

Irrigation's real impact on global water and food security

R code

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```

# 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),
          legend.key.width = unit(0.4, "cm"),
          legend.key.height = unit(0.4, "cm"),
          legend.title = element_text(size = 9))
}

```

1 Network analysis

```

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

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

# READ IN DATASETS AND TURN TO LOWERCAPS #####

```

```

tmp <- list()

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

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

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

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

  } else {

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

names(tmp) <- all.files

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

## [1] "water" "water" "water" "food"  "food"  "food"  "water" "water" "water"
## [10] "food"   "food"   "food"

# CLEAN AND MERGE DATASETS #####
# Work datasets ----

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

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

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

```

```

## 11: food <NA> 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 2007 water  46
## 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      4
## 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 online service 2010 water      1
## 11: faostat online service 2019 water      1
## 12:          faostat 2023 water      1
## 13:          faostat 2012 food       2
## 14:          faostat 2006 food       1
## 15:          faostat 2011 food       1

```



```

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

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

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

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

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

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

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

## Key: <topic>
##      topic    nature.claim      N number.rows      fraction
##      <char>      <char> <int>      <int>      <num>
##  1: food      no citation   192      1041 0.1844380403
##  2: food      citation backup  614      1041 0.5898174832
##  3: food      no claim     91      1041 0.0874159462
##  4: food          <NA>     40      1041 0.0384245917
##  5: food      modelling      1      1041 0.0009606148
##  6: food      citation backup     3      1041 0.0028818444
##  7: food      no claim      1      1041 0.0009606148
##  8: food      no citation     1      1041 0.0009606148
##  9: water      citation backup 2529      4352 0.5811121324
## 10: water      modelling     25      4352 0.0057444853

```

```

## 11: water      no citation    935      4352 0.2148437500
## 12: water          <NA>     123      4352 0.0282628676
## 13: water      no claim     400      4352 0.0919117647
## 14: water citation backup    215      4352 0.0494025735
## 15: water      no claim     34       4352 0.0078125000
## 16: water      no citation    37      4352 0.0085018382
## 17: water      no claim      1       4352 0.0002297794

# Count document type by nature of claim ----

a <- network.dt[, .N, .(nature.claim, document.type, topic)] %>%
  merge(., total.rows, by = "topic") %>%
  .[, proportion:= N / number.rows] %>%
  na.omit() %>%
  ggplot(., aes(reorder(nature.claim, proportion), proportion)) +
  coord_flip() +
  geom_bar(stat = "identity") +
  facet_grid(topic~document.type) +
  scale_y_continuous(breaks = breaks_pretty(n = 2)) +
  labs(x = "", y = "Fraction") +
  theme_AP()

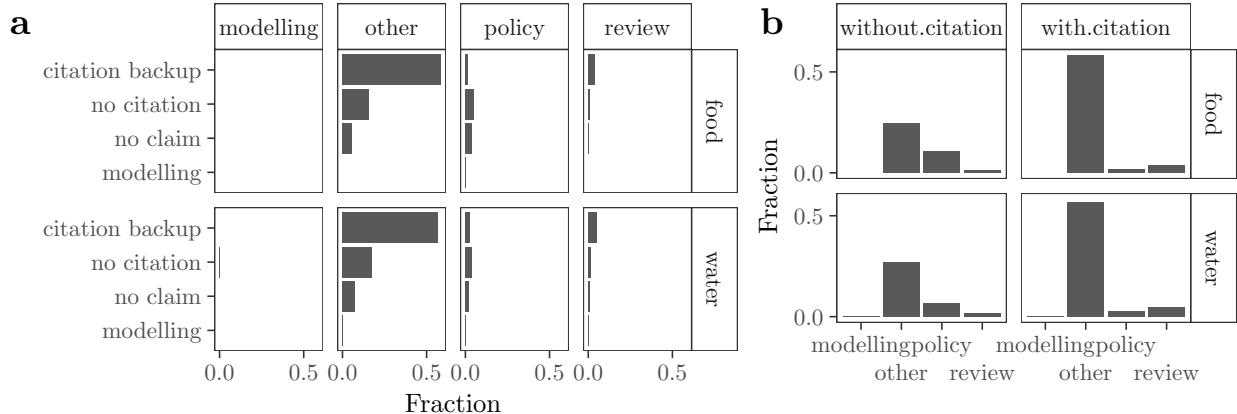
# Count how many documents make the claim and cite / do not cite,
# by document.type ----

b <- network.dt[, .(without.citation = sum(is.na(to)),
                     with.citation = .N - sum(is.na(to))), .(document.type, topic)] %>%
  melt(., measure.vars = c("without.citation", "with.citation")) %>%
  merge(., total.rows, by = "topic") %>%
  .[, proportion:= value / number.rows] %>%
  ggplot(., aes(document.type, proportion)) +
  geom_bar(stat = "identity") +
  scale_y_continuous(breaks = breaks_pretty(n = 2)) +
  scale_x_discrete(guide = guide_axis(n.dodge = 2)) +
  labs(x = "", y = "Fraction") +
  facet_grid(topic~variable) +
  theme_AP()

# merge ----

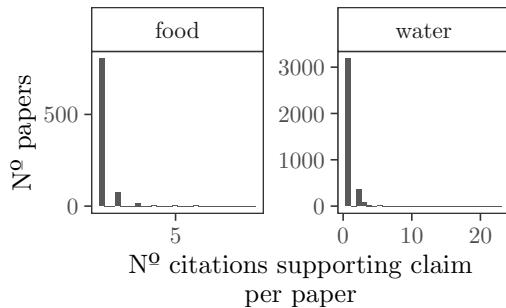
plot_grid(a, b, ncol = 2, rel_widths = c(0.6, 0.4), labels = "auto")

```



```
# PLOT DISTRIBUTION OF CITATION SUPPORTING THE CLAIM #####
network.dt[, .N, .(from, topic)] %>%
  .[order(-N)] %>%
  ggplot(., aes(N)) +
  geom_histogram() +
  facet_wrap(~topic, scale = "free") +
  scale_x_continuous(breaks = breaks_pretty(n = 3)) +
  scale_y_continuous(breaks = breaks_pretty(n = 3)) +
  theme_AP() +
  labs(x = "Nº citations supporting claim \n per paper", y = "Nº papers")
```

`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 -----
```

```

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

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

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

# Calculate network metrics -----
lapply(citation_graph, function(x) edge_density(x))

## $food
## [1] 0.001133923
##
## $water
## [1] 0.0003258099

# 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] 0.9235834
##
## $water
## [1] 0.8766236

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 0.02974953
## 2:           fao 2002     19          0          0       NaN 0.01649633
## 3: morris et al 2003     16          0          0       NaN 0.01139164
##
## $water
##           node degree degree.out betweenness closeness    pagerank
##           <char>  <num>      <num>      <num>      <num>      <num>
## 1:     fao aquastat    175          0      0.0000       NaN 0.056614184
## 2: siebert et al 2010     67          3  219.8333 0.3333333 0.008257298
## 3:     fao 2011        65          1   81.5000 1.0000000 0.011114066
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 0.0007646680
## 2:     pei et al 2017     1          6          4 0.20000000 0.0008946616
## 3: kadigi et al 2004     0          6          0 0.10000000 0.0007646680
##
## $water
##           node degree degree.out betweenness closeness    pagerank
##           <char>  <num>      <num>      <num>      <num>      <num>

```

```

## 1:      wada 2015      0       23      0 0.02702703 0.0001806776
## 2: wada et al 2014a    1       9      10 0.09090909 0.0002113928
## 3: zarei et al 2021    0       9      0 0.06666667 0.0001806776

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: 0.004014507
## 2: 0.008407207
## 3: 0.006645071

##
## $water
##           node degree degree.out betweenness closeness pagerank
##           <char>  <num>     <num>     <num>     <num>     <num>
## 1: siebert et al 2010      67       3   219.8333 0.33333333 0.008257298
## 2: boretti and rosa 2019      12       5   195.0000 0.03703704 0.001661406
## 3: molden et al 2007       42       1   147.0000 0.33333333 0.008518694

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 0.000764668
## 2: du preez et al 2018      0       1       0       1 0.000764668
## 3: meier et al 2018       3       1       3       1 0.002389588

##
## $water
##           node degree degree.out betweenness closeness pagerank
##           <char>  <num>     <num>     <num>     <num>     <num>
## 1: sharma and irmak 2012      0       1       0       1 0.0001806776
## 2: world bank 2007        5       1      46       1 0.0053984194
## 3: brajovic et al 2015      0       1       0       1 0.0001806776

```

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, classification,
    by.x = "name", by.y = "from", all.x = TRUE)
  }])

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

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

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

```

```

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

for (i in names(graph)) {

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

}

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

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

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

## $food
## + 764/764 vertices, named, from 23341a7:
## [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
## + 2931/2931 vertices, named, from fa1e3a3:

```

```

## [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 khilid 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] 661
##
## $water
## [1] 2798

# 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 ----

```

```

stopCluster(cl)

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

results.counts

## $food
## [1] 824 104
##
## $water
## [1] 4976 1008

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

## $food
## [1] 0.1262136
##
## $water
## [1] 0.2025723

# 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")
}

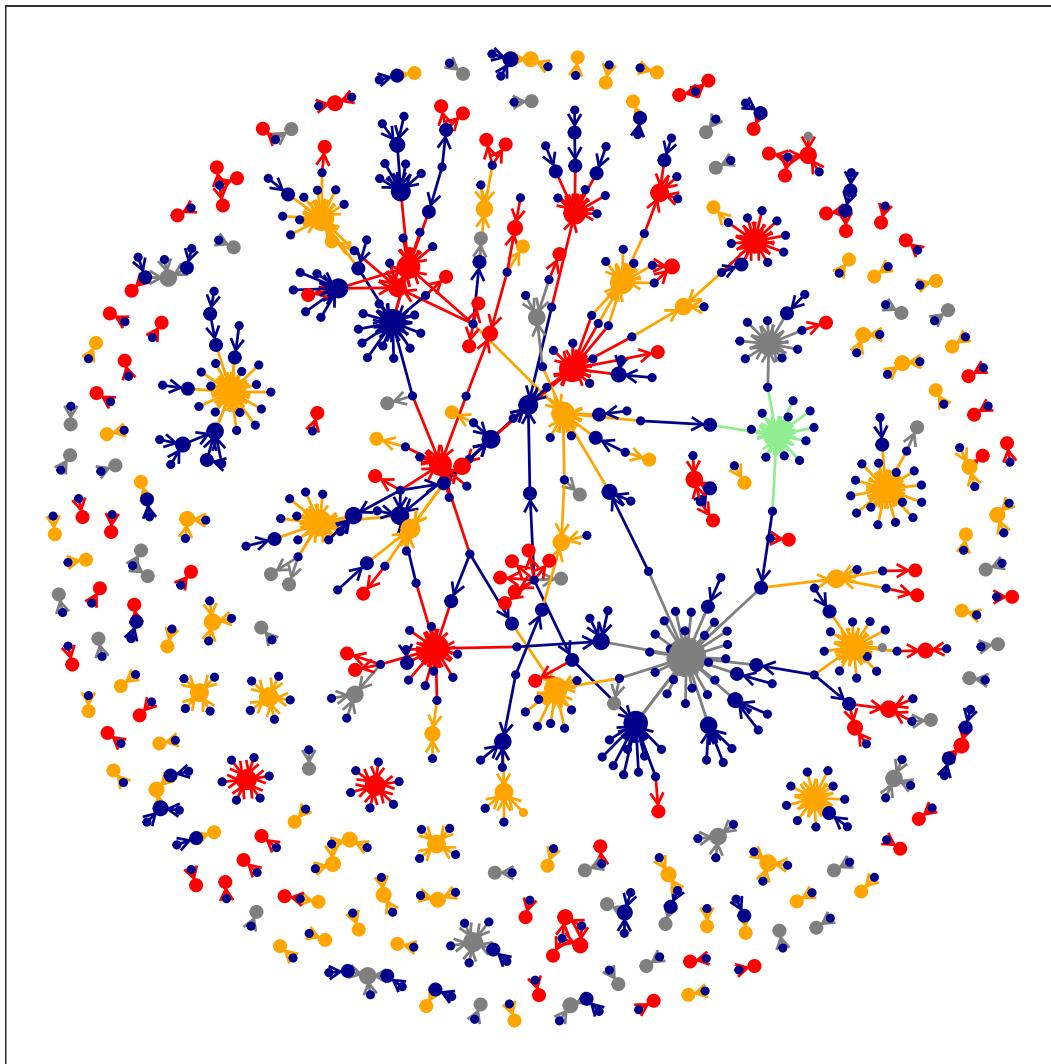
p1

## $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()`).

```

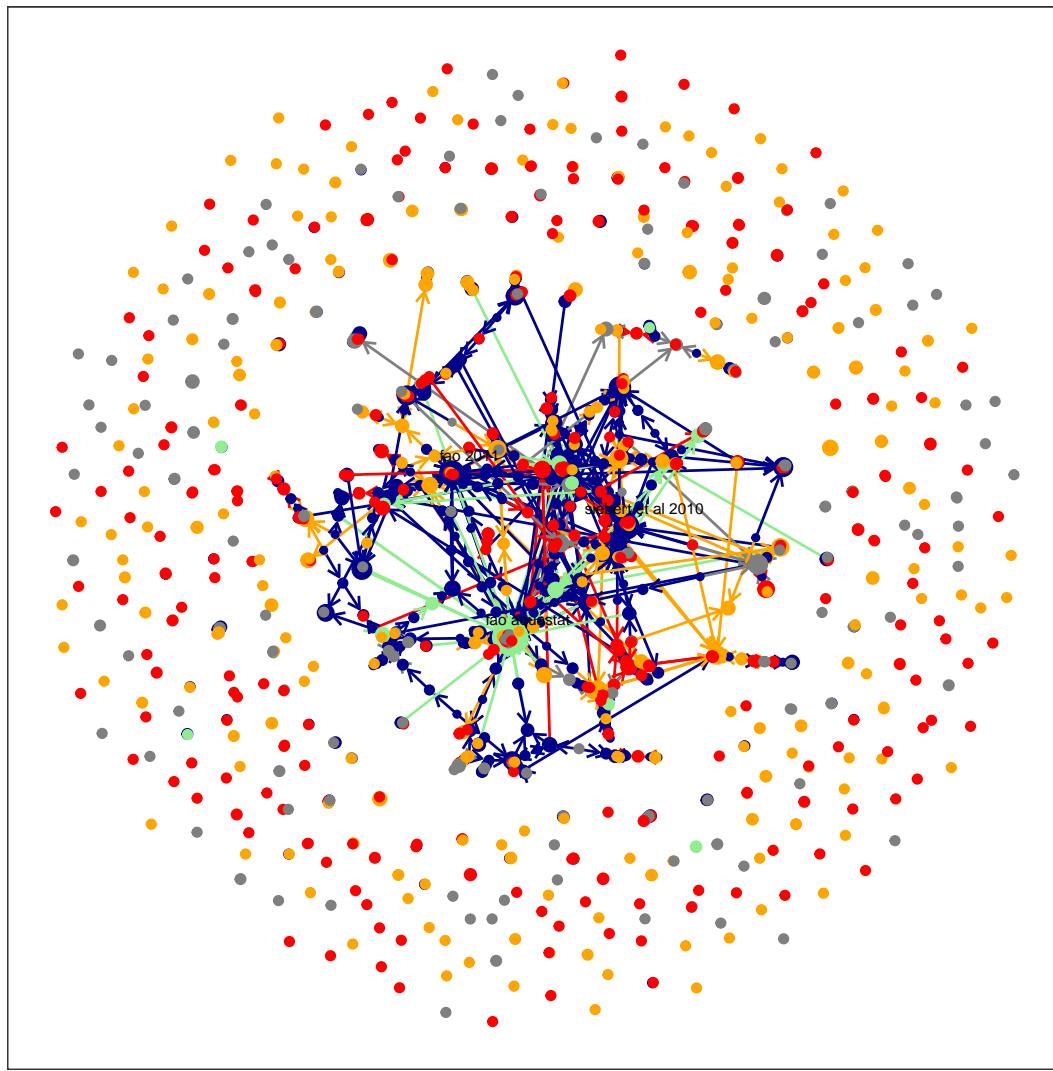


```

## 
## $water

## Warning: Removed 2928 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(arrows = arrow(length = unit(1.8, 'mm')),
                  end_cap = circle(1, "mm"),
                  aes(color = edge_color)) +
    scale_edge_color_manual(values = selected_colors, guide = "none") +
    geom_node_point(aes(color = nature.claim, size = degree)) +
    geom_node_text(aes(label = ifelse(nature.claim == "modelling", name, NA)),
                  repel = TRUE, size = 2.2) +

```

