Irrigated areas drive irrigation water withdrawals

R code

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1 Presentation

This document presents the workflow of the paper "Irrigated areas drive irrigation water withdrawals," by A. Puy, E. Borgonovo, S. Lo Piano, S. Levin and A. Saltelli. The abstract is the following:

A sustainable management of global freshwater resources requires producing reliable estimates of the water demanded by irrigated agriculture. This has been attempted by FAO through country surveys and censuses, or through Global Models (GM), which compute irrigation water withdrawals with sub-models on crop types and calendars, evapotranspiration, irrigation efficiencies, weather data and irrigated areas, among others. Here we demonstrate that these strategies err on the side of excess complexity, as the values reported by FAO and outputted by GM are largely driven by irrigated areas only. Modeling irrigation water withdrawals as a function of irrigated areas yields almost the same results in a much cheaper and parsimonious way, while permitting the exploration of all model uncertainties. Our work offers a more robust and transparent approach to compute one of the most important indicators guiding our policies on water security worldwide.

Once all datasets required for the analysis have been acquired from the appropriate sources, the results of the paper should be fully reproducible in any personal computer. Questions about the code or the computational design should be addressed to A. Puy (apuy@princeton.edu; arnald.puy@pm.me).

1.1 Preliminary functions

We start by creating a function to load all required libraries for the analysis in one go. We also set a checkpoint to ensure that our code is fully reproducible for anyone anytime. Finally, we design a short theme function for all the plots that will be produced in the analysis.

```
# LOAD PACKAGES ------------------------------------------------------------

# Function to read in all required packages in one go:
loadPackages <- function(x) {
  for(i in x) {
    if(!require(i, character.only = TRUE)) {
      install.packages(i, dependencies = TRUE)
      library(i, character.only = TRUE)
    }
  }
}

loadPackages(c("data.table", "sensobol", "ncdf4",
               "rworldmap", "sp", "countrycode",
               "IDPmisc", "boot", "parallel", "scales",
               "MASS", "doParallel", "complmrob",
               "mvoutlier", "sandwich", "lmtest", "mice",
               "ggridges", "broom", "naniar", "cowplot",
               "benchmarkme", "tidyverse", "grid", "gridExtra",
               "robustbase", "rsample"))
```

```
# SET CHECKPOINT ------------------------------------------------------------

dir.create(".checkpoint")

library("checkpoint")

checkpoint("2021-04-07",
           R.version ="4.0.3",
           checkpointLocation = getwd())

# CUSTOM FUNCTION TO DEFINE THE PLOT THEMES ---------------------------------

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))
}
```

2 Load datasets

Here we retrieve the datasets needed to conduct the analysis at the national level. We collect irrigation water withdrawal data outputted by eight Global Hydrological Models (GHM) (PCR-GLOBWB, H08, LPJmL, WaterGap, MPI-HM, DBHM), one Land Surface Model (LSM) (VIC) and one Land Earth Surface Model (LESM) (CLM45). We also retrieve irrigation water withdrawal values reported by two FAO-based datasets, Aquastat and Aquastat without missing values (Liu et al. 2016).

For PCR-GLOBWB, H08, LPMjL and WaterGap we use the `.nc` files prepared by Huang et al. (2018). For DBHM, MPI-HM, CLM45 and VIC we use the `.nc` files available in the Inter-Sectoral Impact Model Intercomparison Project (ISIMIP) webpage, https://www.isimip.org. For the FAO-based datasets, we use the irrigation water withdrawal values reported by Aquastat (Frenken and Gillet 2012) and the dataset by Liu et al. (2016), which is similar to Aquastat's but without missing values.

2.1 Define loading functions

Here we define some functions that will be applied later on to read in and clean the datasets just mentioned.

`country_code` unifies the country names across datasets and provides each country with its United Nations code to avoid any confusion during the processing of the data.

`coords2country` transforms the coordinates of the .nc files to the appropriate country names.

`get_nc_data` is tailored to specifically extract irrigation water withdrawal data at the country level

from the datasets compiled by Huang et al. (2018). Note that there are calls to `country_code` and `coors2country` inside the function to transform each longitude and latitude value to a country name.

`open_nc_files` is tailored to specifically extract irrigation water withdrawal data at the country level from the datasets retrieved from ISIMIP. Again, it includes calls to `country_code` and `coors2country`.

```
# CREATE FUNCTIONS ------------------------------------------------------------

# Function to obtain UN code, Continent and Country names
country_code <- function(dt) {
  dt[, `:=` (Code = countrycode(dt[, Country],
                                origin = "country.name",
                                destination = "un"),
             Continent = countrycode(dt[, Country],
                                     origin = "country.name",
                                     destination = "continent"))]
  dt[, Country:= countrycode(dt[, Code],
                             origin = "un",
                             destination = "country.name")]
  setcolorder(dt, c("Country", "Continent", "Code", "Water.Withdrawn"))
  return(dt)
}

## Function to transform longitude and latitude to country.
# It is borrowed from Andy:
# https://stackoverflow.com/questions/14334970/convert-latitude-and-longitude-coordinates-to-c
coords2country = function(points) {
  countriesSP <- rworldmap::getMap(resolution = 'low')
  pointsSP = sp::SpatialPoints(points, proj4string=CRS(proj4string(countriesSP)))
  indices = sp::over(pointsSP, countriesSP)
  indices$ADMIN
  #indices$ISO3 # returns the ISO3 code
  #indices$continent   # returns the continent (6 continent model)
  #indices$REGION   # returns the continent (7 continent model)
}

# Function to load and extract data from .nc files produced
# by Huang et al. 2018
get_nc_data <- function(nc_file) {
  nc <- nc_open(nc_file)
  ww <- ncvar_get(nc, "withd_irr")
  lon <- ncvar_get(nc, "lon")
  lat <- ncvar_get(nc, "lat")
  out <- lapply(selected.years, function(x) {
    water <- rowSums(ww[, vec[[x]]])
    ww.df <- data.frame(cbind(lon, lat, water))
    ww.df <- data.frame(cbind(lon, lat, water))
```

```
    countries <- coords2country(ww.df[1:nrow(ww.df), 1:2])
    df <- cbind(countries, ww.df)
    setDT(df)
    final <- df[, .(Water.Withdrawn = sum(water)), countries]
    setnames(final, "countries", "Country")
    country_code(final)
    out <- na.omit(final[order(Continent)])
    out[, Water.Withdrawn:= Water.Withdrawn / 1000] # From mm to m
  })
  names(out) <- selected.years
  return(out)
}

# Function to load and extract data from .nc files from ISIMIP
open_nc_files <- function(file, dname, selected.years, vec) {
  ncin <- nc_open(file)
  # get longitude, latitude, time
  lon <- ncvar_get(ncin, "lon")
  lat <- ncvar_get(ncin, "lat")
  # Get variable
  tmp_array <- ncvar_get(ncin, dname)
  m <- lapply(selected.years, function(x) vec[[x]])

  out <- lapply(m, function(x) {
    tmp_slice <- lapply(x, function(y) tmp_array[, , y])
    # create dataframe -- reshape data
    # matrix (nlon*nlat rows by 2 cols) of lons and lats
    lonlat <- as.matrix(expand.grid(lon,lat))
    # vector of `tmp` values
    tmp_vec <- lapply(tmp_slice, function(x) as.vector(x))
    # create dataframe and add names
    tmp_df01 <- lapply(tmp_vec, function(x) data.frame(cbind(lonlat, x)))
    names(tmp_df01) <- x
    da <- lapply(tmp_df01, data.table) %>%
      rbindlist(., idcol = "month") %>%
      na.omit()
    # Convert coordinates to country
    Country <- coords2country(da[1:nrow(da), 2:3])
    df <- cbind(Country, da)
    setDT(df)
    out <- na.omit(df)[, .(Water.Withdrawn = sum(x)), Country]
    out[, Water.Withdrawn:= Water.Withdrawn * 10000]
    out[, Continent:= countrycode(out[, Country],
                                  origin = "country.name",
                                  destination = "continent")] %>%
      .[, Code:= countrycode(out[, Country],
                             origin = "country.name",
```

```
                                destination = "un")] %>%
      .[, Country:= countrycode(out[, Code],
                                origin = "un",
                                destination = "country.name")] %>%
      .[!Continent == "Oceania"]
    setcolorder(out, c("Country", "Continent", "Code", "Water.Withdrawn"))
  })
  return(out)
}
```

2.2 Load Huang et al. datasets

```
# READ IN GHM DATASETS ------------------------------------------------------

# Read in Huang et al. datasets ---------------------------------

# Define vector with the months and the years
vecs <- 1:((2010 - 1970) * 12)
vec <- split(vecs, ceiling(seq_along(vecs) / 12))
names(vec) <- 1971:2010
selected.years <- c("1971", "1980", "1990", "2000", "2005")

# Vector with the files
names_nc_files <- c("withd_irr_lpjml.nc", "withd_irr_pcrglobwb.nc",
                    "withd_irr_h08.nc", "withd_irr_watergap.nc")

# Read in datasets
huang.dt <- mclapply(names_nc_files, function(x) get_nc_data(x), mc.cores = detectCores() * 0.
names.huang <- c("LPJmL", "PCR-GLOBWB", "H08", "WaterGap")
names(huang.dt) <- names.huang

# ISIMIP datasets -----------------------------------------------

files <- list("dbh_wfdei_nobc_hist_varsoc_co2_airrww_global_monthly_1971_2010.nc",
              "mpi-hm_miroc5_ewembi_picontrol_histsoc_co2_airrww_global_monthly_1861_2005.nc",
              "vic_wfdei_nobc_hist_pressoc_co2_airrww_global_monthly_1971_2010.nc",
              "clm45_gfdl-esm2m_ewembi_historical_2005soc_co2_pirrww_global_monthly_1861_2005.

isimip.dt <- mclapply(files, function(x) {
  if(x == "mpi-hm_miroc5_ewembi_picontrol_histsoc_co2_airrww_global_monthly_1861_2005.nc") {
    vecs <- 1:((2005 - 1860) * 12)
    vec <- split(vecs, ceiling(seq_along(vecs) / 12))
    names(vec) <- 1861:2005
    dname <- "airrww"
  } else if (x == "clm45_gfdl-esm2m_ewembi_historical_2005soc_co2_pirrww_global_monthly_1861_2
    vecs <- 1:((2005 - 1860) * 12)
    vec <- split(vecs, ceiling(seq_along(vecs) / 12))
```

```
    names(vec) <- 1861:2005
    dname <- "pirrww"
  } else {
    vecs <- 1:((2010 - 1970) * 12)
    vec <- split(vecs, ceiling(seq_along(vecs) / 12))
    names(vec) <- 1971:2010
    dname <- "airrww"
  }
  open_nc_files(file = x, dname = dname, selected.years = selected.years,
                vec = vec)
},
mc.cores = detectCores() * 0.75)

names.isimip <- c("DBHM", "MPI-HM", "VIC", "CLM45")
names(isimip.dt) <- names.isimip

for(i in names(isimip.dt)) {
  names(isimip.dt[[i]]) <- selected.years
}
```

2.3 Load historic FAO-GMIA

```
# READ IN HISTORIC FAO-GMIA ----------------------------------------------------

gmia.hist <- fread("FAO_GMIA_historic.csv")
gmia.hist <- gmia.hist[, Continent:= countrycode(gmia.hist[, Country],
                                                 origin = "country.name",
                                                 destination = "continent")] %>%
  .[, Code:= countrycode(gmia.hist[, Country],
                         origin = "country.name",
                         destination = "un")] %>%
  .[, Country:= countrycode(gmia.hist[, Code],
                            origin = "un",
                            destination = "country.name")] %>%
  .[!Continent == "Oceania"]
```

```
## Warning in countrycode(gmia.hist[, Country], origin = "country.name", destination = "contine
```

```
## Warning in countrycode(gmia.hist[, Country], origin = "country.name", destination = "un"): S
```

```
# Create list with the columns selected

dt.tmp <- lapply(c("AEI_1970", paste("AEI_", c(seq(1980, 2000, 10), 2005), sep = "")), functio
  gmia.hist[, .SD, .SDcols = c("Country", "Code", "Continent", x)])
names(dt.tmp) <- selected.years

# MERGE GHM AND HISTORIC FAO-GMIA ----------------------------------------------
```

```
all.ghm <- c(huang.dt, isimip.dt)
ghm.dt <- lapply(names(all.ghm), function(x)
  lapply(selected.years, function(y)
    all.ghm[[x]][[y]][, merge(.SD, dt.tmp[[y]], by = c("Country", "Code", "Continent"),
                              all.y = TRUE)])) %>%
  lapply(., function(x) lapply(x, function(y) setnames(y, 5, "AEI") %>%
                                 na.omit()))

names(ghm.dt) <- c(names.huang, names.isimip)

for(i in names(ghm.dt)) {
  names(ghm.dt[[i]]) <- selected.years
}
```

2.4 Long-term trends between irrigated areas and irrigation water withdrawals

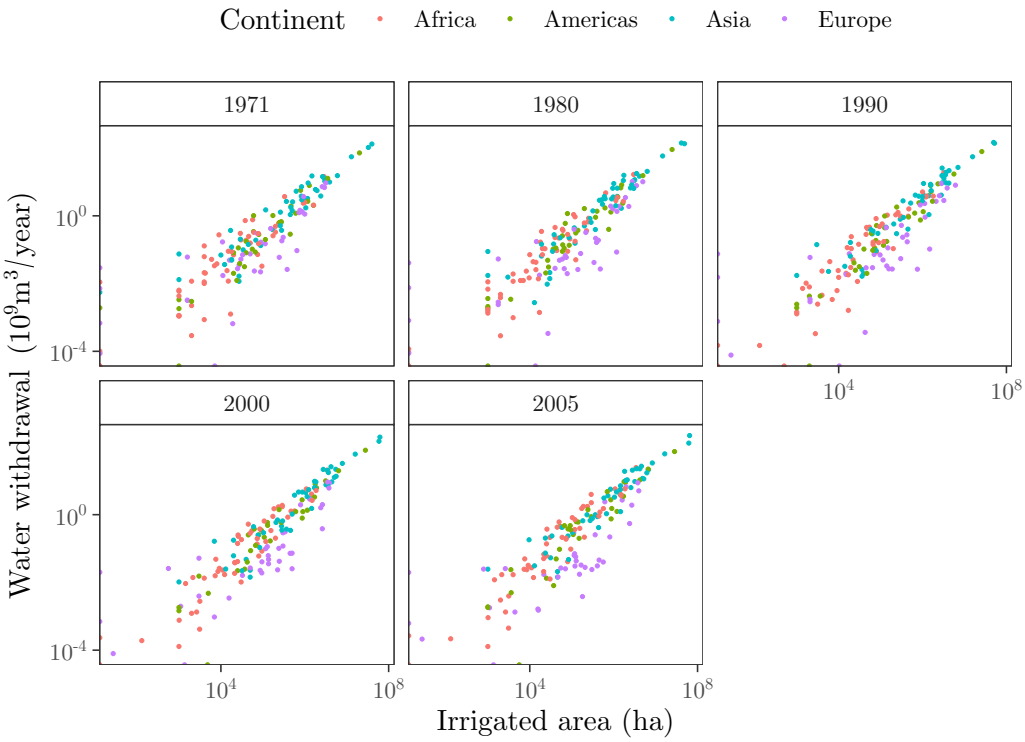
```
# PLOT GHM WATER WITHDRAWALS THROUGH TIME (1970-2005) -----------------------------

tmp <- lapply(ghm.dt, function(x) rbindlist(x, idcol = "Year"))

# Plot
gg <- list()
for(i in 1:length(tmp)) {
  gg[[i]] <- ggplot(tmp[[i]], aes(AEI, Water.Withdrawn,
                                  color = Continent)) +
    geom_point(size = 0.4) +
    scale_x_log10(breaks = trans_breaks("log10", function(x) 10 ^ (2 * x)),
                  labels = trans_format("log10", math_format(10 ^ .x))) +
    scale_y_log10(breaks = trans_breaks("log10", function(x) 10 ^ (2 * x)),
                  labels = trans_format("log10", math_format(10 ^ .x))) +
    labs(x = "Irrigated area (ha)",
         y = expression(paste("Water withdrawal ", " ", "(", 10^9, m^3/year, "", ")"))) +
    facet_wrap(~Year) +
    theme_AP() +
    theme(legend.position = "top",
          strip.background = element_rect(fill = "white")) +
    ggtitle(names(tmp[i]))
}

gg
```

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

```
## Warning: Transformation introduced infinite values in continuous x-axis
```

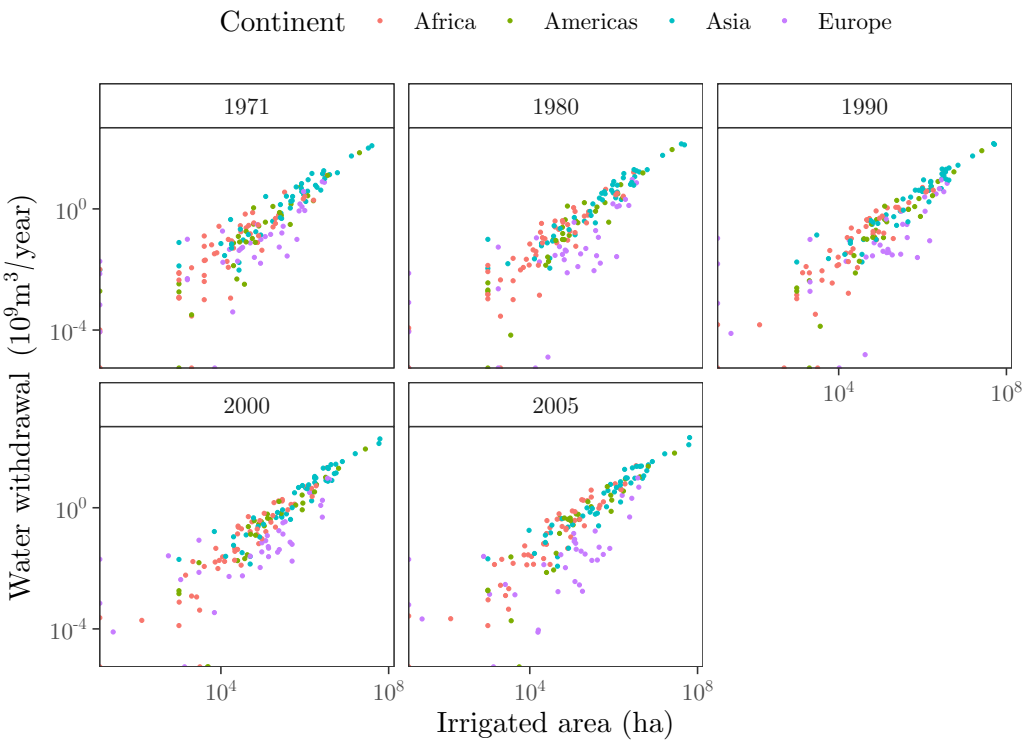
```
## Warning: Transformation introduced infinite values in continuous y-axis
```

LPJmL



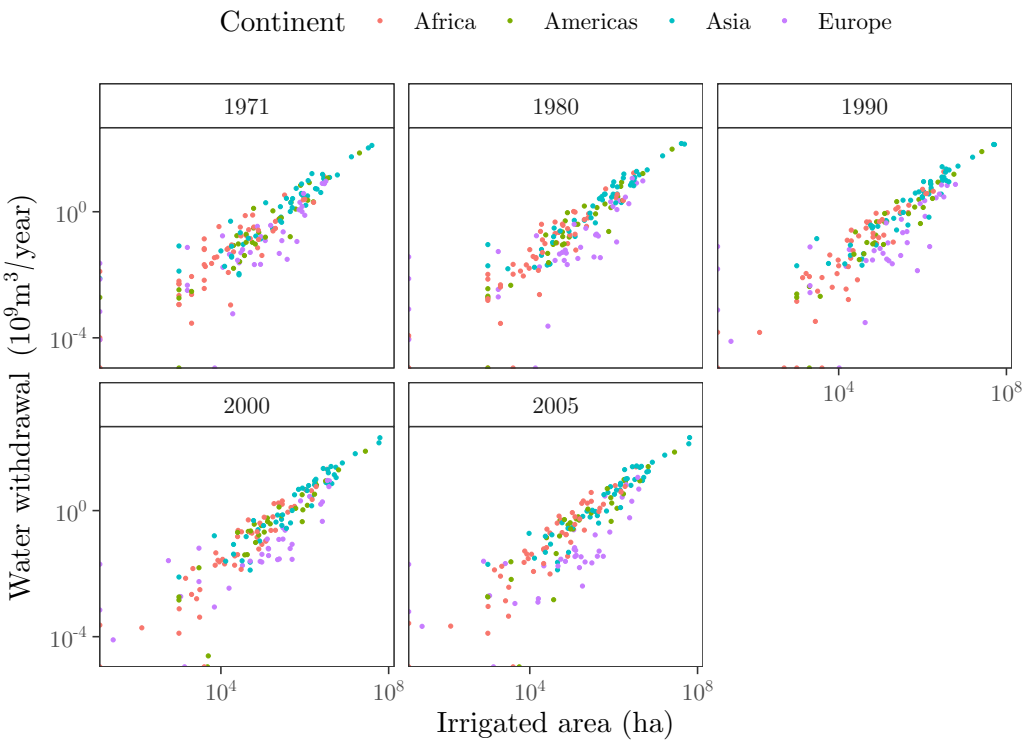

```
##
## [[2]]

## Warning: Transformation introduced infinite values in continuous x-axis

## Warning: Transformation introduced infinite values in continuous y-axis
```

PCR-GLOBWB




```
##
## [[3]]

## Warning: Transformation introduced infinite values in continuous x-axis

## Warning: Transformation introduced infinite values in continuous y-axis
```

