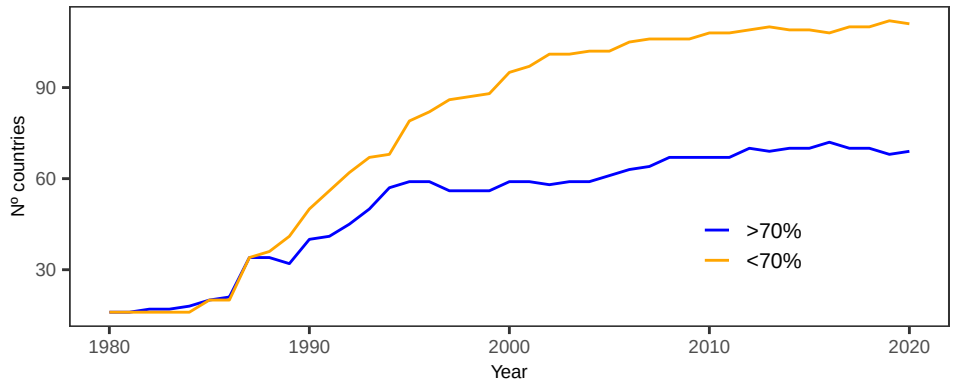
```
  scale_color_discrete(name = "") +
  geom_hline(yintercept = 70, lty = 2) +
  theme_AP() +
  labs(x = "Year", y = "Percentage") +
  theme(legend.position = "none")
```

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%", "<70%"),
                     values = c("blue", "orange")) +

  labs(x = "Year", y = "Nº countries") +
  theme(legend.position = c(0.78, 0.34))
```

b




```
# Fraction of estimated and imputed values ------------------------------------

n.countries <- aquastat.aww[, .(total.countries = .N), Year]
fraction.estimate <- aquastat.aww[, .N, .(Symbol, Year)] %>%
```

```
  merge(., n.countries, by = "Year") %>%
  .[, fraction:= N / total.countries] %>%
  ggplot(., aes(Year, N, color = Symbol)) +
  geom_line() +
  labs(x = "Year", y = "Nº countries") +
  scale_color_discrete(name = "") +
  theme_AP() +
  theme(legend.position = c(0.85, 0.25),
        legend.text = element_text(size = 7))

dt.stats.year <- aquastat.aww.stats %>%
  rbind(weighted.average.dt) %>%
  .[Year == max(Year)]

water.histogram <- aquastat.aww[Year == max(Year)] %>%
  ggplot(., aes(Value)) +
  geom_histogram(color = "black", fill = "grey") +
  geom_vline(xintercept = 70, lty = 2) +
  geom_vline(data = dt.stats.year, aes(xintercept = value, color = variable)) +
  labs(x = "Percentage", y = "Nº countries") +
  theme_AP() +
  theme(legend.position = "none")

water.plots.aquastat <- plot_grid(a, water.histogram, b, fraction.estimate,
                                  ncol = 4, labels = c("b", ""))
```

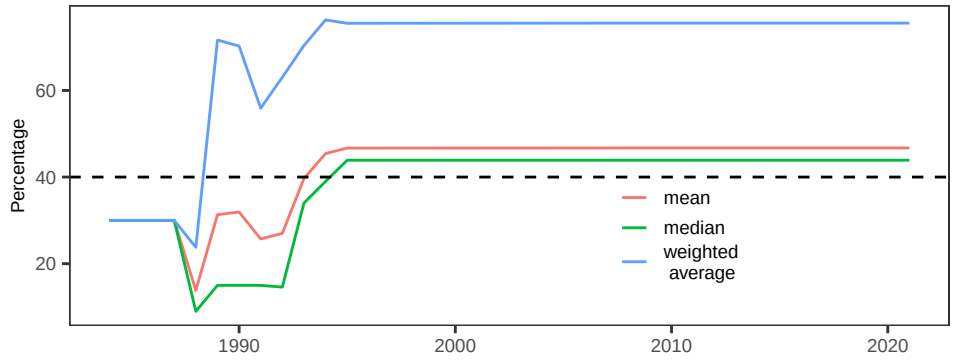
```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

```
# DATA FOR THE FOOD BELIEF ############################################################

dt <- fread("aquastat.fraction.grain.irrigated.csv")

# Check the variable examined ---------------------------------------------------

unique(dt$Variable)
```

