

# Irrigation's real impact on global water and food security

R code

Arnald Puy

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```

# PRELIMINARY FUNCTIONS #####

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

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

```

```

# CREATION OF VECTORS WITH NAMES #####

database <- c("wos", "scopus", "dimensions")
topic <- c("water", "food")

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

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

# READ IN THE DATA #####

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

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

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

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

  } else {

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

  }

}

# vector with new column names -----

new_colnames <- c("doi", "authors", "year", "title", "journal", "abstract", "database")
to_lower <- c("authors", "title", "journal", "abstract")

# Loop to read in the datasets -----

out <- list()

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

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

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

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

```

```

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

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

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

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

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

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

}

```

```

##
## Converting your wos collection into a bibliographic dataframe
##
##
## Warning:
## In your file, some mandatory metadata are missing. Bibliometrix functions may not work properly
##
## Please, take a look at the vignettes:
## - 'Data Importing and Converting' (https://www.bibliometrix.org/vignettes/Data-Importing-and-Converting)
## - 'A brief introduction to bibliometrix' (https://www.bibliometrix.org/vignettes/Introduction-to-Bibliometrix)
##
##
## Missing fields:  C1 CR
## Done!
##
##
## Converting your wos collection into a bibliographic dataframe
##
##
## Warning:
## In your file, some mandatory metadata are missing. Bibliometrix functions may not work properly
##
## Please, take a look at the vignettes:

```

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

```
names(out) <- combinations$topic

# CLEAN THE DATASETS #####

# Arrange -----

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

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

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

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

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

# Filter out duplicated studies by doi -----

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

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

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

}

names(final.dt) <- topic

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

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

## [1] FALSE

# Export to xlsx -----
```

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

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

## 1 Retrieve all corpus

### 1.1 Abstract corpus

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

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

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

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

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

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

}
```

### 1.2 Policy corpus

```
# LOAD IN DIMENSIONS DATASETS (POLICY TEXT) #####

# Function to load and preprocess data -----
```

```

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

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

# Load data -----

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

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

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

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

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

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

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

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

# Export -----

for (i in c("water", "food")) {
  matching.rows.policy[topic == i] %>%
    write.xlsx(paste("policy.corpus", i, "xlsx", sep = "."))
}

```

### 1.3 Full text corpus

```
# LOAD IN DIMENSIONS DATASET (FULL TEXT) #####
```

```
full.text.corpus.water <- fread("full.text.corpus.water.csv")
```

## 2 Split full text corpus for analysis

```
# SPLIT THE DATASET INTO N FOR RESEARCH #####
```

```
# Function to split dataset in n chunks -----
```

```
split_dt_fun <- function(dt, num_parts) {
```

```
  split_dt <- list()
```

```
  # Calculate the number of rows in each part
```

```
  rows_per_part <- nrow(dt) %/% num_parts
```

```
  # Split the data.table into roughly equal parts
```

```
  for (i in 1:num_parts) {
```

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

```
    end_row <- i * rows_per_part
```

```
    if (i == num_parts) {
```

```
      end_row <- nrow(dt)
```

```
    }
```

```
    split_dt[[i]] <- dt[start_row:end_row, ]
```

```
  }
```

```
  return(split_dt)
```

```
}
```

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

```
times.nanxin <- 2
```

```
times.arnald <- 1
```

```
nanxin <- paste(rep("nanxin", times.nanxin), 1:times.nanxin, sep = "")
```

```
arnald <- paste(rep("arnald", times.arnald), 1:times.arnald, sep = "")
```

```
names_surveyors <- c(arnald, nanxin, "seth", paste("student", 1:4, sep = ""))
```

```
n_surveyors <- length(names_surveyors)
```

```
survey.dt.split <- split_dt_fun(dt = full.text.corpus.water, num_parts = n_surveyors)
```

```
names(survey.dt.split) <- names_surveyors
```



```

# Export -----

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

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

}

```

### 3 Network analysis

```

# CREATE VECTORS TO READ IN AND CLEAN THE DATASETS #####

tmp <- list()
names.files <- c("WORK", "NETWORK")
topics <- c("water")
corpus <- c("abstract.corpus", "policy.corpus", "full.text.corpus")
cols_of_interest <- c("title", "author", "claim", "citation")

# 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

# CLEAN AND MERGE DATASETS #####

```

```

dataset.networks <- all.files[str_detect(all.files, "NETWORK")]
network.dt <- tmp[dataset.networks] %>%
  rbindlist() %>%
  .[, policy:= grepl("^policy", doi)]

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

# CHECK NUMBER OF FAO AQUASTAT CITES #####

network.dt[citation %like% "fao aquastat"] %>%
  .[, .N, citation]

##           citation      N
##           <char> <int>
## 1: fao aquastat 2006      1
## 2:      fao aquastat      8
## 3: fao aquastat 2010      5
## 4: fao aquastat 2020      2
## 5: fao aquastat 2011      2
## 6: fao aquastat 2012      2
## 7: fao aquastat 2021      1
## 8: fao aquastat 2017      1
## 9: fao aquastat 2015      1
## 10: fao aquastat 2019      3
## 11: fao aquastat 2016      2
## 12: fao aquastat 2014      1
## 13: fao aquastat 2023      1

# WRITE LOOKUP TABLE TO CHECK ALREADY RETRIEVED STUDIES #####

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

nrow(lookup.dt)

## [1] 344

write.xlsx(lookup.dt, "lookup.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]])]
}