H08

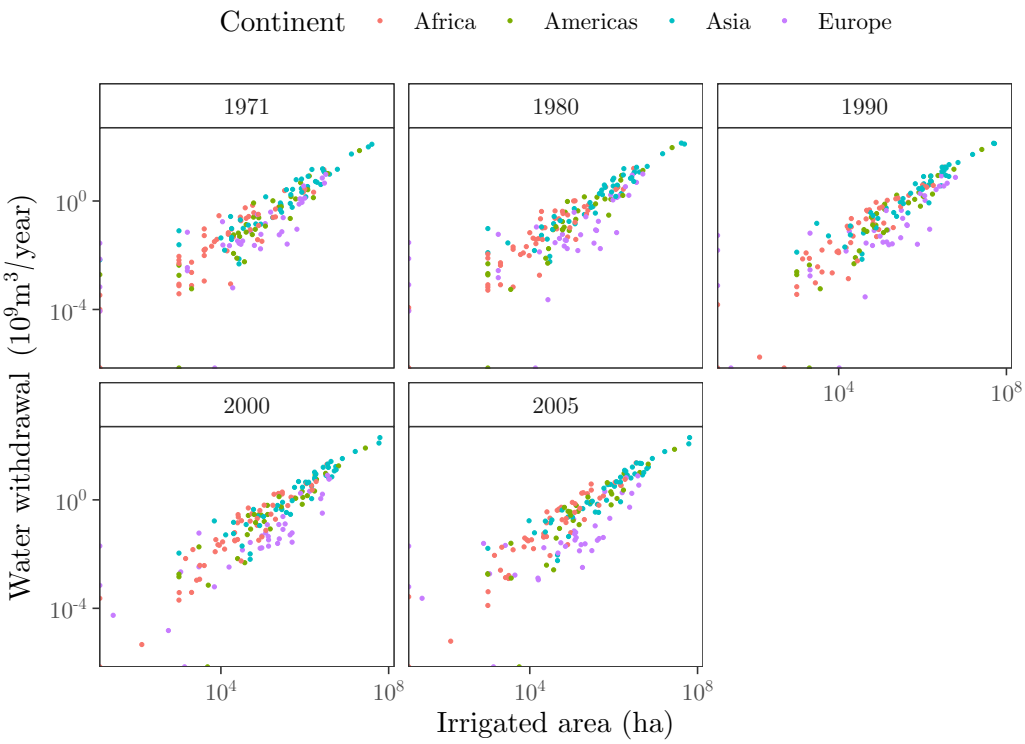



```
##
## [[4]]
```

```
## Warning: Transformation introduced infinite values in continuous x-axis
```

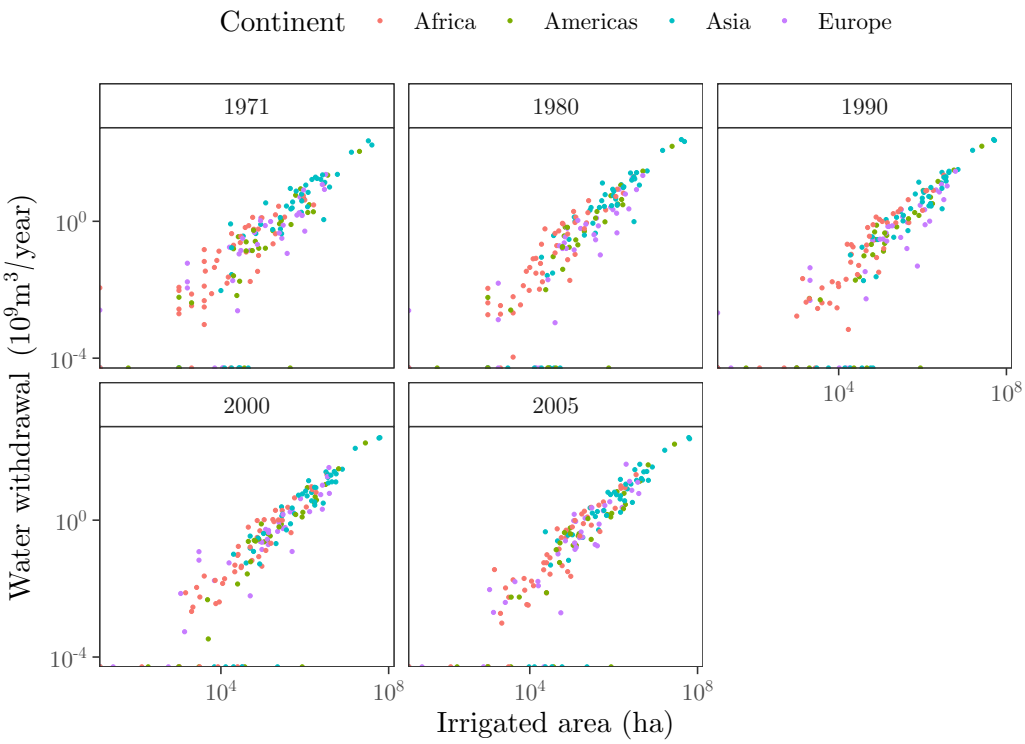
```
## Warning: Transformation introduced infinite values in continuous y-axis
```

WaterGap



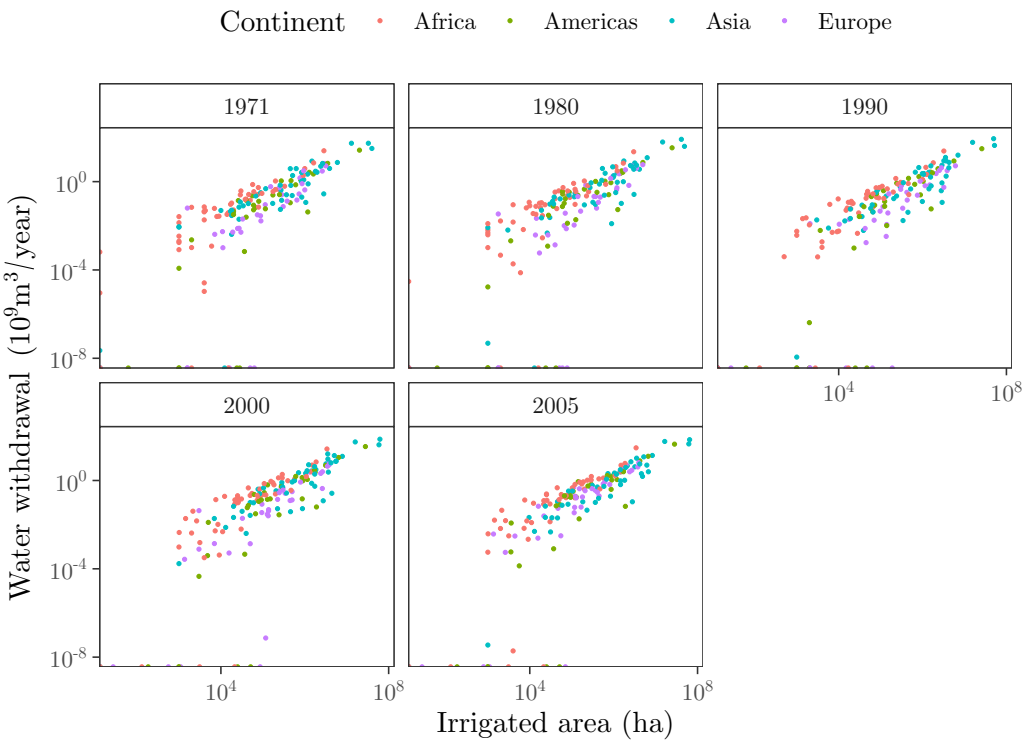

```
##
## [[5]]

## Warning: Transformation introduced infinite values in continuous x-axis

## Warning: Transformation introduced infinite values in continuous y-axis
```

DBHM



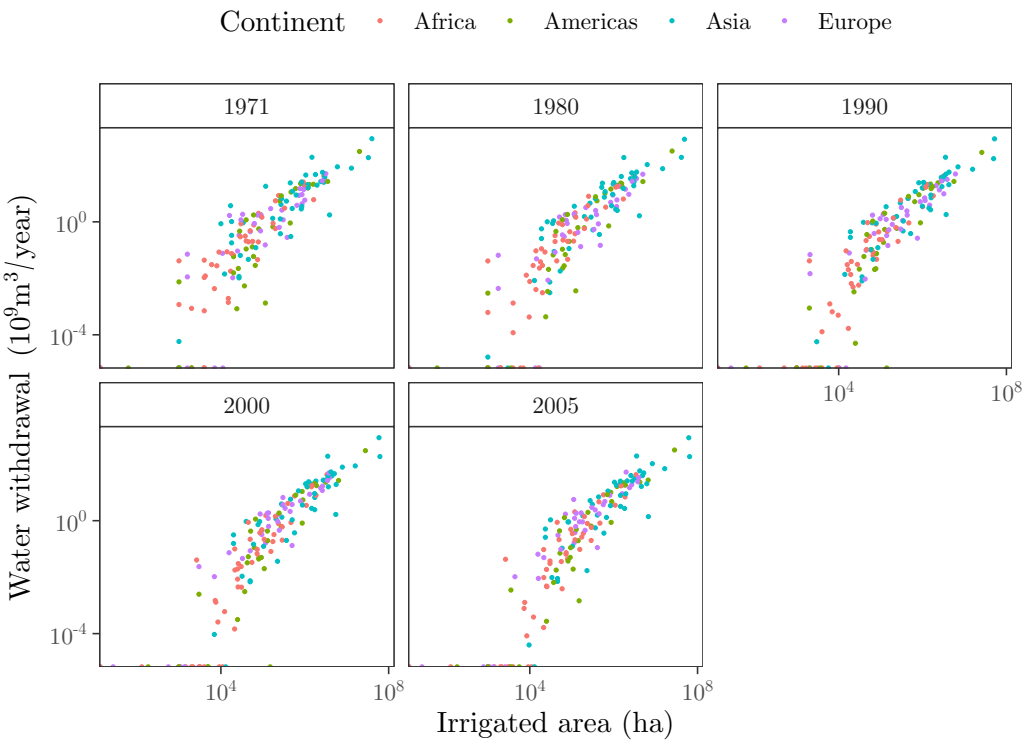

```
##
## [[6]]

## Warning: Transformation introduced infinite values in continuous x-axis

## Warning: Transformation introduced infinite values in continuous y-axis
```

MPI-HM



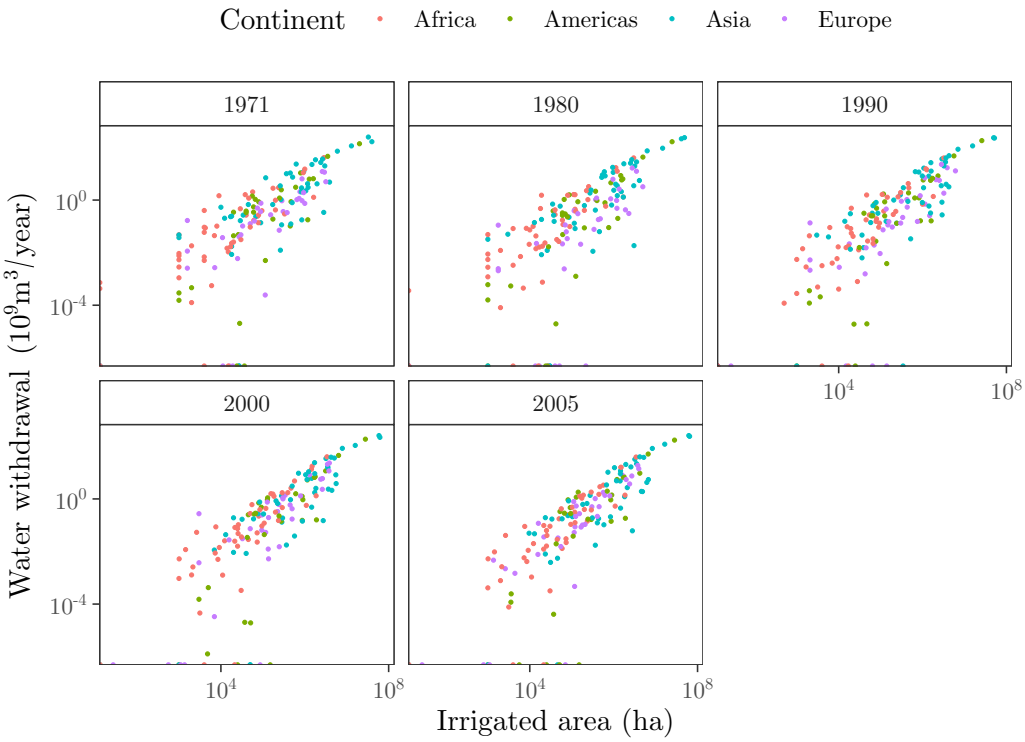

```
##
## [[7]]

## Warning: Transformation introduced infinite values in continuous x-axis

## Warning: Transformation introduced infinite values in continuous y-axis
```

VIC




```
##
## [[8]]

## Warning: Transformation introduced infinite values in continuous x-axis

## Warning: Transformation introduced infinite values in continuous y-axis
```

CLM45




```
# ANALYZE LONG-TERM HISTORICAL TRENDS ------------------------------------------

files <- list("pcr-globwb_gfdl-esm2m_ewembi_historical_histsoc_co2_airrww_global_monthly_1861_
              "mpi-hm_gfdl-esm2m_ewembi_historical_histsoc_co2_airrww_global_monthly_1861_2005
              "lpjml_miroc5_ewembi_historical_histsoc_co2_airrww_global_monthly_1861_2005.nc",
              "h08_miroc5_ewembi_historical_histsoc_co2_airrww_global_monthly_1861_2005.nc")

vecs <- 1:((2005 - 1860) * 12)
vec <- split(vecs, ceiling(seq_along(vecs) / 12))
names(vec) <- 1861:2005
dname <- "airrww"
selected.years <- as.character(seq(1900, 2000, 10))

isimip.hist <- mclapply(files, function(x)
  open_nc_files(file = x, dname = dname, selected.years = selected.years,
                vec = vec), mc.cores = detectCores() * 0.75)

names.isimip.hist <- c("PCR-GLOBWB", "MPI-HM", "LPJmL", "H08")
names(isimip.hist) <- names.isimip.hist

for(i in names(isimip.hist)) {
  names(isimip.hist[[i]]) <- selected.years
}

# Create list with the columns selected
```

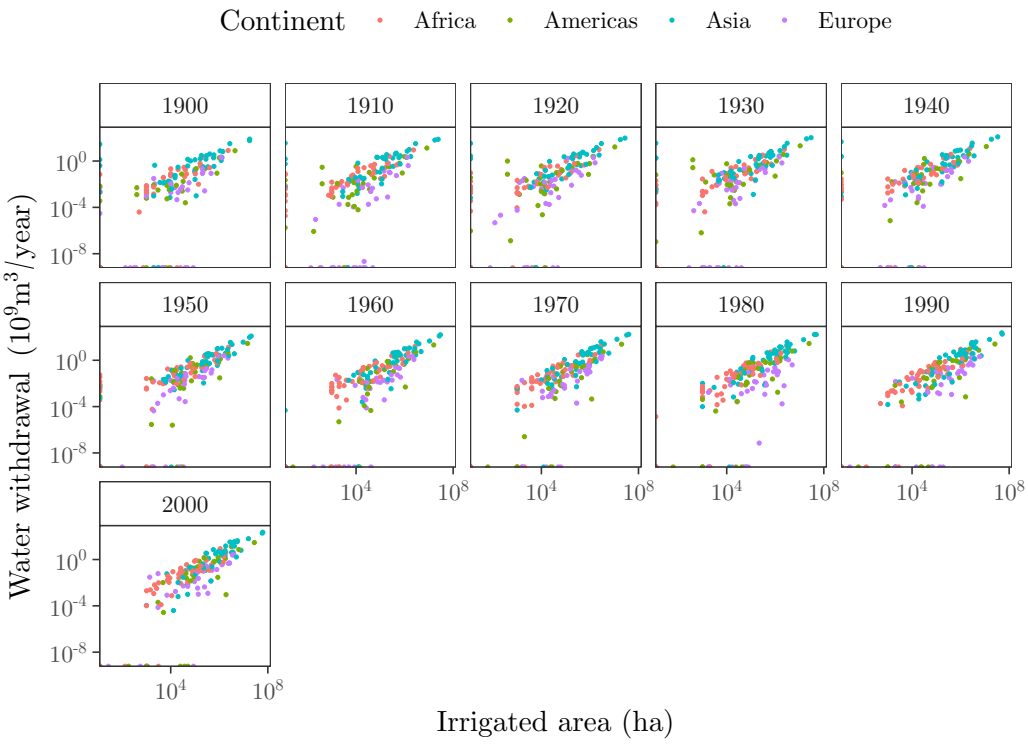
```
dt.tmp <- lapply(paste("AEI_", seq(1900, 2000, 10), sep = ""), function(x)
  gmia.hist[, .SD, .SDcols = c("Country", "Code", "Continent", x)])
names(dt.tmp) <- selected.years


out <- lapply(names(isimip.hist), function(x)
  lapply(selected.years, function(y)
    isimip.hist[[x]][[y]][, merge(.SD, dt.tmp[[y]], by = c("Country", "Code", "Continent"),
                                  all.y = TRUE)])) %>%
  lapply(., function(x) lapply(x, function(y) setnames(y, 5, "AEI") %>%
                                 na.omit()))

names(out) <- c("PCR-GLOBWB", "MPI-HM", "LPJmL", "H08")

for(i in names(out)) {
  names(out[[i]]) <- selected.years
}
```

```
# PLOT GHM WATER WITHDRAWALS THROUGH TIME (1900-1960) -----------------------------

tmp <- lapply(out, function(x) rbindlist(x, idcol = "Year")) %>%
  na.omit()

# Plot
gg <- list()
for(i in 1:length(tmp)) {
  gg[[i]] <- ggplot(tmp[[i]], aes(AEI, Water.Withdrawn,
                                  color = Continent)) +
    geom_point(size = 0.4) +
    scale_x_log10(breaks = trans_breaks("log10", function(x) 10 ^ (2 * x)),
                  labels = trans_format("log10", math_format(10 ^ .x))) +
    scale_y_log10(breaks = trans_breaks("log10", function(x) 10 ^ (2 * x)),
                  labels = trans_format("log10", math_format(10 ^ .x))) +
    labs(x = "Irrigated area (ha)",
         y = expression(paste("Water withdrawal ", " ", "(", 10^9, m^3/year, "", ")"))) +
    facet_wrap(~Year, ncol = 5) +
    theme_AP() +
    theme(legend.position = "top",
          strip.background = element_rect(fill = "white")) +
    ggtitle(names(tmp[i]))
}

gg
```

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

```
## Warning: Transformation introduced infinite values in continuous x-axis
```

```
## Warning: Transformation introduced infinite values in continuous y-axis
```

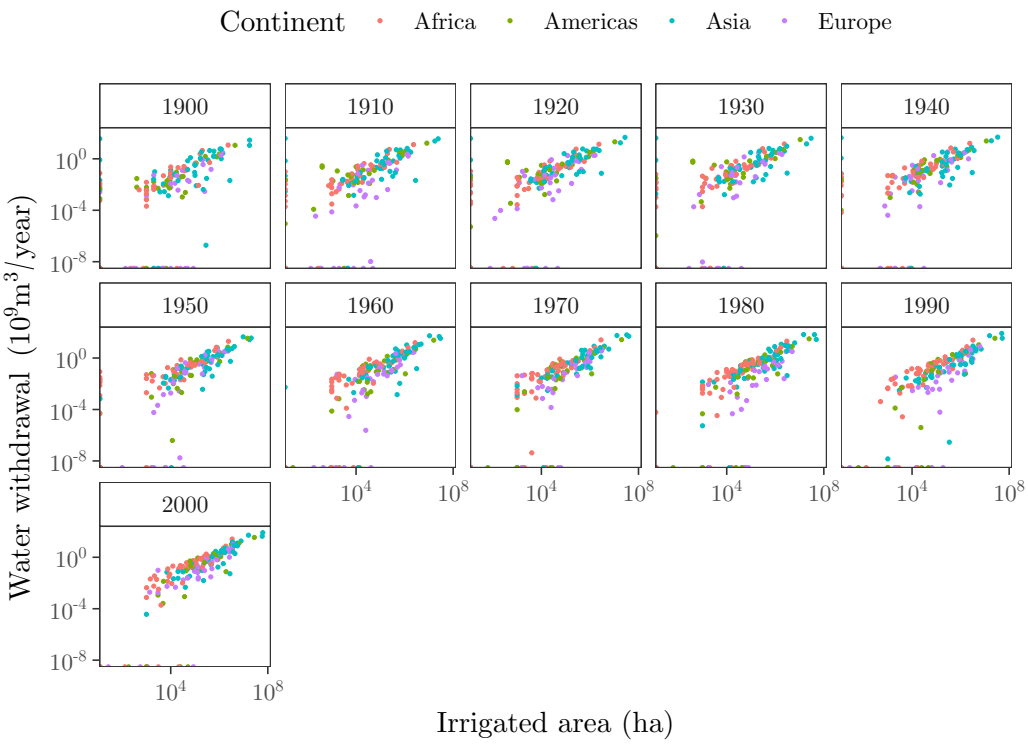



```
##
## [[2]]
```

```
## Warning: Transformation introduced infinite values in continuous x-axis
```

```
## Warning: Transformation introduced infinite values in continuous y-axis
```

MPI-HM

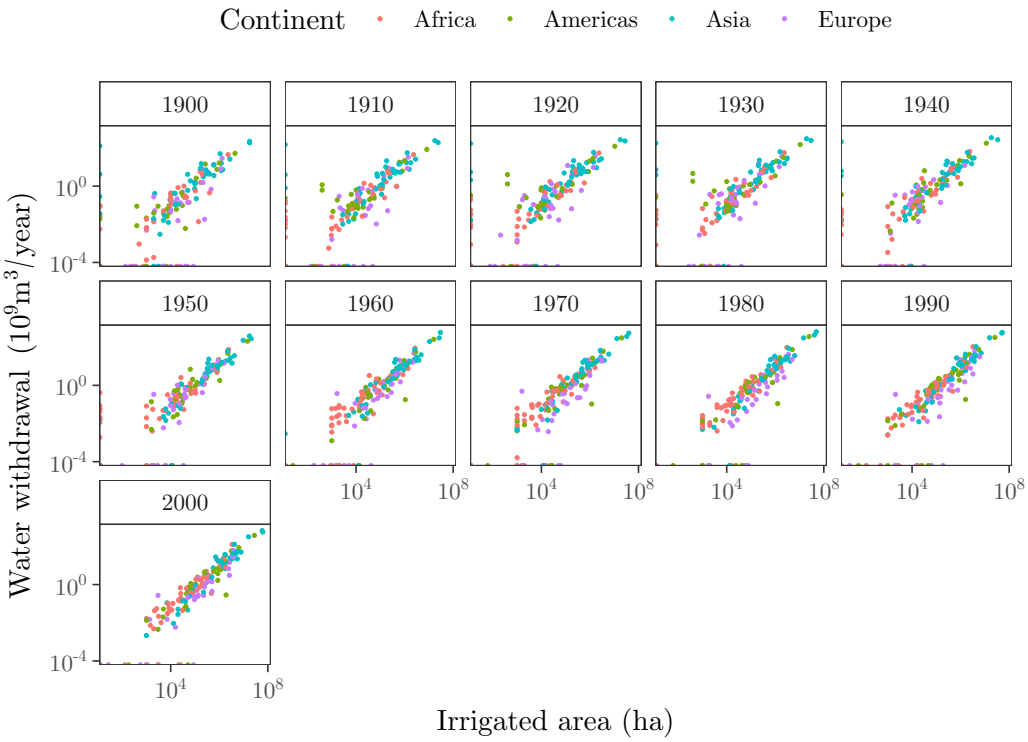



```
##
## [[3]]
```

```
## Warning: Transformation introduced infinite values in continuous x-axis
```

```
## Warning: Transformation introduced infinite values in continuous y-axis
```