```

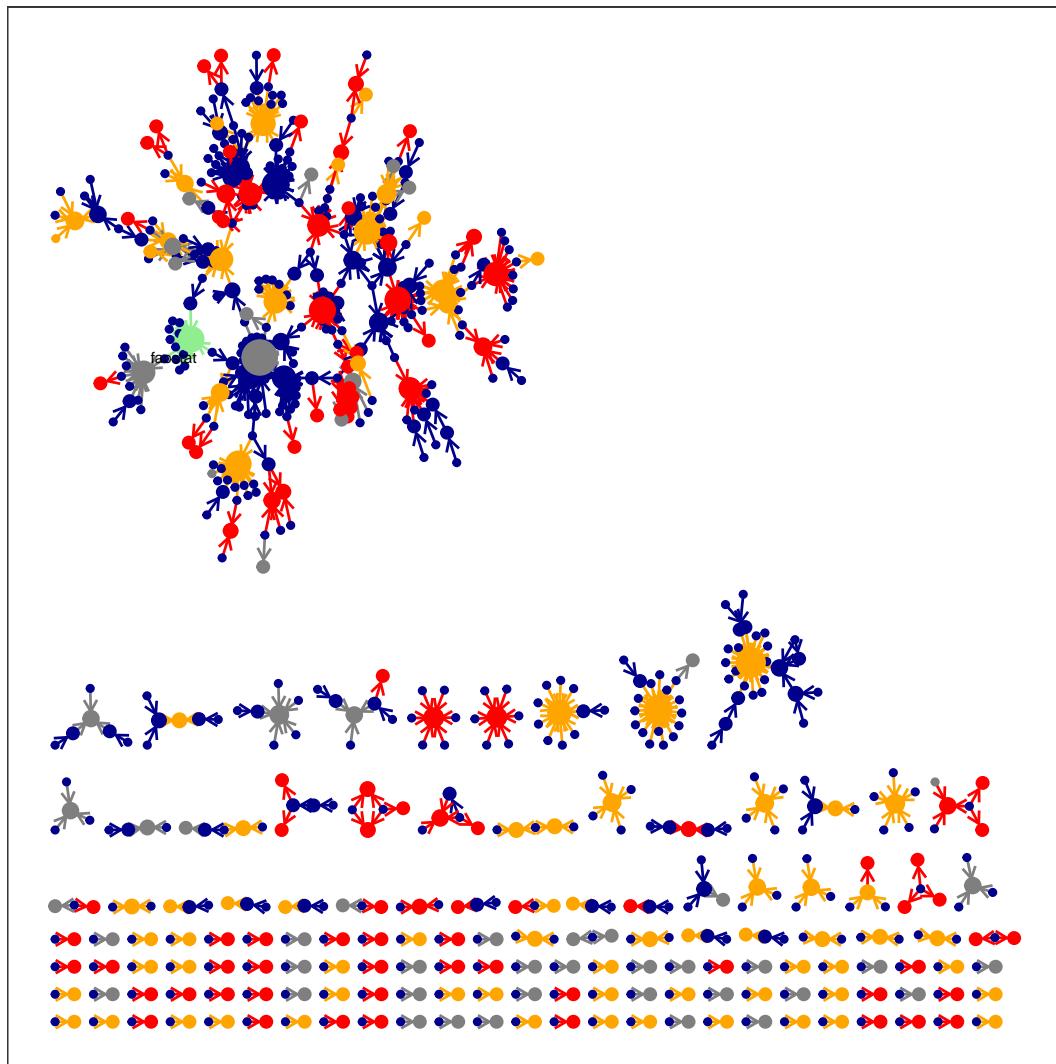
    labs(x = "", y = "") +
    scale_color_manual(name = "",
                       values = selected_colors) +
    theme_AP() +
    theme(axis.text.x = element_blank(),
          axis.ticks.x = element_blank(),
          axis.text.y = element_blank(),
          axis.ticks.y = element_blank(),
         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

p5

## $food

## Warning: Removed 763 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).

```



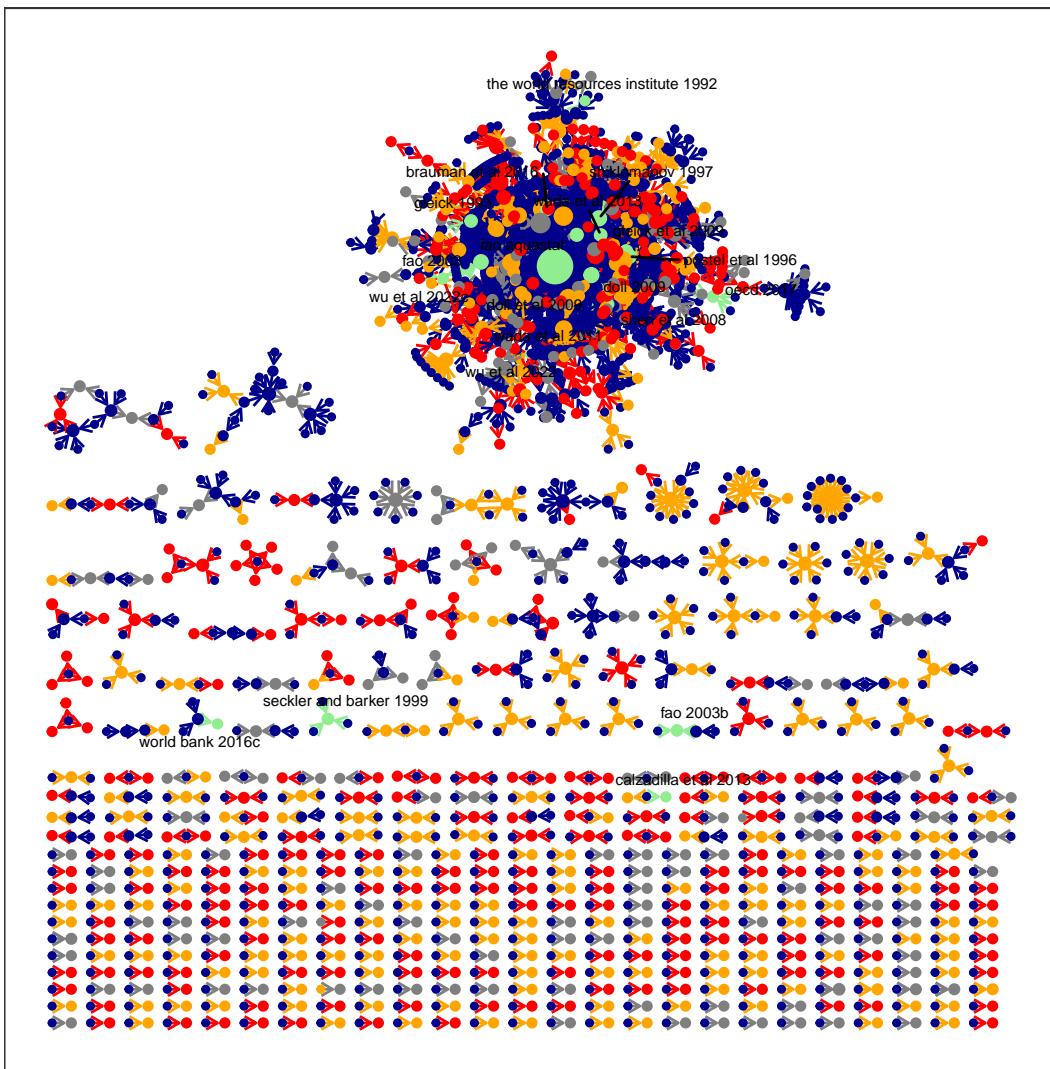
```

## 
## $water

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

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

```



```

# Label the nodes with highest betweenness ----

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

  set.seed(seed)

  p2[[i]] <- ggraph(graph.final[[i]], layout = "igraph", algorithm = "nicely") +
    geom_edge_link(arrows = arrow(length = unit(1.8, 'mm')),
                  end_cap = circle(1, "mm")) +
    geom_node_point(aes(color = nature.claim, size = betweenness)) +

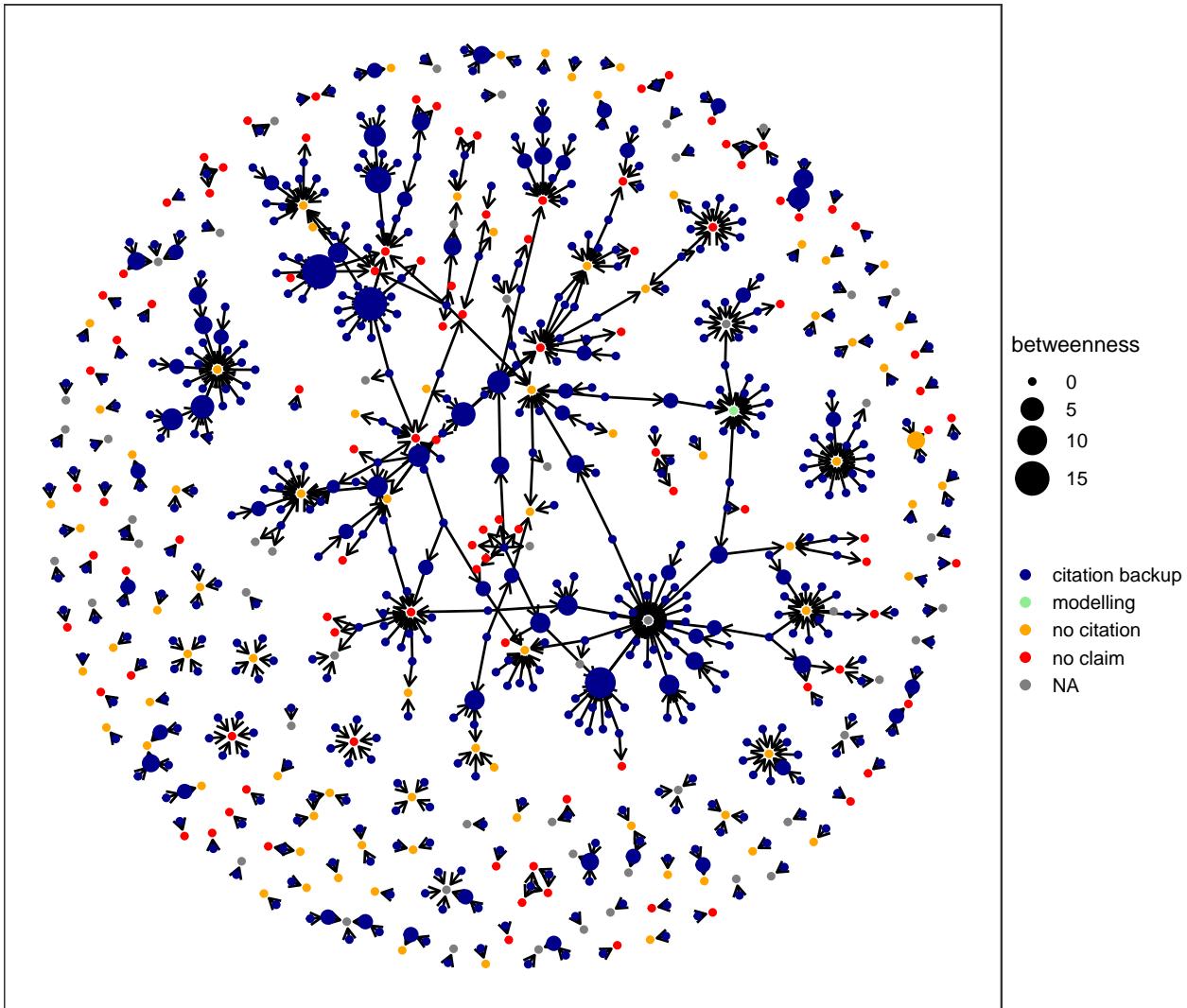
```

```
geom_node_text(aes(label = ifelse(betweenness >= min(betweenness.nodes[[i]]$betweenness),
                                name, NA)),
               repel = TRUE, size = 2.2) +
  labs(x = "", y = "") +
  scale_color_manual(name = "",
                     values = selected_colors) +
  theme_AP() +
  theme(axis.text.x = element_blank(),
        axis.ticks.x = element_blank(),
        axis.text.y = element_blank(),
        axis.ticks.y = element_blank(),
        legend.position = "right")
}
```

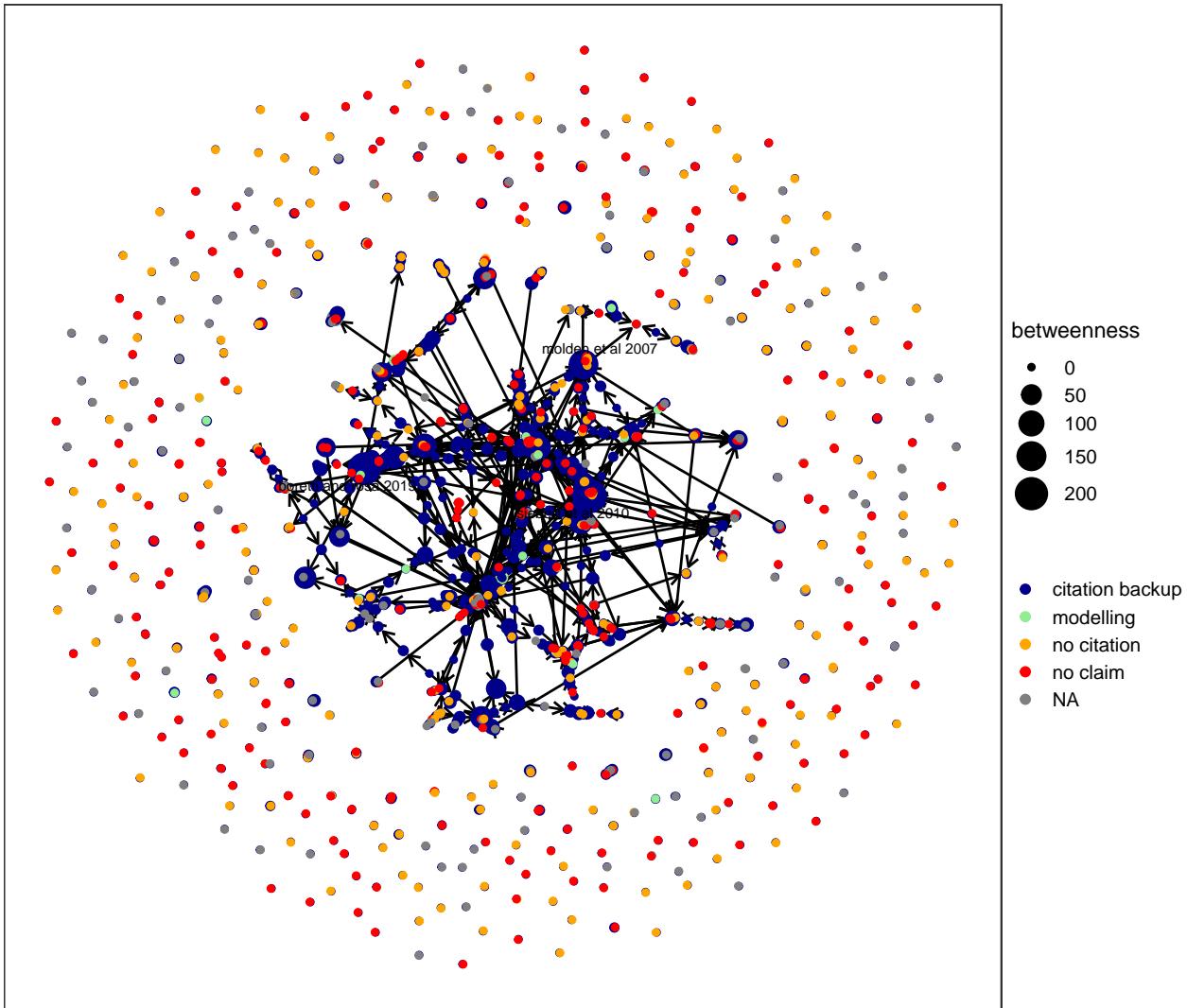
p2

```
## $food

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



```
##  
## $water  
  
## Warning: Removed 2928 rows containing missing values or values outside the scale range  
## (`geom_text_repel()`).
```



```
# by document.type-----
for (i in names(graph.final)) {
  set.seed(seed)

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

```

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

```

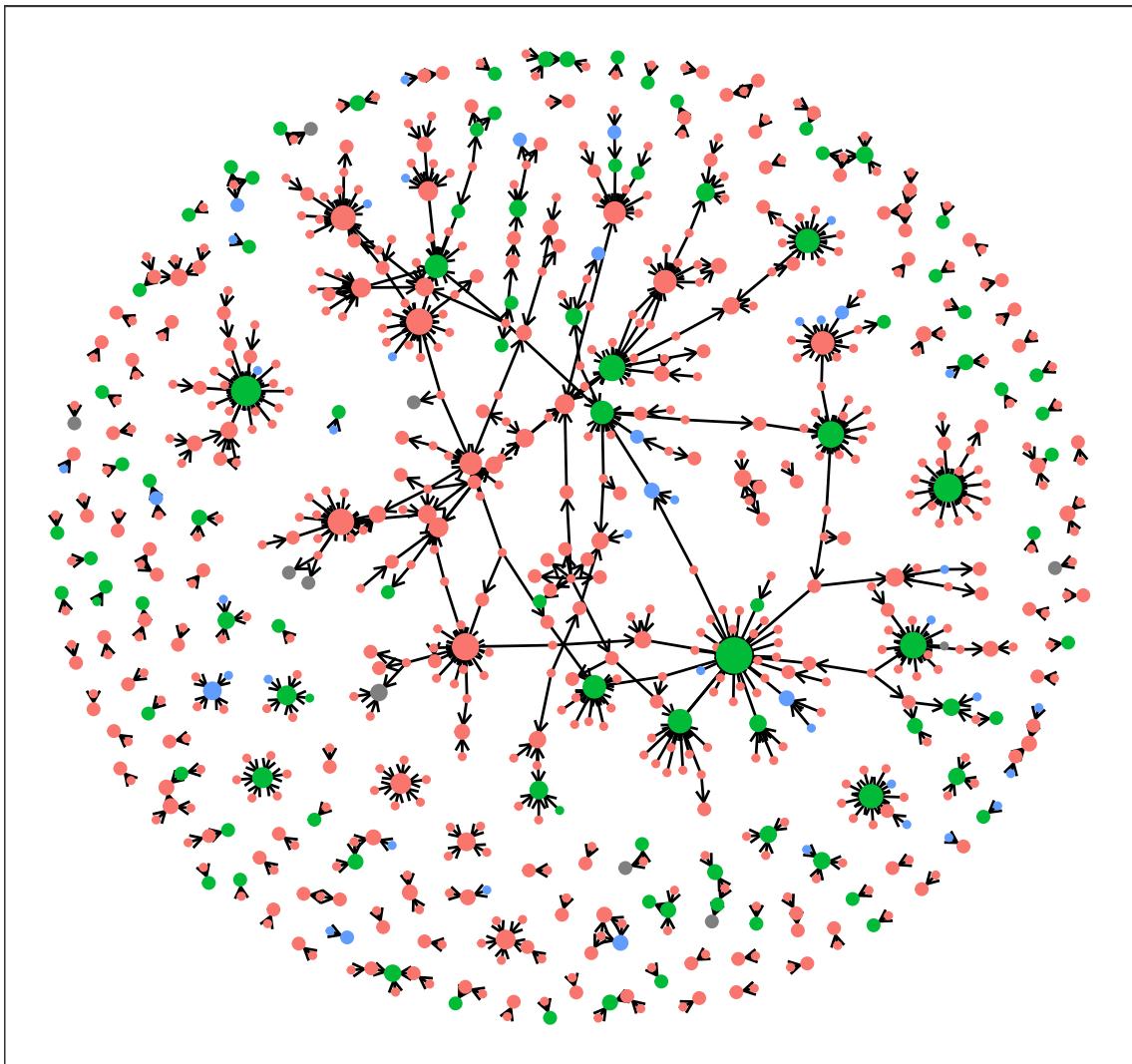
p3

\$food

```

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

```



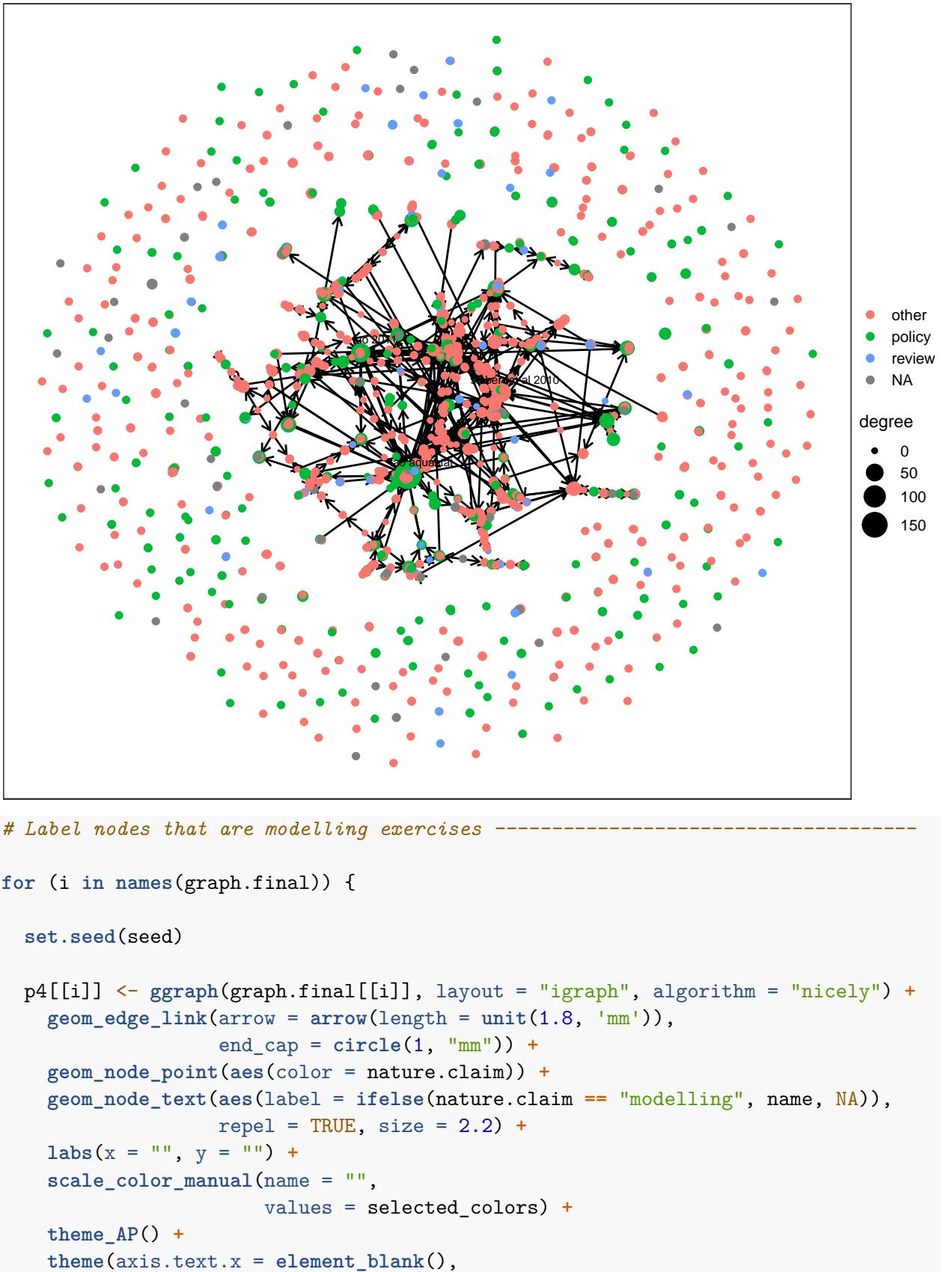
##

\$water