```

```

}

# Rename columns -----

setnames(network.dt, c("author", "citation"), c("from", "to"))

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

# PLOT DESCRIPTIVE STATISTICS #####

# Check proportio of studies making the claim but without providing any citation and
# not being primary papers (!modelling) -----

no.citation.total <- nrow(network.dt.claim[nature.claim == "no citation" &
                                           !document.type == "modelling"])
no.citation.total / nrow(network.dt.claim)

## [1] 0.1651584

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

a <- network.dt[, .N, .(nature.claim, document.type)] %>%
  na.omit() %>%
  ggplot(., aes(reorder(nature.claim, N), N)) +
  coord_flip() +
  geom_bar(stat = "identity") +
  facet_wrap(~document.type) +
  scale_y_continuous(breaks = breaks_pretty(n = 2)) +
  labs(x = "", y = "Counts") +
  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] %>%

```

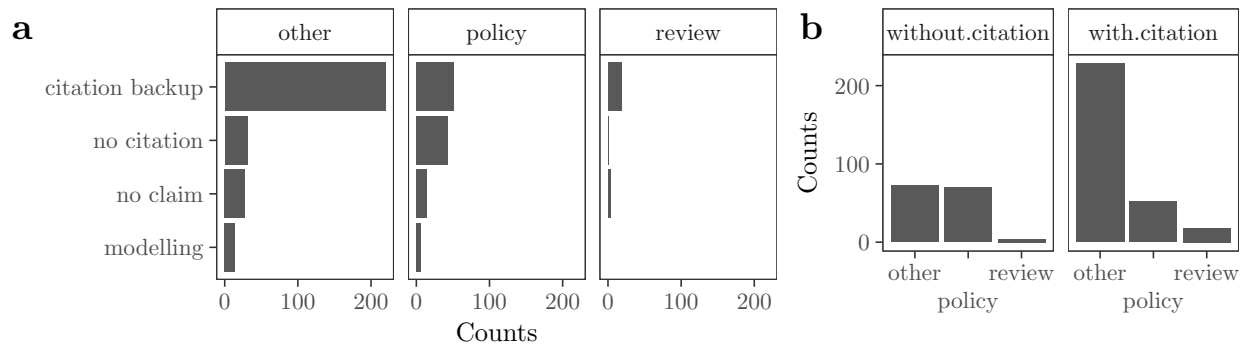
```

melt(., measure.vars = c("without.citation", "with.citation")) %>%
  ggplot(., aes(document.type, value)) +
  geom_bar(stat = "identity") +
  scale_y_continuous(breaks = breaks_pretty(n = 2)) +
  scale_x_discrete(guide = guide_axis(n.dodge = 2)) +
  labs(x = "", y = "Counts") +
  facet_wrap(~variable) +
  theme_AP()

# merge -----

plot_grid(a, b, ncol = 2, rel_widths = c(0.63, 0.37), labels = "auto")

```



### 3.1 Network metrics

```

# CALCULATE NETWORK METRICS #####

# only complete cases -----

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

# Transform to graph -----

citation_graph <- graph_from_data_frame(d = network.dt.complete, directed = TRUE)

# Calculate network metrics -----

edge_density(citation_graph)

```

```
## [1] 0.003459404
```

```

# 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 <- cluster_walktrap(citation_graph)
modularity(wtc)

```

```
## [1] 0.7993277
```

```
network_metrics <- data.table(node = V(citation_graph)$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(citation_graph, mode = "in"),  
  
  # 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(citation_graph),  
  
  # 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(citation_graph),  
  pagerank = pagerank(citation_graph)$vector  
)  
  
# Define the max number of rows  
max.number <- 3  
  
degree.nodes <- network_metrics[order(-degree)][1:max.number]  
betweenness.nodes <- network_metrics[order(-betweenness)][1:max.number]  
pagerank.nodes <- network_metrics[order(-closeness)][1:max.number]  
  
degree.nodes
```

```
##           node degree betweenness closeness  pagerank  
##           <char>  <num>         <num>      <num>      <num>  
## 1:      fao aquastat      30           0         NaN 0.07450656  
## 2: molden et al 2007       9          20 0.33333333 0.01665012  
## 3: shiklomanov 1997        8           0         NaN 0.02667465
```

```
betweenness.nodes
```

```
##           node degree betweenness  closeness  pagerank  
##           <char>  <num>         <num>      <num>      <num>  
## 1:      molden et al 2007       9          20.00 0.33333333 0.016650122  
## 2:      oki and kanae 2006       3          14.25 1.00000000 0.016982956
```

```
## 3: boretti and rosa 2019      1      11.00 0.05555556 0.003442607
```

```
pagerank.nodes
```

```
##           node degree betweenness closeness    pagerank
##           <char>  <num>         <num>      <num>      <num>
## 1: sharma and irmak 2012      0          0          1 0.001860869
## 2:      world bank 2007      3          8          1 0.011344247
## 3:   brajovic et al 2015      0          0          1 0.001860869
```