LPJmL

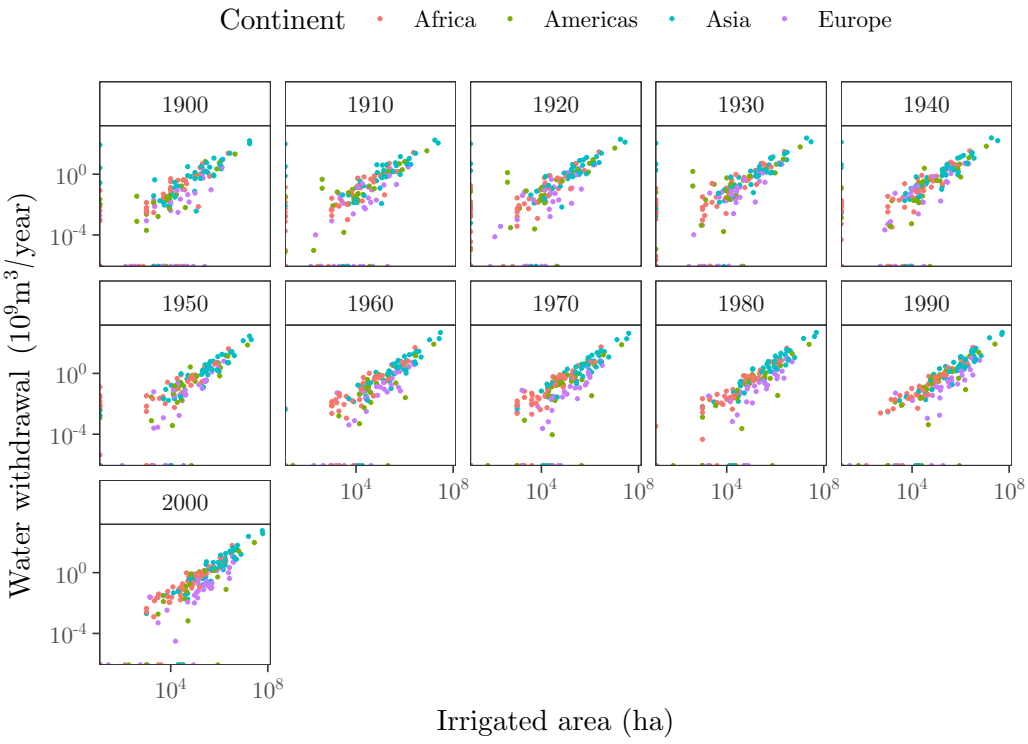



```
##
## [[4]]
```

```
## Warning: Transformation introduced infinite values in continuous x-axis
```

```
## Warning: Transformation introduced infinite values in continuous y-axis
```

H08



2.5 Plot trend between irrigated areas and irrigation water withdrawals

```
# READ IN DATASETS ON IRRIGATION WATER WITHDRAWAL AND MEIER DATASET --------------

# Define vector to reorder columns
cols_order <- c("Continent", "Country", "Code", "Water.Dataset", "Water.Withdrawn")

# FAO data (Table 4) ----------------------------
# UNIT IS KM3/YEAR
table4.tmp <- fread("table_4.csv", skip = 3, nrows = 167) %>%
  .[, .(Country, Year, Water.withdrawal)] %>%
  setnames(., "Water.withdrawal", "Water.Withdrawn")

# Extract the selected years
table4.dt <- country_code(table4.tmp[Year %in% 1999:2012])[
  , Water.Dataset:= "Aquastat"][
    , Year:= NULL] %>%
  country_code(.) %>%
  setcolorder(., cols_order)

# Liu et al. dataset ----------------------------
#UNIT IS 10^9 m3/year = km3/year
liu.dt <- fread("liu.csv")[, .(country, irr)] %>%
  setnames(., c("country", "irr"), c("Country", "Water.Withdrawn")) %>%
```

```
  country_code(.) %>%
  .[, Water.Dataset:= "Liu et al. 2016"] %>%
  country_code(.) %>%
  setcolorder(., cols_order)

# READ IN FAO-GMIA BY MEIER  ----------------------------------------------------

meier.dt <- fread("meier.csv") %>%
  setnames(., "Codes", "Code") %>%
  na.omit() %>%
  .[, .(Country, Continent, Code, `FAO-GMIA`)] %>%
  setnames(., "FAO-GMIA", "Irrigated.Area")

# MERGE WITH MEIER ET AL. FAO-GMIA ----------------------------------------------

water.dt <- lapply(all.ghm, function(x) rbindlist(x, idcol = "Year")) %>%
  rbindlist(., idcol = "Water.Dataset") %>%
  .[Year == 2005] %>%
  .[, Year:= NULL] %>%
  setcolorder(., cols_order) %>%
  rbind(., table4.dt, liu.dt)

# Check if there are duplicated countries
water.dt[, .N, .(Country)][N > 10][, Country]
```

```
## [1] "Cyprus"                  "Palestinian Territories"
## [3] NA
```

```
# Compute the mean
water.dt <- water.dt[, .(Water.Withdrawn = mean(Water.Withdrawn)),
                     .(Continent, Country, Code, Water.Dataset)]

# And check again
water.dt[, .N, .(Country)][N > 10][, Country]
```

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

```
full.dt <- water.dt[, merge(.SD, meier.dt, by = c("Country", "Code", "Continent"),
                        all.y = TRUE), Water.Dataset] %>%
  .[!Continent == "Oceania"]

# Show countries with missing values in Water Withdrawal
full.dt[is.na(Water.Withdrawn), ] %>%
  .[, unique(Country), Water.Dataset] %>%
  print(n = Inf)
```

```
##       Water.Dataset                 V1
##  1:           LPJmL            Grenada
##  2:           LPJmL              Malta
```

```
##  3:           LPJmL          Saint Lucia
##  4:           LPJmL           Seychelles
##  5:           LPJmL            Swaziland
##  6:      PCR-GLOBWB            Argentina
##  7:      PCR-GLOBWB               Canada
##  8:      PCR-GLOBWB              Grenada
##  9:      PCR-GLOBWB                Malta
## 10:      PCR-GLOBWB             Portugal
## 11:      PCR-GLOBWB               Russia
## 12:      PCR-GLOBWB          Saint Lucia
## 13:      PCR-GLOBWB           Seychelles
## 14:      PCR-GLOBWB            Swaziland
## 15:             H08              Grenada
## 16:             H08                Malta
## 17:             H08          Saint Lucia
## 18:             H08           Seychelles
## 19:             H08            Swaziland
## 20:        WaterGap              Grenada
## 21:        WaterGap                Malta
## 22:        WaterGap          Saint Lucia
## 23:        WaterGap           Seychelles
## 24:        WaterGap            Swaziland
## 25:            DBHM              Grenada
## 26:            DBHM                Malta
## 27:            DBHM            Mauritius
## 28:            DBHM          Saint Lucia
## 29:            DBHM           Seychelles
## 30:            DBHM            Swaziland
## 31:          MPI-HM              Grenada
## 32:          MPI-HM                Malta
## 33:          MPI-HM          Saint Lucia
## 34:          MPI-HM           Seychelles
## 35:          MPI-HM            Swaziland
## 36:             VIC              Grenada
## 37:             VIC                Malta
## 38:             VIC          Saint Lucia
## 39:             VIC           Seychelles
## 40:             VIC            Swaziland
## 41:           CLM45           Cape Verde
## 42:           CLM45              Grenada
## 43:           CLM45                Malta
## 44:           CLM45          Saint Lucia
## 45:           CLM45           Seychelles
## 46:           CLM45            Swaziland
## 47:        Aquastat               Belize
## 48:        Aquastat Bosnia & Herzegovina
## 49:        Aquastat           Cape Verde
## 50:        Aquastat              Croatia
```

```
## 51:        Aquastat                 Cuba
## 52:        Aquastat          El Salvador
## 53:        Aquastat              Grenada
## 54:        Aquastat               Guyana
## 55:        Aquastat                Haiti
## 56:        Aquastat              Ireland
## 57:        Aquastat              Lebanon
## 58:        Aquastat           Luxembourg
## 59:        Aquastat             Malaysia
## 60:        Aquastat               Panama
## 61:        Aquastat                 Peru
## 62:        Aquastat          Saint Lucia
## 63:        Aquastat                Sudan
## 64:        Aquastat             Suriname
## 65:        Aquastat            Swaziland
## 66:        Aquastat    Trinidad & Tobago
## 67:        Aquastat              Uruguay
## 68: Liu et al. 2016          Saint Lucia
## 69: Liu et al. 2016            Swaziland
##       Water.Dataset                   V1
```

```
# Show unique countries missing
full.dt[is.na(Water.Withdrawn), ] %>%
  .[, unique(Country)]
```

```
##  [1] "Grenada"              "Malta"                "Saint Lucia"
##  [4] "Seychelles"           "Swaziland"            "Argentina"
##  [7] "Canada"               "Portugal"             "Russia"
## [10] "Mauritius"            "Cape Verde"           "Belize"
## [13] "Bosnia & Herzegovina" "Croatia"              "Cuba"
## [16] "El Salvador"          "Guyana"               "Haiti"
## [19] "Ireland"              "Lebanon"              "Luxembourg"
## [22] "Malaysia"             "Panama"               "Peru"
## [25] "Sudan"                "Suriname"             "Trinidad & Tobago"
## [28] "Uruguay"
```

```
# PLOT ------------------------------------------------------------------------

full.dt %>%
  na.omit() %>%
  ggplot(., aes(Irrigated.Area, Water.Withdrawn,
                color = Continent)) +
  geom_point(size = 0.4) +
  scale_x_log10(breaks = trans_breaks("log10", function(x) 10 ^ (4 * x)),
                labels = trans_format("log10", math_format(10 ^ .x))) +
  scale_y_log10(breaks = trans_breaks("log10", function(x) 10 ^ (2 * x)),
                labels = trans_format("log10", math_format(10 ^ .x))) +
  labs(x = "Irrigated area (ha)",
       y = expression(paste("Water withdrawal ", " ", "(", 10^9, m^3/year, "", ")"))) +
```

```
  facet_wrap(~Water.Dataset, ncol = 5) +
  theme_AP() +
  theme(legend.position = "top",
        strip.background = element_rect(fill = "white"))
```

```
## Warning: Transformation introduced infinite values in continuous x-axis
```

```
## Warning: Transformation introduced infinite values in continuous y-axis
```

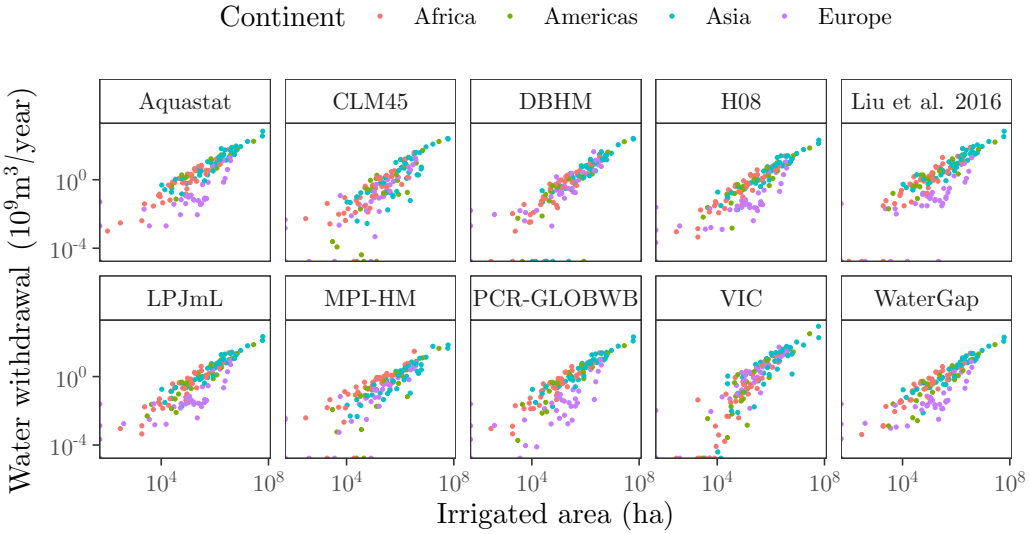


Figure 1: Scatterplots of irrigated areas reported by FAO-GMIA against irrigation water withdrawals. Each dot is a country.

3 The influence of other parameters

3.1 Potential evapotranspiration

```
# CHECK THE INFLUENCE OF POTENTIAL EVAPOTRANSPIRATION ----------------------------

full.dt <- full.dt[, div:= Water.Withdrawn / Irrigated.Area]

# Create function to access the evapotranspiration data from ISIMIP
open_nc_totevap <- function(file, dname) {
ncin <- nc_open(file)
# get longitude, latitude, time
lon <- ncvar_get(ncin, "lon")
lat <- ncvar_get(ncin, "lat")
# Get variable
tmp_array <- ncvar_get(ncin, dname)
m <- (dim(tmp_array)[3] - 11):dim(tmp_array)[3]
tmp_slice <- lapply(m, function(m) tmp_array[, , m])
lonlat <- as.matrix(expand.grid(lon,lat))
# vector of `tmp` values
```

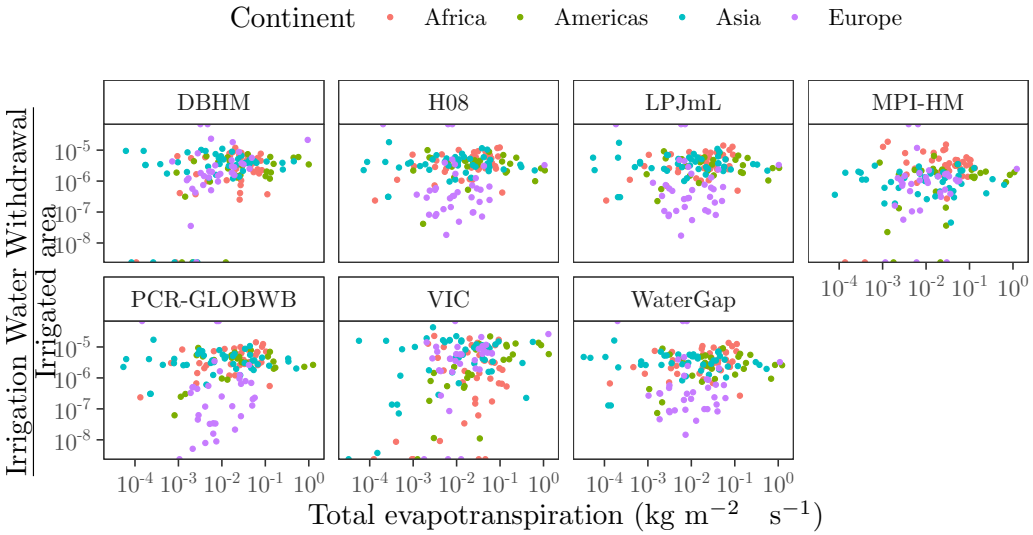
```
tmp_vec <- lapply(tmp_slice, function(x) as.vector(x))
# create dataframe and add names
tmp_df01 <- lapply(tmp_vec, function(x) data.frame(cbind(lonlat, x)))
names(tmp_df01) <- m
da <- lapply(tmp_df01, data.table) %>%
  rbindlist(., idcol = "month") %>%
  na.omit()
# Convert coordinates to country
countries <- coords2country(da[1:nrow(da), 2:3])
dt <- cbind(countries, da)
setDT(dt)
dt <- na.omit(dt)[, .(totevap = sum(x)), countries]
setnames(dt, "countries", "Country")
dt[, `:=` (Code = countrycode(dt[, Country],
                              origin = "country.name",
                              destination = "un"),
           Continent = countrycode(dt[, Country],
                                   origin = "country.name",
                                   destination = "continent"))]
dt[, Country:= countrycode(dt[, Code],
                           origin = "un",
                           destination = "country.name")]
return(dt)
}

# List of files to access
files <- list("watergap2_wfdei_nobc_hist_varsoc_co2_evap_global_monthly_1971_2010.nc",
              "pcr-globwb_wfdei_nobc_hist_varsoc_co2_evap_global_monthly_1971_2010.nc",
              "mpi-hm_wfdei_nobc_hist_pressoc_co2_evap_global_monthly_1971_2010.nc",
              "lpjml_wfdei_nobc_hist_varsoc_co2_evap_global_monthly_1971_2010.nc",
              "h08_wfdei_nobc_hist_varsoc_co2_evap_global_monthly_1971_2010.nc",
              "vic_wfdei_nobc_hist_varsoc_co2_evap_global_monthly_1971_2010.nc",
              "dbh_wfdei_nobc_hist_varsoc_co2_evap_global_monthly_1971_2010.nc")

# Retrieve and arrange the data
dname <- "evap"
totevap.dt <- mclapply(files, function(x)
  open_nc_totevap(file = x,
                  dname = dname),
  mc.cores = detectCores() * 0.75)
gm_list <- c("WaterGap", "PCR-GLOBWB", "MPI-HM", "LPJmL", "H08", "VIC", "DBHM")
names(totevap.dt) <- gm_list
```

```
# PLOT EVAPOTRANSPIRATION ----------------------------------------------------

rbindlist(totevap.dt, idcol = "Water.Dataset") %>%
  na.omit() %>%
```

```
  merge(full.dt[Water.Dataset %in% gm_list], ., by = c("Continent", "Country",
                                                       "Code", "Water.Dataset")) %>%
  ggplot(., aes(totevap, div,
                color = Continent)) +
  geom_point(size = 0.6) +
  scale_x_log10(labels = trans_format("log10", math_format(10 ^ .x))) +
  scale_y_log10(labels = trans_format("log10", math_format(10 ^ .x))) +
  labs(x = "Total evapotranspiration (kg $\\textrm{m}^{-2} \\quad \\textrm{s}^{-1}$)",
       y = "$\\frac{\\textrm{Irrigation Water Withdrawal}}{\\textrm{Irrigated area}}$") +
  facet_wrap(~Water.Dataset, ncol = 4) +
  theme_AP() +
  theme(legend.position = "top",
        strip.background = element_rect(fill = "white"))
```

```
## Warning: Transformation introduced infinite values in continuous y-axis
```

```
## Warning: Removed 16 rows containing missing values (geom_point).
```



3.2 Potential evaporation

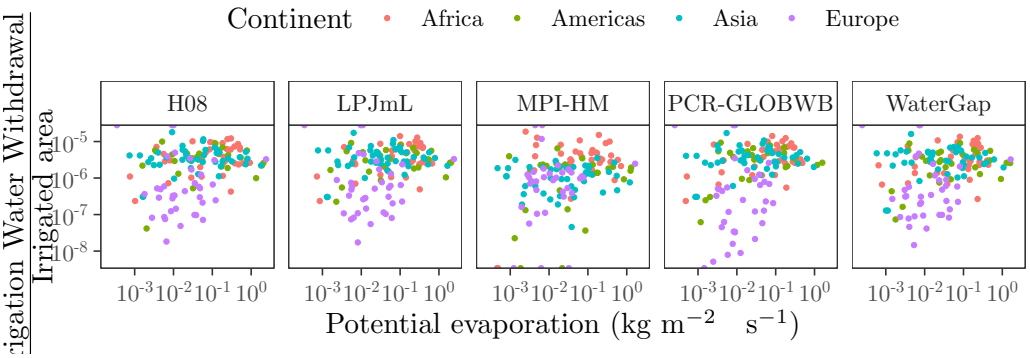
```
# CHECK THE INFLUENCE OF POTENTIAL EVAPORATION ---------------------------------

files <- c("watergap2_wfdei_nobc_hist_pressoc_co2_potevap_global_monthly_1971_2010.nc",
           "h08_wfdei_nobc_hist_pressoc_co2_potevap_global_monthly_1971_2010.nc",
           "pcr-globwb_wfdei_nobc_hist_pressoc_co2_potevap_global_monthly_1971_2010.nc",
           "mpi-hm_wfdei_nobc_hist_pressoc_co2_potevap_global_monthly_1971_2010.nc",
           "lpjml_wfdei_nobc_hist_pressoc_co2_potevap_global_monthly_1971_2010.nc")

# Retrieve and arrange the data
dname <- "potevap"
potevap.dt <- mclapply(files, function(x)
  open_nc_totevap(file = x,
```

```
                    dname = dname),
  mc.cores = detectCores() * 0.75)
gm_list <- c("WaterGap", "H08", "PCR-GLOBWB", "MPI-HM", "LPJmL")
names(potevap.dt) <- gm_list
```

```
# PLOT POTENTIAL EVAPORATION ----------------------------------------------------

rbindlist(potevap.dt, idcol = "Water.Dataset") %>%
  na.omit() %>%
  merge(full.dt[Water.Dataset %in% gm_list], ., by = c("Continent", "Country",
                                                       "Code", "Water.Dataset")) %>%
  ggplot(., aes(totevap, div,
                color = Continent)) +
  geom_point(size = 0.6) +
  scale_x_log10(labels = trans_format("log10", math_format(10 ^ .x))) +
  scale_y_log10(labels = trans_format("log10", math_format(10 ^ .x))) +
  labs(x = "Potential evaporation (kg $\\textrm{m}^{-2} \\quad  \\textrm{s}^{-1}$)",
       y = "$\\frac{\\textrm{Irrigation Water Withdrawal}}{\\textrm{Irrigated area}}$") +
  facet_wrap(~Water.Dataset, ncol = 5) +
  theme_AP() +
  theme(legend.position = "top",
        strip.background = element_rect(fill = "white"))
```

```
## Warning: Transformation introduced infinite values in continuous y-axis
```

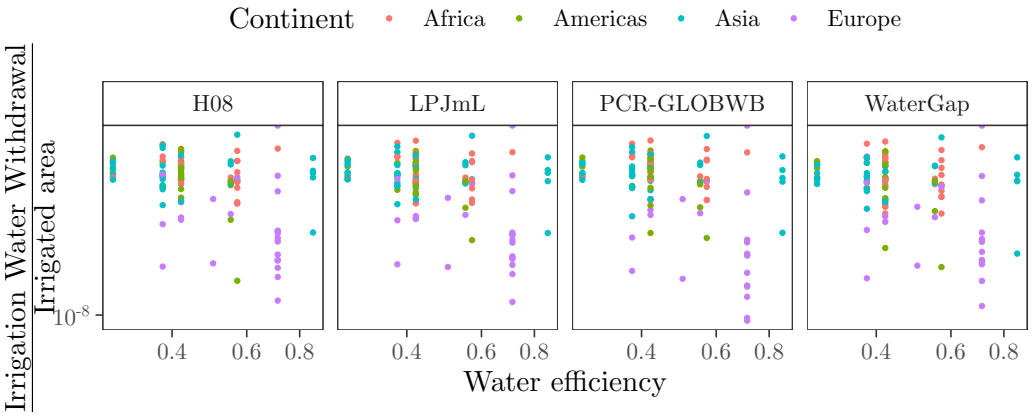
```
## Warning: Removed 10 rows containing missing values (geom_point).
```