```

## Warning: Removed 2928 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).

```



```

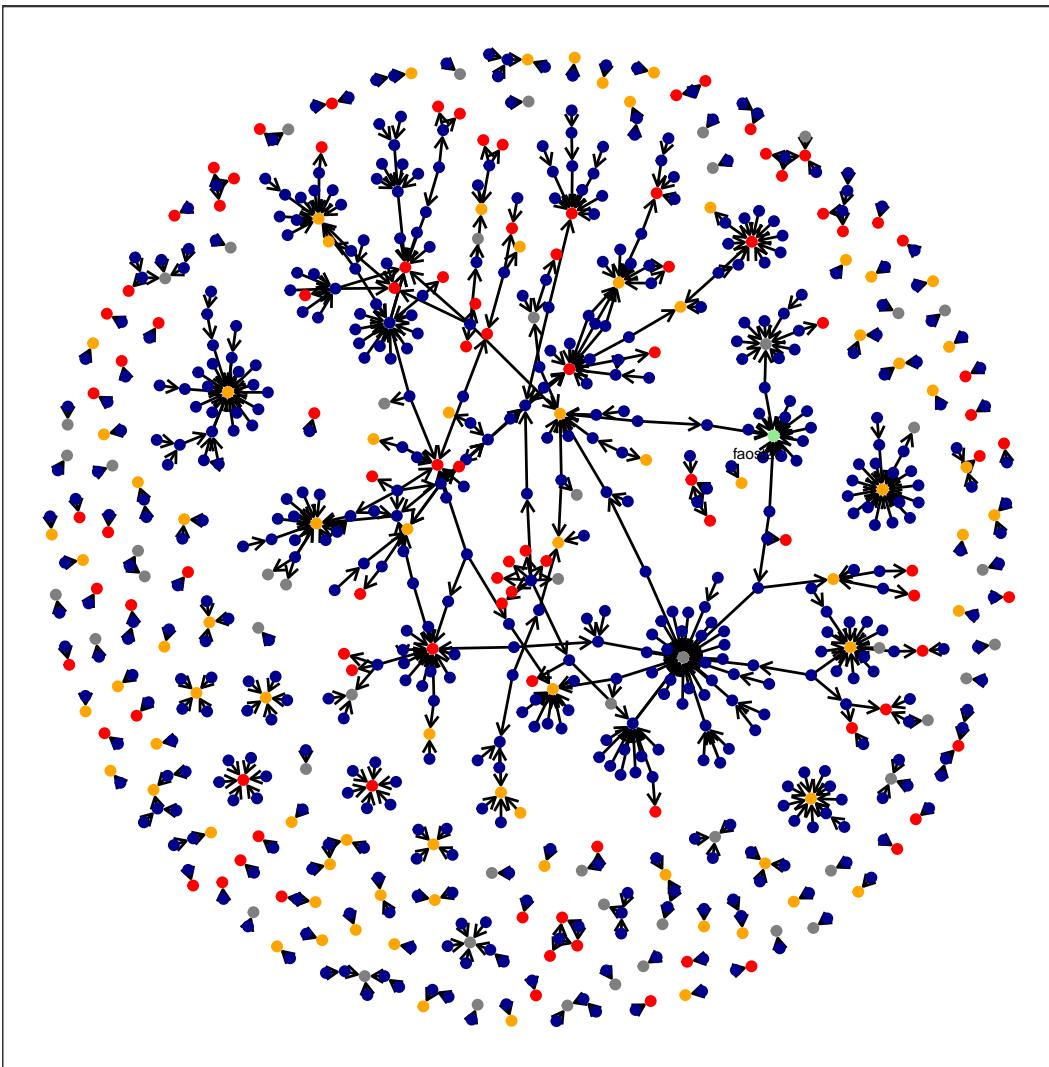
        axis.ticks.x = element_blank(),
        axis.text.y = element_blank(),
        axis.ticks.y = element_blank(),
        legend.position = "right")
}

p4

## $food

## Warning: Removed 763 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).

```

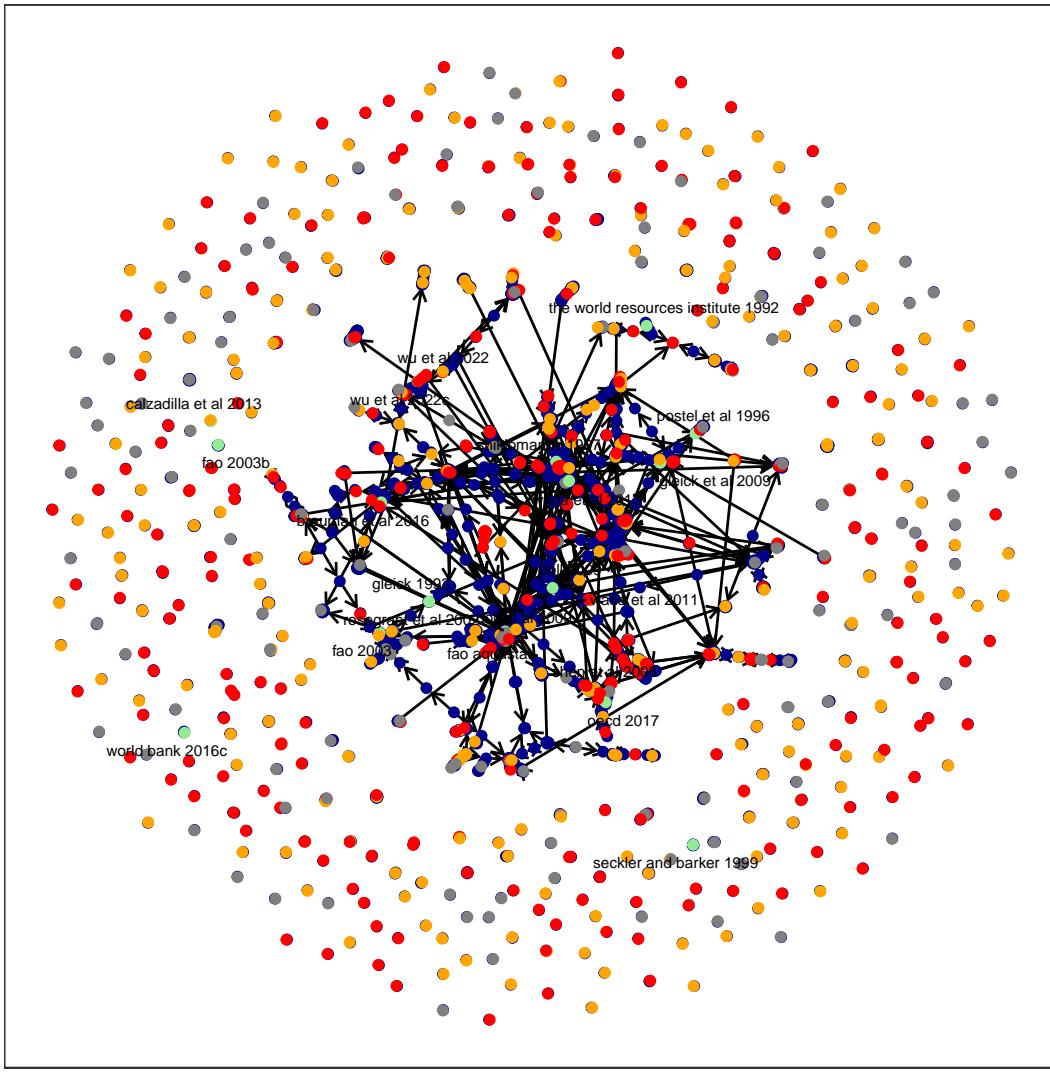


```

## 
## $water

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

```



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(name %in% all.names)
```

```

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

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

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

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

})

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

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

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

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

```

```

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

  return(output)
}

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

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

p7 <- list()

for (i in names(out)) {

  set.seed(seed)

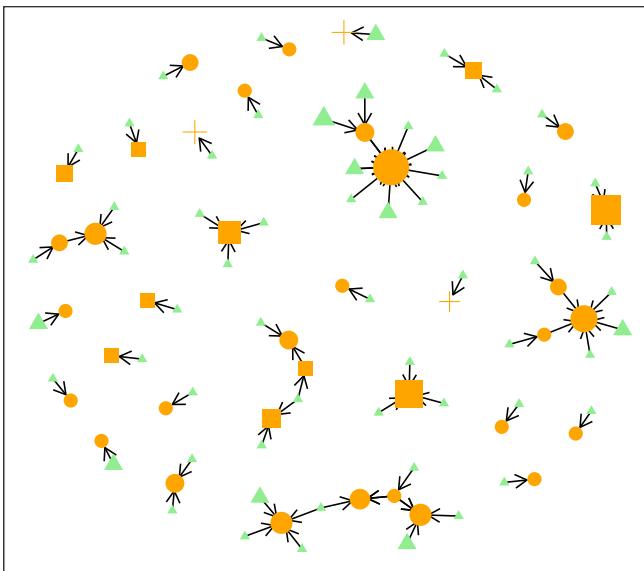
  p7[[i]] <- ggraph(out[[i]], layout = "igraph", algorithm = "nicely") +
    geom_edge_link(arrow = arrow(length = unit(1.8, 'mm')),
                   end_cap = circle(1, "mm")) +
    geom_node_point(aes(color = category, size = degree, shape = classification)) +
    scale_color_manual(values = c("lightgreen",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

p7

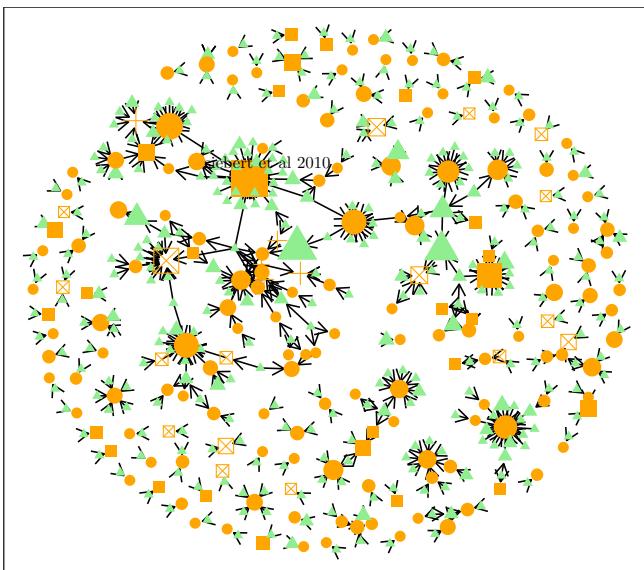
## $food

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

```



```
##  
## $water  
  
## Warning: Removed 488 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] 0.08719346
## [1] 0.0940041

```

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:  0.3846154 0.3905325 0.02071006 0.204142
##
## $water
##      no citation no claim modelling       NA
##          <num>     <num>     <num>     <num>
## 1:  0.2787183 0.269347 0.3116687 0.140266

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

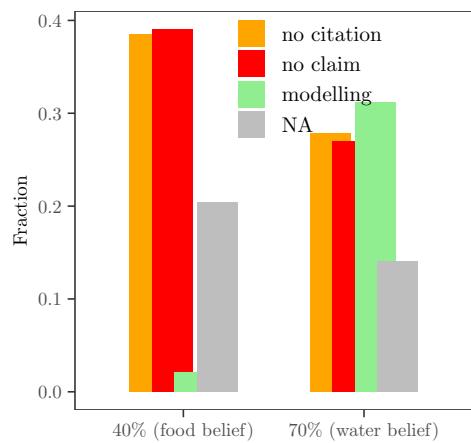
```

```

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

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

```



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", .)

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

```

```

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

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

v_years[location_aquastat] <- oldest.aquastat.cite

# Find NA values ----

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

# Generate random values to replace NA ----

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

# Replace NA with random values ----

v_years[na_indices] <- random_values

# Define the coordinates-----

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

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

set.seed(seed)

# Plot ----

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

```

```

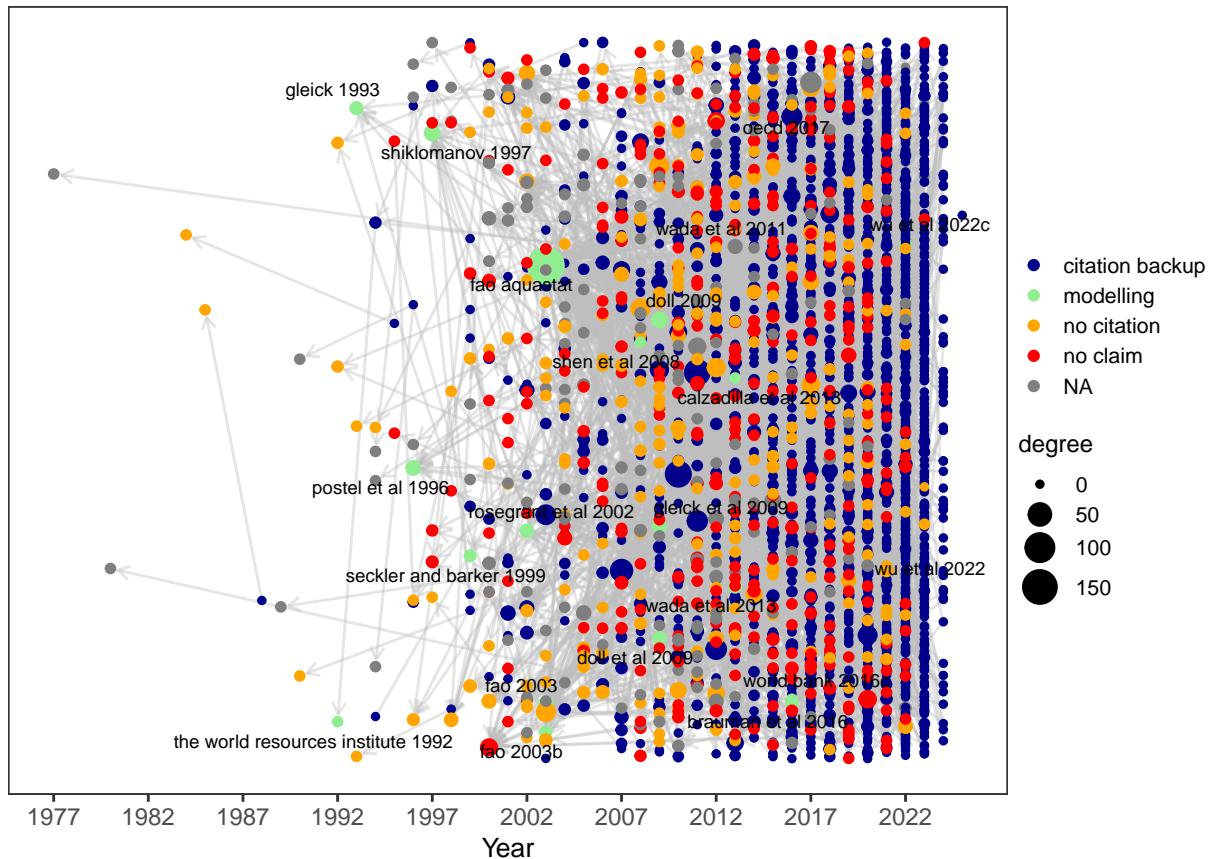
        breaks = seq(min(v_years),
                      max(v_years), by = 5)) +
      labs(x = "Year", y = "") +
      theme_AP() +
      theme(axis.text.y = element_blank(),
            axis.ticks.y = element_blank())
    }

plot.years

## $water

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

```

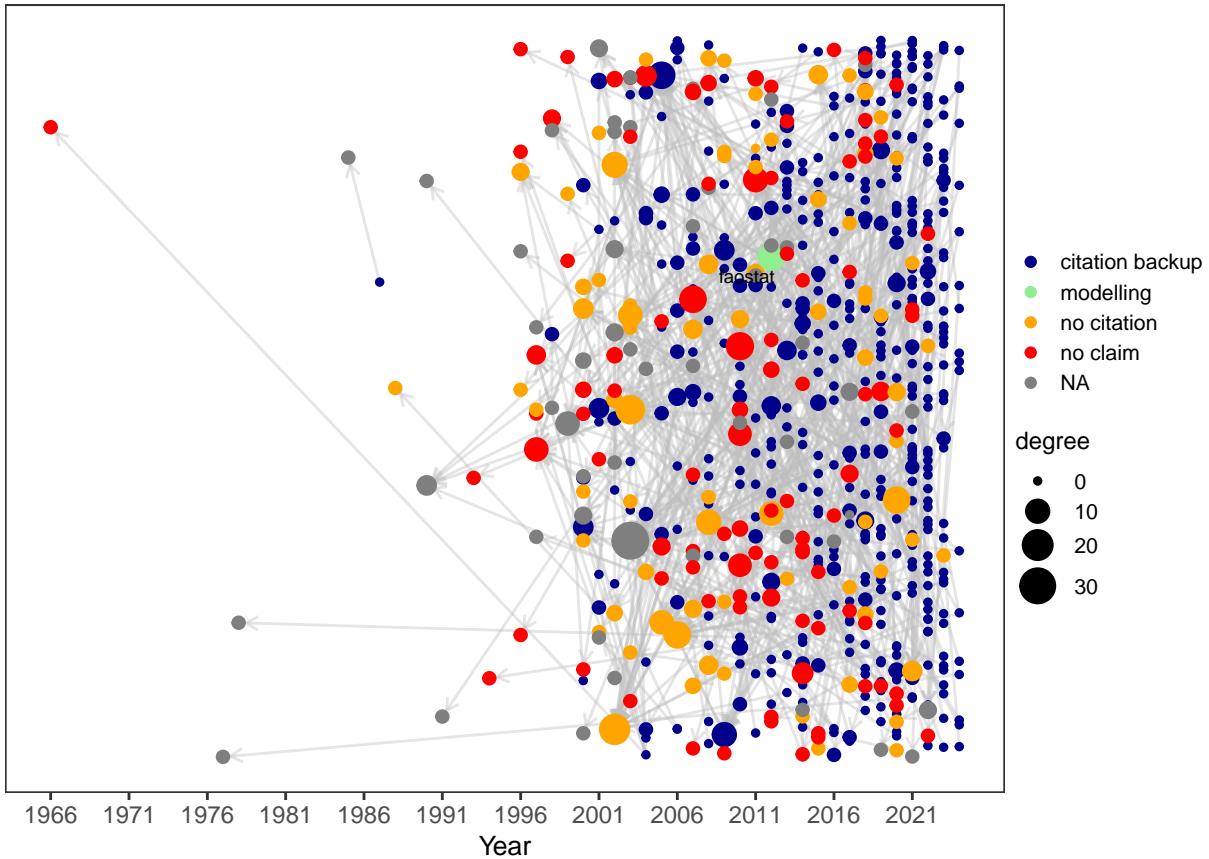


```

## $food

## Warning: Removed 763 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).