## 3.2 Network plots

```
# ADD FEATURES TO NODES #####

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

graph <- tidygraph::as_tbl_graph(network.dt.complete, directed = TRUE)
vec.names <- graph %>%
  activate(nodes) %>%
  pull() %>%
  data.table(name = .)

# Merge with info from the network.dt -----

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

# Merge with the correct order -----

order_indices <- match(vec.names$name, vec.nature.claim$name)
final.vec.nature.claim <- vec.nature.claim[order_indices, ] %>%
  .[, nature.claim]
final.vec.document.type <- vec.nature.claim[order_indices, ] %>%
  .[, document.type]

# Attach to the graph -----

graph <- graph %>%
  activate(nodes) %>%
  mutate(nature.claim = final.vec.nature.claim,
         document.type = final.vec.document.type,
         degree = network_metrics$degree,
         betweenness = network_metrics$betweenness,
         pagerank = network_metrics$pagerank)
```

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

```
seed <- 123
```

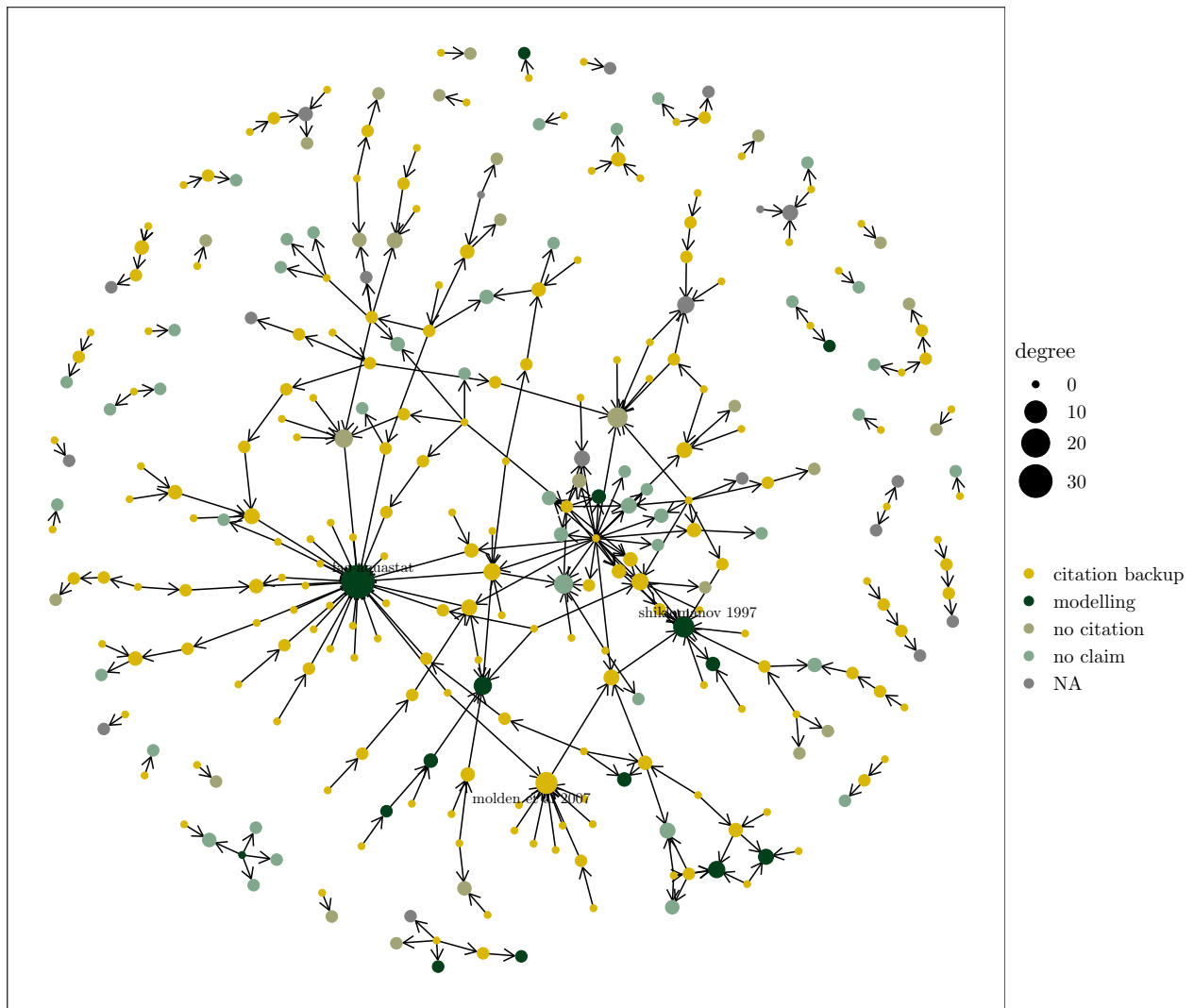
```
# by nature of claim -----
```

```
set.seed(seed)
```