3.3 Water efficiency

```
# CHECK INFLUENCE OF WATER EFFICIENCY -------------------------------------------

# Retrieve the data from Rohwer
rohwer_data <- fread("rohwer_data.csv")

# Plot
merge(full.dt[Water.Dataset %in% c("WaterGap", "H08", "LPJmL",
                                   "PCR-GLOBWB")],
      rohwer_data, by = "Country") %>%
```

```
  na.omit() %>%
  ggplot(., aes(Project.efficiency, div,
                color = Continent)) +
  geom_point(size = 0.6) +
  scale_y_log10(breaks = trans_breaks("log10", function(x) 10 ^ (2 * x)),
                labels = trans_format("log10", math_format(10 ^ .x))) +
  scale_x_log10(breaks = pretty_breaks(n = 3)) +
  labs(x = "Water efficiency",
       y = "$\\frac{\\textrm{Irrigation Water Withdrawal}}{\\textrm{Irrigated area}}$") +
  facet_wrap(~Water.Dataset, ncol = 4) +
  theme_AP() +
  theme(legend.position = "top",
        strip.background = element_rect(fill = "white"))
```



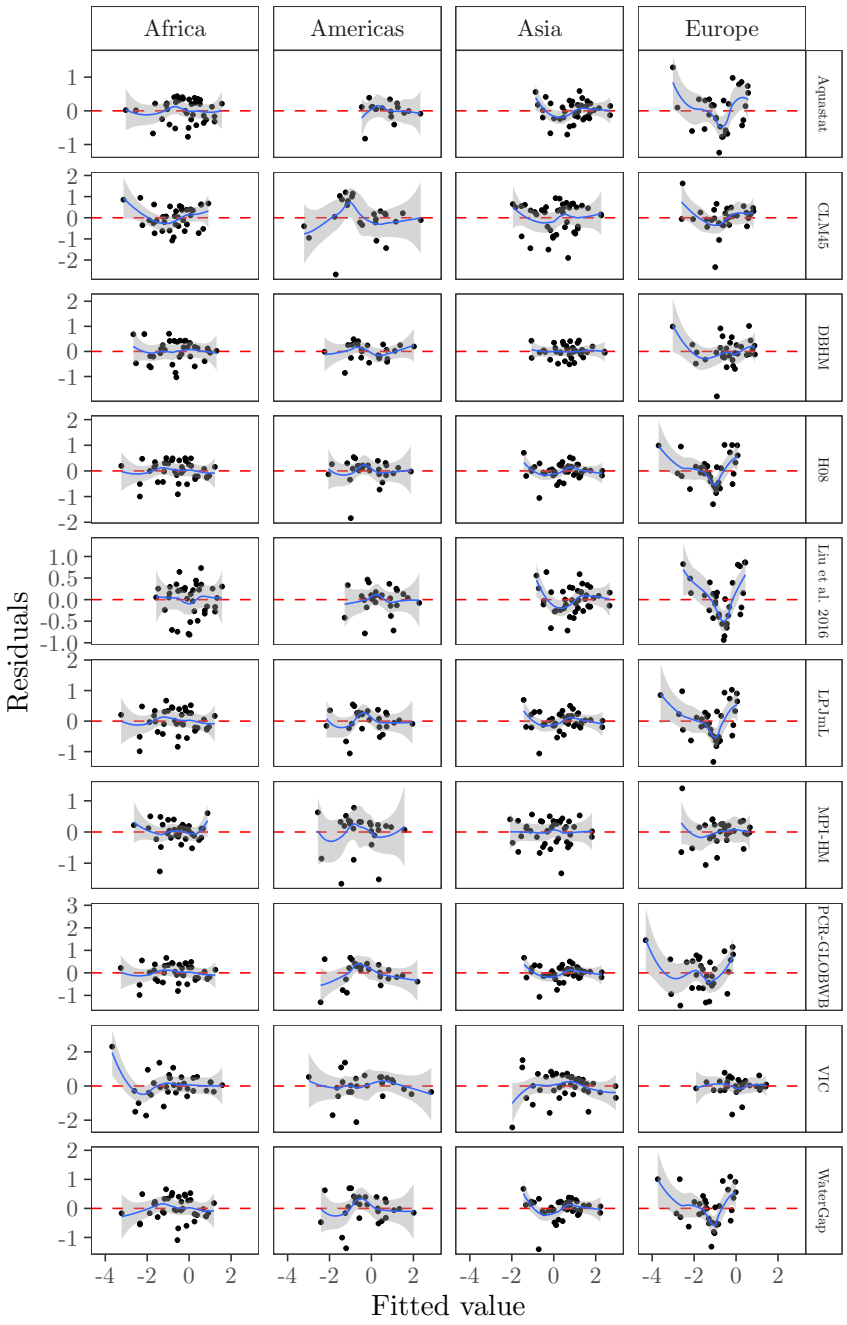
4 Creation of the final dataset

```
# TRANSFORM DATASET ------------------------------------------------------------

cols <- c("Water.Withdrawn", "Irrigated.Area")
col_names <- c("Continent", "Water.Dataset", "Area.Dataset", "Regression",
               "Imputation.Method", "Iteration")
cols_group <- c("Continent", "Water.Dataset")
full.dt <- full.dt[, (cols):= lapply(.SD, log10), .SDcols = (cols)]
full.dt <- full.dt[, Country:= str_replace(Country, "\\&", "and")]
```

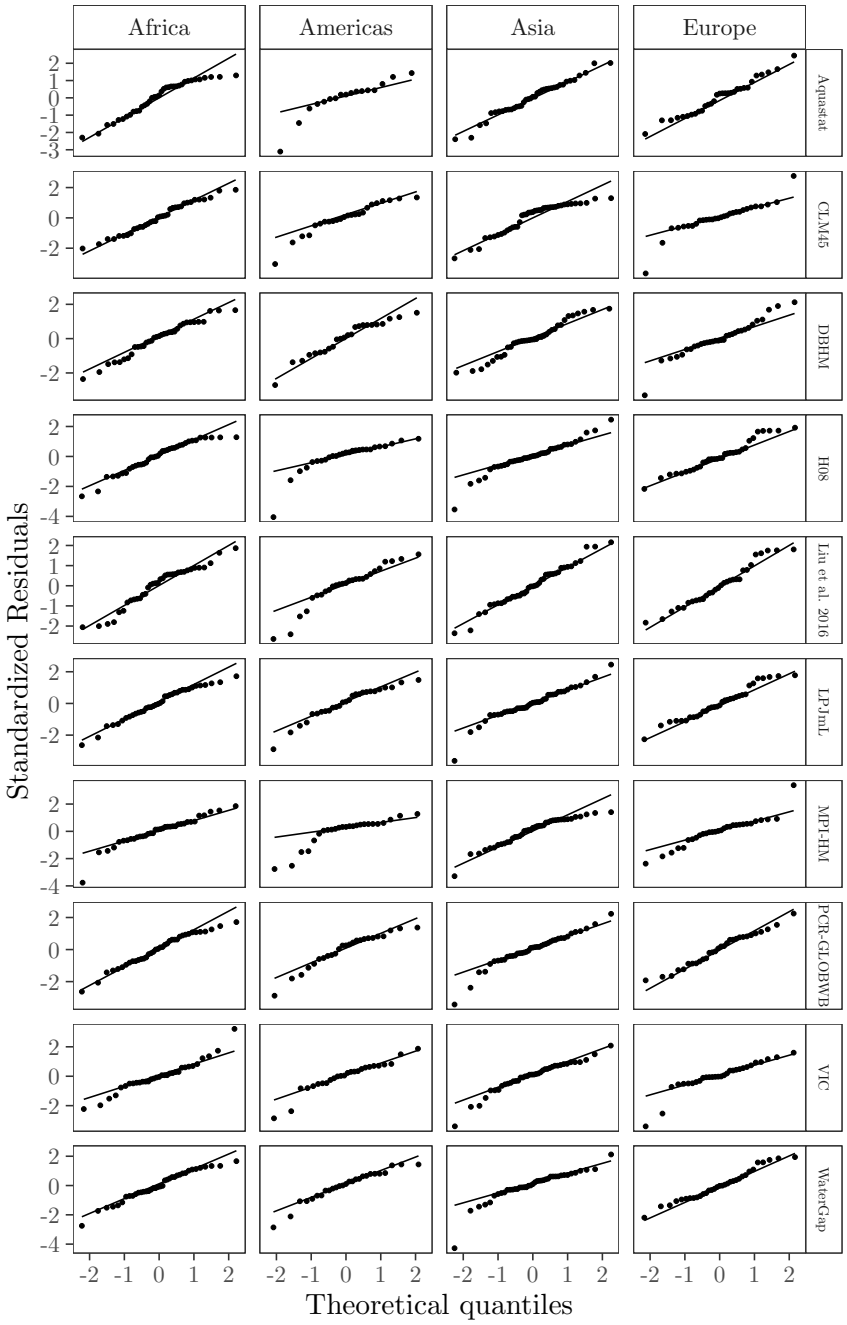
```
# REGRESSION DIAGNOSTICS -------------------------------------------------------

# Conduct regressions
regression.diag <- full.dt %>%
  NaRV.omit() %>%
  group_by(Continent, Water.Dataset) %>%
  nest() %>%
  mutate(fit = map(.x = data, .f = ~lm(Water.Withdrawn ~ Irrigated.Area, data = .)),
         results = map(fit, glance),
         residuals = map(fit, augment))
```

```r
# Prepare dataset
diagnostics.dt <- regression.diag %>%
  dplyr::select(Continent, Water.Dataset, residuals) %>%
  unnest(residuals) %>%
  data.table()

# Residuals versus fitted
ggplot(diagnostics.dt, aes(.fitted, .resid)) +
  geom_point(size = 0.5) +
  geom_hline(yintercept = 0, lty = 2, color = "red") +
  geom_smooth(size = 0.5) +
  labs(x = "Fitted value", y = "Residuals") +
  facet_grid(Water.Dataset ~ Continent,
             scales = "free_y") +
  theme_AP() +
  theme(strip.text.y = element_text(size = 5.5),
        strip.background = element_rect(fill = "white"))
```

```
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
```



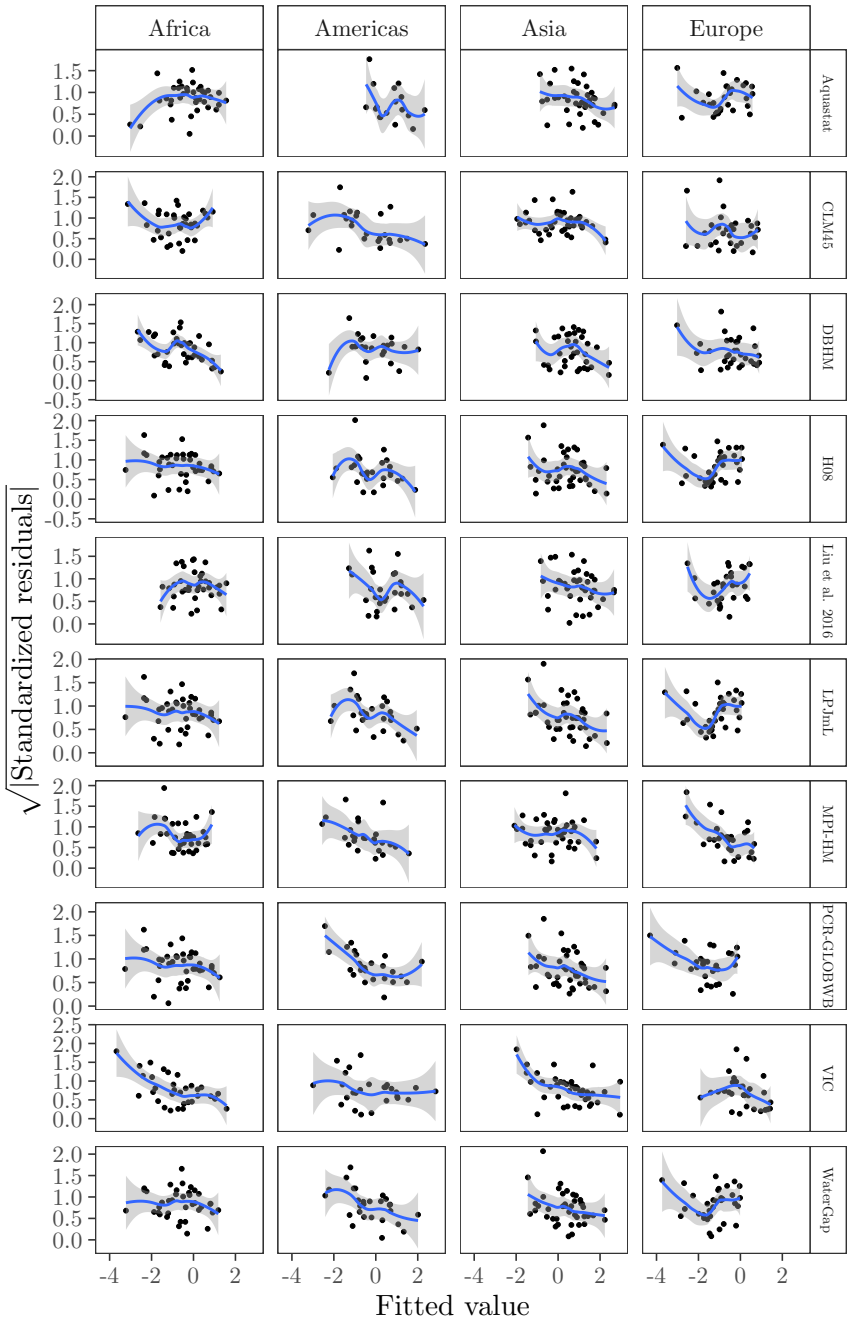

```
# QQ plot
ggplot(diagnostics.dt, aes(sample = .std.resid)) +
  stat_qq(size = 0.5) +
  stat_qq_line() +
  facet_grid(Water.Dataset ~ Continent,
             scales = "free_y") +
  labs(x = "Theoretical quantiles",
       y = "Standardized Residuals") +
  theme_AP() +
  theme(strip.text.y = element_text(size = 5.5),
        strip.background = element_rect(fill = "white"))
```




```
# Scale location plot
ggplot(diagnostics.dt, aes(.fitted, sqrt(abs(.std.resid)))) +
  geom_point(size = 0.5) +
  geom_smooth() +
  facet_grid(Water.Dataset ~ Continent,
             scales = "free_y") +
  labs(x = "Fitted value",
       y = "$\\sqrt{|\\textrm{Standardized residuals}|}$") +
  theme_AP() +
```

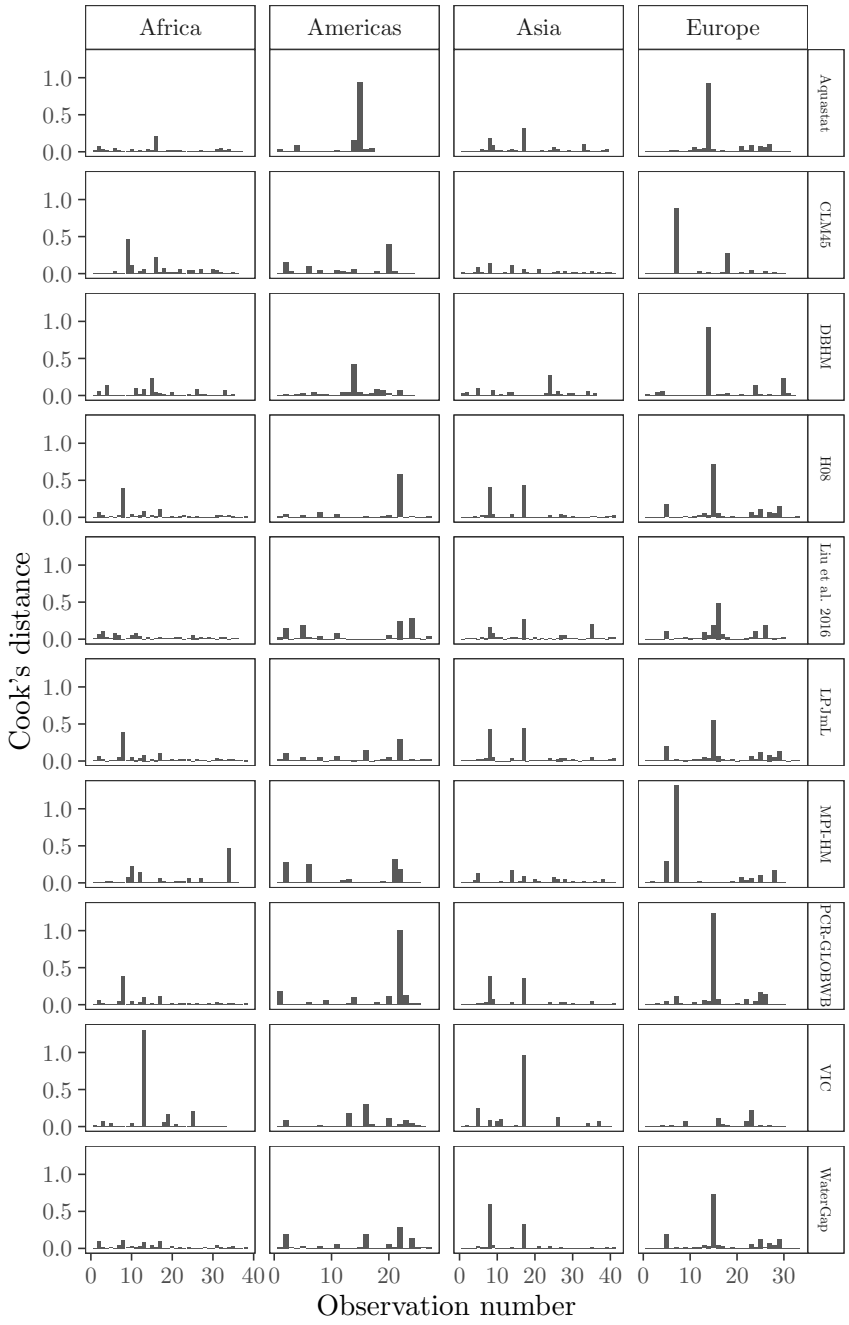
```
  theme(strip.text.y = element_text(size = 5.5),
        strip.background = element_rect(fill = "white"))
```

```
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
```




```
# Cook's distance
ID <- diagnostics.dt[, .N, .(Continent, Water.Dataset)]
diagnostics.dt <- diagnostics.dt[, ID:= unlist(sapply(ID[, N], function(x) 1:x))]
ggplot(diagnostics.dt, aes(ID, .cooksd)) +
  geom_col() +
  facet_grid(Water.Dataset ~ Continent,
```

```
            scales = "free_x") +
  theme_AP() +
  labs(x = "Observation number", y = "Cook's distance") +
  theme(strip.text.y = element_text(size = 5.5),
        strip.background = element_rect(fill = "white"))
```




```
# EXPORT FULL DATASET WITH MISSING VALUES ------------------------------------

fwrite(full.dt, "full.dt.csv")
fwrite(water.dt, "water.dt.csv")
```

5 Missing values

```
# PLOT PERCENTAGE OF MISSING 2 ------------------------------------------------

full.dt[, sum(is.na(.SD) == TRUE) / .N,
        .(Continent, Water.Dataset),
        .SDcols = "Water.Withdrawn"] %>%
  ggplot(., aes(Continent, V1, fill = Water.Dataset)) +
  geom_bar(stat = "identity",
           position = position_dodge(0.7),
           color = "black") +
  labs(x = "",
       y = "Proportion of missing values") +
  scale_fill_discrete(name = "") +
  theme_AP() +
  theme(legend.position = "top")
```

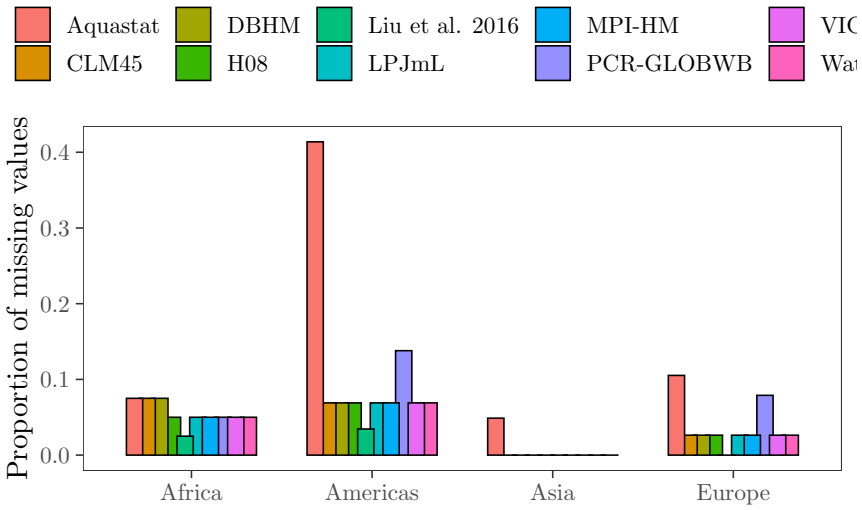


Figure 2: Proportion of missing values in irrigation water withdrawal per dataset.