```



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

plot.years <- list()

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

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

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

```

)

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

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

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

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

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

```

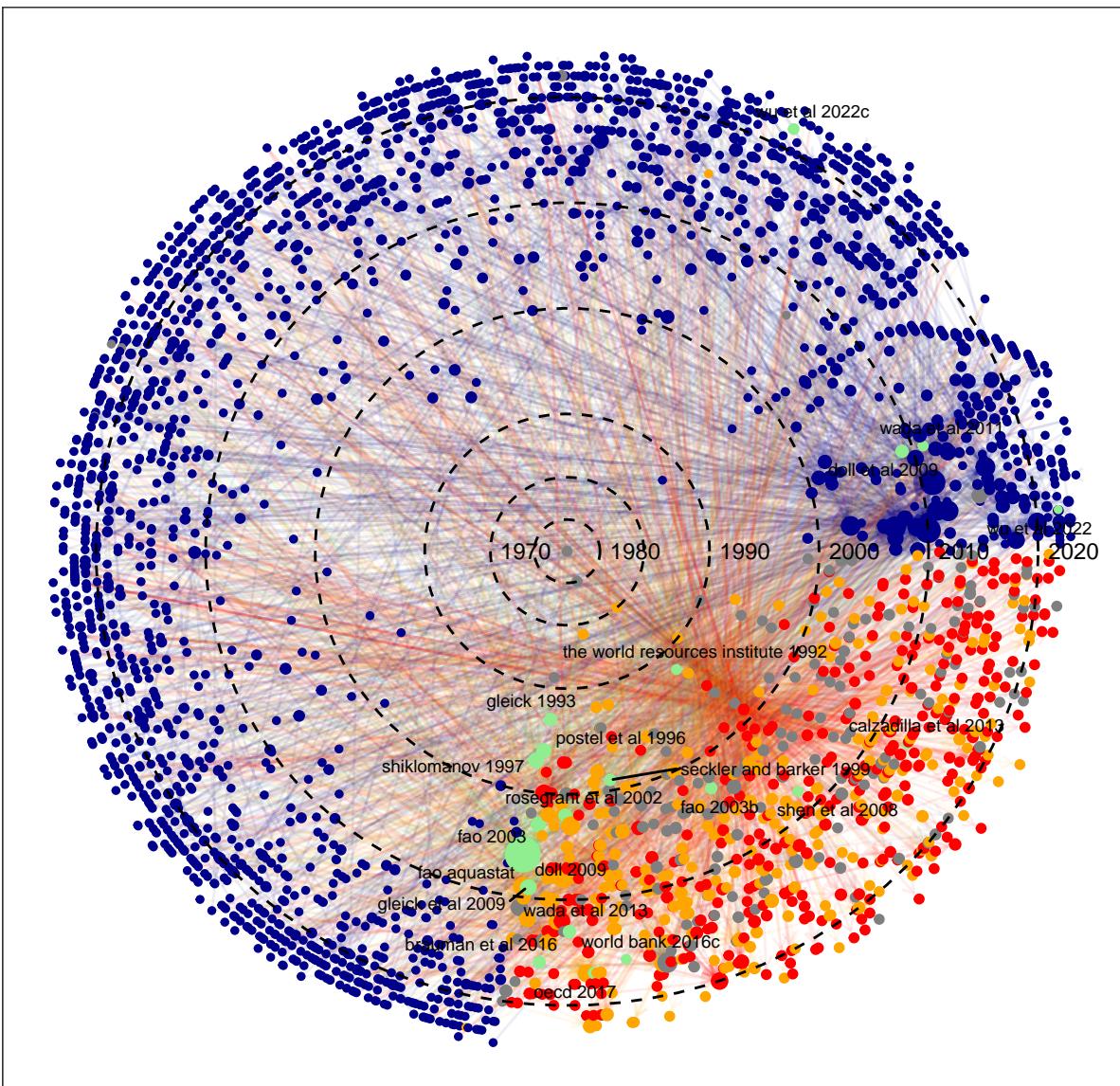
```
theme(axis.text.y = element_blank(),
      axis.ticks.y = element_blank(),
      axis.text.x = element_blank(),
      axis.ticks.x = element_blank(),
      legend.position = "top")
}

plot.years

## $water

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

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



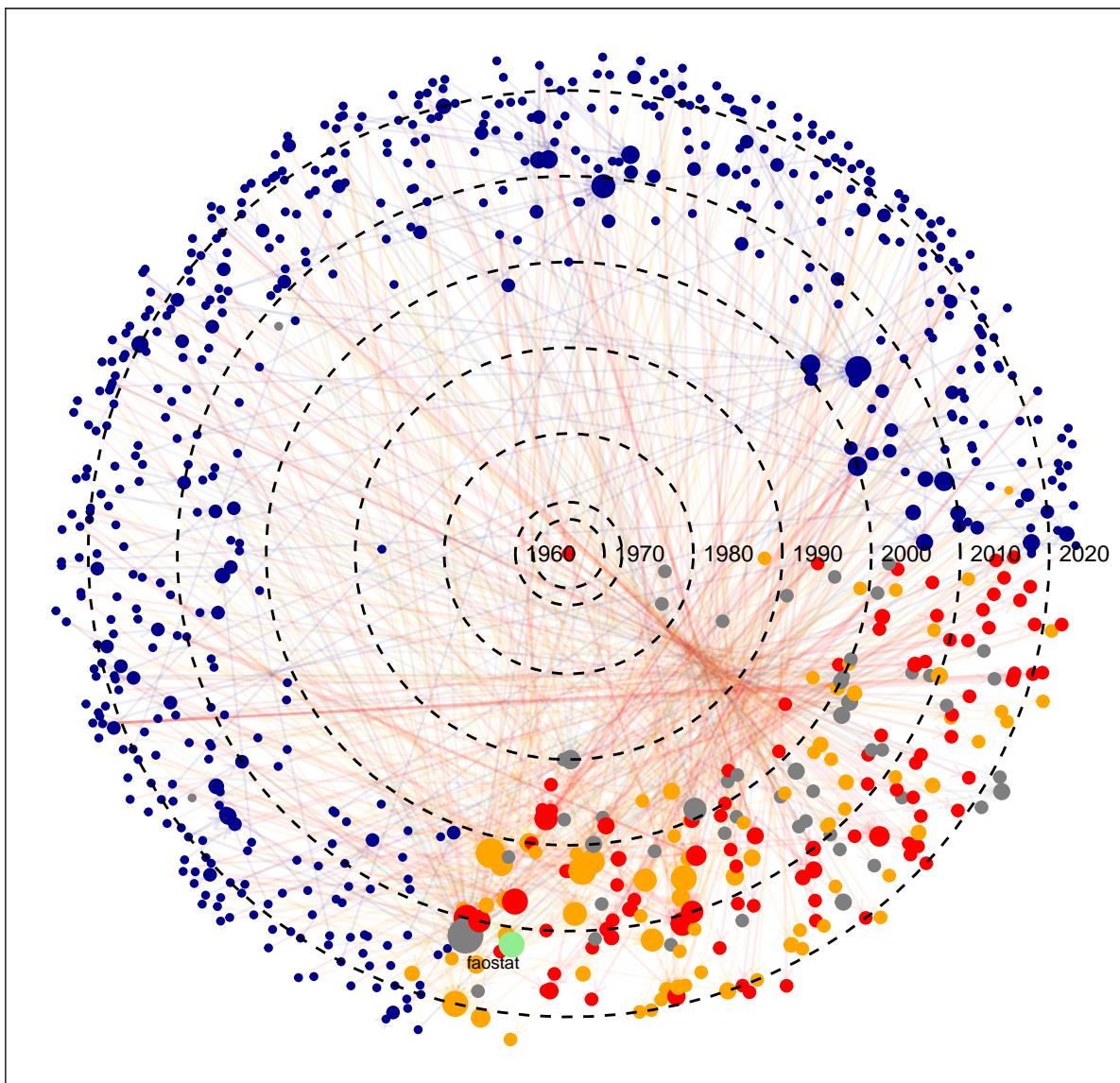
```

## 
## $food

## Warning: Removed 763 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).

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

```



```

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

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

```

```

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

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

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

set.seed(seed)

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

return(out)
}

```

```

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

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

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

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

da <- list()

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

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

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

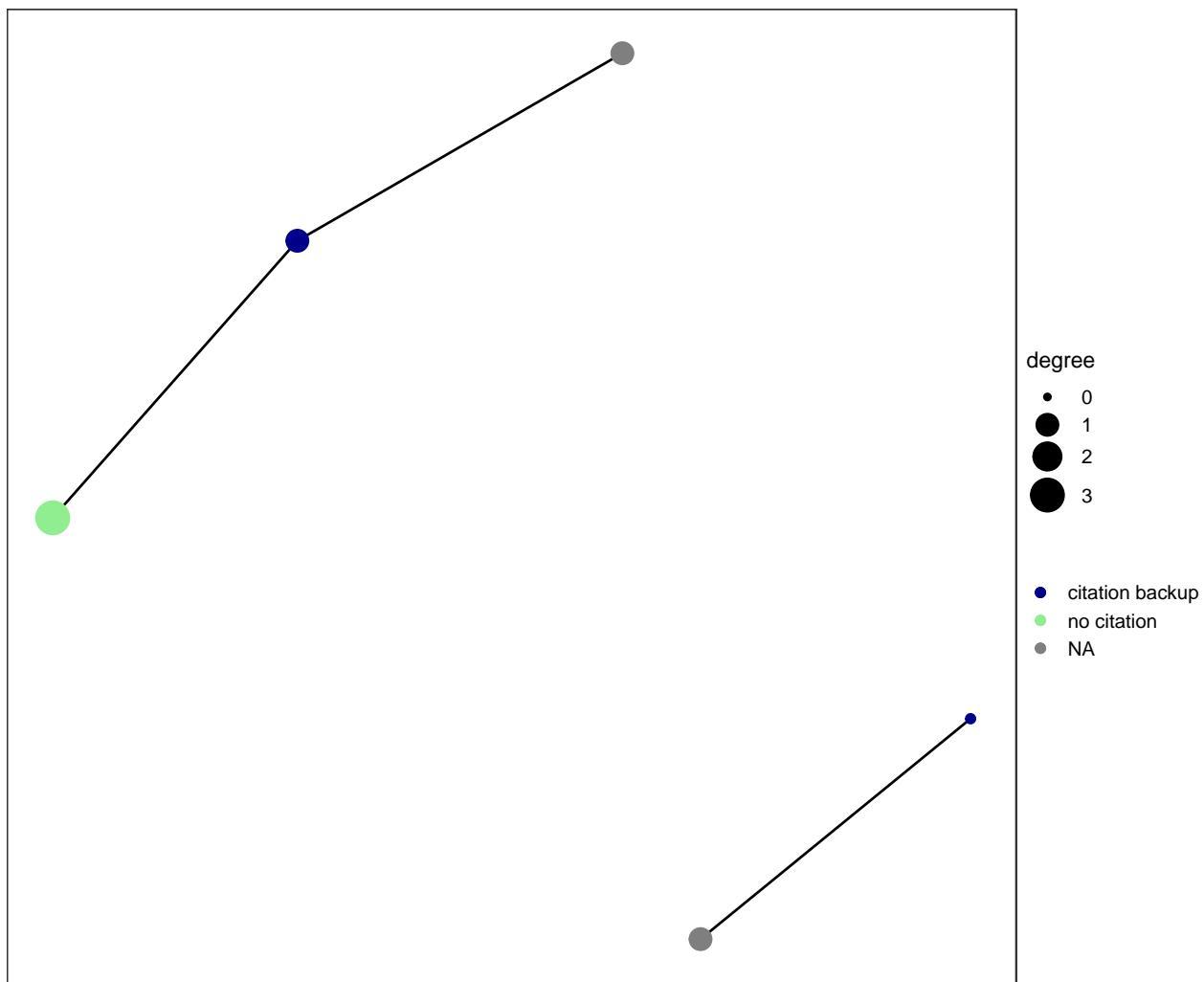
da

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

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

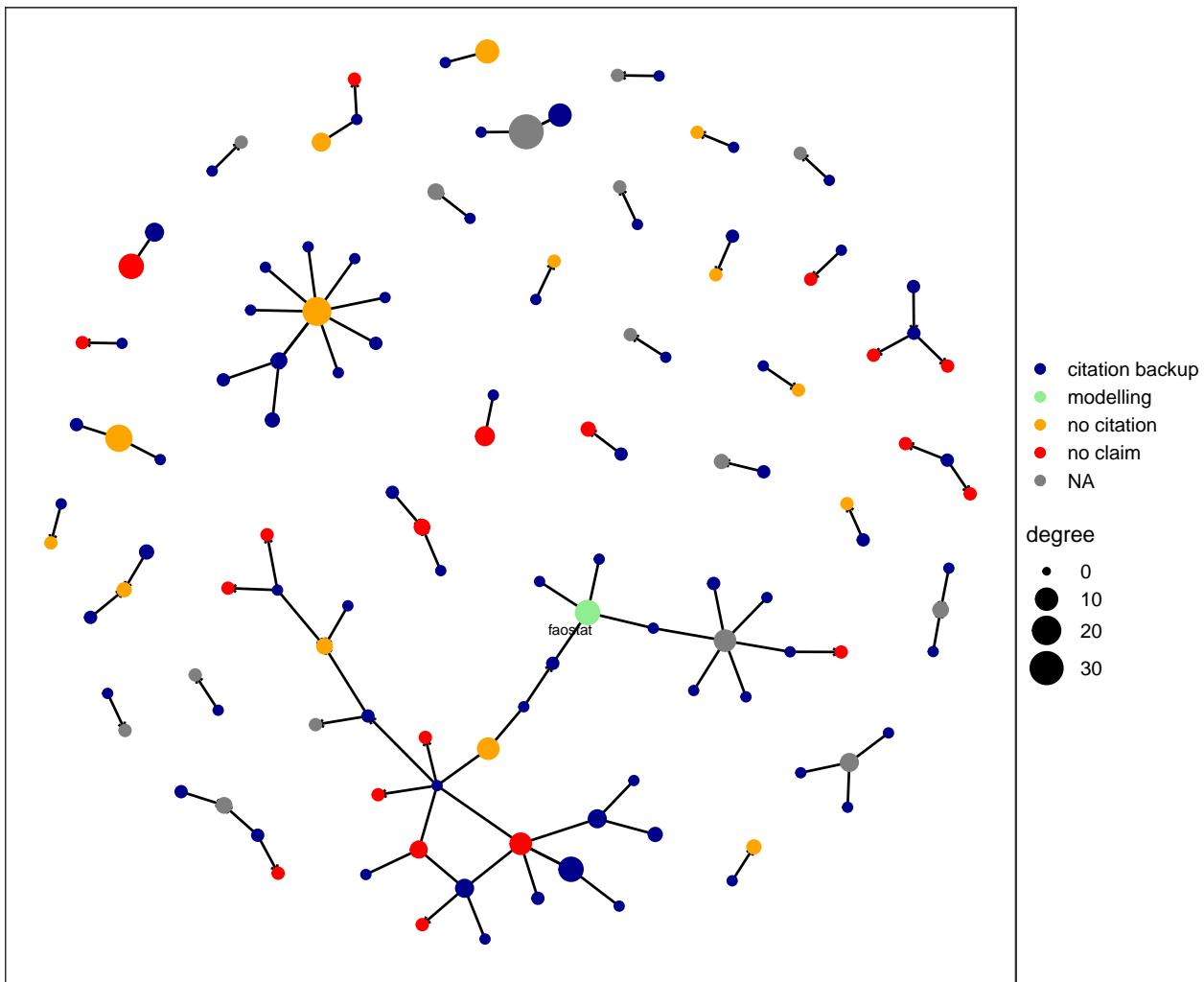
```

2000



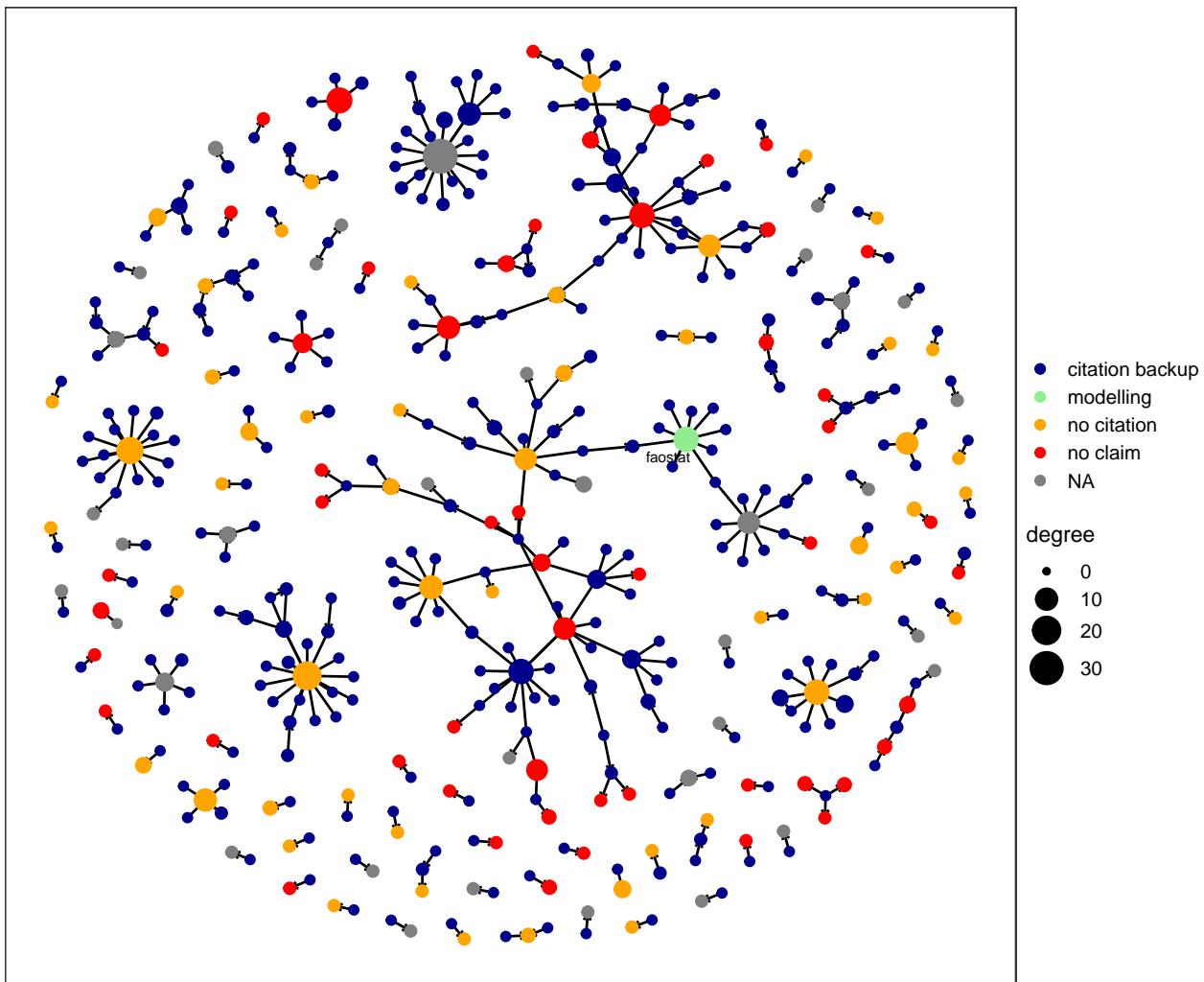
```
##  
## $food[[2]]  
  
