Irrigation's real impact on global water and food security

R code

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

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

# 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))
}
```

```r
# 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 prope
##
## Please, take a look at the vignettes:
## - 'Data Importing and Converting' (https://www.bibliometrix.org/vignettes/Data-Importing-and
## - 'A brief introduction to bibliometrix' (https://www.bibliometrix.org/vignettes/Introductio
##
##
## 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 prope
##
## Please, take a look at the vignettes:
```

```
## - 'Data Importing and Converting' (https://www.bibliometrix.org/vignettes/Data-Importing-and
## - 'A brief introduction to bibliometrix' (https://www.bibliometrix.org/vignettes/Introductio
##
##
## 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)

# Filer 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 --------------------------------------------------------------
```

```r
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 Abstract corpus

```r
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
```

```r
# 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 = "."))

}
```

2 Full text corpus

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

# Load dataset of the full text ----------------------------------------------

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

```r
keywords <- c("water", "irrigat")

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

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

# Load and preprocess water data ----------------------------------------------

dimensions.full.text.water <- load_and_preprocess_data("dimensions_dt_full_text_water_2022_2023

dimensions.full.text.food <- rbind(
  load_and_preprocess_data("dimensions_dt_full_text_food_2022.csv", "food"),
  load_and_preprocess_data("dimensions_dt_full_text_food_2023.csv", "food")
)

# Combine water and food data -------------------------------------------------

result <- rbind(dimensions.full.text.water, dimensions.full.text.food) %>%
  .[, .(DOI, PubYear, Title, `Source title`, topic)] %>%
  setnames(., colnames(.), colnames.full.text) %>%
  # remove the references that are included in the dataset that
  # collects mentions in the abstracts
  .[!.$doi %in% final.dt.water.screened$doi]

# Create a logical condition for pattern matching using grepl -----------------

pattern_condition <- sapply(keywords, function(keyword)
  grepl(keyword, result$title, ignore.case = TRUE))

full.text.dt <- result[rowSums(pattern_condition) > 0]

# Sample just 50% for the analysis --------------------------------------------

# Create function
random_sample <- function(input_dt) {
  set.seed(123)  # Set a seed for reproducibility
  sampled_dt <- input_dt[sample(.N, .N * 0.5), ]
  return(sampled_dt)
}

# sample
full.text.sampled <- full.text.dt[, random_sample(.SD), topic]

full.text.sampled[, .N, topic]
```

```
##     topic     N
##    <char> <int>
## 1:  water  4607
## 2:   food  8108
```

```
# Export ------------------------------------------------------------------

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

  full.text.sampled[topic == i] %>%
    write.xlsx(paste("full.text.corpus", i, "xlsx", sep = "."))
}
```

3 Policy corpus

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

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 = "."))
}
```

4 Split datasets for analysis

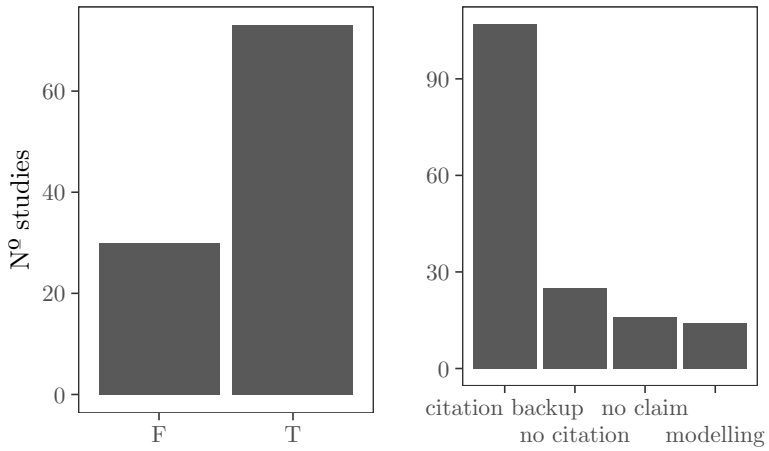
```
# SPLIT THE DATASET INTO N FOR RESEARCH ########################################

# 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 <- 4
times.arnald <- 2
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)

full.text.corpus.water <- read.xlsx("full.text.corpus.water.xlsx")

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

```r
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"))

}
```

```r
# 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"), al
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
```

```r
# 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 = "Nº 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()

plot_grid(a, b, ncol = 2)
```




```
# 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
```