5.1 Imputation of missing values

```
# IMPUTATION OF MISSING VALUES ------------------------------------------------

# Substitute Inf values for NA
for (j in 1:ncol(full.dt)) set(full.dt, which(is.infinite(full.dt[[j]])), j, NA)

full.dt[, lapply(.SD, function(x) sum(is.infinite(x)))] # Check
```

```
##    Water.Dataset Country Code Continent Water.Withdrawn Irrigated.Area div
## 1:             0       0    0         0               0              0   0
```

```
# Imputation settings
m.iterations <- 40
```

```r
imputation.methods <- c("norm.boot", "norm", "norm.nob")

# Run
full.dt <- full.dt[, div:= NULL]

imput <- full.dt[, .(Group = lapply(imputation.methods, function(x)
  mice(.SD, m = m.iterations, maxit = m.iterations, method = x, seed = 500,
       print = FALSE))),
  cols_group]

imput <- imput[, Imputation.Method:= rep(imputation.methods, .N /
                                           length(imputation.methods))]

# Extract iterations
imput <- imput[, Datasets:= lapply(Group, function(x)
  lapply(1:m.iterations, function(y) data.table(mice::complete(x, y))))] %>%
  .[, Data:= lapply(Datasets, function(x) rbindlist(x, idcol = "Iteration"))]

# Vector to loop onto
columns_add <- c("Country", "Iteration", "Irrigated.Area", "Water.Withdrawn")
tmp <- as.list(columns_add)
names(tmp) <- columns_add

# Extract columns
for(i in names(tmp)) {
  imput <- imput[, tmp[[i]]:= lapply(.SD, function(x)
    lapply(x, function(y) y[, ..i])), .SDcols = "Data"]
}

# Unlist
full.imput <- imput[, lapply(.SD, unlist),
                    .SDcols = columns_add,
                    .(Continent,Water.Dataset, Imputation.Method)]
```

6 Compute linear regressions

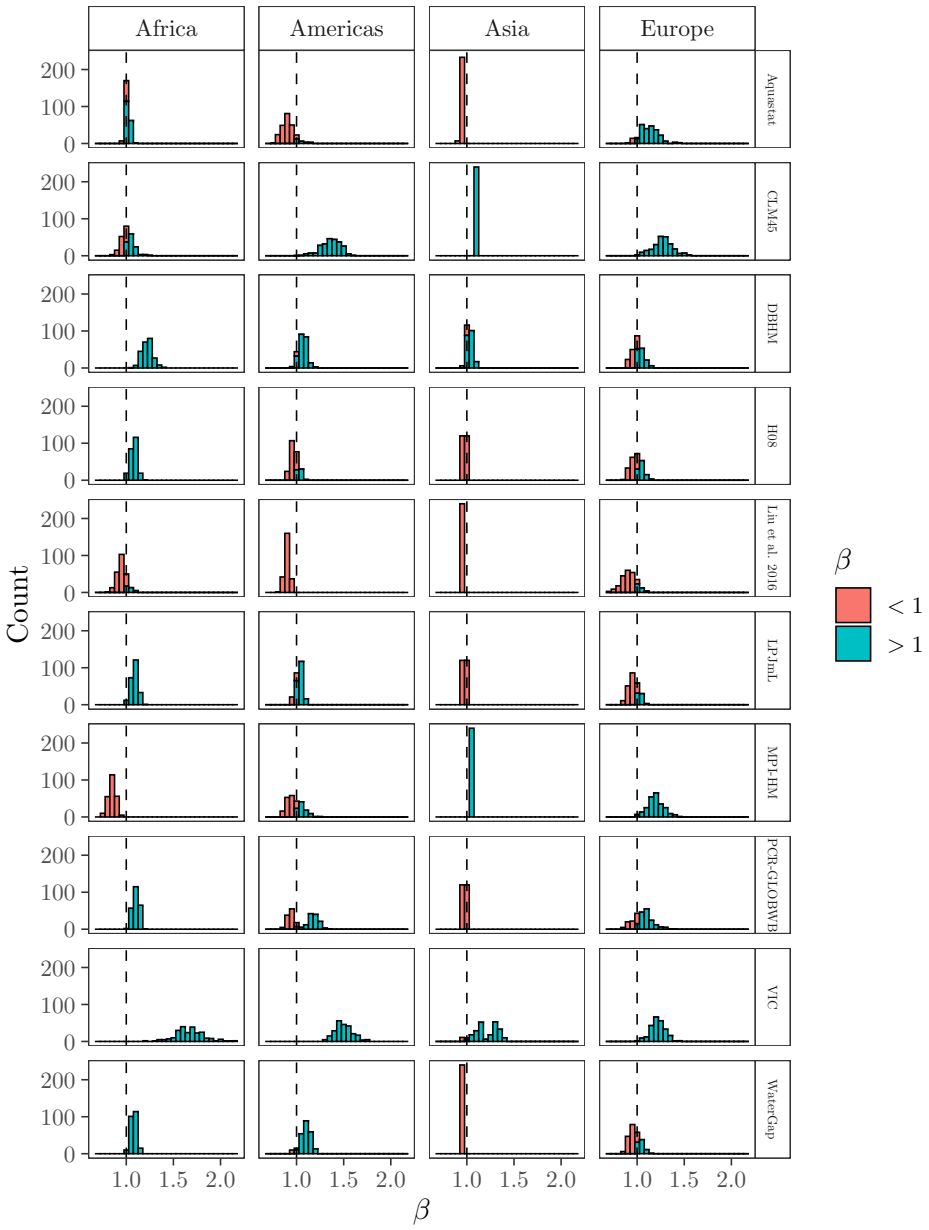
```r
# COMPUTE LINEAR REGRESSIONS ----------------------------------------------------

# Compute regressions in each combination
# Settings for robust regressions
a1<-lmrob.control()
a1$k.max <- 1000

# Compute regressions
regressions <- full.imput %>%
  group_by(Continent, Water.Dataset, Imputation.Method, Iteration) %>%
```

```
  nest() %>%
  mutate(fit = map(.x = data, .f = ~lm(Water.Withdrawn ~ Irrigated.Area, data = .)),
         fit.robust = map(.x = data, .f = ~lmrob(Water.Withdrawn ~ Irrigated.Area, data = .,
                                                 control = a1)),
         results = map(fit, glance),
         results.robust = map(fit.robust, glance),
         residuals = map(fit, augment))

# EXTRACT R SQUARED ----------------------
# Regular r squared
results <- regressions %>%
  dplyr::select(Continent, Water.Dataset,
                Imputation.Method, Iteration, results,) %>%
  unnest(results) %>%
  data.table() %>%
  .[, Regression:= "Normal"] %>%
  .[, index:= paste(Continent, Water.Dataset, Imputation.Method,
                    Iteration, Regression, sep = "_")]

# Robust r squared
results.robust <- regressions %>%
  dplyr::select(Continent, Water.Dataset,
                Imputation.Method, Iteration, results.robust) %>%
  unnest(results.robust) %>%
  data.table() %>%
  .[, Regression:= "Robust"] %>%
  .[, index:= paste(Continent, Water.Dataset, Imputation.Method,
                    Iteration, Regression, sep = "_")]

cols_extract <- c("Continent", "Water.Dataset", "Imputation.Method",
                  "Iteration", "Regression", "r.squared",
                  "index")

# Bind regular and robust
all.results <- rbind(results[, ..cols_extract],
                     results.robust[, ..cols_extract])
```

```
# EXTRACT SLOPE (BETA) ------------------------------------------------------

# Extract regular slope
slope <- regressions %>%
  mutate(slope = map(fit, tidy)) %>%
  unnest(slope) %>%
  dplyr::select(Continent, Water.Dataset,
                Imputation.Method, Iteration, term, estimate) %>%
  data.table() %>%
  .[term == "Irrigated.Area"]
```

```r
# Extract robust slope
slope.robust <- regressions %>%
  mutate(slope = map(fit.robust, tidy)) %>%
  unnest(slope) %>%
  dplyr::select(Continent, Water.Dataset,
                Imputation.Method, Iteration, term, estimate) %>%
  data.table() %>%
  .[term == "Irrigated.Area"]

# Plot
rbind(slope, slope.robust) %>%
  ggplot(., aes(estimate)) +
  geom_histogram(color = "black", aes(fill = estimate > 1)) +
  geom_vline(xintercept = 1, lty = 2) +
  labs(x = "$\\beta$",
       y = "Count") +
  scale_fill_discrete(name = "$\\beta$",
                      labels = c("$<1$", "$>1$")) +
  scale_y_continuous(breaks = pretty_breaks(n = 3)) +
  facet_grid(Water.Dataset~Continent) +
  theme_AP() +
  theme(strip.text.y = element_text(size = 5),
        strip.background = element_rect(fill = "white"))
```

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



7 Predictions

7.1 Compare our approach with estimates by GHM

```
# PREDICT WATER WITHDRAWALS ------------------------------------------------

size.gmia <- meier.dt[, .(Country, Continent, Irrigated.Area)] %>%
  .[!Irrigated.Area == 0] %>%
  .[, Irrigated.Area:= log10(Irrigated.Area)] %>%
  .[!Continent == "Oceania"] %>%
  .[order(Continent)]
```

```
countries <- split(size.gmia, size.gmia$Continent) %>%
  lapply(., function(x) x[, Country]) %>%
  lapply(., data.table)

areas <- split(size.gmia, size.gmia$Continent) %>%
  lapply(., function(x) x[, Irrigated.Area]) %>%
  lapply(., data.frame) %>%
  lapply(., function(x) setnames(x, "X..i..", "Irrigated.Area"))

tmp.regressions <- regressions %>%
  split(., .$Continent)

out <- out.robust <- list()
for(i in names(tmp.regressions)) {
  out[[i]] <- mutate(tmp.regressions[[i]],
                     pred = map(fit, .f = ~predict(., areas[[i]])))
  out.robust[[i]] <- mutate(tmp.regressions[[i]],
                            pred = map(fit.robust, .f = ~predict(., areas[[i]])))
}

water.predicted <- lapply(out, function(x) {
  select(x, Continent, Water.Dataset, Imputation.Method, Iteration, pred) %>%
  unnest(pred) %>%
  data.table()
})

water.predicted.rob <- lapply(out.robust, function(x) {
  select(x, Continent, Water.Dataset, Imputation.Method, Iteration, pred) %>%
    unnest(pred) %>%
    data.table()
})

out <- out.robust <- list()
for(i in names(water.predicted)) {
  out[[i]] <- water.predicted[[i]][, Country:= rep(countries[[i]][, V1],
                                                   times = nrow(water.predicted[[i]]) /
                                                           nrow(countries[[i]]))]
  out.robust[[i]] <- water.predicted.rob[[i]][, Country:= rep(countries[[i]][, V1],
                                                              times = nrow(water.predicted[[i]]) /
                                                                nrow(countries[[i]]))]
}

water.predicted <- rbindlist(water.predicted) %>%
  .[, pred:= 10 ^ pred]

water.predicted.rob <- rbindlist(water.predicted.rob) %>%
  .[, pred:= 10 ^ pred]
```

```
# Compute quantiles
water.quantiles <- rbind(water.predicted, water.predicted.rob) %>%
  .[, .(min = min(pred),
                                        max = max(pred),
                                        q0.025 = quantile(pred, 0.025),
                                        q0.1 = quantile(pred, 0.1),
                                        q0.25 = quantile(pred, 0.25),
                                        q0.5 = quantile(pred, 0.5),
                                        q0.75 = quantile(pred, 0.75),
                                        q0.975 = quantile(pred, 0.975),
                                        q0.99 = quantile(pred, 0.99),
                                        q1 = quantile(pred, 1),
                                        mean = mean(pred),
                                        median = median(pred)),
                                    .(Continent, Country)] %>%
  .[order(Country, Continent)]

water.quantiles <- water.quantiles[, Country:= str_replace(Country, "\\&", "and")]
```

```
# PLOT PREDICTIONS AGAINST GHM AND FAO OUTPUTS ---------------------------------

water.tmp <- water.dt[Country %in% water.quantiles[, Country]]
Cont <- c("Africa", "Americas", "Asia", "Europe")
gg <- list()
for(i in Cont) {
  gg[[i]] <- water.quantiles[Continent == i] %>%
    ggplot(., aes(reorder(Country, median), median)) +
    geom_point() +
    geom_point(data = water.tmp[Continent == i],
               aes(Country, Water.Withdrawn, color = Water.Dataset)) +
    geom_errorbar(aes(ymin = min,
                      ymax = max)) +
    scale_y_log10(breaks = trans_breaks("log10", function(x) 10 ^ (2 * x)),
                  labels = trans_format("log10", math_format(10 ^ .x))) +
    scale_color_discrete(name = "Water dataset") +
    labs(y = expression(paste("Water withdrawal ", " ", "(", 10^9, m^3/year, "", ")")),
         x = "") +
    coord_flip() +
    theme_AP()
}

all.plots <- lapply(1:4, function(x)
  gg[[x]] +
    theme(legend.position = "none") +
    labs(x = "", y = ""))

legend <- get_legend(gg[[1]] + theme(legend.position = "top",
```

```
                                        legend.key.size = unit(0.5, 'lines')))
```

```
## Warning: Transformation introduced infinite values in continuous y-axis
```

```
bottom1 <- plot_grid(all.plots[[1]], all.plots[[2]], ncol = 2, labels = "auto", align = "hv")
```

```
## Warning: Transformation introduced infinite values in continuous y-axis
```

```
## Warning: Transformation introduced infinite values in continuous y-axis
```

```
all1 <- plot_grid(legend, bottom1, ncol = 1, rel_heights = c(0.1, 1))

grid.arrange(arrangeGrob(all1, bottom = grid::textGrob(
  label = expression(paste("Irrigation water withdrawal ", " ", "(", 10^9, m^3/year, "", ")")))
```

```
bottom2 <- plot_grid(all.plots[[3]], all.plots[[4]], ncol = 2, labels = "auto", align = "hv")
```

```
## Warning: Transformation introduced infinite values in continuous y-axis
```

```
## Warning: Transformation introduced infinite values in continuous y-axis
```

```
all <- plot_grid(legend, bottom2, ncol = 1, rel_heights = c(0.1, 1))

grid.arrange(arrangeGrob(all, bottom = grid::textGrob(
  label = expression(paste("Irrigation water withdrawal ", " ", "(", 10^9, m^3/year, "", ")")))
```

```
# CHECK HOW MANY ESTIMATES FIT WITHIN THE REGRESSION BOUNDS ----------------------

da <- merge(water.tmp, water.quantiles[, .(Continent, Country, min, max)],
            by = c("Continent", "Country")) %>%
  .[, fit:= ifelse(Water.Withdrawn >= min & Water.Withdrawn <= max, TRUE, FALSE)]

# Check which GHM or FAO-based dataset shows more estimates
# beyond or below our predictions
da[, .(N = sum(Water.Withdrawn < min | Water.Withdrawn > max),
       prop = sum(Water.Withdrawn < min | Water.Withdrawn > max) / .N),
   .(Water.Dataset, Continent)]
```

```
##       Water.Dataset Continent  N       prop
##  1:           LPJmL    Africa  3 0.07894737
##  2:      PCR-GLOBWB    Africa  2 0.05263158
##  3:             H08    Africa  2 0.05263158
##  4:        WaterGap    Africa  4 0.10526316
##  5:            DBHM    Africa  5 0.13513514
##  6:          MPI-HM    Africa  5 0.13157895
##  7:             VIC    Africa 17 0.44736842
##  8:           CLM45    Africa  8 0.21621622
##  9:        Aquastat    Africa 13 0.35135135
## 10: Liu et al. 2016    Africa 18 0.46153846
## 11:           LPJmL  Americas  2 0.07692308
```

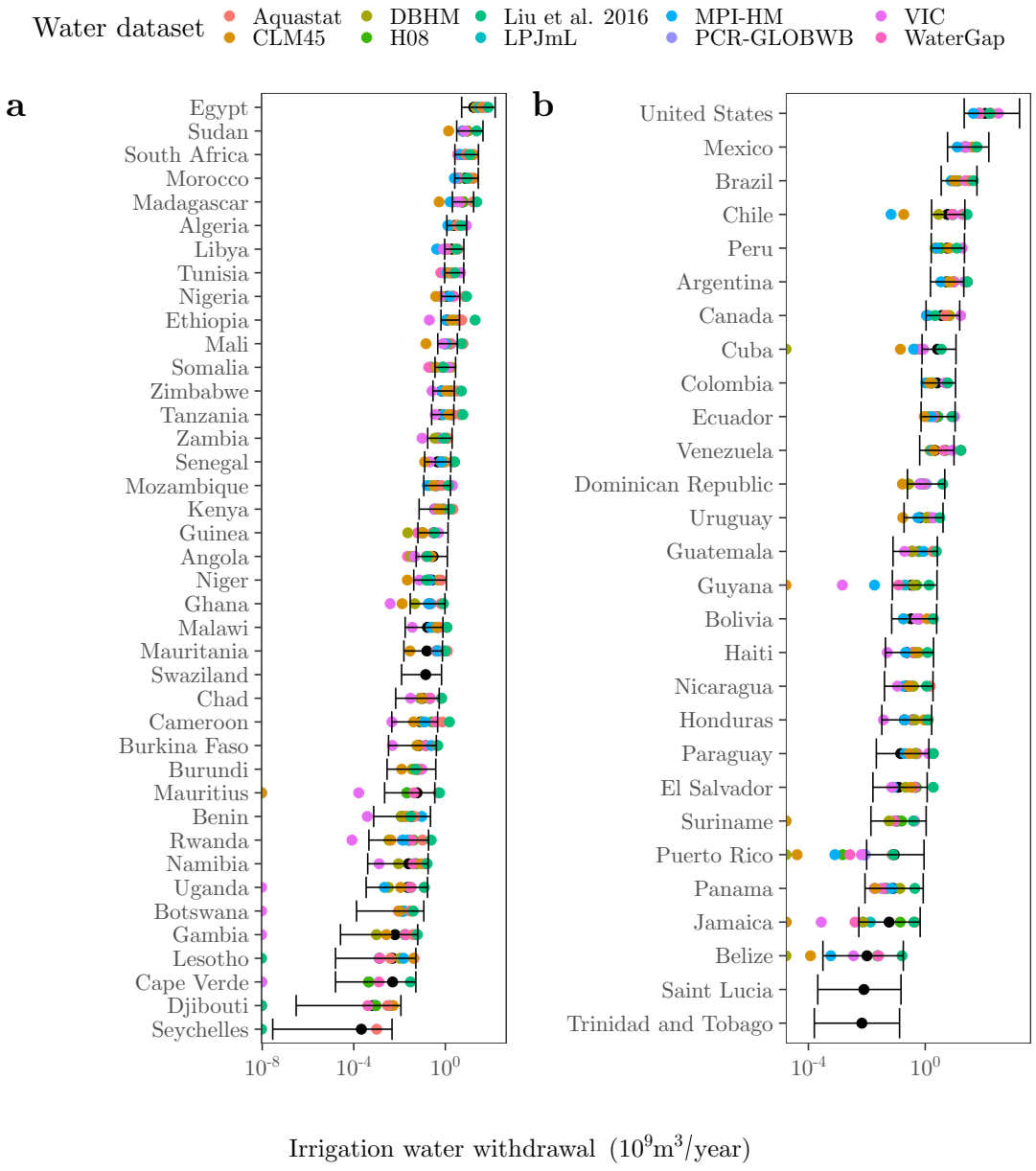


Figure 3: Validation of our approach. The black dots and the error bars show the range of irrigation water withdrawal values predicted from irrigated areas only. The colored dots show the irrigation water withdrawal values outputted by Global Hydrological Models (DBHM, Ho8, LPJmL, MPI-HM, PCR-GLOBWB, WaterGap) and FAO-based datasets (Aquastat, Liu et al. 2016).

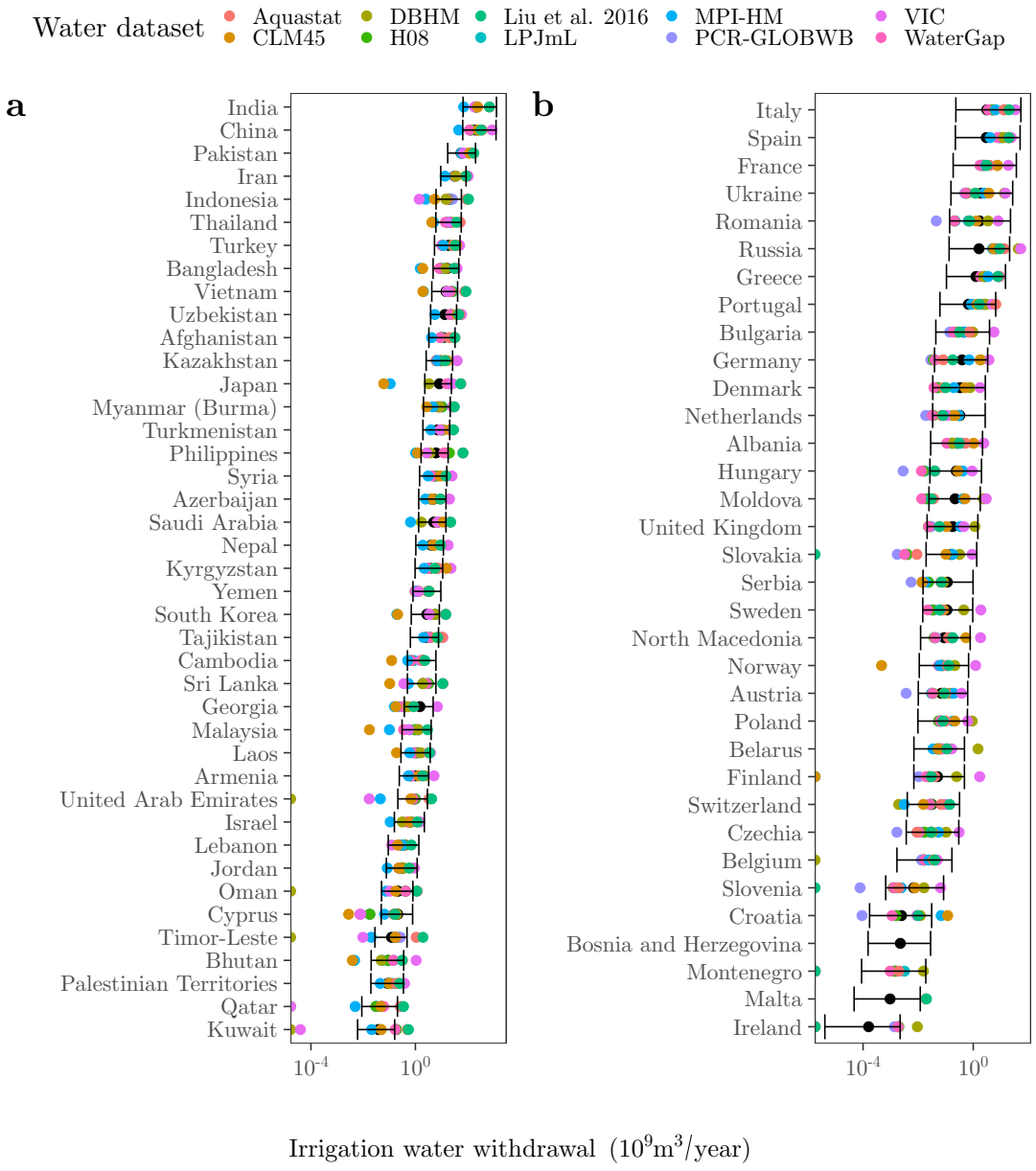
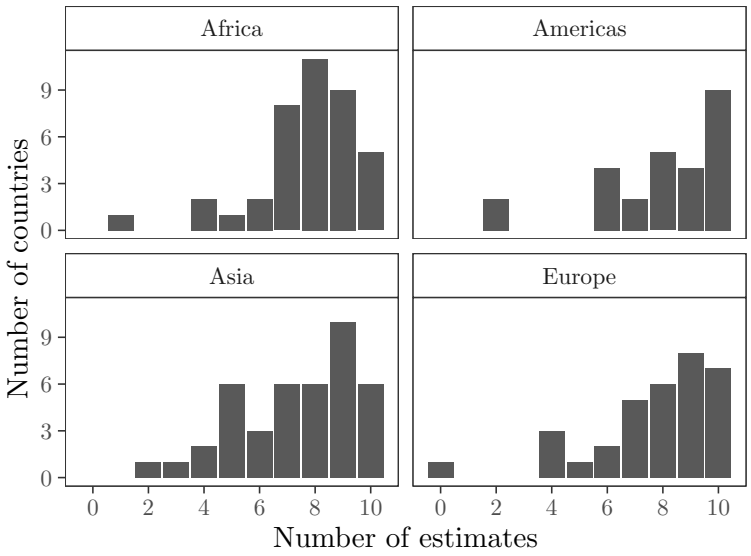