## Warning: Removed 123 rows containing missing values or values outside the scale range  
## (`geom_text_repel()`).
```

2010



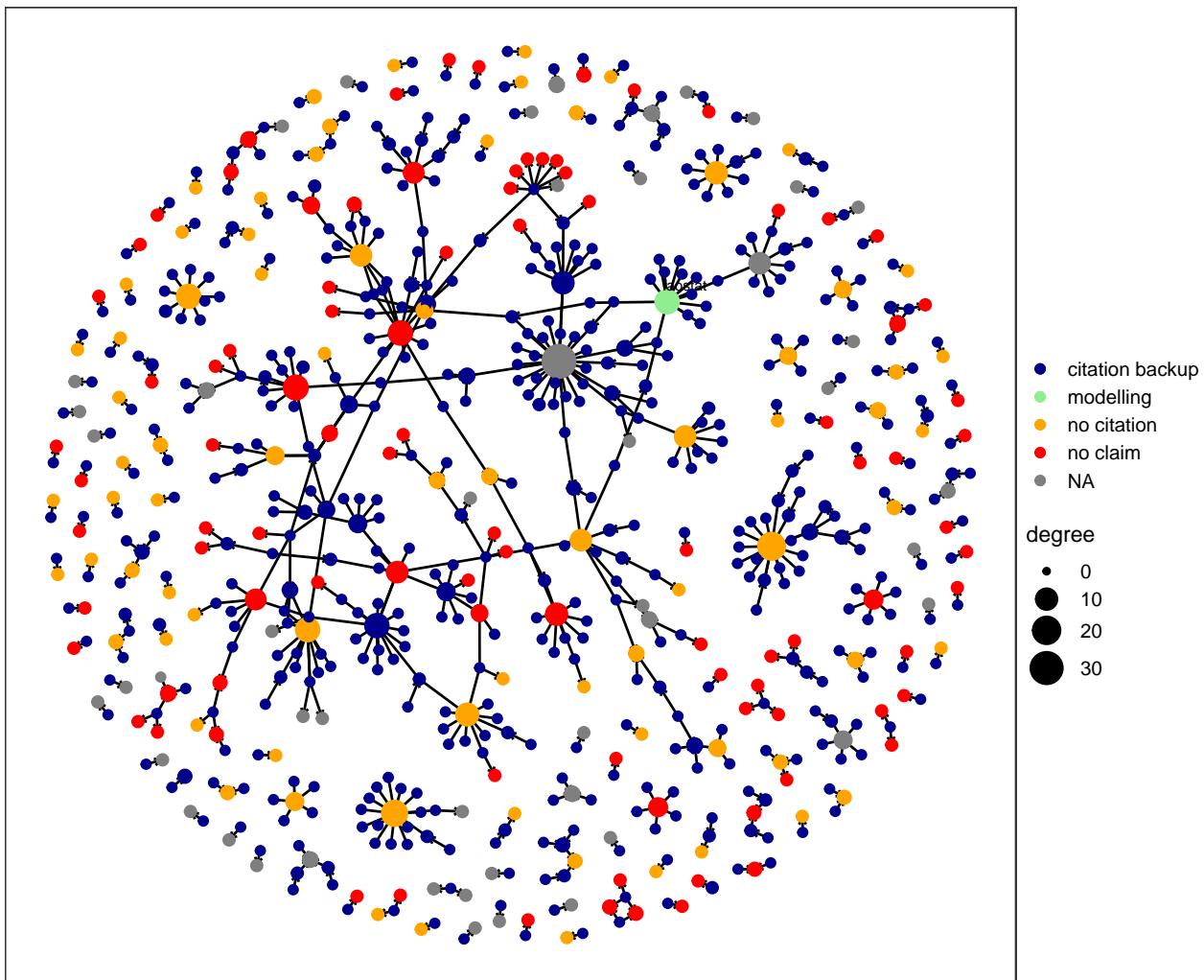
```
##  
## $food[[3]]  
  
## Warning: Removed 450 rows containing missing values or values outside the scale range  
## (`geom_text_repel()`).
```

2020



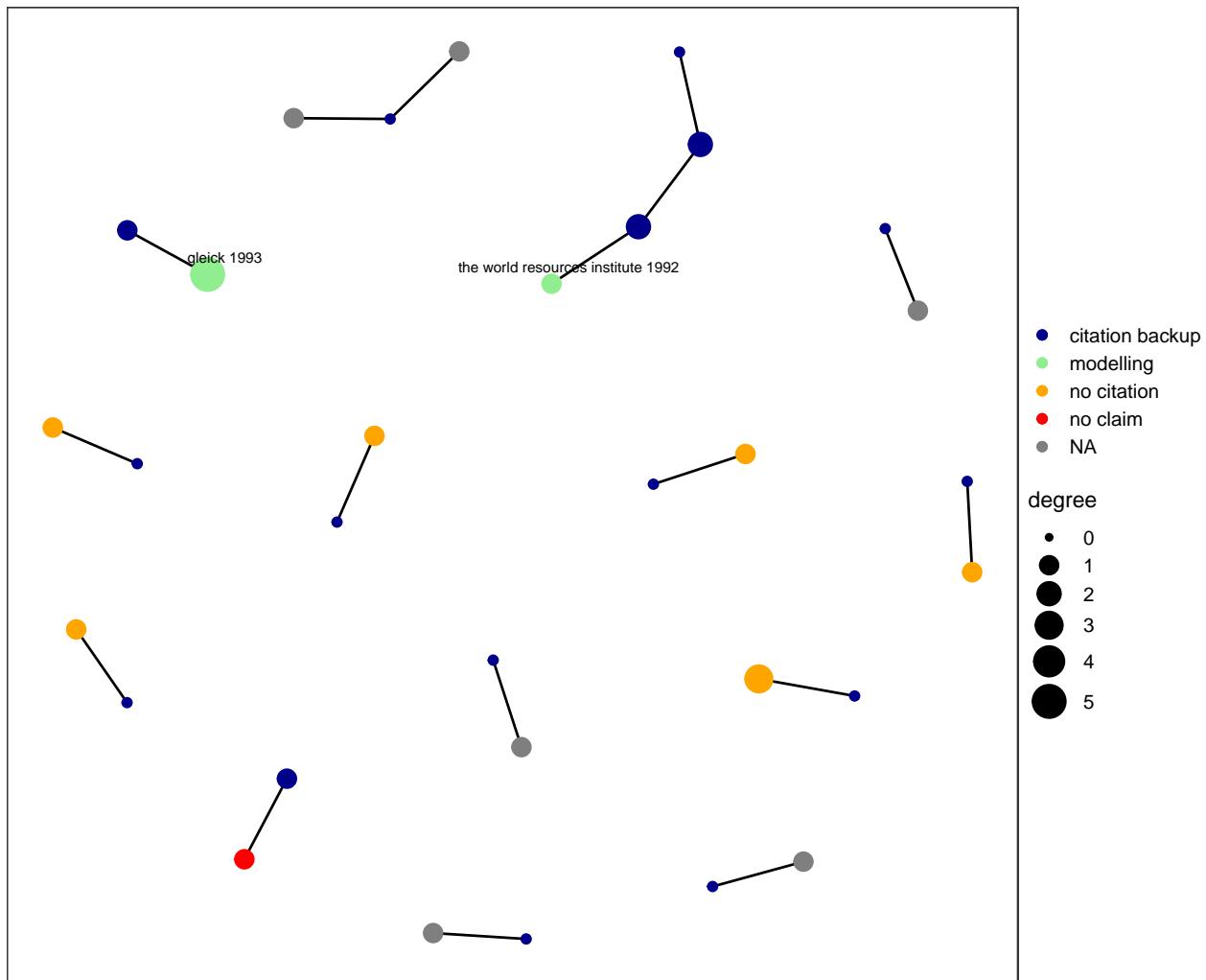
```
##  
## $food[[4]]  
  
## Warning: Removed 725 rows containing missing values or values outside the scale range  
## (`geom_text_repel()`).
```

2024



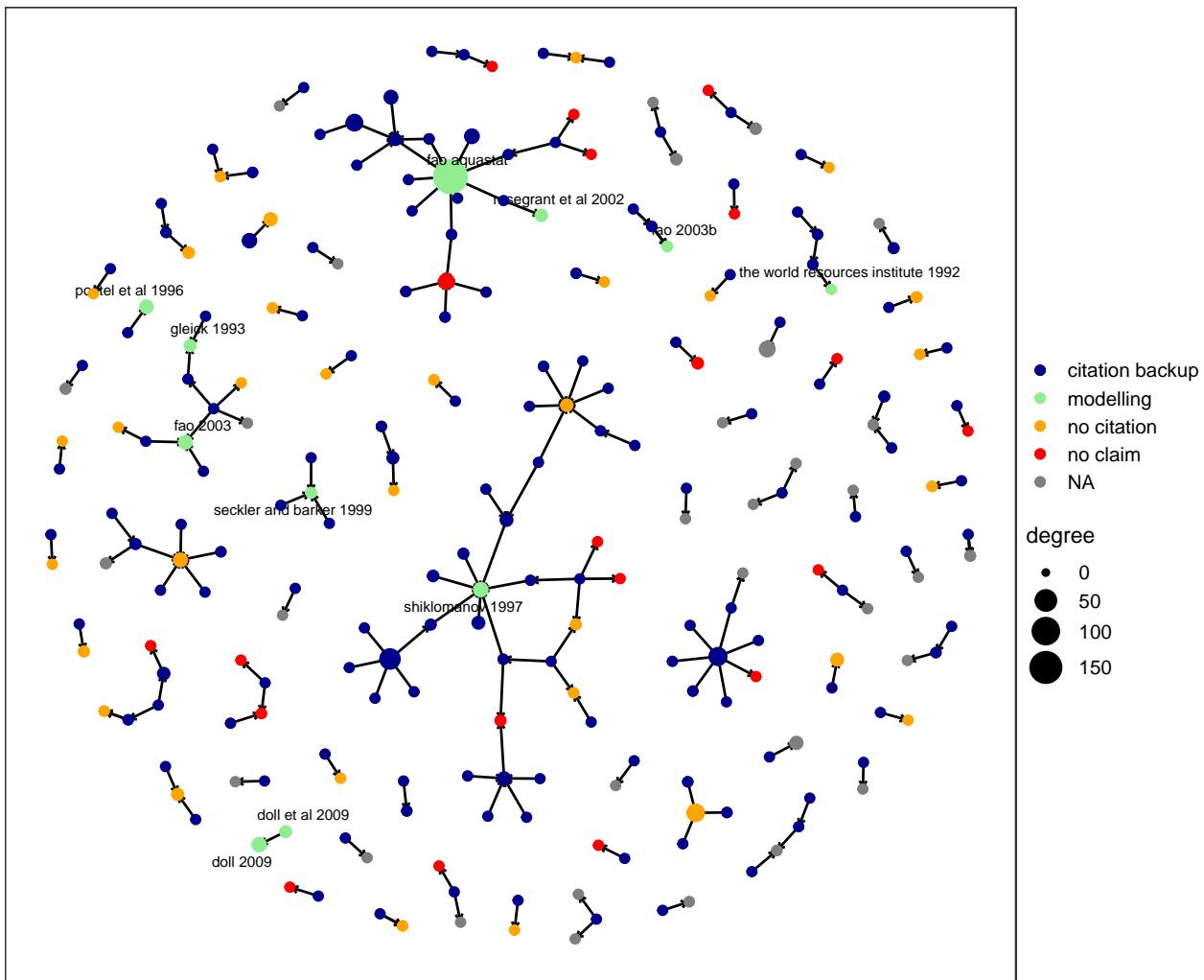
```
##  
##  
## $water  
## $water[[1]]  
  
## Warning: Removed 29 rows containing missing values or values outside the scale range  
## (`geom_text_repel()`).
```

2000



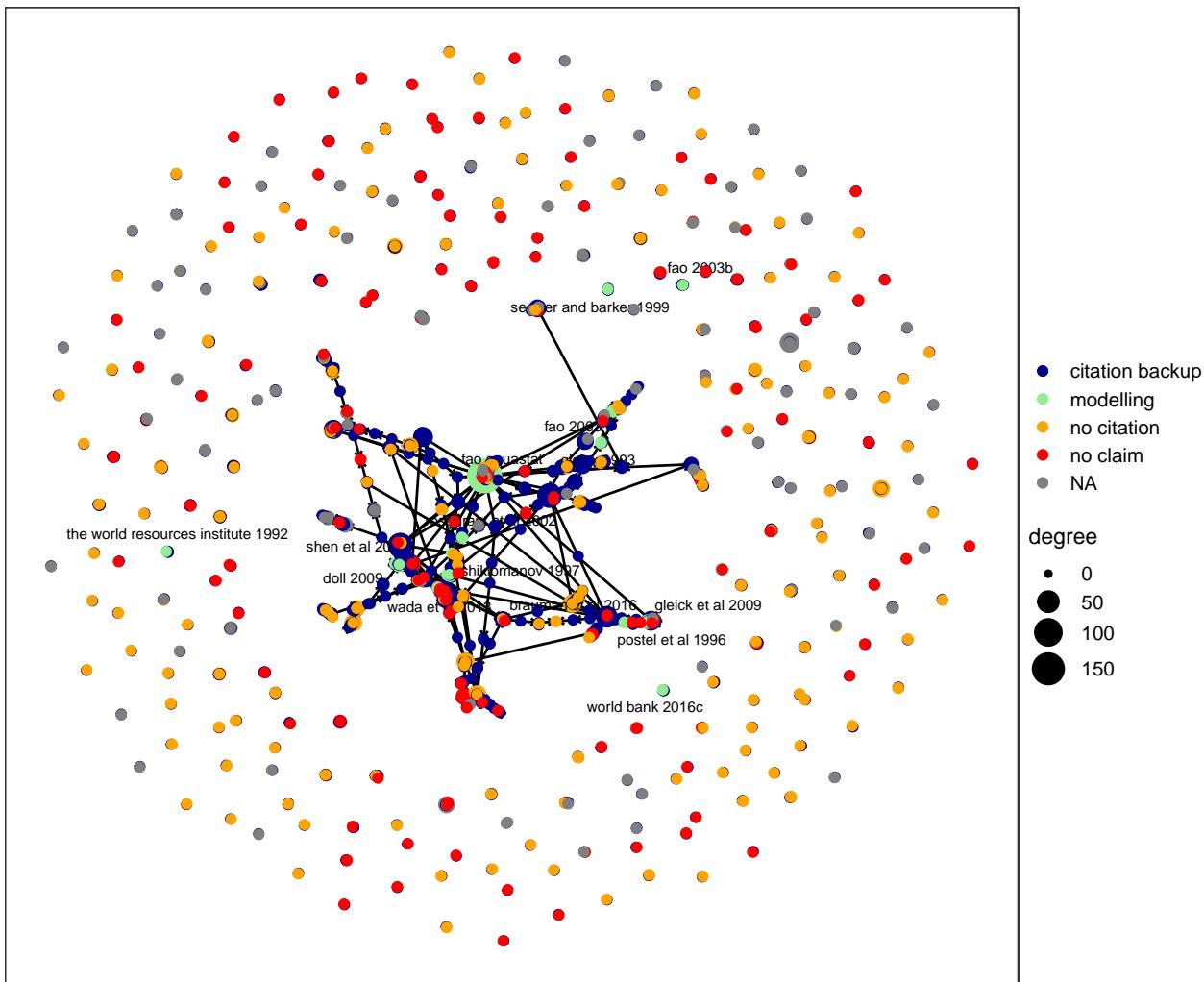
```
##  
## $water[[2]]  
  
## Warning: Removed 233 rows containing missing values or values outside the scale range  
## (`geom_text_repel()`).
```

2010



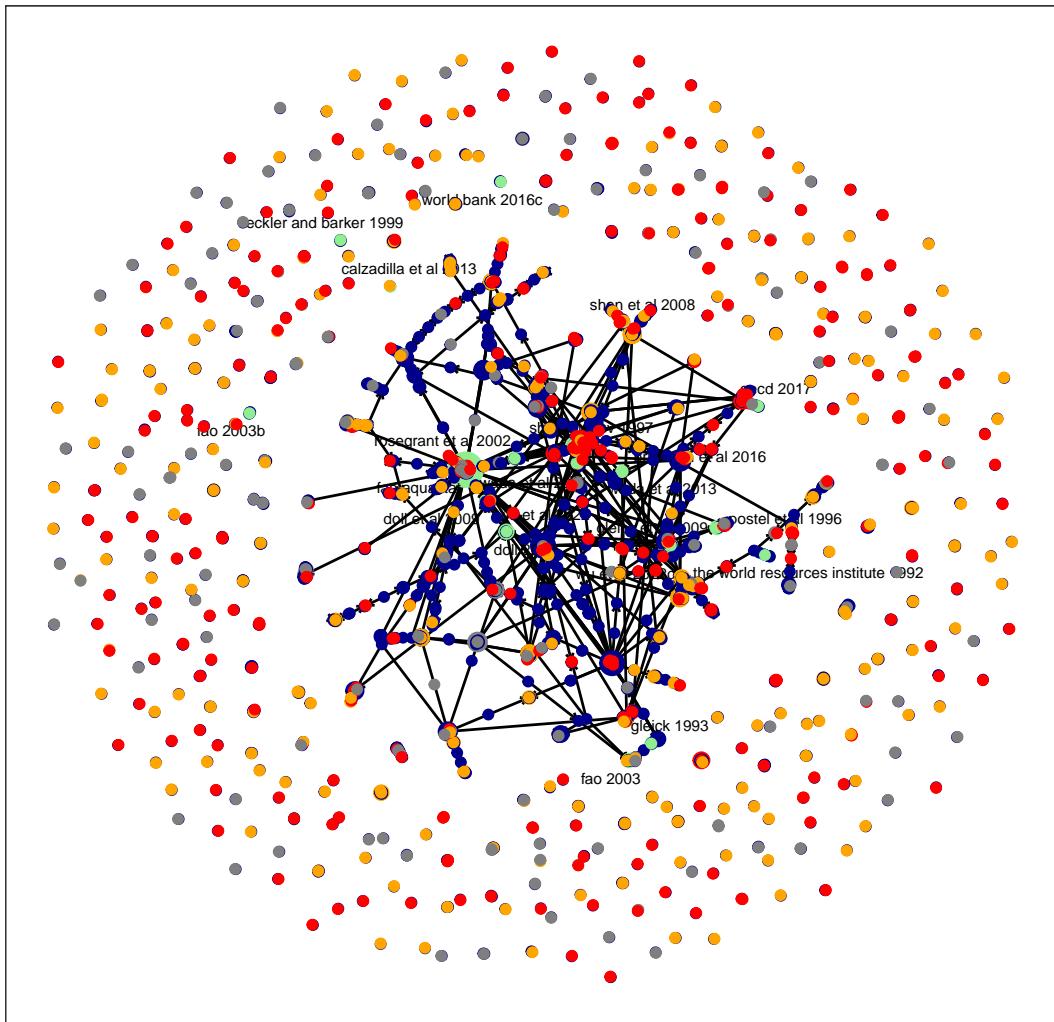
```
##
## $water[[3]]
## Warning: Removed 1476 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).
## Warning: ggrepel: 2 unlabeled data points (too many overlaps). Consider
## increasing max.overlaps
```

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 725 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 450 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).

## Warning: Removed 725 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).

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

## Warning: Removed 233 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()`).

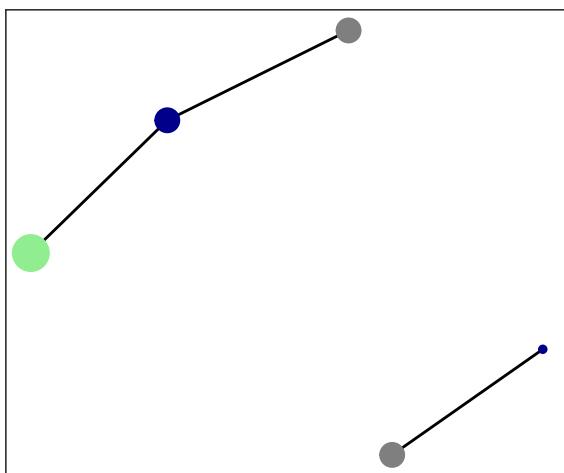
## Warning: Removed 2781 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).

out.plot

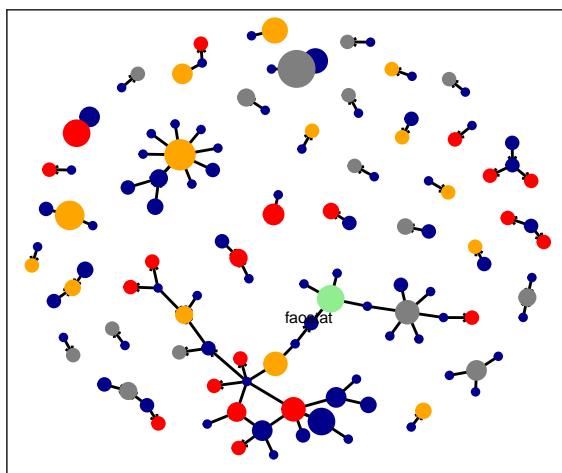
## $food