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

```
ggraph(graph, 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 = degree)) +  
  geom_node_text(aes(label = ifelse(degree >= min(degree.nodes$degree), name, NA)),  
                repel = TRUE, size = 2.2) +  
  labs(x = "", y = "") +  
  scale_color_manual(name = "",  
                     values = wes_palette(name = "Cavalcanti1", 5)) +  
  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 291 rows containing missing values (`geom_text_repel()`).
```



```

set.seed(seed)

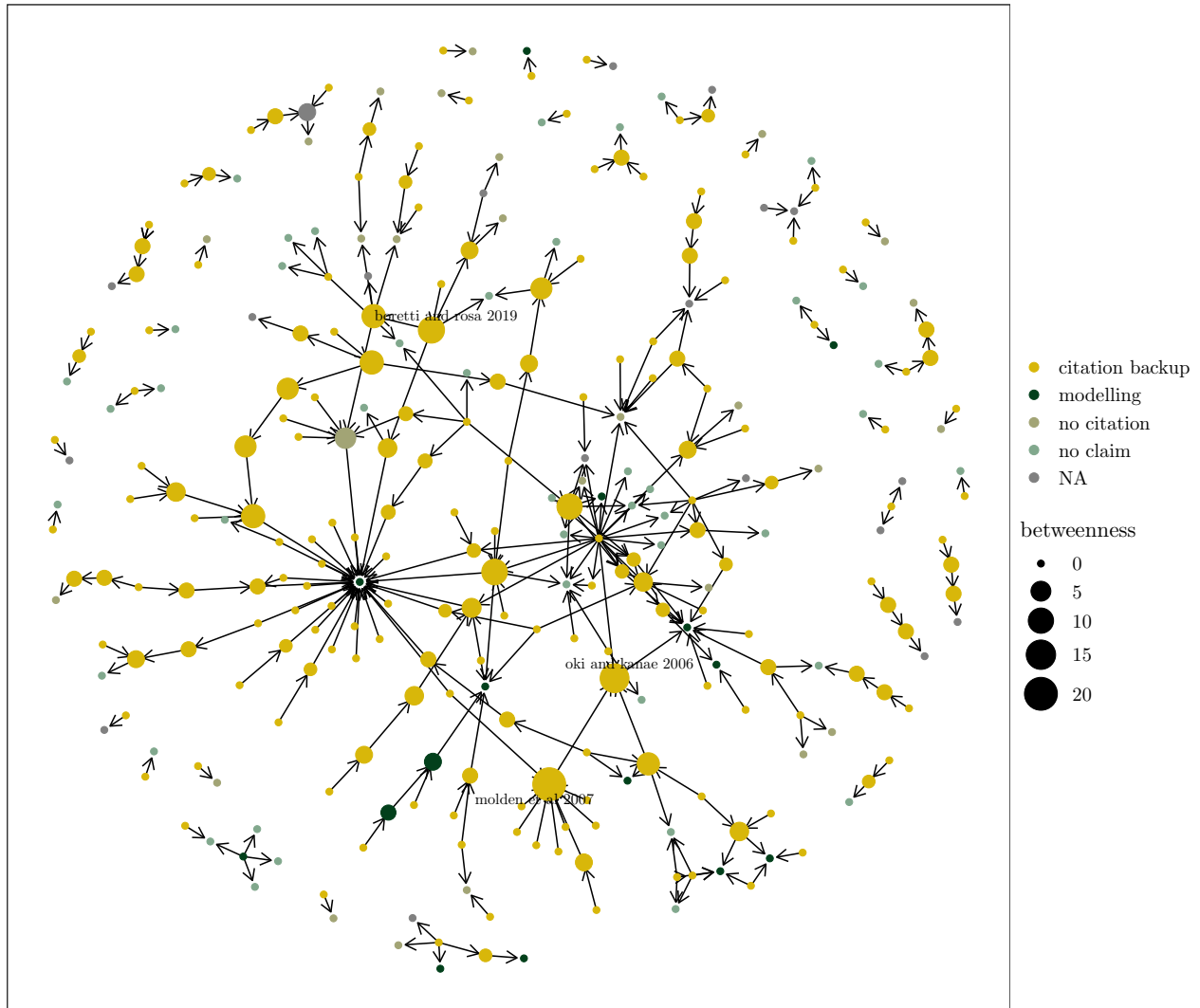
# Label the nodes with highest betweenness -----

ggraph(graph, 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$betweenness), name, NA),
    repel = TRUE, size = 2.2)) +
  labs(x = "", y = "") +
  scale_color_manual(name = "",
    values = wes_palette(name = "Cavalcanti1", 5)) +
  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 291 rows containing missing values (`geom_text_repel()`).
```