Figure 4: Validation of our approach. The black dots and the error bars show the range of irrigation water withdrawal values predicted from irrigated areas only. The colored dots show the irrigation water withdrawal values outputted by Global Hydrological Models (DBHM, Ho8, LPJmL, MPI-HM, PCR-GLOBWB, WaterGap) and FAO-based datasets (Aquastat, Liu et al. 2016).

```
## 12:             H08  Americas  2 0.07692308
## 13:        WaterGap  Americas  3 0.11538462
## 14:            DBHM  Americas  3 0.11538462
## 15:          MPI-HM  Americas  6 0.23076923
## 16:             VIC  Americas  5 0.19230769
## 17:           CLM45  Americas  9 0.34615385
## 18:        Aquastat  Americas  4 0.23529412
## 19: Liu et al. 2016  Americas  5 0.19230769
## 20:      PCR-GLOBWB  Americas  2 0.08333333
## 21:           LPJmL      Asia  3 0.07317073
## 22:      PCR-GLOBWB      Asia  4 0.09756098
## 23:             H08      Asia  4 0.09756098
## 24:        WaterGap      Asia  3 0.07317073
## 25:            DBHM      Asia  6 0.14634146
## 26:          MPI-HM      Asia 16 0.39024390
## 27:             VIC      Asia 22 0.53658537
## 28:           CLM45      Asia 17 0.41463415
## 29:        Aquastat      Asia 16 0.41025641
## 30: Liu et al. 2016      Asia 16 0.39024390
## 31:           LPJmL    Europe  4 0.12500000
## 32:      PCR-GLOBWB    Europe 12 0.40000000
## 33:             H08    Europe  4 0.12500000
## 34:        WaterGap    Europe  4 0.12500000
## 35:            DBHM    Europe  7 0.21875000
## 36:          MPI-HM    Europe  5 0.15625000
## 37:             VIC    Europe 14 0.43750000
## 38:           CLM45    Europe  6 0.18750000
## 39:        Aquastat    Europe  3 0.09677419
## 40: Liu et al. 2016    Europe  5 0.15151515
##       Water.Dataset Continent  N       prop
```

```
# Plot bars
prove <- da[, sum(fit), .(Country, Continent)]

ggplot(prove, aes(V1)) +
  geom_bar() +
  facet_wrap(~Continent) +
  theme_AP() +
  labs(x = "Number of estimates",
       y = "Number of countries") +
  scale_x_continuous(breaks = seq(0, 10, 2)) +
  theme(strip.background = element_rect(fill = "white"))
```




```
# Check how many countries show more than 7 or 10 estimates
# bounded by our predictions
lapply(c(7, 10), function(x)
  prove[, .(Total.countries = .N,
            Bounded = sum(V1 >= x),
            Proportion = sum(V1 >= x) / .N)])
```

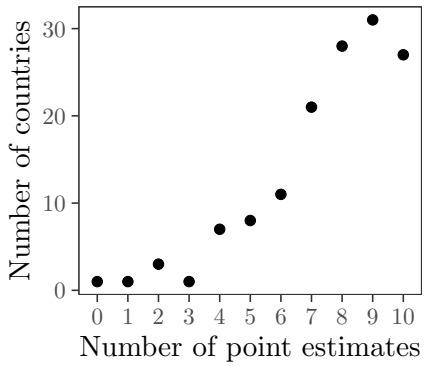
```
## [[1]]
##    Total.countries Bounded Proportion
## 1:             139     107  0.7697842
##
## [[2]]
##    Total.countries Bounded Proportion
## 1:             139      27  0.1942446
```

```
# Which countries do not show any framed estimate, or only 1, 2 or 3
lapply(c(0:3), function(x) prove[V1 == x])
```

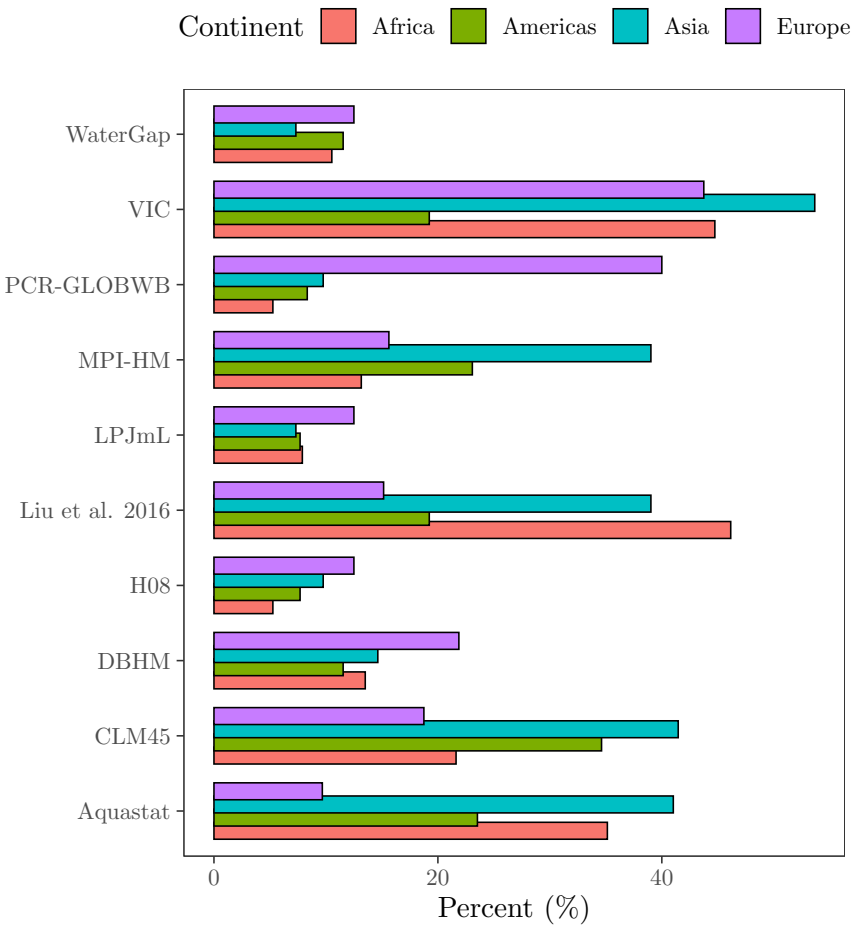
```
## [[1]]
##    Country Continent V1
## 1:   Malta    Europe  0
##
## [[2]]
##       Country Continent V1
## 1: Seychelles    Africa  1
##
## [[3]]
##        Country Continent V1
## 1:        Cuba  Americas  2
## 2: Puerto Rico  Americas  2
## 3:      Kuwait      Asia  2
##
## [[4]]
```

```
##        Country Continent V1
## 1: Philippines      Asia  3
```

```
# PLOT ALL ESTIMATES TOGETHER ------------------------------------------------

data.table(table(prove$V1)) %>%
  .[, V1:= factor(V1, levels = 0:10)] %>%
  ggplot(., aes(V1, N)) +
  geom_point() +
  labs(x = "Number of point estimates",
       y = "Number of countries") +
  theme_AP()
```




```
# CHECK BIASED POINT ESTIMATES BY DATASET ------------------------------------

da[, .(N = sum(Water.Withdrawn < min | Water.Withdrawn > max),
       prop = sum((Water.Withdrawn < min | Water.Withdrawn > max) / .N) * 100),
   .(Water.Dataset, Continent)] %>%
  ggplot(., aes(Water.Dataset, prop, fill = Continent)) +
  geom_bar(stat = "identity",
           position = position_dodge(0.7),
           color = "black") +
  labs(x = "",
       y = "Percent (\\%)") +
  coord_flip() +
  theme_AP() +
  theme(legend.position = "top")
```



7.2 Can future irrigation water withdrawals be estimated as a function of irrigated areas?

```
# FUTURE IRRIGATION WATER WITHDRAWALS ------------------------------------------

files <- list(
  "pcr-globwb_miroc5_ewembi_rcp60_2005soc_co2_airrww_global_monthly_2006_2099.nc",
  "pcr-globwb_miroc5_ewembi_rcp26_2005soc_co2_airrww_global_monthly_2006_2099.nc",
  "lpjml_miroc5_ewembi_rcp60_2005soc_co2_airrww_global_monthly_2006_2099.nc",
  "lpjml_miroc5_ewembi_rcp26_2005soc_co2_airrww_global_monthly_2006_2099.nc",
  "lpjml_miroc5_ewembi_rcp60_rcp60soc_co2_airrww_global_monthly_2006_2099.nc",
  "lpjml_miroc5_ewembi_rcp26_rcp26soc_co2_airrww_global_monthly_2006_2099.nc",
  "h08_miroc5_ewembi_rcp60_2005soc_co2_airrww_global_monthly_2006_2099.nc",
  "h08_miroc5_ewembi_rcp26_2005soc_co2_airrww_global_monthly_2006_2099.nc",
  "h08_miroc5_ewembi_rcp60_rcp60soc_co2_airrww_global_monthly_2006_2099.nc",
  "h08_miroc5_ewembi_rcp26_rcp26soc_co2_airrww_global_monthly_2006_2099.nc",
  "mpi-hm_miroc5_ewembi_rcp60_2005soc_co2_airrww_global_monthly_2006_2099.nc",
  "mpi-hm_miroc5_ewembi_rcp26_2005soc_co2_airrww_global_monthly_2006_2099.nc"
)

vecs <- 1:((2099 - 2005) * 12)
```

```
vec <- split(vecs, ceiling(seq_along(vecs) / 12))
names(vec) <- 2006:2099
dname <- "airrww"
selected.years <- as.character(seq(2030, 2050, 10))

# Read in datasets
isimip.future <- mclapply(
  files, function(x)
    open_nc_files(file = x, dname = dname, selected.years = selected.years,
                  vec = vec), mc.cores = detectCores() * 0.75
)
```

```
# PLOT ------------------------------------------------------------------------

# Create vector to name the slots
ghms <- c(c("PCR-GLOBWB", "PCR-GLOBWB"), rep(c("LPJmL", "H08"), each = 4), c("MPI-HM", "MPI-HM"
climate_scenario <- rep(c(60, 26), 6)
climate2 <- c(rep(2005, 4), rep(c(60, 26, 2005, 2005), 2))
names.isimip.future <- paste(paste(ghms, climate_scenario, sep = "/"), climate2, sep = ".")

# Name the slots
names(isimip.future) <- names.isimip.future

for(i in names(isimip.future)) {
  names(isimip.future[[i]]) <- selected.years
}

# Arrange data
isimip.future.dt <- lapply(isimip.future, function(x) rbindlist(x, idcol = "Year")) %>%
  rbindlist(., idcol = "Model") %>%
  .[!Continent == "Oceania"] %>%
  separate(., "Model", c("Model", "Climate scenario"), "/") %>%
  na.omit()

Cont <- unique(isimip.future.dt$Continent)
water.tmp <- isimip.future.dt[Country %in% data.table(water.quantiles)[, Country]]

gg <- list()
for(j in Cont) {
  gg[[j]] <- water.quantiles[Continent == j] %>%
    ggplot(., aes(reorder(Country, median), median)) +
    geom_point() +
    geom_point(data = water.tmp[Year == "2050" & Continent == j],
               aes(reorder(Country, Water.Withdrawn), Water.Withdrawn,
                   shape = `Climate scenario`,
                   color = Model)) +
    geom_errorbar(aes(ymin = min,
```

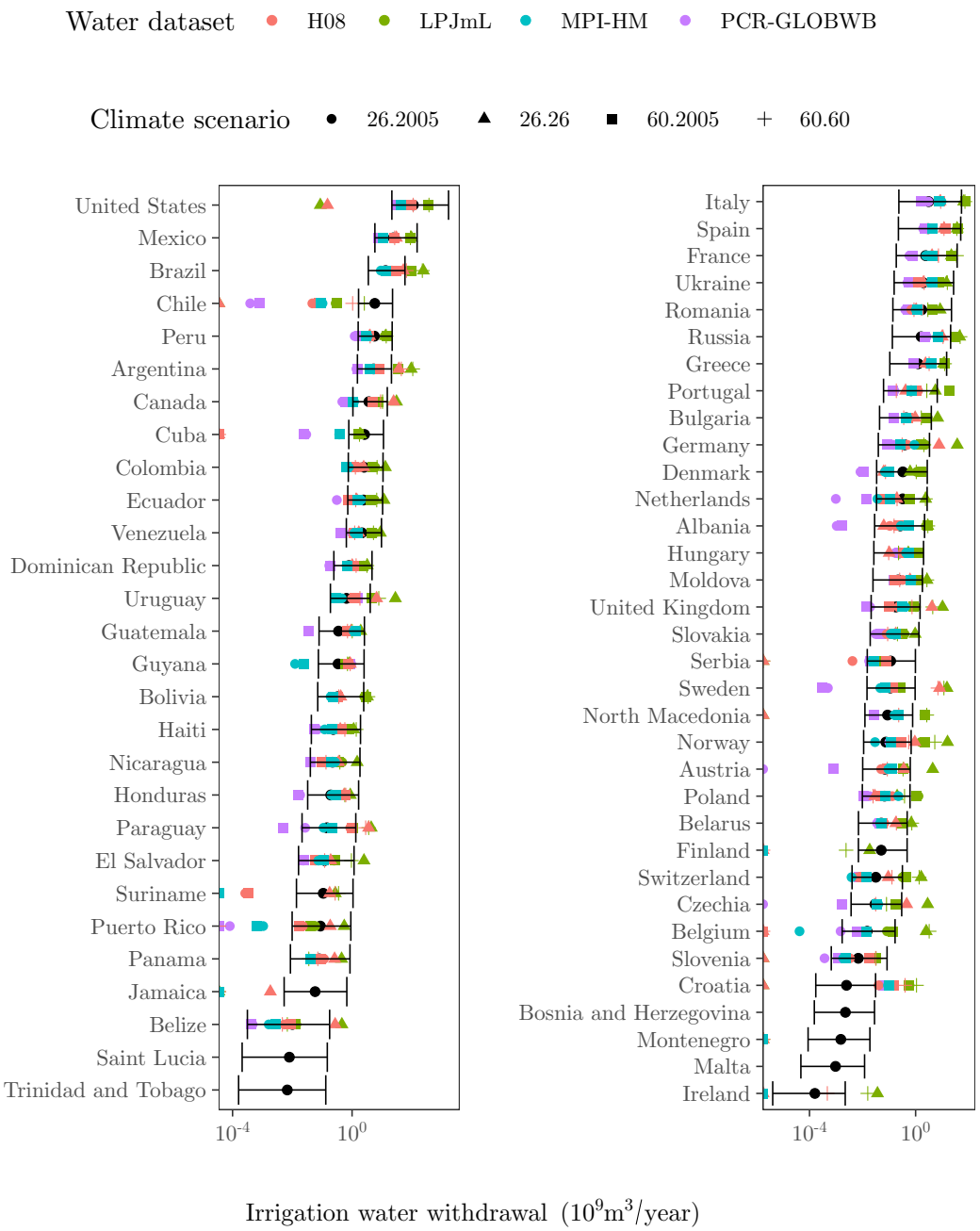
```
                      ymax = max)) +
    scale_y_log10(breaks = trans_breaks("log10", function(x) 10 ^ (2 * x)),
                  labels = trans_format("log10", math_format(10 ^ .x))) +
    scale_color_discrete(name = "Water dataset") +
    labs(y = "", x = "") +
    coord_flip() +
    theme_AP() +
    theme(legend.position = "none")
}

legend <- get_legend(gg[[1]] +
                       theme(legend.position = "top",
                             legend.box = "vertical"))
```

```
## Warning: Transformation introduced infinite values in continuous y-axis
```

```
bottom1 <- plot_grid(gg[[1]] + theme(legend.position = "none"),
                     gg[[2]] + theme(legend.position = "none"), ncol = 2)
```

```
## Warning: Transformation introduced infinite values in continuous y-axis

## Warning: Transformation introduced infinite values in continuous y-axis
```

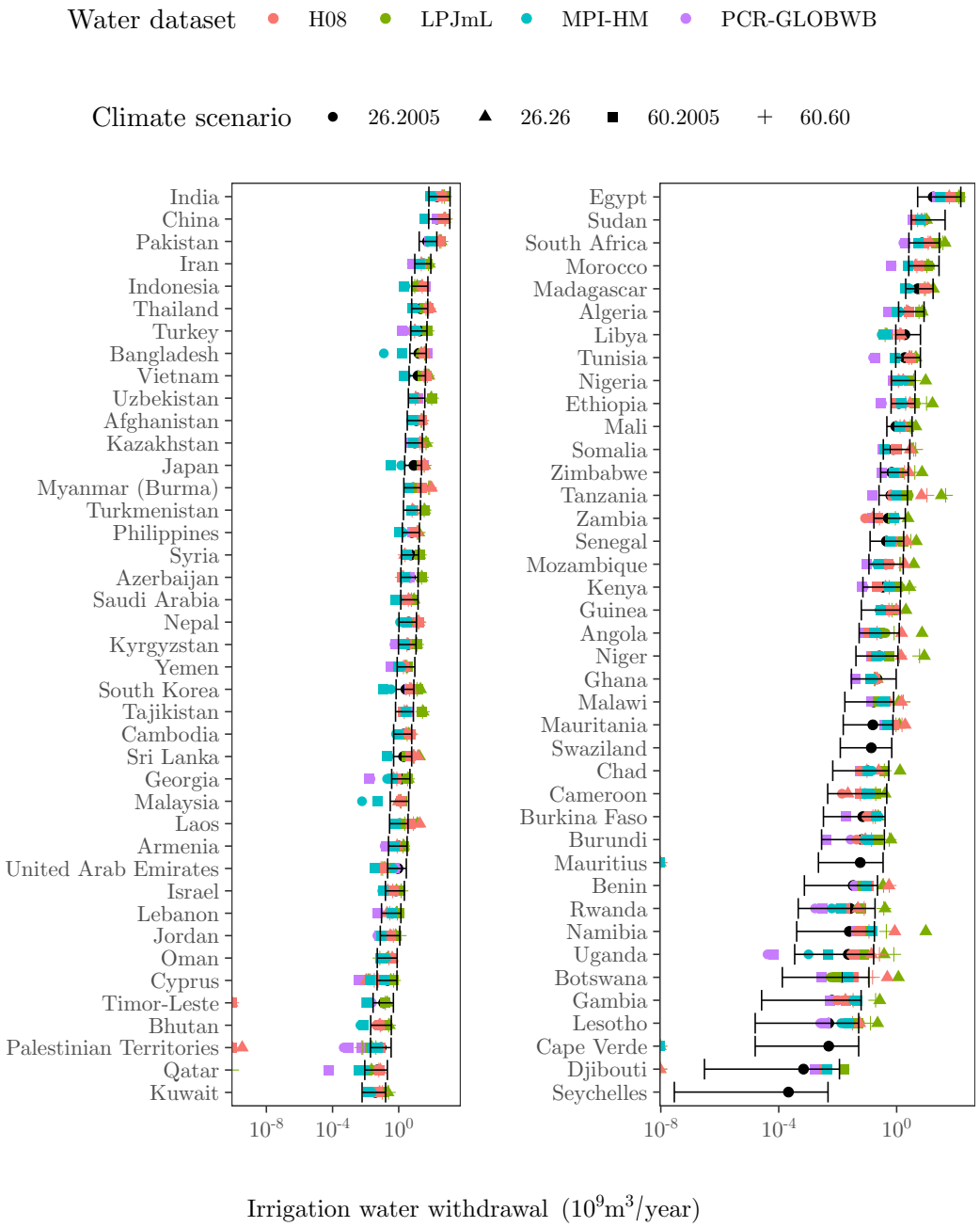
```
all1 <- plot_grid(legend, bottom1, rel_heights = c(0.2, 1), ncol = 1)
grid.arrange(arrangeGrob(all1, bottom = grid::textGrob(
  label = expression(paste("Irrigation water withdrawal ", " ", "(", 10^9, m^3/year, "", ")")))
```




```
bottom2 <- plot_grid(gg[[3]] + theme(legend.position = "none"),
                     gg[[4]] + theme(legend.position = "none"), ncol = 2)
```

```
## Warning: Transformation introduced infinite values in continuous y-axis

## Warning: Transformation introduced infinite values in continuous y-axis
```

```
all2 <- plot_grid(legend, bottom2, rel_heights = c(0.2, 1), ncol = 1)
grid.arrange(arrangeGrob(all2, bottom = grid::textGrob(
  label = expression(paste("Irrigation water withdrawal ", " ", "(", 10^9, m^3/year, "", ")")))
```



8 The model

8.1 Create lookup table

```
# CREATE LOOKUP TABLE ----------------------------------------------------------

lookup <- setkey(all.results, index)

# EXPORT DATASETS --------------------------------------------------------------

fwrite(full.imput, "full.imput.csv")
```

```
fwrite(results, "results.csv")
fwrite(lookup, "lookup.csv")
fwrite(water.quantiles, "water.quantiles.csv")
```

8.2 Sample matrix

```
# DEFINE THE SETTINGS OF THE SAMPLE MATRIX ------------------------------------

Continents <- c("Africa", "Americas", "Asia", "Europe")

# Create a vector with the name of the columns
parameters <- paste("X", 1:4, sep = "")

# Select sample size
n <- 2 ^ 13

# Define order
order <- "third"
```

```
# CREATE THE SAMPLE MATRIX ----------------------------------------------------

# Create an A, B and AB matrices for each continent
sample.matrix <- lapply(Continents, function(Continents)
  sobol_matrices(N = n,
                 params = parameters,
                 order = order) %>%
    data.table())

# Name the slots, each is a continent
names(sample.matrix) <- Continents

# Name the columns
sample.matrix <- lapply(sample.matrix, setnames, parameters)
```

```
# TRANSFORM THE SAMPLE MATRIX -------------------------------------------------

# Function to transform sample matrix to appropriate distributions
transform_sample_matrix <- function(dt) {
  dt[, X1:= floor(X1 * (10 - 1 + 1)) + 1] %>%
    .[, X1:= ifelse(X1 == 1, "LPJmL",
                    ifelse(X1 == 2, "H08",
                           ifelse(X1 == 3, "PCR-GLOBWB",
                                  ifelse(X1 == 4, "WaterGap",
                                         ifelse(X1 == 5, "Aquastat",
                                                ifelse(X1 == 6, "Liu et al. 2016",
                                                       ifelse(X1 == 7, "DBHM",
                                                              ifelse(X1 == 8, "VIC",
                                                                     ifelse(X1 == 9, "MPI-HM",
```