```

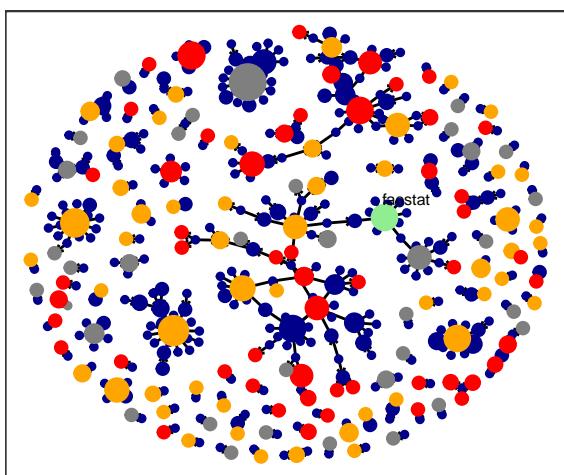
2000



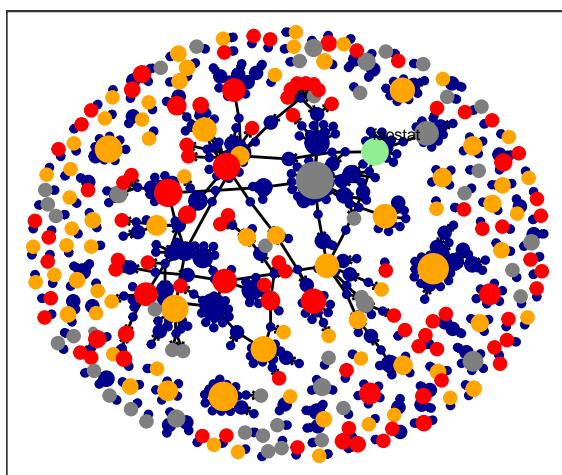
2010



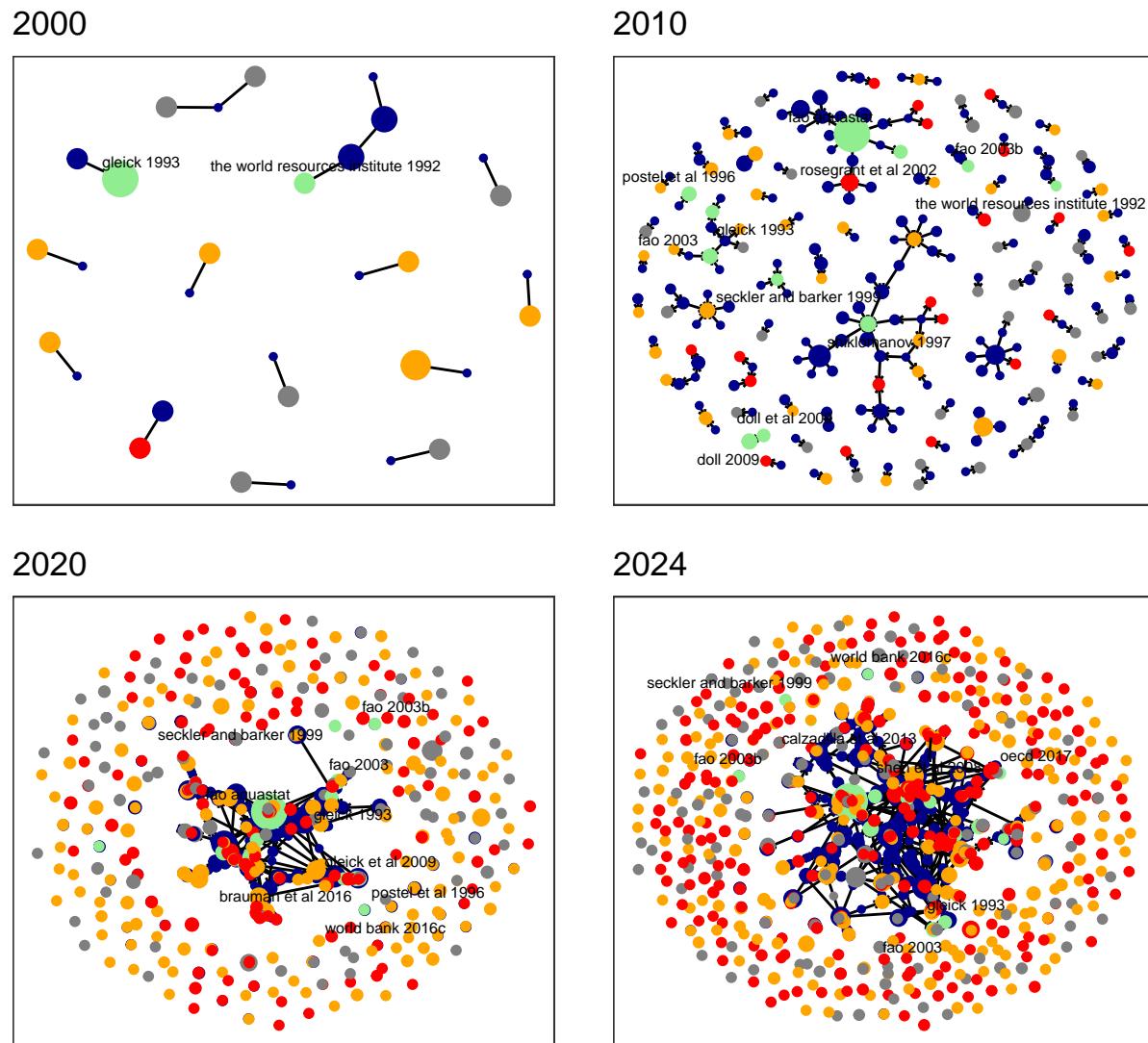
2020



2024



```
##  
## $water  
  
## Warning: ggrepel: 8 unlabeled data points (too many overlaps). Consider  
## increasing max.overlaps  
  
## Warning: ggrepel: 13 unlabeled data points (too many overlaps). Consider  
## increasing max.overlaps
```



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")
}

tmp

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

```

```

## [30] "chen et al 2017"
## [31] "chen et al 2018a"
## [32] "chowdhury et al 2022"
## [33] "clay 2004"
## [34] "cody 2018"
## [35] "cotera et al 2023"
## [36] "cruse et al 2016"
## [37] "dalin et al 2017"
## [38] "das et al 2018"
## [39] "de vrese et al 2016"
## [40] "defries 2008"
## [41] "dinar et al 2019"
## [42] "dong et al 2023"
## [43] "dos santos et al 2016"
## [44] "drastig et al 2016"
## [45] "du et al 2015"
## [46] "elbakidze and cobourn 2014"
## [47] "emami and koch 2018"
## [48] "ertas et al 2021"
## [49] "es'haghi et al 2022"
## [50] "falkenmark 2013"
## [51] "famiglietti et al 2011"
## [52] "fao 1999d"
## [53] "fao 2002e"
## [54] "fao 2008b"
## [55] "fao 2011"
## [56] "fao 2012"
## [57] "fao 2012f"
## [58] "fao 2012g"
## [59] "fao 2012i"
## [60] "fao 2014c"
## [61] "fao 2014d"
## [62] "fao 2015d"
## [63] "fao 2016e"
## [64] "fao 2017c"
## [65] "fao 2018g"
## [66] "fao 2019"
## [67] "fao 2019d"
## [68] "farooq et al 2024"
## [69] "farrag et al 2015"
## [70] "fereres and connor 2004"
## [71] "fereres and soriano 2006"
## [72] "fernandez garcia et al 2018"
## [73] "finkenbiner et al 2019"
## [74] "flemer and champ 2006"
## [75] "foley et al 1996"
## [76] "foley et al 2011"
## [77] "gebul 2021"

```

```

## [78] "gerber et al 2013"
## [79] "gheewala et al 2014"
## [80] "gibson et al 2017"
## [81] "gibson et al 2018"
## [82] "gleick 1993"
## [83] "godfray et al 2010"
## [84] "goel et al 2007"
## [85] "grados et al 2022"
## [86] "grassini et al 2011"
## [87] "guimberteau et al 2011"
## [88] "guo et al 2023a"
## [89] "hamdani et al 2023"
## [90] "hammond and dubé 2012"
## [91] "hando 2022"
## [92] "hanjra and qureshi 2010"
## [93] "hardie 2020"
## [94] "harmel et al 2020a"
## [95] "harmel et al 2020b"
## [96] "hassan et al 2022"
## [97] "hubert et al 2010"
## [98] "huffaker 2008"
## [99] "hussain et al 2010"
## [100] "jain et al 2021"
## [101] "jambo et al 2021"
## [102] "jenkins et al 2021"
## [103] "johansson 2000"
## [104] "johnson et al 2001"
## [105] "jury and vaux jr 2005"
## [106] "kadigi et al 2004"
## [107] "karimzadeh et al 2024"
## [108] "kataoka et al 2017"
## [109] "knapp and schwabe 2008"
## [110] "knorr and augustin 2023"
## [111] "koch et al 2020"
## [112] "konikow 2015"
## [113] "kundzewicz et al 2007"
## [114] "lado et al 2024"
## [115] "lawston et al 2017"
## [116] "lele et al 2013"
## [117] "leng et al 2016"
## [118] "leng et al 2017"
## [119] "li et al 2021f"
## [120] "li et al 2023f"
## [121] "liagre et al 2015"
## [122] "lin et al 2024"
## [123] "lipan et al 2019"
## [124] "liu et al 2018"
## [125] "liu et al 2022"

```

```

## [126] "liu et al 2023 b"
## [127] "machibya and mdemu 2005"
## [128] "madramootoo and fyles 2012"
## [129] "magidi et al 2021"
## [130] "mahapatra et al 2020"
## [131] "manjunatha et al 2016"
## [132] "mao et al 2003"
## [133] "mao et al 2024"
## [134] "maponya et al 2015"
## [135] "martins et al 2023"
## [136] "mathur and achutaraao 2019"
## [137] "mazengo et al 2022"
## [138] "mccabe and wolock 2007"
## [139] "mcdermid et al 2023"
## [140] "mebrahtu et al 2018"
## [141] "mehta et al 2024"
## [142] "millenium ecosystem assessment 2005"
## [143] "mitchell et al 2018"
## [144] "molden 2007"
## [145] "molden and de fraiture 2010"
## [146] "molden et al 2007"
## [147] "molden et al 2007b"
## [148] "molden et al 2010"
## [149] "moyo et al 2020"
## [150] "mueller et al 2012"
## [151] "mukherji et al 2009"
## [152] "muratoglu et al 2023"
## [153] "mutambara 2016"
## [154] "ngouajio et al 2008"
## [155] "nikolaou et al 2020"
## [156] "ning et al 2023"
## [157] "niu et al 2022"
## [158] "niu et al 2023"
## [159] "norton et al 2021"
## [160] "obembe et al 2023"
## [161] "oecd 2012b"
## [162] "oecd and fao 2020"
## [163] "onishi et al 2019"
## [164] "owens et al 2022"
## [165] "ozdogan 2011"
## [166] "panettieri et al 2013"
## [167] "papdopoulos et al 2005"
## [168] "pawlak and kołodziejczak 2020"
## [169] "pei et al 2017"
## [170] "peña-guerrero et al 2020"
## [171] "perry and steduto 2017"
## [172] "pokhrel et al 2016"
## [173] "pomoni et al 2023"

```

```
## [174] "pool et al 2021"
## [175] "portmann et al 2010"
## [176] "postel et al 1996"
## [177] "postel et al 2001"
## [178] "potopova et al 2022"
## [179] "pradipta et al 2022"
## [180] "qi et al 2021"
## [181] "ragettli et al 2018"
## [182] "raheem et al 2023"
## [183] "ramlow et al 2018"
## [184] "rashed 2014"
## [185] "ray et al 2023"
## [186] "ribeiro et al 2016"
## [187] "rigby et al 2010"
## [188] "rockstrom and barron 2007"
## [189] "rockstrom and falkenmark 2000"
## [190] "rockstrom et al 2007b"
## [191] "rosa et al 2018"
## [192] "rosegrant et al 2002c"
## [193] "rosegrant et al 2009"
## [194] "rosenzweig et al 2019"
## [195] "rost et al 2008"
## [196] "rulli et al 2013"
## [197] "sadeghi et al 2020"
## [198] "sam-amoaah et al 2016"
## [199] "san-millan et al 2017"
## [200] "scanlon et al 2007"
## [201] "scanlon et al 2012"
## [202] "scheierling and treguer 2018"
## [203] "scheierling et al 2014"
## [204] "scott et al 2018"
## [205] "seckler et al 1998"
## [206] "selvam and sivasubramanian 2012"
## [207] "selvam et al 2014"
## [208] "sengsourivong and ichihashi 2019"
## [209] "shao et al 2014"
## [210] "shehata and abdrabboh 2023"
## [211] "shen et al 2013"
## [212] "shiklomanov 1996"
## [213] "shiklomanov 1997"
## [214] "shiklomanov and rodda 2003"
## [215] "shyam et al 2022"
## [216] "sidibe et al 2012"
## [217] "siebert and doll 2010"
## [218] "siebert et al 2005"
## [219] "siebert et al 2010"
## [220] "siebert et al 2013"
## [221] "singh 2014"
```

```
## [222] "singh 2014b"
## [223] "singh 2015c"
## [224] "smedema et al 2000"
## [225] "somerville and briscoe 2001"
## [226] "soylu and bras 2024"
## [227] "stanley et al 2011"
## [228] "suebsombut et al 2021"
## [229] "supe et al 2024"
## [230] "swett 2020"
## [231] "taguta et al 2022"
## [232] "terwisscha van scheltinga et al 2021"
## [233] "thenkabail et al 2005"
## [234] "thenkabail et al 2009a"
## [235] "thorslund et al 2022"
## [236] "tian et al 2024"
## [237] "tijjani et al 2022"
## [238] "tilman et al 2002"
## [239] "tiri et al 2018"
## [240] "tiwari et al 2023"
## [241] "tomaz et al 2020"
## [242] "tsur 2005"
## [243] "united nations 1966"
## [244] "united nations 2003"
## [245] "united nations 2014"
## [246] "united nations 2015b"
## [247] "united nations 2016b"
## [248] "united nations 2018c"
## [249] "united nations 2019"
## [250] "united nations environment program 1999"
## [251] "usman et al 2021"
## [252] "van der ploeg 2014"
## [253] "van schilfgaarde 1994"
## [254] "velasco-sanchez et al 2021"
## [255] "verhulst et al 2010"
## [256] "vico and porporato 2011"
## [257] "vlek et al 2017"
## [258] "vorosmarty and sahagian 2000"
## [259] "walczak 2021"
## [260] "wang et al 2012"
## [261] "wang et al 2014"
## [262] "wang et al 2021e"
## [263] "wei et al 2023b"
## [264] "wilson et al 2021"
## [265] "wiltshire et al 2013"
## [266] "wisser et al 2008"
## [267] "wmo 1997"
## [268] "wondzell 2010"
## [269] "world bank 1997"
```

```

## [270] "world bank 2001"
## [271] "world water assessment programme 2021"
## [272] "wri 2000"
## [273] "xiang et al 2019"
## [274] "xiao et al 2017"
## [275] "xie and lark 2021"
## [276] "xu et al 2019b"
## [277] "xu et al 2023"
## [278] "yang et al 2015"
## [279] "yao et al 2022"
## [280] "yao et al 2024"
## [281] "zabel et al 2014"
## [282] "zappa et al 2021"
## [283] "zappa et al 2024"
## [284] "zareie et al 2020"
## [285] "zhai et al 2015"
## [286] "zhang et al 2015"
## [287] "zhang et al 2017b"
## [288] "zhang et al 2017c"
## [289] "zhang et al 2018d"
## [290] "zhang et al 2021"
## [291] "zhang et al 2022"
## [292] "zhang et al 2022c"
## [293] "zhang et al 2022e"
## [294] "zhang et al 2022m"
## [295] "zhu and burney 2022 b"
## [296] "zingaro et al 2017"
## [297] "zohaib et al 2019"
## [298] "zou et al 2012"
##
## $food$`path ending in no claim or no citation`
## [1] "aaac 2018"
## [2] "abafe et al 2022"
## [3] "abd-elghany et al 2021"
## [4] "abdelmoneim et al 2023"
## [5] "abdullah 2006"
## [6] "adamala et al 2014"
## [7] "adeyemi et al 2017"
## [8] "ahmad et al 2004"
## [9] "ahmad et al 2018"
## [10] "ahmad et al 2022"
## [11] "ahmed et al 2022"
## [12] "akoteyon and soladoye 2011"
## [13] "al tenaiji et al 2019"
## [14] "al-agele et al 2021"
## [15] "alcon et al 2021"
## [16] "alexandratos and bruinsma 2012"
## [17] "ali et al 2017"

```

```

## [18] "anderies 2017"
## [19] "anderson et al 2012"
## [20] "appiah and asomani-boateng 2018"
## [21] "aseyehregn et al 2012"
## [22] "attia et al 2022"
## [23] "avellan and gremillion 2019"
## [24] "azedo et al 2022"
## [25] "bai et al 2023"
## [26] "baniasadi et al 2019"
## [27] "barberena et al 2022"
## [28] "barbier 2016"
## [29] "barbosa et al 2022"
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## [1813] "wong et al 2021"
## [1814] "wood et al 2000"
## [1815] "world bank 1992"
## [1816] "world bank 2001"
## [1817] "world bank 2001b"
## [1818] "world bank 2017a"
## [1819] "world bank 2017c"
## [1820] "world bank 2020"
## [1821] "world bank 2021"
## [1822] "world bank 2022"
## [1823] "world economic forum 2010a"
## [1824] "world economic forum 2011"
## [1825] "world economic forum 2014"
## [1826] "world resources institute 2001"
## [1827] "world resources institute 2010"
## [1828] "world resources institute 2020"
## [1829] "world watch institute 2004"
## [1830] "world water assessment programme 2003"
## [1831] "world water assessment programme 2006"
## [1832] "world water assessment programme 2012b"
## [1833] "world water vision"
## [1834] "worldometers 2019"
## [1835] "wri 1994"
## [1836] "wri 1996"
## [1837] "wri 2000"
## [1838] "wri 2016"
```