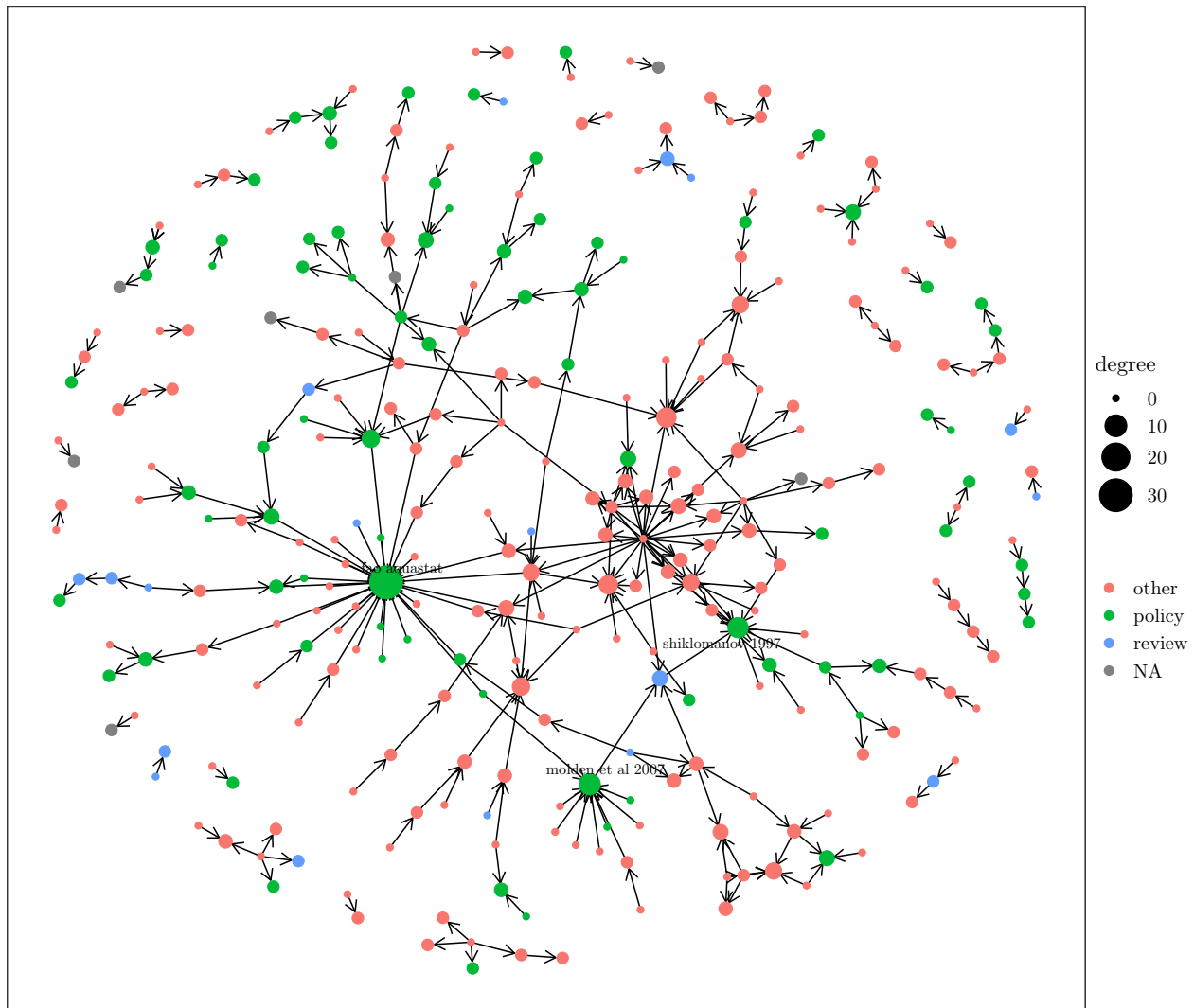
```
# by document.type-----

set.seed(seed)

ggraph(graph, 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$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")
```

## Warning: Removed 291 rows containing missing values (`geom\_text\_repel()`).



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

```
set.seed(seed)

ggraph(graph, 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)) +
```

```
## Warning: Removed 279 rows containing missing values (`geom_text_repel()`).
```



```

# CREATE VECTORS TO READ IN AND CLEAN THE DATASETS #####

tmp <- list()
names.files <- c("WORK", "NETWORK")
cols_of_interest <- c("title", "author", "claim", "citation")
files.abstract.water <- paste(paste("abstract.corpus.water2_", names.files, sep = ""), "xlsx",

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

for (i in 1:length(files.abstract.water)) {

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

  if (i == 1) {

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

  } else {

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

names(tmp) <- names.files

# CLEAN DATASET #####

abstract.water.dt <- merge(tmp[[1]][claim.in.text == "F"], tmp[[2]], by = c("doi", "title"), a
abstract.water.dt[, claim.in.text:= ifelse(is.na(claim.in.text), "TRUE", "FALSE")]
abstract.water.dt[, c(cols_of_interest, "nature.claim"):= lapply(.SD, trimws), .SDcols = c(cols
abstract.water.dt[, year:= ifelse(is.na(year), as.numeric(gsub("\\D", "", abstract.water.dt$au

# PRELIMINARY ANALYSIS #####

a <- tmp$WORK[claim.in.text %in% c("T", "F")] %>%
  .[, .N, claim.in.text] %>%
  ggplot(., aes(claim.in.text, N)) +
  geom_bar(stat = "identity") +
  labs(x = "", y = "N° studies") +
  theme_AP()

b <- tmp$NETWORK %>%
  .[, complete.cases(.$nature.claim), ] %>%
  .[, nature.claim:= trimws(nature.claim)] %>%
  .[, .N, nature.claim] %>%
  ggplot(., aes(reorder(nature.claim, -N), N)) +
  scale_x_discrete(guide = guide_axis(n.dodge = 2)) +