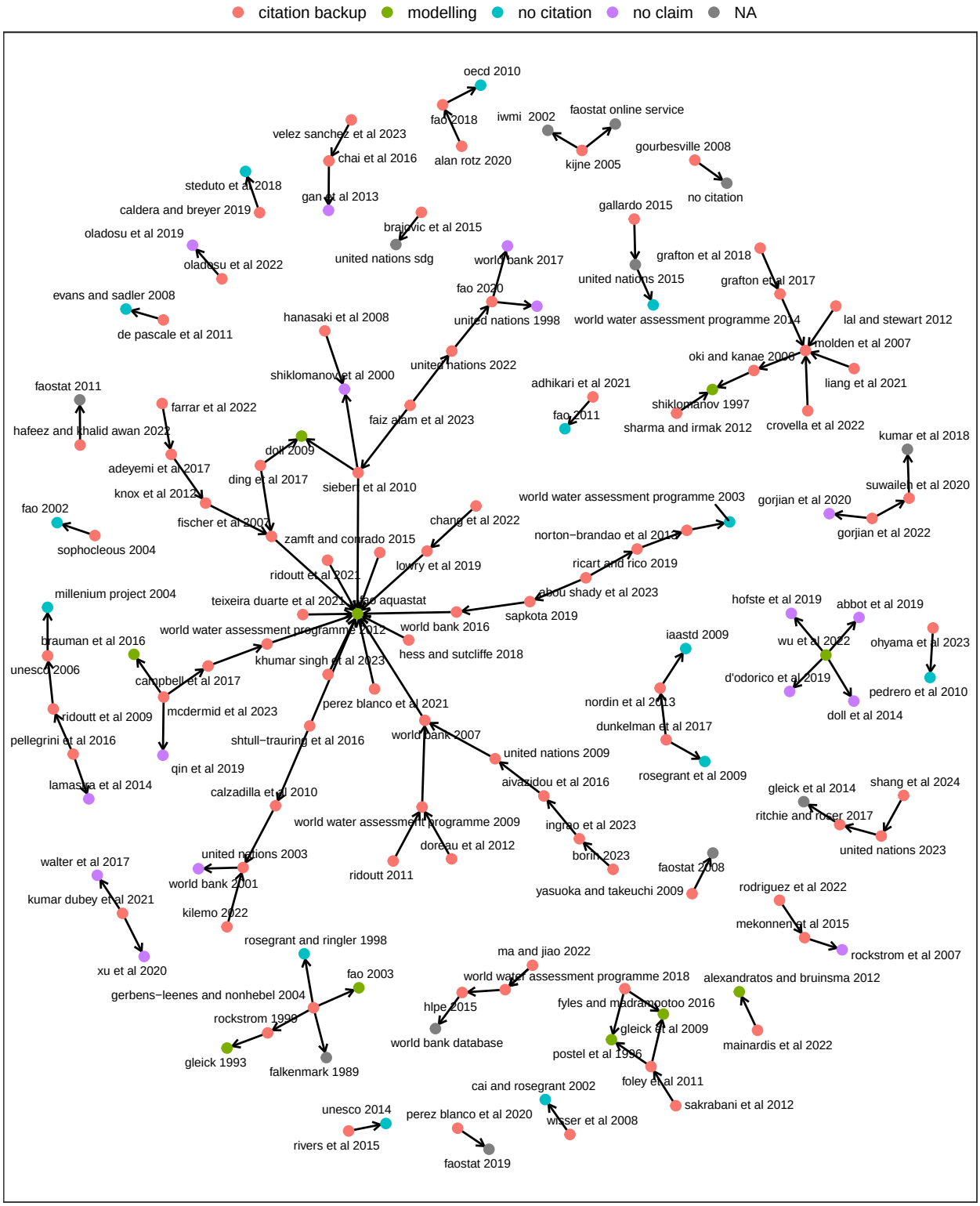
```
network_metrics[order(-closeness)][1:5]
```

```
##                          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")
```

```
## 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.
```