```
## [1839] "wu and zheng 2023"
## [1840] "wu et al 2018"
## [1841] "wu et al 2019"
## [1842] "wu et al 2020"
## [1843] "wu et al 2022"
## [1844] "wu et al 2022a"
## [1845] "wu et al 2022c"
## [1846] "wu et al 2023"
## [1847] "wu et al 2024"
## [1848] "wwf 2006"
## [1849] "wwf 2019"
## [1850] "xia et al 2022a"
## [1851] "xia et al 2022b"
## [1852] "xiang et al 2020"
## [1853] "xiao et al 2005"
## [1854] "xiao et al 2024"
## [1855] "xiaogang et al 2020"
## [1856] "xie and lark 2021"
## [1857] "xie et al 2014"
## [1858] "xinchun et al 2017"
## [1859] "xing yuan et al 2024"
## [1860] "xiu et al 2022"
## [1861] "xiu et al 2022b"
## [1862] "xu et al 2020"
## [1863] "xu et al 2022"
## [1864] "xu et al 2023a"
## [1865] "xu et al 2023c"
## [1866] "xue et al 2016"
## [1867] "xue et al 2017"
## [1868] "xue et al 2018"
## [1869] "yan et al 2022"
## [1870] "yan et al 2023b"
## [1871] "yanes et al 2020"
## [1872] "yang et al 2003"
## [1873] "yang et al 2006"
## [1874] "yang et al 2015a"
## [1875] "yang et al 2015b"
## [1876] "yang et al 2016"
## [1877] "yang et al 2021"
## [1878] "yang et al 2022a"
## [1879] "yang et al 2022b"
## [1880] "yang et al 2023a"
## [1881] "yang et al 2023c"
## [1882] "yannopoulos et al 2015"
## [1883] "yao et al 2022"
## [1884] "yasin et al 2022"
## [1885] "ye et al 2023"
## [1886] "yetik and sen 2023"
```

```
## [1887] "yigezu et al 2021"
## [1888] "yilmaz 2023"
## [1889] "yilmazkuday et al 2021"
## [1890] "yin et al 2022a"
## [1891] "yin et al 2022c"
## [1892] "yip et al 2024"
## [1893] "yoshida et al 2013"
## [1894] "younes et al 2024"
## [1895] "young et al 2019"
## [1896] "yu 2014"
## [1897] "yu and songhao 2020"
## [1898] "yu et al 2015"
## [1899] "yu et al 2017"
## [1900] "yu et al 2019"
## [1901] "yu et al 2020"
## [1902] "yu et al 2021"
## [1903] "yu et al 2022a"
## [1904] "yu et al 2022b"
## [1905] "yuli et al 2018"
## [1906] "zarei and mahmoudi 2020"
## [1907] "zarei and moghimi 2019a"
## [1908] "zarei and moghimi 2019b"
## [1909] "zarei et al 2021"
## [1910] "zeng and cai 2014"
## [1911] "zeng et al 2022"
## [1912] "zeraatkar et al 2016"
## [1913] "zhang 2011"
## [1914] "zhang 2013"
## [1915] "zhang and guo 2017"
## [1916] "zhang and guo 2018"
## [1917] "zhang et al 2015"
## [1918] "zhang et al 2015b"
## [1919] "zhang et al 2017"
## [1920] "zhang et al 2018b"
## [1921] "zhang et al 2019b"
## [1922] "zhang et al 2019c"
## [1923] "zhang et al 2021"
## [1924] "zhang et al 2021c"
## [1925] "zhang et al 2021f"
## [1926] "zhang et al 2022a"
## [1927] "zhang et al 2022b"
## [1928] "zhang et al 2022c"
## [1929] "zhang et al 2022e"
## [1930] "zhang et al 2022f"
## [1931] "zhang et al 2022g"
## [1932] "zhang et al 2022h"
## [1933] "zhang et al 2022j"
## [1934] "zhang et al 2022l"
```

```

## [1935] "zhang et al 2023a"
## [1936] "zhang et al 2023b"
## [1937] "zhao et al 2021c"
## [1938] "zhao et al 2022a"
## [1939] "zheng et al 2020a"
## [1940] "zheng et al 2020b"
## [1941] "zhi et al 2022"
## [1942] "zhou et al 2015"
## [1943] "zhou et al 2021"
## [1944] "zhou et al 2022"
## [1945] "zhu et al 2018"
## [1946] "zhu et al 2023a"
## [1947] "zhu et al 2023c"
## [1948] "zhuang et al 2023"
## [1949] "zhuo et al 2022"
## [1950] "zhupley et al 2021"
## [1951] "zia et al 2021"
## [1952] "zisopoulou et al 2022"
## [1953] "zong et al 2023"
## [1954] "zou and he 2016"
## [1955] "zou et al 2013"
## [1956] "zucchinelli et al 2021"

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

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

out

## $food
## $food$path ending in no claim
## [1] 0.3900524
##
## $food$path ending in no claim or no citation
## [1] 0.776178
##
## 
## $water
## $water$path ending in no claim
## [1] 0.353463
##
## $water$path ending in no claim or no citation
## [1] 0.667349

```

3.2 Calculation of amplification

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

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

```
amplification_fun <- function(graph) {
```

Convert *tbl_graph* to *igraph* object -----

```
ig <- as.igraph(graph)
nature_claims <- V(ig)$nature.claim
```

initialize counter to store results for each paper -----

```
results <- numeric(vcount(ig))
```

Loop over each paper -----

```
for (P in V(ig)) {
```

Initialize counter for valid paths

```
path_count <- 0
```

Traverse through all nodes and count paths avoiding direct "modelling"

```
for (target in V(ig)) {
```

if ($P \neq target$) {

```
    all_paths <- all_simple_paths(ig, from = P, to = target, mode = "out")
```

Filter out paths of length 1 that end in a "modelling" node

```
    valid_paths <- Filter(function(path) {
        !(length(path) == 2 && nature_claims[path[2]] == "modelling")
    }, all_paths)
```

path_count <- path_count + length(valid_paths)

```
}
```

```
}
```

results[P] <- path_count
}

```

return(results)
}
```

```

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

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

## $food
## [1] 0.9253927
##
## $water
## [1] 1.510065

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

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

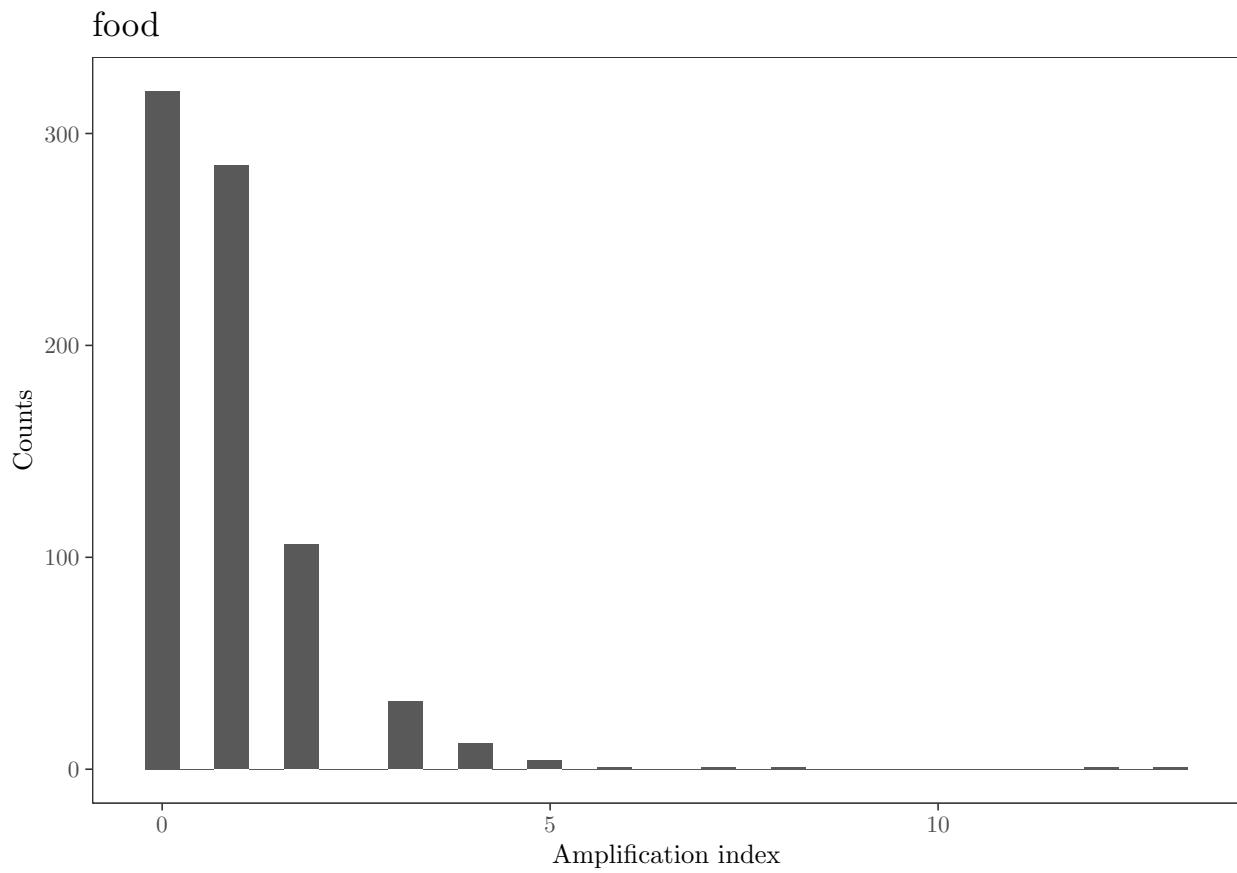
  plot.amplification[[i]] <- amplification.indices[[i]] %>%
    data.frame("index" = .) %>%
    ggplot(., aes(index)) +
    geom_histogram() +
    theme_AP() +
    labs(y = "Counts", x = "Amplification index") +
    ggtitle(names(amplification.indices[i]))

}

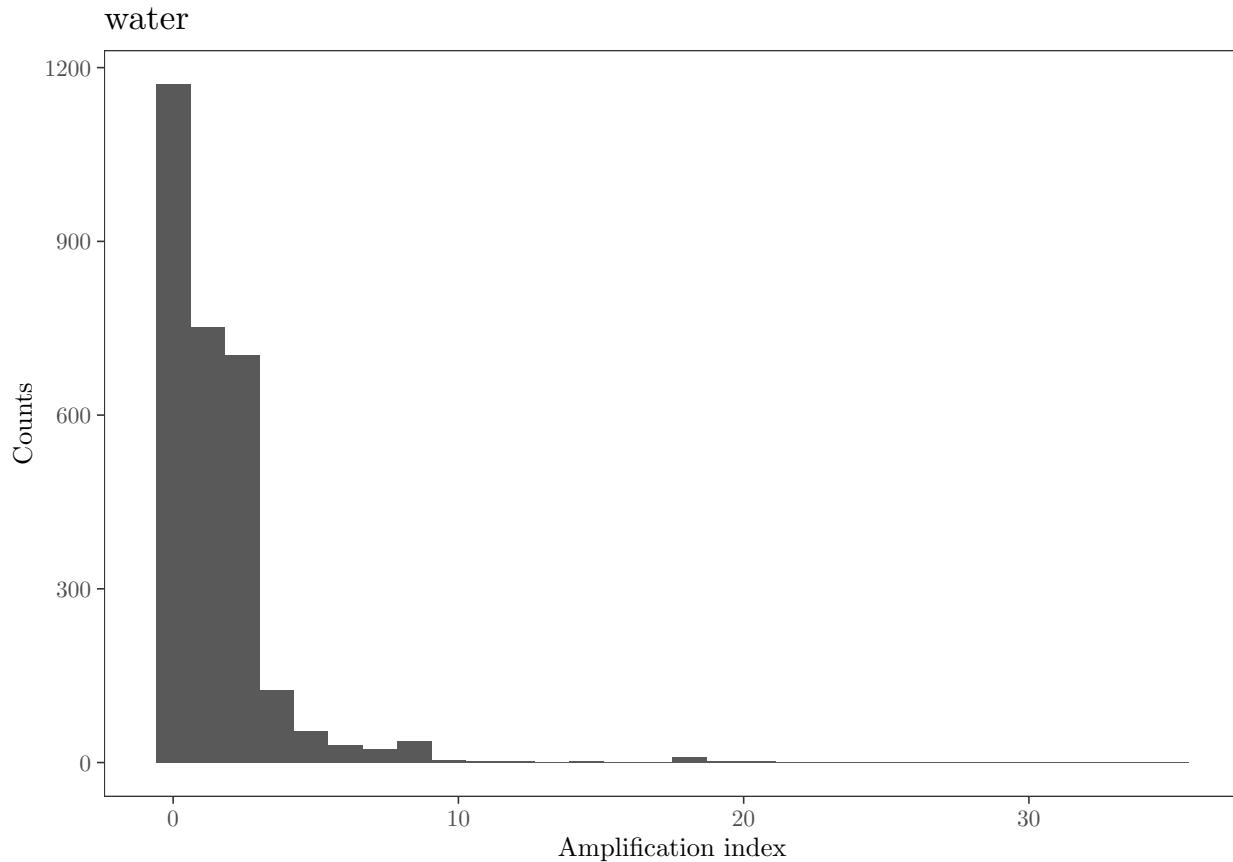
plot.amplification

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

```



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



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]
```

```

# 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  2117  0.61061436
## 2:    water   1046  0.30170176
## 3:    both    125  0.03605423
## 4:    food    179  0.05162965

# 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)) +

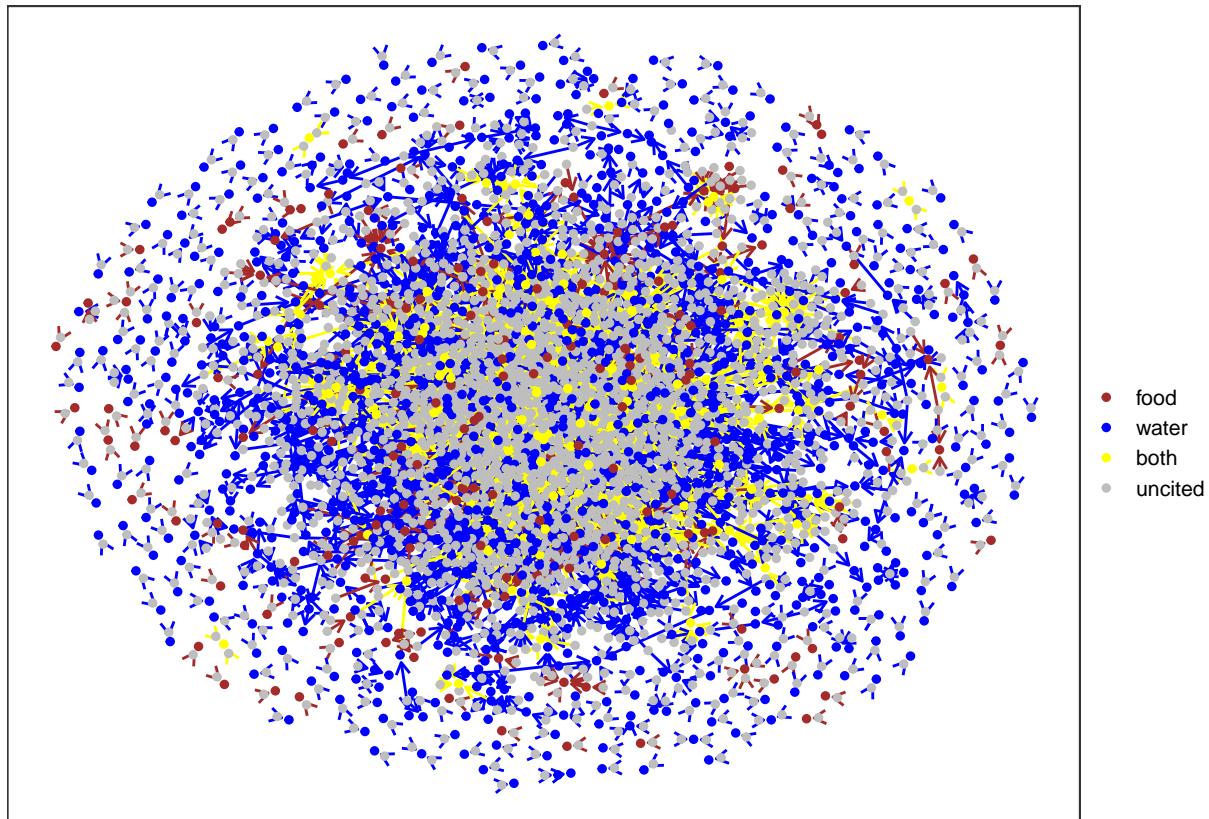
```

```

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")

## 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.