```

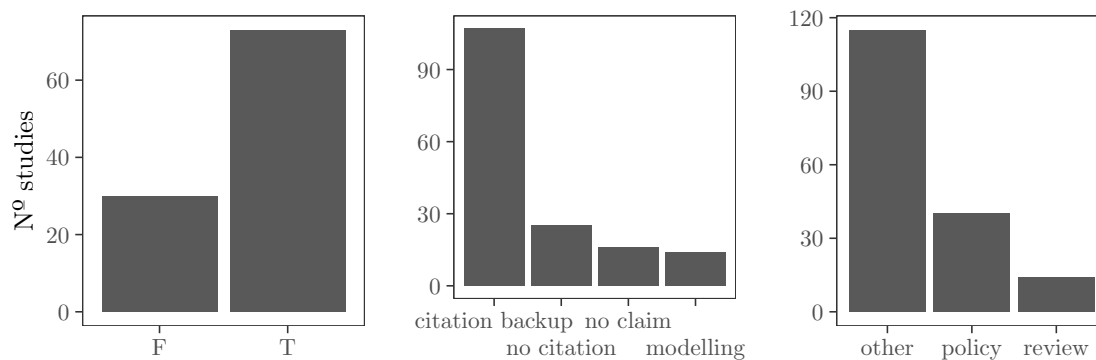
```

geom_bar(stat = "identity") +
labs(x = "", y = "") +
theme_AP()

c <- tmp$NETWORK %>%
  .[, .N, document.type] %>%
  ggplot(., aes(reorder(document.type, -N), N)) +
  geom_bar(stat = "identity") +
  labs(x = "", y = "") +
  theme_AP()

plot_grid(a, b, c, ncol = 3)

```



*# NETWORK ANALYSIS #####*

*# Arrange data -----*

```

network.dt <- copy(tmp$NETWORK)
setnames(network.dt, c("author", "citation"), c("from", "to"))
network.dt <- network.dt[, .(from, to, document.type, nature.claim)]
cols_to_change <- colnames(network.dt)
network.dt[, (cols_to_change):= lapply(.SD, trimws), .SDcols = (cols_to_change)]

```

*# only complete cases -----*

```

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

```

*# Transform to graph -----*

```

citation_graph <- graph_from_data_frame(d = network.dt.complete, directed = TRUE)

```

*# Calculate network metrics -----*

```

edge_density(citation_graph)

```

```

## [1] 0.005838807

```

```

network_metrics <- data.table(node = V(citation_graph)$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(citation_graph, mode = "in"),

# 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(citation_graph),

# 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(citation_graph),
pagerank = page_rank(citation_graph)$vector
)

```

```
network_metrics[order(-degree)][1:5]
```

```

##                node degree betweenness closeness
##                <char>  <num>         <num>      <num>
## 1:                fao aquastat      13           0      NaN
## 2:                molden et al 2007    4          10 0.3333333
## 3: world water assessment programme 2009    2           4 0.3333333
## 4:                world bank 2007      2           7 1.0000000
## 5: world water assessment programme 2018    2           2 0.3333333
##      pagerank
##      <num>
## 1: 0.079718516
## 2: 0.020085501
## 3: 0.010586794
## 4: 0.023540448
## 5: 0.007253915

```

```
network_metrics[order(-betweenness)][1:5]
```

```

##                node degree betweenness closeness  pagerank
##                <char>  <num>         <num>      <num>      <num>
## 1:    molden et al 2007    4          10 0.3333333 0.02008550
## 2:    world bank 2007      2           7 1.0000000 0.02354045
## 3: aivazidou et al 2016    1           6 0.1666667 0.01008686
## 4: united nations 2009      1           6 0.3333333 0.01249487
## 5: oki and kanae 2006      1           6 1.0000000 0.02099371

```

```
network_metrics[order(-closeness)][1:5]
```

```
##           node degree betweenness closeness    pagerank
##           <char>  <num>         <num>         <num>         <num>
## 1:      sharma and irmak 2012         0           0           1 0.003921035
## 2:           world bank 2007         2           7           1 0.023540448
## 3:      brajovic et al 2015         0           0           1 0.003921035
## 4:      rivers et al 2015         0           0           1 0.003921035
## 5: hafeez and khalid awan 2022         0           0           1 0.003921035
```