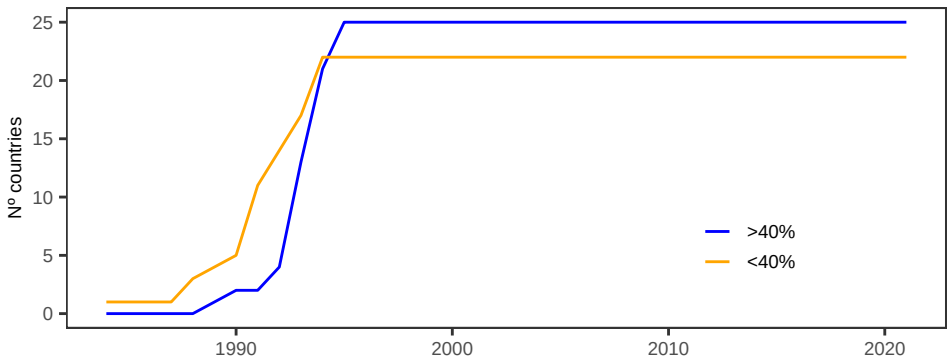
```
## [1] "% of total grain production irrigated"
```

```
# Calculate mean and median -----------------------------------------------------

aquastat.grain.stats <- dt[, .(mean = mean(Value),
                               median = median(Value),
                               N.countries = .N), Year] %>%
  melt(., measure.vars = c("mean", "median"))

# Calculated weighted average ---------------------------------------------------

dt[, weights:= Value / sum(Value), Year]
weighted.average.dt <- dt[, .(value = sum(Value * weights),
```

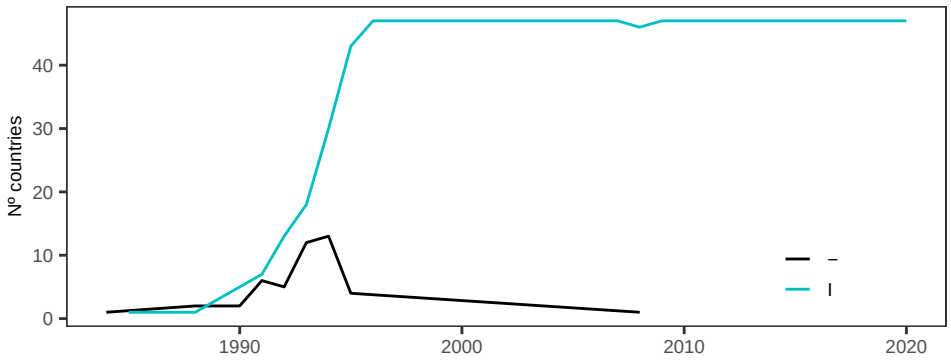
```
                                N.countries = .N), Year] %>%
  .[, variable:= "weighted \n average"]

# Plot ------------------------------------------------------------------------

a.crop <- aquastat.grain.stats %>%
  rbind(weighted.average.dt) %>%
  ggplot(., aes(Year, value, group = variable, color = variable)) +
  geom_line() +
  scale_color_discrete(name = "") +
  geom_hline(yintercept = 40, lty = 2) +
  theme_AP() +
  labs(x = "", y = "Percentage") +
  theme(legend.position = c(0.7, 0.38),
        legend.text = element_text(size = 7))

a.crop
```




```
b.crop <- dt[, .(above.40 = sum(Value > 40),
                 below.40 = sum(Value < 40)), Year] %>%
  melt(., measure.vars = c("above.40", "below.40")) %>%
  ggplot(., aes(Year, value, color = variable)) +
  geom_line() +
  theme_AP() +
  scale_color_manual(name = "", labels = c(">40%", "<40%"),
                     values = c("blue", "orange")) +

  labs(x = "", y = "Nº countries") +
  theme(legend.position = c(0.78, 0.34),
        legend.text = element_text(size = 7))

b.crop
```