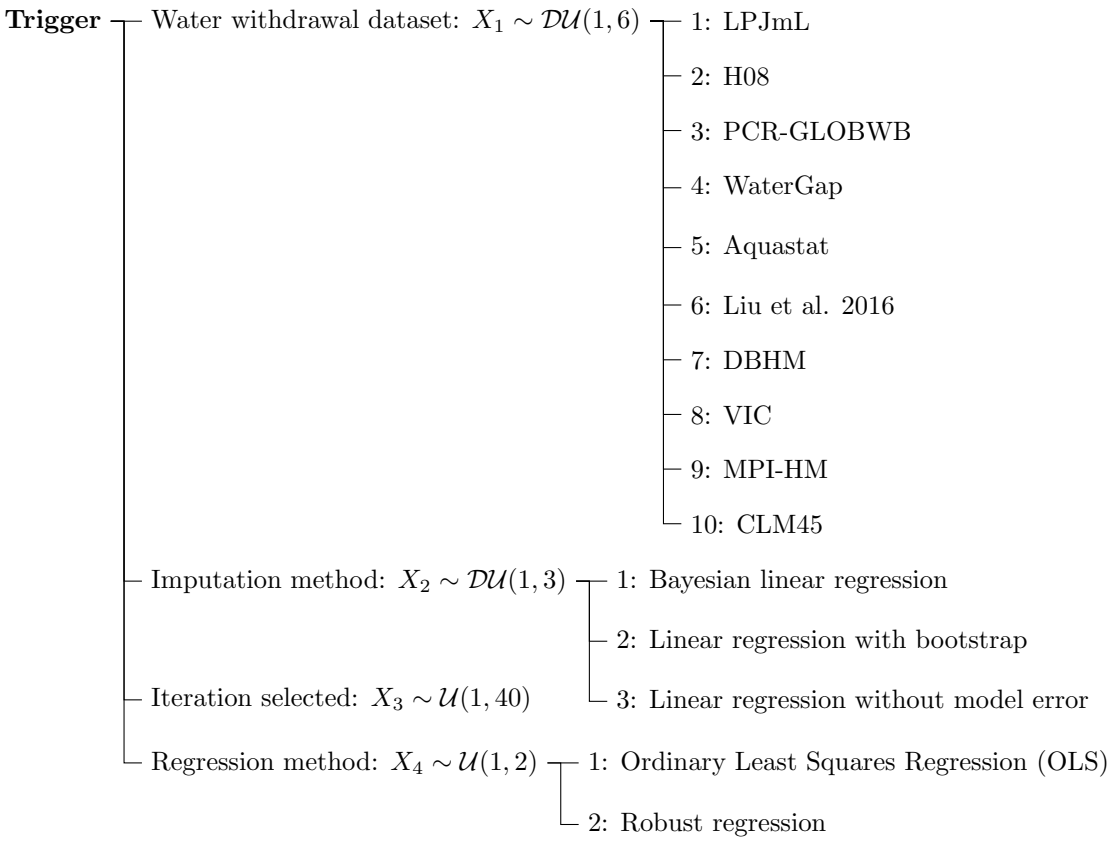


Figure 5: Tree diagram coding the discrete probability distributions of each trigger into each uncertainty level.

```
    .[, X2:= floor(X2 * (length(imputation.methods) - 1 + 1)) + 1] %>%
    .[, X2:= ifelse(X2 == 1, imputation.methods[1],
                    ifelse(X2 == 2, imputation.methods[2], imputation.methods[3]))] %>%
    .[, X3:= floor(X3 * (m.iterations - 1 + 1)) + 1] %>%
    .[, X4:= floor(X4 * (2 - 1 + 1)) + 1] %>%
    .[, X4:= ifelse(X4 == 1, "Normal", "Robust")]
}

sample.matrix <- lapply(sample.matrix, transform_sample_matrix)
sample.matrix.dt <- rbindlist(sample.matrix, idcol = "Continent")
```

We then print out the sample matrix to allow the reader understand its organization.

```
# PRINT SAMPLE MATRIX ------------------------------------------------------------

print(sample.matrix.dt)
```

```
##         Continent              X1        X2 X3     X4
##      1:    Africa Liu et al. 2016      norm 21 Robust
##      2:    Africa             VIC norm.boot 31 Normal
##      3:    Africa      PCR-GLOBWB  norm.nob 11 Robust
##      4:    Africa        WaterGap      norm 26 Normal
##      5:    Africa          MPI-HM  norm.nob  6 Robust
##     ---
## 524284:    Europe      PCR-GLOBWB  norm.nob 21 Robust
## 524285:    Europe             VIC norm.boot  1 Normal
## 524286:    Europe Liu et al. 2016  norm.nob 11 Robust
## 524287:    Europe           LPJmL      norm 31 Normal
## 524288:    Europe           LPJmL  norm.nob 36 Robust
```

8.3 Run the model

```
# THE MODEL ----------------------------------------------------------------------

model <- function(X) lookup[.(paste0(X[, 1:5], collapse = "_"))][, r.squared]
```

```
# RUN THE MODEL------------------------------------------------------------------

# Set number of cores at 75%
n_cores <- floor(detectCores() * 0.75)

# Create cluster
cl <- makeCluster(n_cores)
registerDoParallel(cl)

# Run model in parallel
r.squared <- foreach(i=1:nrow(sample.matrix.dt),
             .packages = "data.table",
```

```
              .combine = "c") %dopar%
  {
    model(sample.matrix.dt[i])
  }

# Stop parallel cluster
stopCluster(cl)
```

```
# ARRANGE MODEL OUTPUT ------------------------------------------------------

sample.matrix.dt <- cbind(sample.matrix.dt, r.squared)

# Select the A and B matrix only (for uncertainty analysis)
AB.dt <- sample.matrix.dt[, .SD[1:(n * 2)], Continent]

# Export results
fwrite(sample.matrix.dt, "sample.matrix.dt.csv")
fwrite(AB.dt, "AB.dt.csv")
```

9 Uncertainty analysis

```
# COMPUTE QUANTILES AND MEAN ------------------------------------------------

AB.dt[, .(q0.025 = quantile(r.squared, 0.025),
          q0.1 = quantile(r.squared, 0.1),
          q0.25 = quantile(r.squared, 0.25),
          q0.5 = quantile(r.squared, 0.5),
          q0.75 = quantile(r.squared, 0.75),
          q0.975 = quantile(r.squared, 0.975),
          q0.99 = quantile(r.squared, 0.99),
          q1 = quantile(r.squared, 1),
          mean = mean(r.squared),
          median = median(r.squared)), Continent]
```

```
##    Continent    q0.025      q0.1     q0.25      q0.5     q0.75    q0.975
## 1:    Africa 0.7547564 0.8005998 0.8620280 0.8852212 0.8942089 0.9087420
## 2:  Americas 0.6834208 0.7433140 0.8283374 0.8846235 0.9129680 0.9473124
## 3:      Asia 0.6774377 0.7280933 0.8642012 0.8912723 0.9185866 0.9340638
## 4:    Europe 0.5787127 0.6548570 0.7136559 0.7569199 0.8331306 0.9341776
##        q0.99        q1      mean    median
## 1: 0.9117541 0.9336117 0.8691079 0.8852212
## 2: 0.9576745 0.9810536 0.8602771 0.8846235
## 3: 0.9367093 0.9427824 0.8643384 0.8912723
## 4: 0.9414859 0.9569898 0.7679499 0.7569199
```

```
# PLOT UNCERTAINTY ----------------------------------------------------------
```

```r
# Plot r2
unc.plot <- ggplot(AB.dt, aes(r.squared)) +
      geom_histogram(color = "black", fill = "white") +
      theme_AP() +
      labs(x = expression(italic(r) ^ 2),
           y = "Count") +
      scale_y_continuous(breaks = pretty_breaks(n = 2)) +
      scale_x_continuous(breaks = pretty_breaks(n = 3)) +
      facet_wrap(~Continent, ncol = 1) +
      theme(panel.spacing.x = unit(4, "mm"),
            strip.background = element_rect(fill = "white"))

unc.plot
```

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

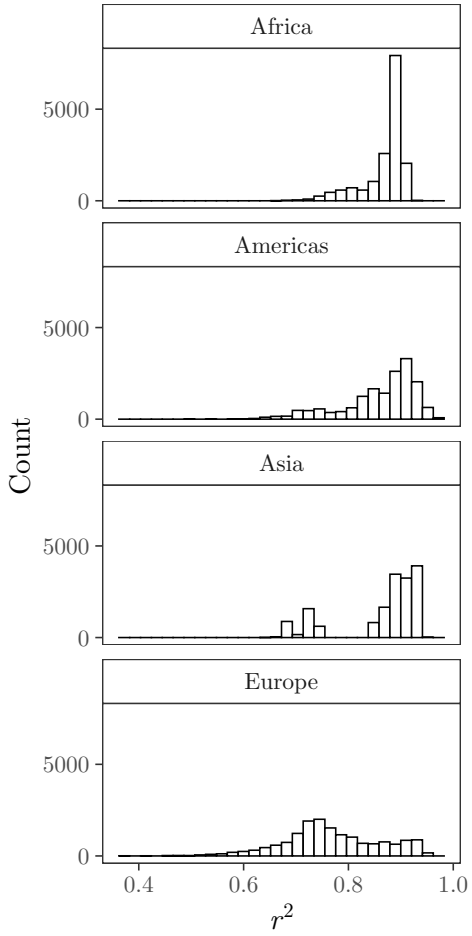


Figure 6: Uncertainty in the empirical distribution of r^2.

```r
# PLOT UNCERTAINTY IN EACH GHM AND FAO-BASED DATASET ----------------------------

unc.GHM <- AB.dt %>%
  ggplot(., aes(reorder(X1, r.squared), r.squared, fill = Continent)) +
```

```
  geom_boxplot(position = position_dodge(0.6),
               outlier.size = 0.3) +
  theme_AP() +
  labs(y = expression(italic(r)^2),
       x = "") +
  scale_x_discrete(labels = c("PCR-GLOBWB" = expression(bold(PCR-GLOBWB)),
                              "DBHM" = expression(bold(DBHM)),
                              "MPI-HM" = expression(bold(MPI-HM)),
                              "LPJmL" = expression(bold(LPJmL)),
                              "H08" = expression(bold(H08)),
                              "WaterGap" = expression(bold(WaterGap)),
                              "CLM45" = expression(bold(CLM45)),
                              "VIC" = expression(bold(VIC)))) +
  theme(legend.position = "none") +
  coord_flip()

# Get legend
legend <- get_legend(unc.GHM + theme(legend.position = "top"))
```

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

bottom <- plot_grid(unc.plot, unc.GHM, ncol = 2,
                    rel_widths = c(0.5, 1), labels = "auto")
```

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

```
all <- plot_grid(legend, bottom, ncol = 1, rel_heights = c(0.1, 1))
```

```
# PLOT CUMULATIVE EMPIRICAL DISTRIBUTION FOR R2 ---------------------------------

ggplot(AB.dt, aes(r.squared, colour = Continent)) +
  stat_ecdf() +
  labs(x = "$r^2$",
       y = "y") +
  scale_y_continuous(breaks = pretty_breaks(n = 3)) +
  theme_AP()
```

10 Sensitivity analysis

```
# PLOT SCATTERPLOTS OF PARAMETERS VS MODEL OUTPUT -------------------------------

AB.dt <- AB.dt[, X3:= factor(X3, levels = as.factor(1:m.iterations))]

scatter.dt <- melt(AB.dt[, .SD[1:n], Continent],
                   measure.vars = paste("X", 1:4, sep = ""))

# R squared
ggplot(scatter.dt, aes(r.squared, value)) +
```

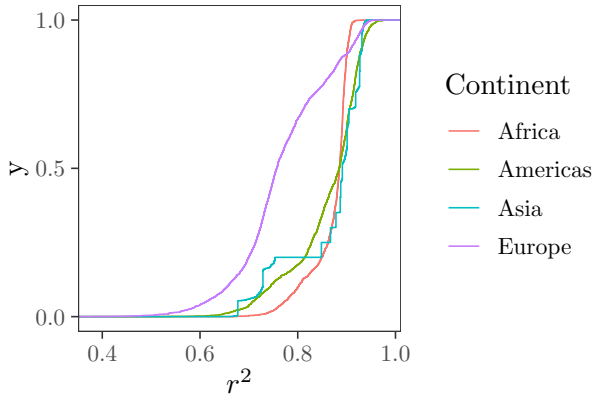


Figure 7: Cumulative empirical distribution for r^2.

```
  geom_point(alpha = 0.05, size = 0.5) +
  facet_grid(variable ~ Continent,
             scales = "free_y",
             space = "free_y") +
  labs(y = "",
       x = expression(italic(r)^2)) +
  scale_x_continuous(breaks = pretty_breaks(n = 3)) +
  scale_color_manual(values = c("#00BFC4", "#F8766D")) +
  theme_AP() +
  theme(axis.text.y = element_text(angle = 45, hjust = 1, size = 6),
        legend.position = "top")
```

```
# SENSITIVITY ANALYSIS ----------------------------------------------------

# Number of bootstrap replicas
R <- 10^3

parameters.recoded <- c("$X_1$", "$X_2$", "$X_3$", "$X_4$")

# Sobol' indices for r2
indices <- sample.matrix.dt[, sobol_indices(Y = r.squared,
                                            N = n,
                                            params = parameters.recoded,
                                            first = "jansen",
                                            R = R,
                                            boot = TRUE,
                                            parallel = "multicore",
                                            ncpus = n_cores,
                                            order = order)$results,
                            Continent]
```

```
# EXPORT SENSITIVITY INDICES ----------------------------------------------

fwrite(indices, "indices.csv")
```

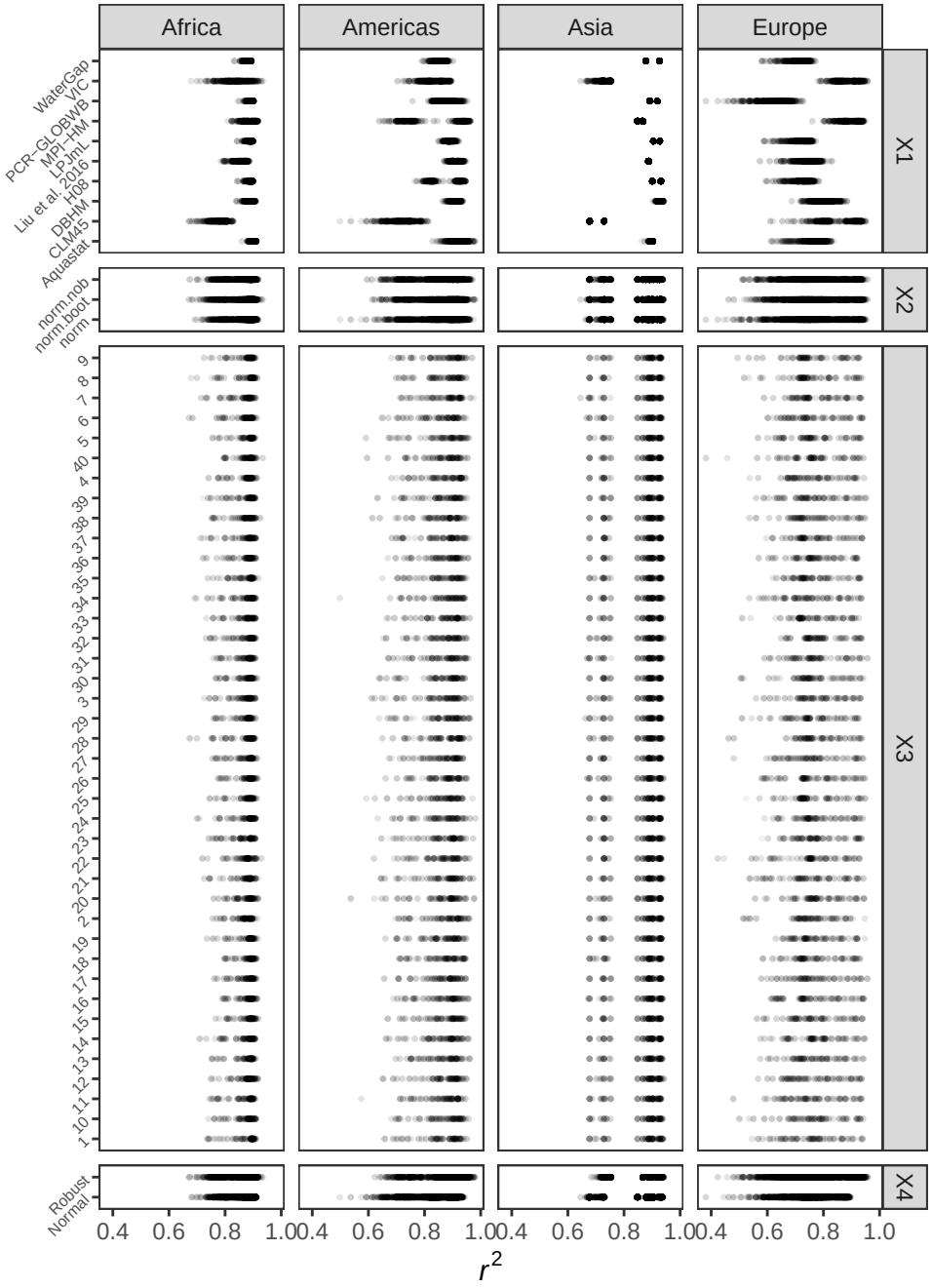


Figure 8: Scatterplots of r^2 against the triggers' levels.

```
# PLOT UNCERTAINTY AND SOBOL' INDICES ------------------------------------------

bottom <- indices[sensitivity %in% c("Si", "Ti")] %>%
  ggplot(., aes(parameters, original, fill = sensitivity)) +
    geom_bar(stat = "identity",
             position = position_dodge(0.6),
             color = "black") +
    geom_errorbar(aes(ymin = low.ci,
                      ymax = high.ci),
                  position = position_dodge(0.6)) +
    scale_y_continuous(breaks = scales::pretty_breaks(n = 3)) +
    facet_wrap(~Continent,
               ncol = 4) +
    labs(x = "",
         y = "Sobol' index") +
    scale_fill_discrete(name = "Sobol' indices",
                        labels = c(expression(S[italic(i)]),
                                   expression(T[italic(i)]))) +
    theme_AP() +
    theme(legend.position = "top",
          strip.background = element_rect(fill = "white"))

bottom
```

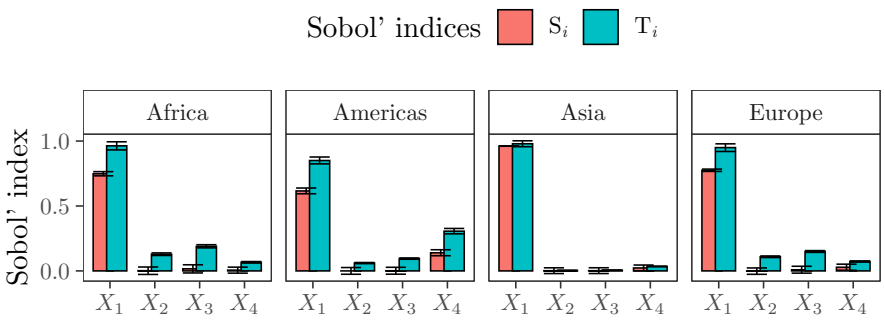


Figure 9: Sobol' indices. S_i and T_i refer respectively to Sobol' first and total order indices. S_i measures the influence of a parameter in the model output, while T_i measures the influence of a parameter jointly with its interactions.

```
# MERGE UNCERTAINTY AND SENSITIVITY ANALYSIS PLOTS -----------------------------

plot_grid(all, bottom, align = "hv", rel_heights = c(0.8, 0.4),
          labels = c("", "c"), ncol = 1)
```

```
## Warning: Graphs cannot be vertically aligned unless the axis parameter is set.
## Placing graphs unaligned.
```

```
## Warning: Graphs cannot be horizontally aligned unless the axis parameter is set.
## Placing graphs unaligned.
```

```
# CHECK SUM OF FIRST-ORDER INDICES ----------------------------------------------
```

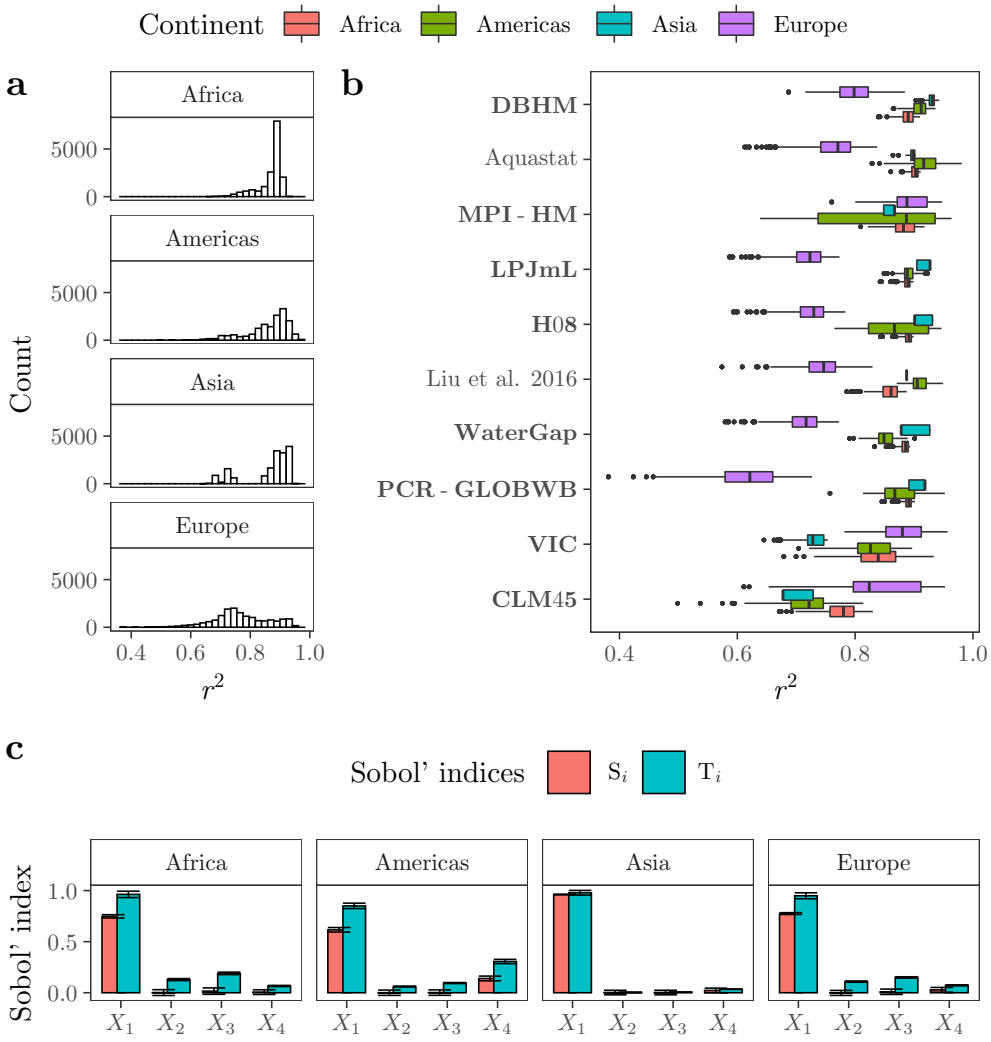


Figure 10: Uncertainty and sensitivity analysis. a) Empirical distribution for r^2 at the continental level. b) Boxplots of r^2 values obtained when regressions where run with GHM (in bold) and FAO-based datasets. c) Sobol' indices. S_i and T_i refer respectively to Sobol' first and total order indices. S_i measures the influence of a parameter in the model output, while T_i measures the influence of a parameter jointly with its interactions.