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

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

```
graph <- tidygraph::as_tbl_graph(network.dt.complete, directed = TRUE)
vec.names <- graph %>%
  activate(nodes) %>%
  pull() %>%
  data.table(name = .)
```

```
# Merge with info from the network.dt -----
```

```
vec.nature.claim <- merge(vec.names, unique(network.dt[, .(from, nature.claim)]),
  by.x = "name", by.y = "from", all.x = TRUE)
```

```
# Merge with the correct order -----
```

```
order_indices <- match(vec.names$name, vec.nature.claim$name)
final.vec.nature.claim <- vec.nature.claim[order_indices, ] %>%
  .[, nature.claim]
```

```
# Attach to the graph -----
```

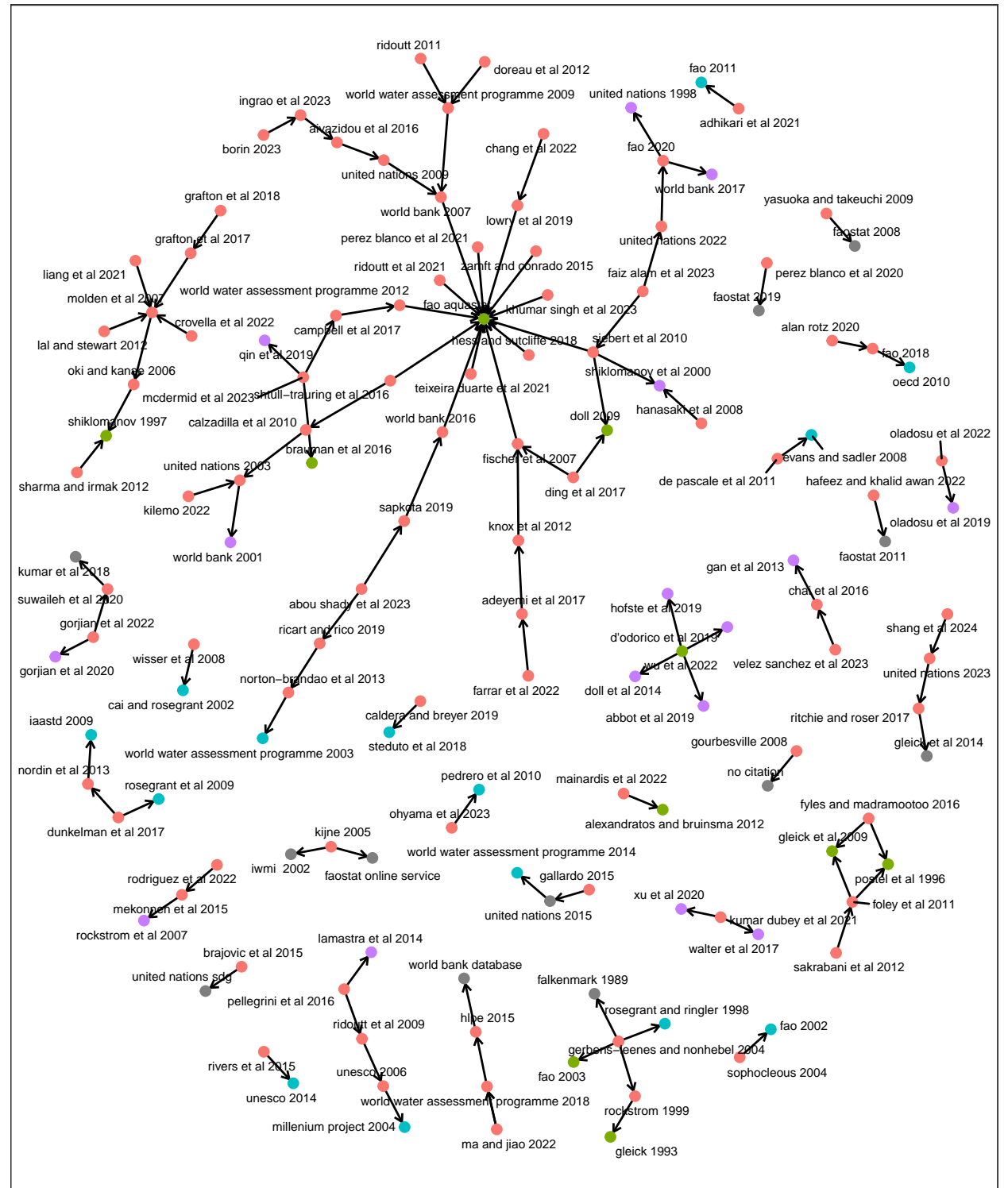
```
graph <- graph %>%
  activate(nodes) %>%
  mutate(nature.claim = final.vec.nature.claim)
```

```
# Plot network -----
```

```
ggraph(graph, layout = "igraph", algorithm = "nicely") +
  geom_edge_link(arrow = arrow(length = unit(1.5, 'mm')),
    end_cap = circle(1, "mm")) +
  geom_node_point(size = 2, aes(color = nature.claim)) +
  geom_node_text(aes(label = name), repel = TRUE, size = 2.1) +
  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 = "top")
```