```



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)

```

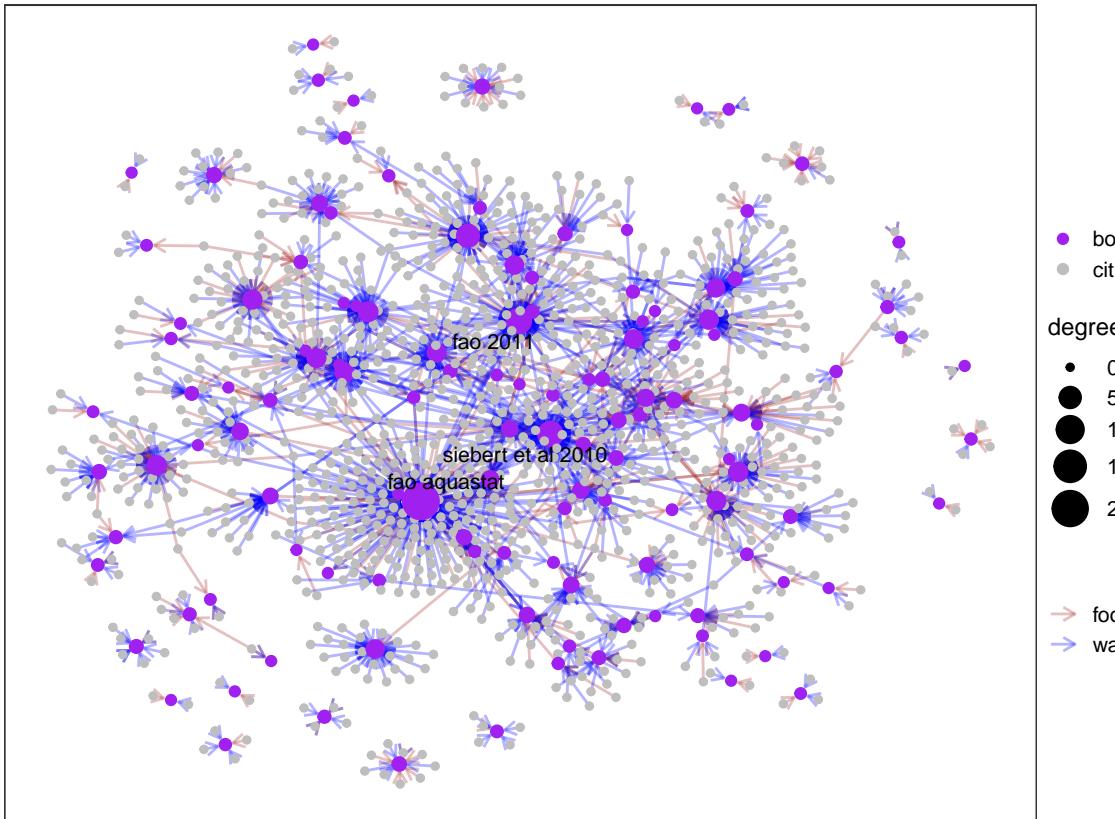
```

ggraph(intersect.graph.final, layout = "graphopt") +
  geom_edge_link(arrows = 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: 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 1275 rows containing missing values or values outside the scale range
## (`geom_text_repel()`).

```



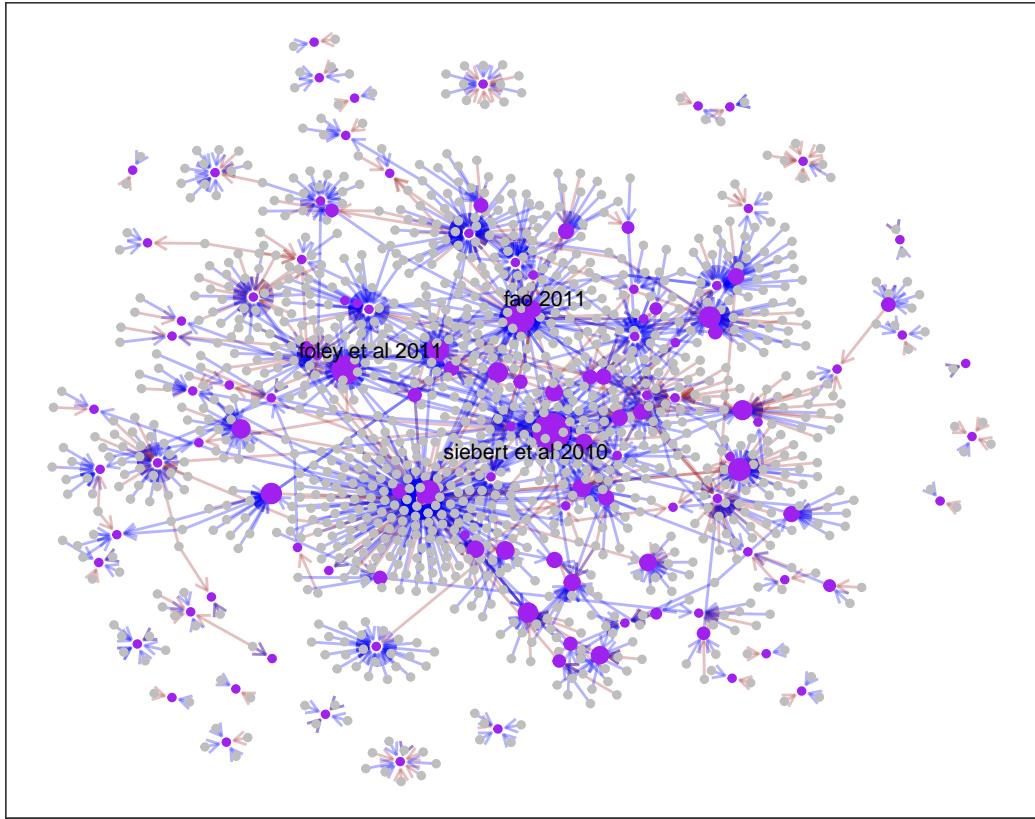
```

set.seed(12)

ggraph(intersect.graph.final, layout = "graphopt") +
  geom_edge_link(arrows = 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 1275 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 = "continent")]

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

```
wri <- fread("world_resources_institut_guide_to_the_global_environment_1994.csv") %>%
  .[order(country)] %>%
  .[, data:= "wri 1994"] %>%
  .[, country:= countrycode(country, origin = "country.name", destination = "country.name")]

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

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

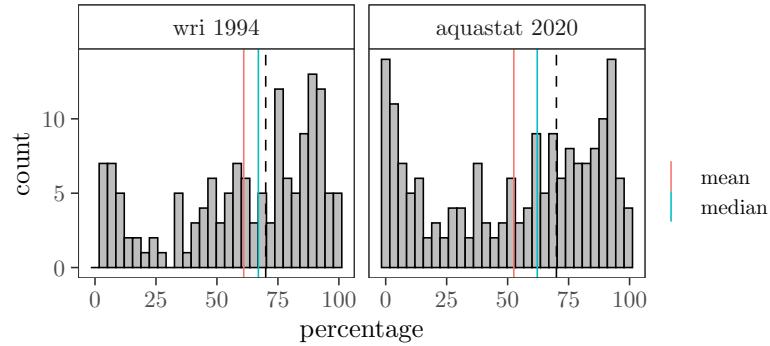
dt.comparison <- rbind(aquastat.dt, wri) %>%
  .[, data:= factor(data, levels = c("wri 1994", "aquastat 2020"))]

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

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

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

Warning: Removed 1 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)) {

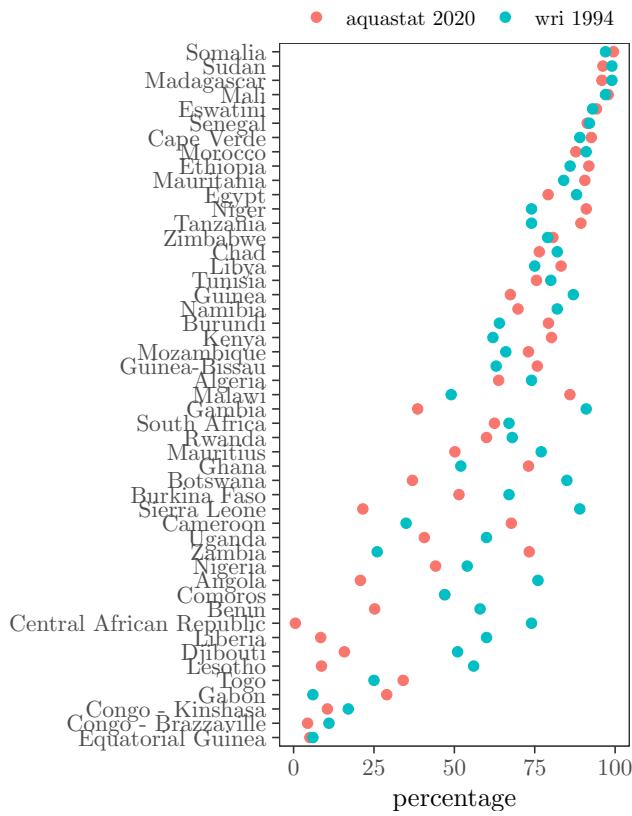
  out[[i]] <- ggplot(tmp[[i]], aes(reorder(country, value),
                                    value, color = variable)) +
    coord_flip() +
    scale_color_discrete(name = "") +
    geom_point() +
    theme_AP() +
    theme(legend.position = "top") +
    labs(x = "", y = "percentage") +
    ggtitle(names(tmp[i]))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

out

## $Africa

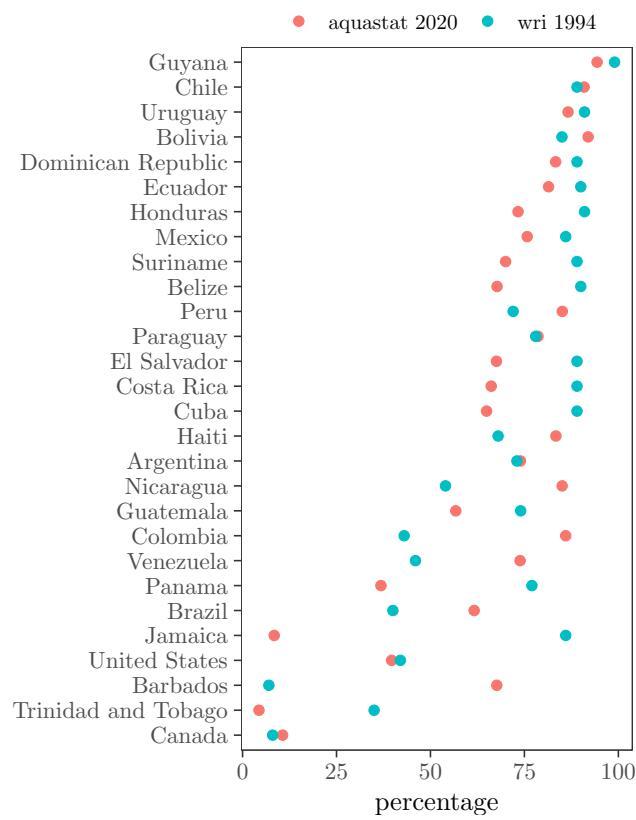
```

Africa



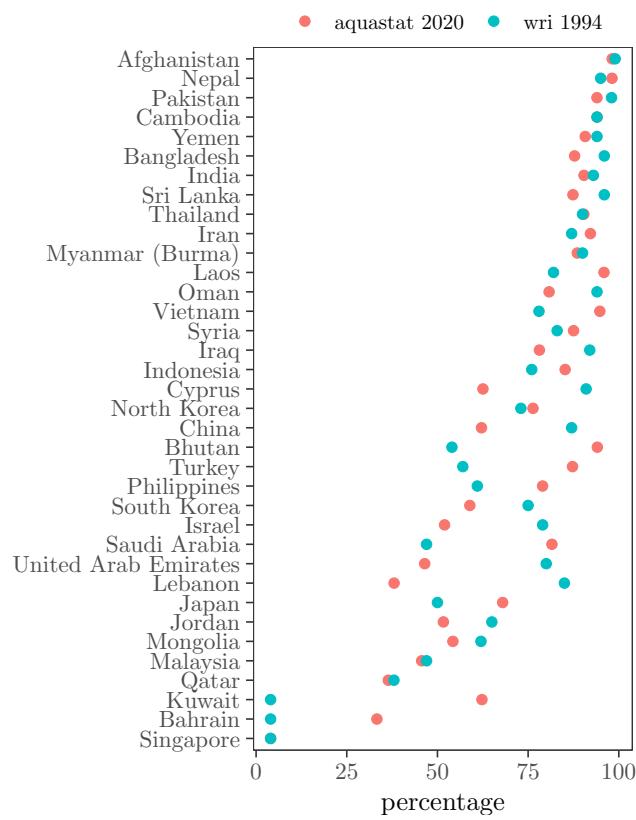
```
##  
## $Americas
```

Americas



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

Asia



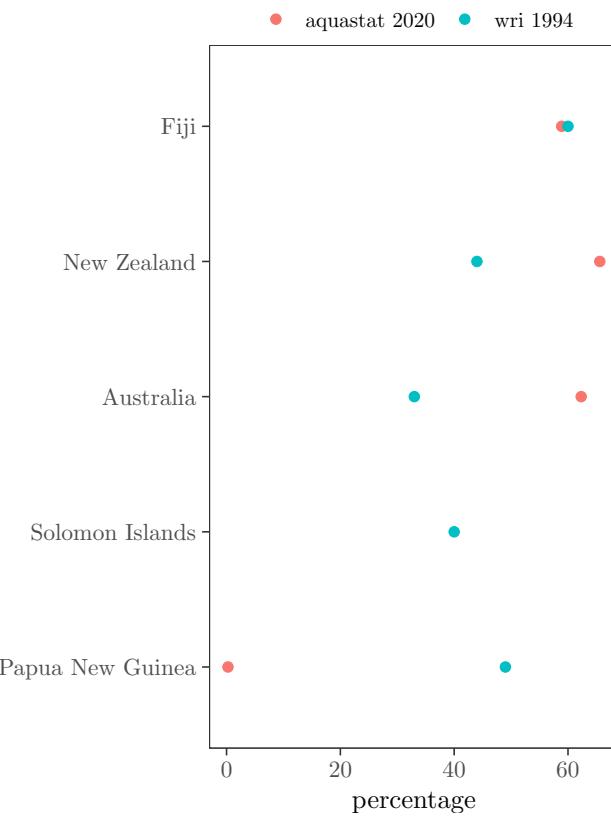
```
##  
## $Europe
```

Europe



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

Oceania



```

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

name.variables <- unique(aquastat$Variable)

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

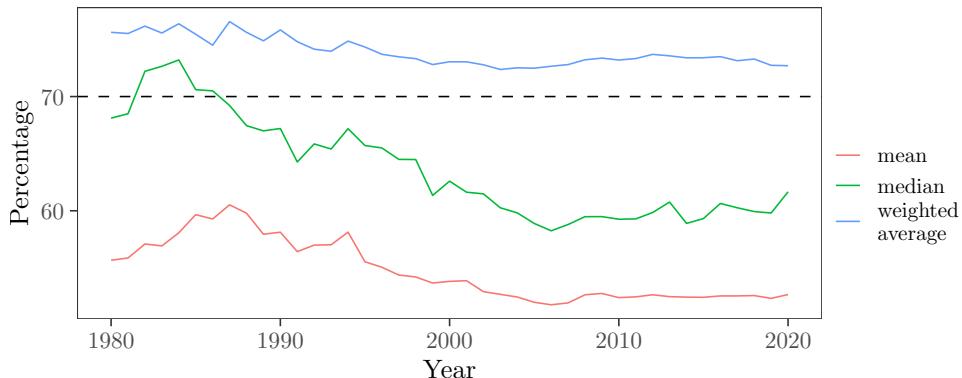
# Weighted average -----
aquastat.aww[, weights:= Value / sum(Value), Year]
weighted.average.dt <- aquastat.aww[, .(value = sum(Value * weights)), Year] %>%
  .[, variable:= "weighted \n average"]

```

```
# Plot ---

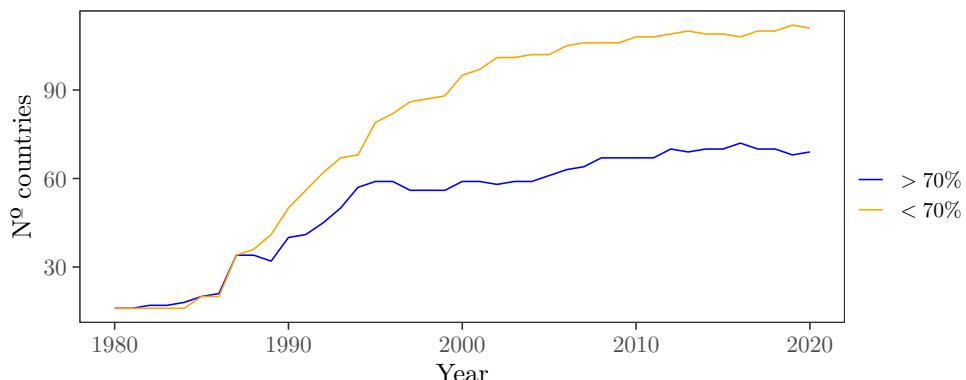
a <- aquastat.aww.stats %>%
  rbind(weighted.average.dt) %>%
  ggplot(., aes(Year, value, group = variable, color = variable)) +
  geom_line() +
  scale_color_discrete(name = "") +
  geom_hline(yintercept = 70, lty = 2) +
  theme_AP() +
  labs(x = "Year", y = "Percentage")
```

a

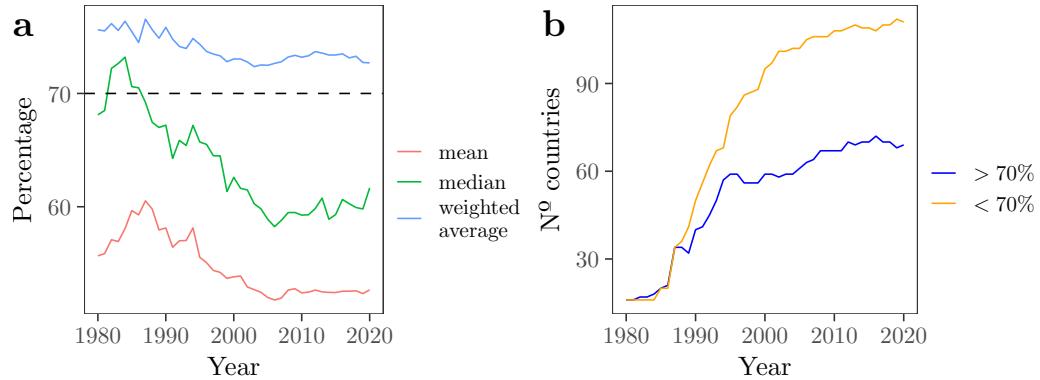


```
b <- aquastat.aww[, .(above.70 = sum(Value > 70),
                     below.70 = sum(Value < 70)), Year] %>%
  melt(., measure.vars = c("above.70", "below.70")) %>%
  ggplot(., aes(Year, value, color = variable)) +
  geom_line() +
  theme_AP() +
  scale_color_manual(name = "", labels = c("$>70$\%",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

b



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



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] purrrr_1.0.2    readr_2.1.4      tidyverse_2.0.0  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            crayon_1.5.2        pkgconfig_2.0.3
## [10] fastmap_1.1.1         ellipsis_0.3.2      labeling_0.4.3
## [13] utf8_1.2.4             promises_1.2.0.1    rmarkdown_2.21
## [16] tzdb_0.3.0              tinytex_0.45        xfun_0.39
## [19] jsonlite_1.8.4         flashClust_1.01-2   highr_0.10
## [22] SnowballC_0.7.1       later_1.3.0        tweenr_2.0.2
## [25] cluster_2.1.6          R6_2.5.1           stringi_1.8.3
## [28] RColorBrewer_1.1-3    cellranger_1.1.0   estimability_1.4.1
## [31] Rcpp_1.0.12             knitr_1.42          filehash_2.4-5
## [34] httpuv_1.6.9            rentrez_1.2.3      Matrix_1.6-5
## [37] timechange_0.2.0       tidyselect_1.2.0   rstudioapi_0.15.0
## [40] stringdist_0.9.10     pubmedR_0.0.3      yaml_2.3.7
## [43] viridis_0.6.4          codetools_0.2-19   lattice_0.22-5
```

```

## [46] plyr_1.8.8           shiny_1.7.4          withr_3.0.0
## [49] benchmarkmeData_1.0.4 coda_0.19-4        evaluate_0.20
## [52] polyclip_1.10-6      zip_2.3.0          pillar_1.9.0
## [55] janeaustenr_1.0.0     DT_0.27           plotly_4.10.1
## [58] generics_0.1.3         hms_1.1.3          munsell_0.5.1
## [61] xtable_1.8-4          leaps_3.1          glue_1.7.0
## [64] tikzDevice_0.12.4     emmeans_1.8.5       scatterplot3d_0.3-43
## [67] lazyeval_0.2.2         tools_4.3.3         tokenizers_0.3.0
## [70] mvtnorm_1.1-3         graphlayouts_1.1.1 XML_3.99-0.14
## [73] grid_4.3.3            rscopus_0.6.6       colorspace_2.1-0
## [76] dimensionsR_0.0.3     ggforce_0.4.1       bibliometrixData_0.3.0
## [79] cli_3.6.3             fansi_1.0.6         viridisLite_0.4.2
## [82] gtable_0.3.5          digest_0.6.34       ggrepel_0.9.5
## [85] FactoMiner_2.8         htmlwidgets_1.6.2    farver_2.1.2
## [88] htmltools_0.5.5        factoextra_1.0.7    lifecycle_1.0.4
## [91] httr_1.4.5             multcompView_0.1-9  mime_0.12
## [94] 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

```