citation backup
modelling
no citation
no claim
NA
oecd 2010
fao 2018
iwmi 2002
faostat online service
kijne 2005
alan rotz 2020
velez sanchez et al 2023
chai et al 2016
gourbesville 2008
no citation
steduto et al 2018
gan et al 2013
caldera and breyer 2019
gallardo 2015
brajovic et al 2015
oladosu et al 2019
oladosu et al 2022
united nations sdg
world bank 2017
grafton et al 2018
united nations 2015
grafton et al 2017
fao 2020
evans and sadler 2008
de pascale et al 2011
united nations 1998
world water assessment programme 2014
lal and stewart 2012
hanasaki et al 2008
molden et al 2007
united nations 2022
oki and kanae 2006
shiklomanov et al 2000
adhikari et al 2021
liang et al 2021
faostat 2011
farrar et al 2022
shiklomanov 1997
fao 2011
sharma and irmak 2012
crovella et al 2022
hafeez and khalid awan 2022
faiz alam et al 2023
kumar et al 2018
doll 2009
adeyemi et al 2017
ding et al 2017
siebert et al 2010
suwailem et al 2020
knox et al 2012
world water assessment programme 2003
gorjian et al 2020
fao 2002
fischer et al 2007
chang et al 2022
norton−brandao et al 2013
gorjian et al 2022
sophocleous 2004
zamft and conrado 2015
ricart and rico 2019
lowry et al 2019
ridoutt et al 2021
millenium project 2004
abou shady et al 2023
hofste et al 2019
abbot et al 2019
teixeira duarte et al 2021
fao aquastat
sapkota 2019
brauman et al 2016
world water assessment programme 2012
world bank 2016
iaastd 2009
wu et al 2022
ohyama et al 2023
unesco 2006
khumar singh et al 2023
hess and sutcliffe 2018
campbell et al 2017
d'odorico et al 2019
nordin et al 2013
pedrero et al 2010
ridoutt et al 2009
mcdermid et al 2023
perez blanco et al 2021
doll et al 2014
dunkelman et al 2017
pellegrini et al 2016
shtull−trauring et al 2016
world bank 2007
united nations 2009
rosegrant et al 2009
qin et al 2019
lamastra et al 2014
aivazidou et al 2016
gleick et al 2014
shang et al 2024
calzadilla et al 2010
ritchie and roser 2017
world water assessment programme 2009
ingrao et al 2023
united nations 2023
doreau et al 2012
walter et al 2017
united nations 2003
borin 2023
faostat 2008
world bank 2001
ridoutt 2011
yasuoka and takeuchi 2009
rodriguez et al 2022
kumar dubey et al 2021
kilemo 2022
mekonnen et al 2015
rockstrom et al 2007
rosegrant and ringler 1998
ma and jiao 2022
xu et al 2020
fao 2003
world water assessment programme 2018
alexandratos and bruinsma 2012
gerbens−leenes and nonhebel 2004
hlpe 2015
fyles and madramootoo 2016
rockstrom 1999
world bank database
gleick et al 2009
mainardis et al 2022
gleick 1993
falkenmark 1989
postel et al 1996
foley et al 2011
cai and rosegrant 2002
sakrabani et al 2012
unesco 2014
perez blanco et al 2020
wisser et al 2008
rivers et al 2015
faostat 2019

5 Session information

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

sessionInfo()
```

```
## R version 4.3.2 (2023-10-31)
## 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] benchmarkme_1.0.8  tidygraph_1.3.0    cowplot_1.1.1      ggraph_2.1.0
##  [5] igraph_1.6.0       bibliometrix_4.0.1 lubridate_1.9.2    forcats_1.0.0
##  [9] stringr_1.5.1      dplyr_1.1.4        purrr_1.0.2        readr_2.1.4
## [13] tidyr_1.3.0        tibble_3.2.1       ggplot2_3.4.4      tidyverse_2.0.0
## [17] 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_4.3.2         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_2.1.4
##  [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_1.6-1.1
##  [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_0.21-9         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] scales_1.3.0           sensobol_1.1.4          xtable_1.8-4
##  [70] leaps_3.1              glue_1.7.0              tikzDevice_0.12.4
##  [73] emmeans_1.8.5          scatterplot3d_0.3-43    lazyeval_0.2.2
##  [76] tools_4.3.2            tokenizers_0.3.0        mvtnorm_1.1-3
##  [79] graphlayouts_1.0.2     XML_3.99-0.14           grid_4.3.2
##  [82] rbibutils_2.2.16       rscopus_0.6.6           colorspace_2.1-0
##  [85] dimensionsR_0.0.3      ggforce_0.4.1           bibliometrixData_0.3.0
##  [88] cli_3.6.2              fansi_1.0.6             viridisLite_0.4.2
##  [91] gtable_0.3.4           digest_0.6.34           ggrepel_0.9.5
##  [94] FactoMineR_2.8         htmlwidgets_1.6.2       farver_2.1.1
##  [97] htmltools_0.5.5        factoextra_1.0.7        lifecycle_1.0.4
## [100] httr_1.4.5             multcompView_0.1-9      mime_0.12
## [103] bit64_4.0.5            MASS_7.3-60
```

```
## 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
```