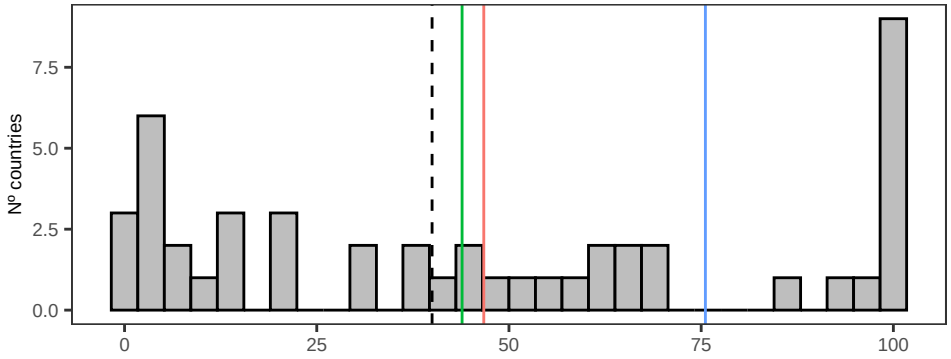

```
n.countries.crop <- dt[, .(total.countries = .N), Year]
fraction.estimate <- dt[, .N, .(Symbol, Year)] %>%
  merge(., n.countries, by = "Year") %>%
  .[, fraction:= N / total.countries] %>%
  ggplot(., aes(Year, N, color = Symbol)) +
  geom_line() +
  labs(x = "", y = "Nº countries") +
  scale_color_manual(name = "", values = c("black", "#00BFC4")) +
  theme_AP() +
  theme(legend.position = c(0.85, 0.25),
        legend.text = element_text(size = 7))

fraction.estimate
```




```
dt.stats.year.crops <- aquastat.grain.stats %>%
  rbind(weighted.average.dt) %>%
  .[Year == max(Year)]

crop.histogram <- dt[Year == max(Year)] %>%
  ggplot(., aes(Value)) +
  geom_histogram(color = "black", fill = "grey") +
  geom_vline(xintercept = 40, lty = 2) +
  geom_vline(data = dt.stats.year.crops, aes(xintercept = value, color = variable)) +
  labs(x = "", y = "Nº countries") +
  theme_AP() +
  theme(legend.position = "none")
```

```
crop.histogram
```

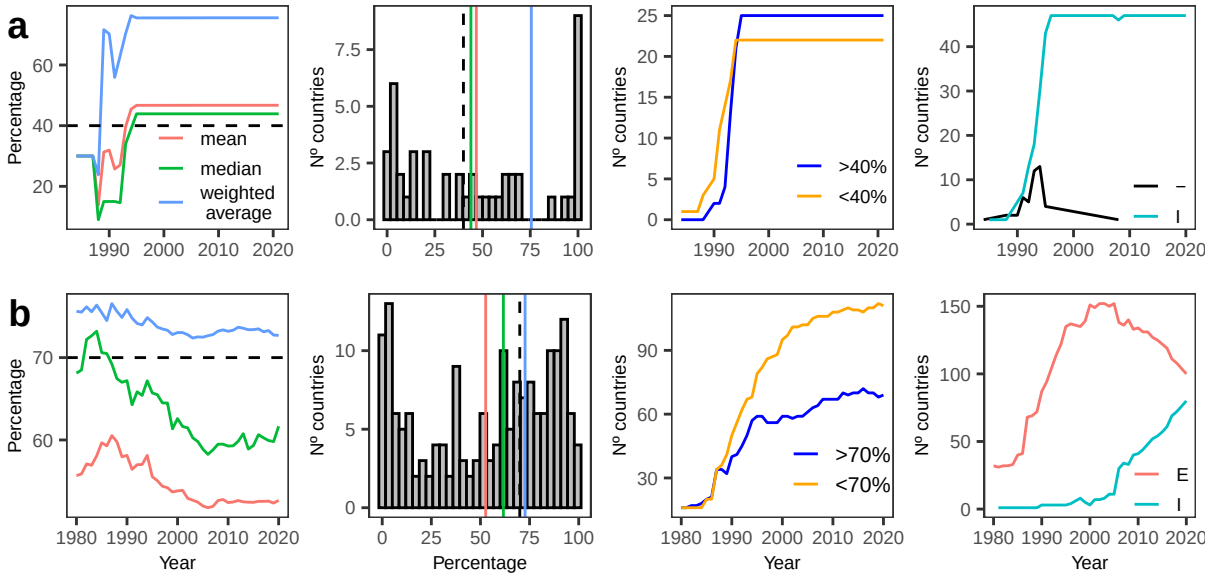
```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```