● citation backup ● modelling ● no citation ● no claim ● NA





## 4 Aquastat data

```
# AQUASTAT DATA #####

# Read in dataset -----

aquastat <- data.table(read.xlsx("aquastat_dt.xlsx"))
aquastat.dt <- aquastat[Variable == "Agricultural water withdrawal as % of total water withdrawal",
  .[, .(Area, Year, Value, Symbol)] %>%
  .[Year == 2020] %>%
  .[, Symbol := ifelse(Symbol == "E", "estimated", "imputed")]

# Count proportion of estimated and imputed values
# E: Estimate either calculated as sum or identify (yield) from
# official values or from an AQUASTAT estimation.
# I: Imputed (carry forward, vertical imputation, linear interpolation)

# Calculate mean and median -----

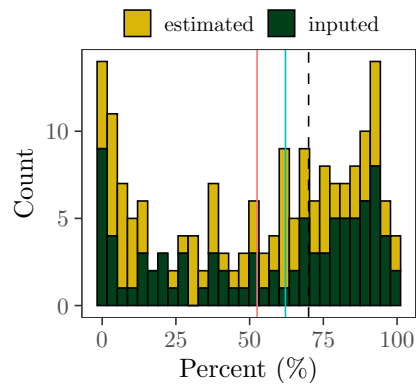
mean.and.median <- aquastat.dt[, .(mean = mean(Value), median = median(Value))] %>%
  melt(., measure.vars = colnames())

# Plot histogram -----

a <- ggplot(aquastat.dt, aes(Value)) +
  geom_histogram(color = "black", aes(fill = Symbol)) +
  geom_vline(data = mean.and.median, aes(xintercept = value, color = variable),
    show.legend = FALSE) +
  geom_vline(xintercept = 70, lty = 2) +
  scale_fill_manual(name = "",
    values = wes_palette(name = "Cavalcanti1", 5)) +
  theme_AP() +
  labs(x = "Percent (\\%)", y = "Count") +
  theme(legend.position = "top")

a

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



## 5 Session information

```
# SESSION INFORMATION #####
```

```
sessionInfo()
```

```
## R version 4.3.3 (2024-02-29)
## Platform: aarch64-apple-darwin20 (64-bit)
## Running under: macOS Sonoma 14.2.1
##
## Matrix products: default
## BLAS:   /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/lib/libRblas.0.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/lib/libRlapack.dylib;
##
## locale:
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## time zone: Europe/London
## tzcode source: internal
##
## attached base packages:
## [1] parallel stats      graphics grDevices utils      datasets methods
## [8] base
##
## other attached packages:
##  [1] scales_1.3.0      wesanderson_0.3.6 benchmarkme_1.0.8 tidygraph_1.3.0
##  [5] cowplot_1.1.1     ggraph_2.1.0      igraph_1.6.0      bibliometrix_4.0.1
##  [9] lubridate_1.9.2   forcats_1.0.0     stringr_1.5.1     dplyr_1.1.4
## [13] purrr_1.0.2       readr_2.1.4       tidyr_1.3.0       tibble_3.2.1
## [17] ggplot2_3.4.4     tidyverse_2.0.0   data.table_1.14.99 openxlsx_4.2.5.2
##
## loaded via a namespace (and not attached):
##  [1] Rdpack_2.6          gridExtra_2.3      readxl_1.4.2
##  [4] rlang_1.1.3         magrittr_2.0.3     tidytext_0.4.1
##  [7] compiler_4.3.3      vctrs_0.6.5        crayon_1.5.2
## [10] pkgconfig_2.0.3     fastmap_1.1.1      ellipsis_0.3.2
## [13] labeling_0.4.3      utf8_1.2.4         promises_1.2.0.1
## [16] rmarkdown_2.21      tzdb_0.3.0         tinytex_0.45
## [19] bit_4.0.5           xfun_0.39          jsonlite_1.8.4
## [22] flashClust_1.01-2   highr_0.10         SnowballC_0.7.1
## [25] later_1.3.0         tweenr_2.0.2        cluster_2.1.6
## [28] R6_2.5.1            stringi_1.8.3       RColorBrewer_1.1-3
## [31] cellranger_1.1.0    estimability_1.4.1  iterators_1.0.14
## [34] Rcpp_1.0.12         knitr_1.42          filehash_2.4-5
## [37] httpuv_1.6.9        rentrez_1.2.3       Matrix_1.6-5
## [40] timechange_0.2.0     tidyselect_1.2.0    viridis_0.6.4
## [43] rstudioapi_0.15.0   stringdist_0.9.10   pubmedR_0.0.3
## [46] yaml_2.3.7          codetools_0.2-19    doParallel_1.0.17
```

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

```
## Return the machine CPU
```

```
cat("Machine:      "); print(get_cpu())$model_name)
```

```
## Machine:
```

```
## [1] "Apple M1 Max"
```

```
## Return number of true cores
```

```
cat("Num cores:    "); print(detectCores(logical = FALSE))
```

```
## Num cores:
```

```
## [1] 10
```

```
## Return number of threads
```

```
cat("Num threads: "); print(detectCores(logical = FALSE))
```

```
## Num threads:
```

```
## [1] 10
```