```
crop.plots.aquastat <- plot_grid(a.crop, crop.histogram, b.crop, fraction.estimate,
                                 labels = c("a", ""), ncol = 4)
```

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

```
plot_grid(crop.plots.aquastat, water.plots.aquastat, ncol = 1)
```



6 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] doParallel_1.0.17  iterators_1.0.14   foreach_1.5.2      countrycode_1.5.0
##  [5] scales_1.3.0       wesanderson_0.3.6  benchmarkme_1.0.8  tidygraph_1.3.0
##  [9] cowplot_1.1.3      ggraph_2.1.0       igraph_2.0.3       bibliometrix_4.0.1
## [13] lubridate_1.9.2    forcats_1.0.0      stringr_1.5.1      dplyr_1.1.4
## [17] purrr_1.0.2        readr_2.1.4        tidyr_1.3.1        tibble_3.2.1
## [21] ggplot2_3.5.1      tidyverse_2.0.0    data.table_1.14.99 openxlsx_4.2.5.2
##
## loaded via a namespace (and not attached):
##  [1] gridExtra_2.3          readxl_1.4.2           rlang_1.1.4
##  [4] magrittr_2.0.3         tidytext_0.4.1         compiler_4.3.3
##  [7] vctrs_0.6.5            pkgconfig_2.0.3        fastmap_1.1.1
## [10] ellipsis_0.3.2         utf8_1.2.4             promises_1.2.0.1
## [13] rmarkdown_2.21         tzdb_0.3.0             xfun_0.39
## [16] jsonlite_1.8.4         flashClust_1.01-2      SnowballC_0.7.1
## [19] later_1.3.0            tweenr_2.0.2           cluster_2.1.6
## [22] R6_2.5.1               stringi_1.8.3          RColorBrewer_1.1-3
## [25] cellranger_1.1.0       estimability_1.4.1     Rcpp_1.0.12
## [28] knitr_1.42             filehash_2.4-5         httpuv_1.6.9
## [31] rentrez_1.2.3          Matrix_1.6-5           timechange_0.2.0
## [34] tidyselect_1.2.0       rstudioapi_0.15.0      stringdist_0.9.10
## [37] pubmedR_0.0.3          yaml_2.3.7             viridis_0.6.4
## [40] codetools_0.2-19       lattice_0.22-5         plyr_1.8.8
## [43] shiny_1.7.4            withr_3.0.0            benchmarkmeData_1.0.4
```

```
## [46] coda_0.19-4            evaluate_0.20          polyclip_1.10-6
## [49] zip_2.3.0              pillar_1.9.0           janeaustenr_1.0.0
## [52] DT_0.27                plotly_4.10.1          generics_0.1.3
## [55] hms_1.1.3              munsell_0.5.1          xtable_1.8-4
## [58] leaps_3.1              glue_1.7.0             tikzDevice_0.12.4
## [61] emmeans_1.8.5          scatterplot3d_0.3-43   lazyeval_0.2.2
## [64] tools_4.3.3            tokenizers_0.3.0       mvtnorm_1.1-3
## [67] graphlayouts_1.1.1     XML_3.99-0.14          grid_4.3.3
## [70] rscopus_0.6.6          colorspace_2.1-0       dimensionsR_0.0.3
## [73] ggforce_0.4.1          bibliometrixData_0.3.0 cli_3.6.3
## [76] fansi_1.0.6            viridisLite_0.4.2      gtable_0.3.5
## [79] digest_0.6.34          ggrepel_0.9.5          FactoMineR_2.8
## [82] htmlwidgets_1.6.2      farver_2.1.2           htmltools_0.5.5
## [85] factoextra_1.0.7       lifecycle_1.0.4        httr_1.4.5
## [88] multcompView_0.1-9     mime_0.12              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
```