```
indices[sensitivity == "Si",  sum(original), Continent]
```

```
##    Continent        V1
## 1:    Africa 0.7720726
## 2:  Americas 0.7566790
## 3:      Asia 0.9877018
## 4:    Europe 0.8099094
```

```
# PLOT SOBOL' INDICES (SECOND AND THIRD ORDER) ------------------------------------

indices[sensitivity == "Sij" | sensitivity == "Sijk"] %>%
  .[low.ci > 0] %>%
  .[, sensitivity:= ifelse(sensitivity %in% "Sij", "$S_{ij}$",
                           "$S_{ijk}$")] %>%
  ggplot(., aes(reorder(parameters, original), original, color = Continent)) +
  geom_point(position = position_dodge(0.6)) +
  geom_errorbar(aes(ymax = high.ci, ymin = low.ci),
                position = position_dodge(0.6)) +
  geom_hline(yintercept = 0,
             lty = 2,
             color = "red") +
  facet_grid(~sensitivity,
             scales = "free_x",
             space = "free_x") +
  scale_color_discrete(name = "Continent") +
  scale_y_continuous(breaks = pretty_breaks(n = 3)) +
  labs(x = "",
       y = "Sobol' index") +
  theme_AP()
```

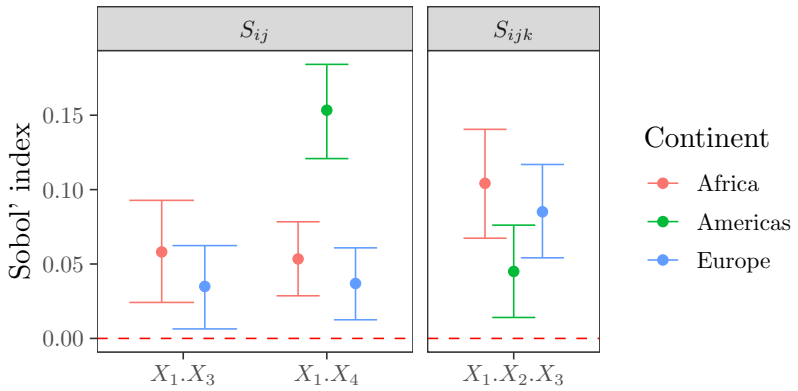


Figure 11: High-order interactions between the triggers. The dots and the errorbars show the mean and the 95% confidence intervals after bootstraping (R=1000).

11 Irrigated areas vs irrigation water withdrawals at different scales

11.1 Australia (scheme level), USA (State level) and Colorado (County level)

```
# RETRIEVE DATA FROM DIFFERENT SCALES ------------------------------------------

# Australia irrigation schemes -------------------------------------

australia.scheme <- fread("australia_scheme.csv")

# Filter out NA and rows with 0
australia.dt <- australia.scheme[, lapply(.SD, function(x)
  ifelse(x == 0, NA, x))] %>%
  na.omit() %>%
  .[, Year:= factor(Year, levels = c("97.98", "2002.2003"))] %>%
  .[, Year:= gsub("\\.", "-", Year)] %>%
  .[, Scale:= "Australian \n irrigation systems"]

# USA level ---------------------------------------------------------

# Irrigated area is in thousand acres
# Water withdrawals in thousand acres feet

# To convert from acre feet to cubic meters, multiply IWW by 1233.48.
# To convert from acre to ha, divide the area value by 2.471.

col_transf <- c("Irrigated.Area", "Water.Withdrawal")

solley.dt <- fread("solley.dt.csv") %>%
  .[, Scale:= "USA states"] # state level

colorado.dt <- fread("colorado_data.csv") # colorado
colorado.dt <- colorado.dt[, `:=`(Irrigated.Area = Flood + Sprinkler + Micro,
                                  Water.Withdrawal = Groundwater + Surface.water)] %>%
  .[, .SD, .SDcols = (col_transf)] %>%
  .[, Scale:= "Colorado counties"]

# Merge both data sets
usa.dt <- rbind(solley.dt, colorado.dt) %>%
  .[, Irrigated.Area:= (Irrigated.Area * 1000) / 2.471] %>%
  .[, Water.Withdrawal:= Water.Withdrawal * 1000 * 1233.48]
```

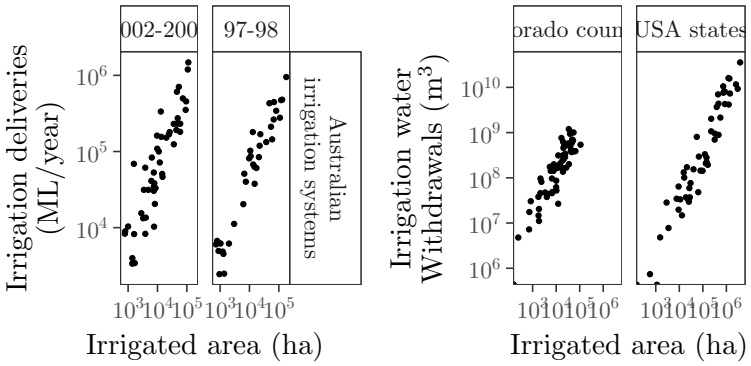
```
# PLOT SCATTERPLOT -------------------------------------------------------------

scatter_usa <- ggplot(usa.dt, aes(Irrigated.Area, Water.Withdrawal)) +
  geom_point(size = 0.6) +
  scale_x_log10(labels = trans_format("log10", math_format(10 ^ .x))) +
```

```
  scale_y_log10(labels = trans_format("log10", math_format(10 ^ .x))) +
  labs(x = "Irrigated area (ha)",
       y = "Irrigation water \n Withdrawals (m$^3$)") +
  facet_wrap(~Scale) +
  theme_AP() +
  theme(strip.background = element_rect(fill = "white"))

scatter_australia <- ggplot(australia.dt, aes(Irrigated.Area, Water.Withdrawal)) +
  geom_point(size = 0.6) +
  scale_x_log10(labels = trans_format("log10", math_format(10 ^ .x))) +
  scale_y_log10(labels = trans_format("log10", math_format(10 ^ .x))) +
  facet_grid(Scale~Year) +
  labs(x = "Irrigated area (ha)",
       y = "Irrigation deliveries \n (ML/year)") +
  theme_AP() +
  theme(strip.background = element_rect(fill = "white"))

all_scatters <- plot_grid(scatter_australia, scatter_usa, ncol = 2)
```

```
## Warning: Transformation introduced infinite values in continuous x-axis
```

```
## Warning: Transformation introduced infinite values in continuous y-axis
```

```
all_scatters
```




```
# COMPUTE REGRESSIONS AND BOOTSTRAP ------------------------------------------

# AUSTRALIA IRRIGATION SYSTEMS ----------------------------------

australia.dt <- australia.dt[, (col_transf):= lapply(.SD, log10), .SDcols = col_transf]

australia.regressions <- australia.dt %>%
  group_by(Year) %>%
  nest() %>%
  mutate(fit = map(.x = data, .f = ~lm(Water.Withdrawal~ Irrigated.Area,
                                       data = .)),
         results = map(fit, glance),
         residuals = map(fit, augment))
```

```r
# Bootstrap
foo <- boot(australia.dt, function(data,indices)
  summary(lm(Water.Withdrawal ~ Irrigated.Area,
             data[indices, ] ))$r.squared, R = 5000)

# Confidence intervals
ci_plot <- boot.ci(foo, type = "all")
```

```
## Warning in boot.ci(foo, type = "all"): bootstrap variances needed for
## studentized intervals
```

```r
# USA LEVEL (COLORADO COUNTY AND COUNTY LEVEL) -------------------

usa.dt.lm <- usa.dt[, (col_transf):= lapply(.SD, log10), .SDcols = col_transf] %>%
  NaRV.omit()

usa.regressions <- usa.dt.lm %>%
  group_by(Scale) %>%
  nest() %>%
  mutate(fit = map(.x = data, .f = ~lm(Water.Withdrawal~ Irrigated.Area,
                                       data = .)),
         results = map(fit, glance),
         residuals = map(fit, augment))

# Bootstrap
usa.loop <- c("USA states", "Colorado counties")
foo.usa <- lapply(usa.loop, function(x)
  boot(usa.dt.lm[Scale == x], function(data,indices)
    summary(lm(Water.Withdrawal ~ Irrigated.Area,
               data[indices, ] ))$r.squared, R = 5000))

names(foo.usa) <- usa.loop

# Confidence intervals
ci_plot2 <- lapply(foo.usa, function(x) boot.ci(x, type = "all"))
```

```
## Warning in boot.ci(x, type = "all"): bootstrap variances needed for studentized
## intervals
```

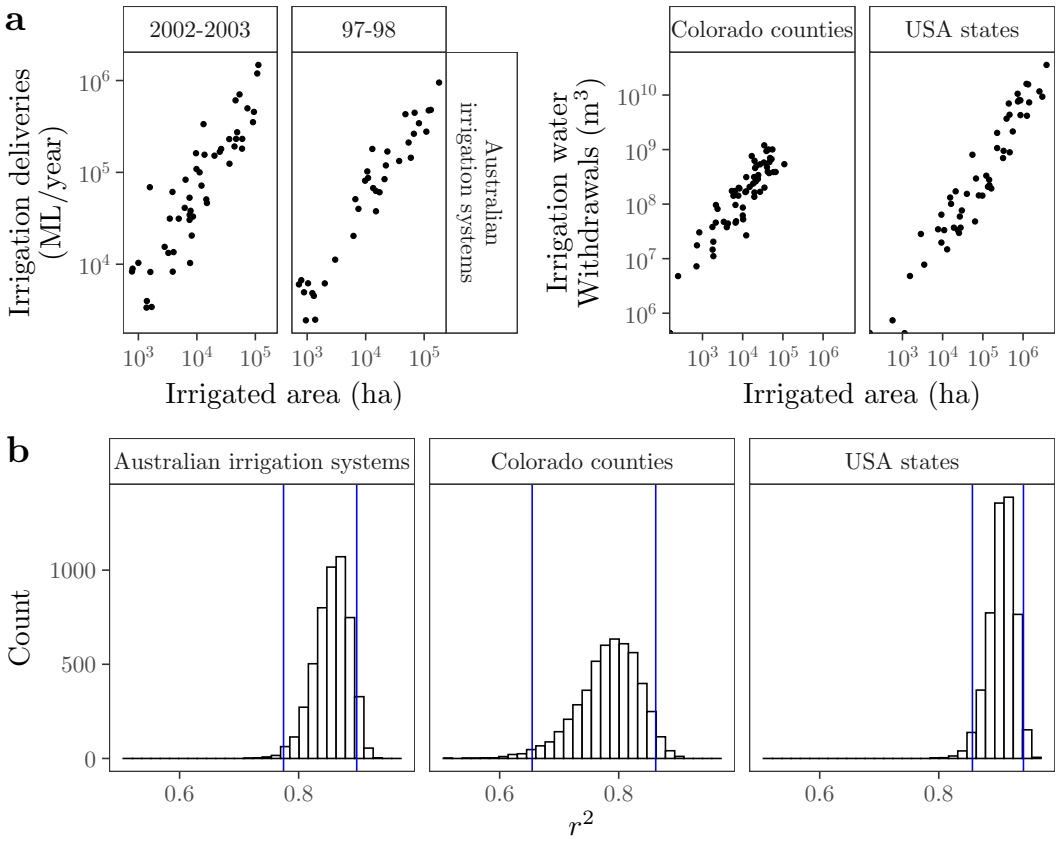
```
## Warning in boot.ci(x, type = "all"): bootstrap variances needed for studentized
## intervals
```

```r
ci.dt <- data.table(Scale = c("USA states", "Colorado counties", "Australian irrigation systems
                    low.ci = c(ci_plot2$`USA states`$bca[[4]],
                               ci_plot2$`Colorado counties`$bca[[4]],
                               ci_plot$bca[[4]]),
                    high.ci = c(ci_plot2$`USA states`$bca[[5]],
                                ci_plot2$`Colorado counties`$bca[[5]],
                                ci_plot$bca[[5]])) %>%
```

```
  melt(., measure.vars = c("low.ci", "high.ci"))
```

```
# PLOT ALL ------------------------------------------------------------------

tmp <- lapply(usa.loop, function(x) foo.usa[[x]]$t) %>%
  lapply(., data.table)

names(tmp) <- usa.loop

all.histo <- rbindlist(tmp, idcol = "Scale") %>%
  rbind(., data.table(foo$t) %>%
          .[, Scale:= "Australian irrigation systems"] %>%
          setcolorder(., c("Scale", "V1"))) %>%
  .[, Scale:= factor(Scale, levels = c("Colorado counties", "USA states",
                                       "Australian irrigation systems"))] %>%
  ggplot(., aes(V1, group = Scale)) +
  geom_histogram(color = "black", fill = "white") +
  geom_vline(data = ci.dt, aes(xintercept = value), color = "blue") +
  labs(x = "$r^2$",
       y = "Count") +
  facet_wrap(~Scale) +
  scale_x_continuous(breaks = pretty_breaks(n = 3)) +
  theme_AP() +
  theme(strip.background = element_rect(fill = "white"))

plot_grid(all_scatters, all.histo, ncol = 1, labels = "auto")
```

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

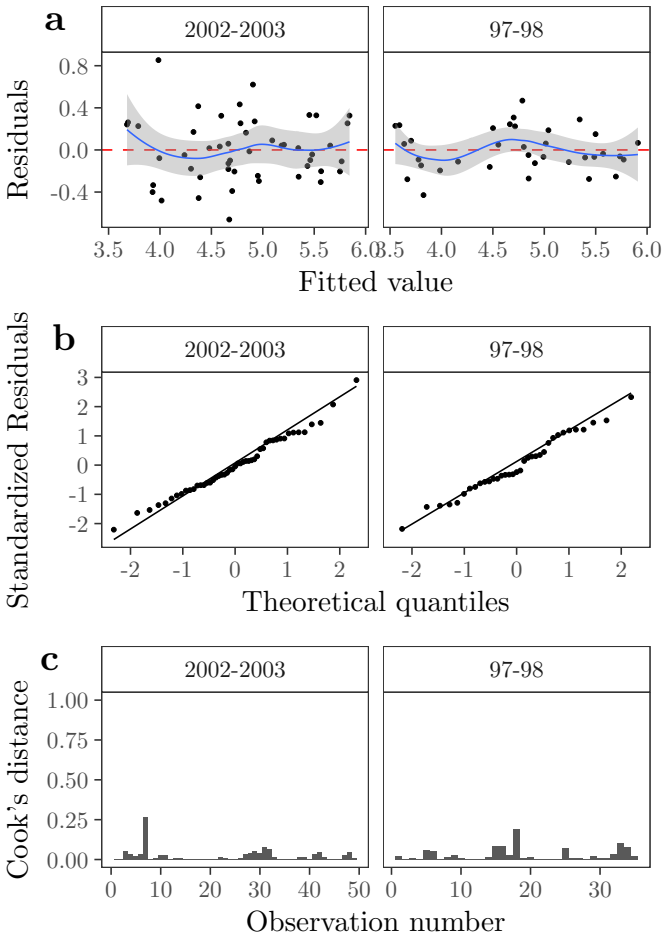


11.2 Regression diagnostics

```
# REGRESSION DIAGNOSTICS ------------------------------------------------------

# AUSTRALIA -------------------------------------
australia.residuals <- australia.regressions  %>%
  dplyr::select(Year, residuals) %>%
  unnest(residuals) %>%
  data.table()

# USA  ------------------------------------------
usa.residuals <- usa.regressions  %>%
  dplyr::select(Scale, residuals) %>%
  unnest(residuals) %>%
  data.table()

# functions to plot:

# residuals versus fitted
plot_res <- function(dt) {
  gg <- ggplot(dt, aes(.fitted, .resid)) +
    geom_point(size = 0.5) +
    geom_hline(yintercept = 0, lty = 2, color = "red") +
```

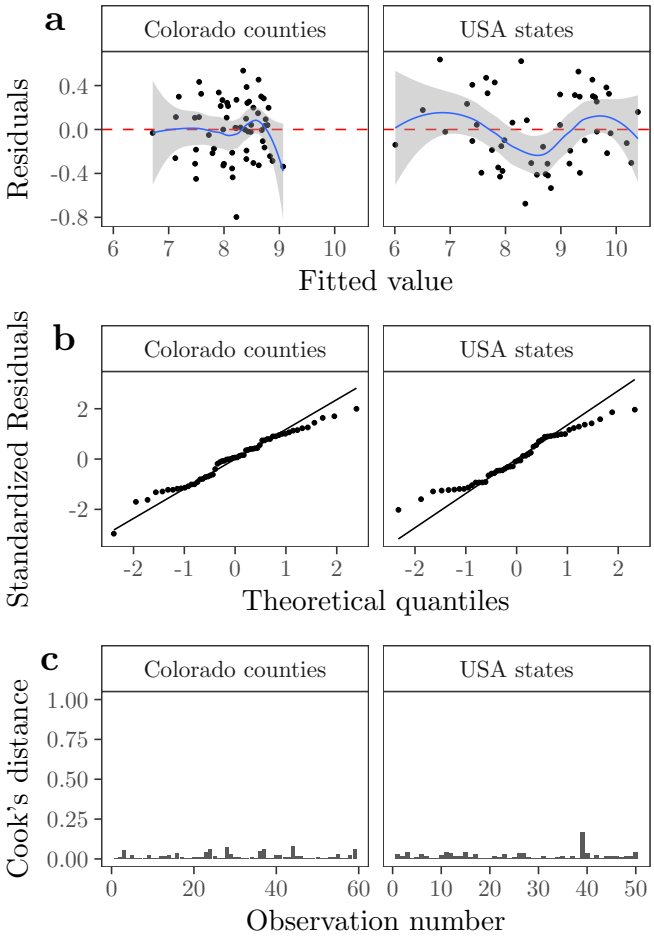
```
    geom_smooth(size = 0.5) +
    labs(x = "Fitted value", y = "Residuals") +
    theme_AP() +
    theme(strip.text.y = element_text(size = 6.4),
          strip.background = element_rect(fill = "white"))
  return(gg)
}

# qq plot
plot_qq <- function(dt) {
  gg <- ggplot(dt, aes(sample = .std.resid)) +
    stat_qq(size = 0.5) +
    stat_qq_line() +
    labs(x = "Theoretical quantiles",
         y = "Standardized Residuals") +
    theme_AP() +
    theme(strip.text.y = element_text(size = 6.4),
          strip.background = element_rect(fill = "white"))
  return(gg)
}

# PLOT FOR AUSTRALIA ------------------

a <- plot_res(australia.residuals) +
  facet_grid(~Year, scales = "free_y")

b <- plot_qq(australia.residuals) +
  facet_grid(~Year, scales = "free_y")

ID <- australia.residuals[, .N, Year]
numb <- unlist(sapply(ID[, N], function(x) 1:x))
c <- cbind(australia.residuals, numb) %>%
  ggplot(., aes(numb, .cooksd)) +
  geom_col() +
  scale_y_continuous(limits = c(0, 1)) +
  facet_grid(~Year, scales = "free_x") +
  theme_AP() +
  labs(x = "Observation number", y = "Cook's distance") +
  theme(strip.text.y = element_text(size = 6.4),
        strip.background = element_rect(fill = "white"))

plot_grid(a, b, c, labels = "auto", ncol = 1, align = "hv", hjust = -2.5)
```

```
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
```




```r
# PLOT FOR USA ------------------------

a <- plot_res(usa.residuals) +
  facet_grid(~Scale, scales = "free_y")

b <- plot_qq(usa.residuals) +
  facet_grid(~Scale, scales = "free_y")

ID <- usa.residuals[, .N, Scale]
numb <- unlist(sapply(ID[, N], function(x) 1:x))
c <- cbind(usa.residuals, numb) %>%
  ggplot(., aes(numb, .cooksd)) +
  geom_col() +
  scale_y_continuous(limits = c(0, 1)) +
  facet_grid(~Scale, scales = "free_x") +
  theme_AP() +
  labs(x = "Observation number", y = "Cook's distance") +
  theme(strip.text.y = element_text(size = 6.4),
        strip.background = element_rect(fill = "white"))

plot_grid(a, b, c, labels = "auto", ncol = 1, align = "hv", hjust = -2.5)
```

```
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
```



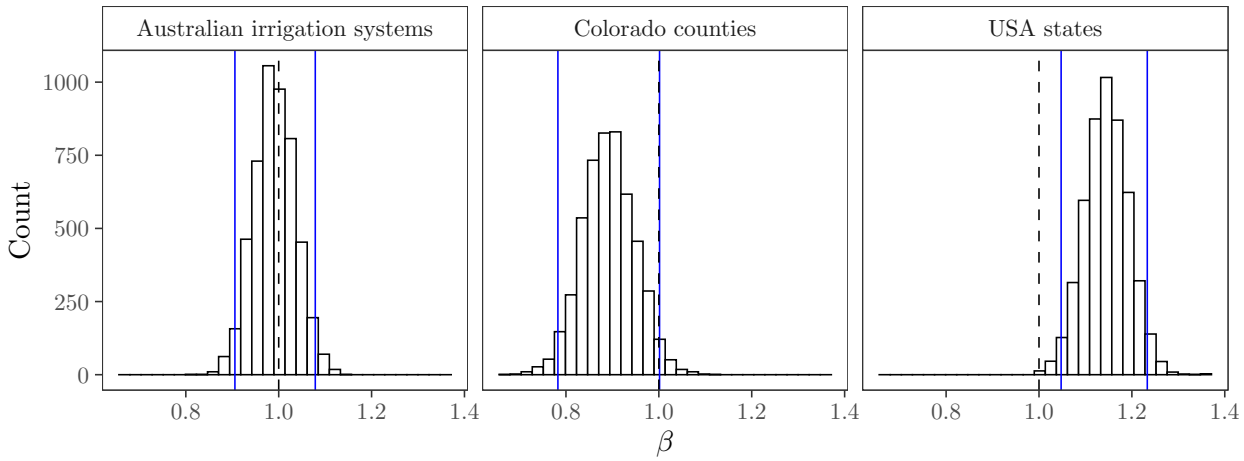

```
# BOOTSTRAP BETA  ----------------------------------------------------------------

# Australia
foo.beta <- boot(australia.dt, function(data,indices)
  coef(lm(Water.Withdrawal ~ Irrigated.Area,
          data[indices, ]))[[2]], R = 5000)

# USA
foo.states <- boot(usa.dt.lm[Scale == "USA states"], function(data,indices)
  coef(lm(Water.Withdrawal ~ Irrigated.Area,
          data[indices, ]))[[2]], R = 5000)

foo.counties <- boot(usa.dt.lm[Scale == "Colorado counties"], function(data,indices)
  coef(lm(Water.Withdrawal ~ Irrigated.Area,
          data[indices, ]))[[2]], R = 5000)

# Confidence intervals
ci_plot2 <- lapply(list(foo.states,
                        foo.counties,
                        foo.beta), function(x) boot.ci(x, type = "all"))
```

```
## Warning in boot.ci(x, type = "all"): bootstrap variances needed for studentized
## intervals

## Warning in boot.ci(x, type = "all"): bootstrap variances needed for studentized
## intervals

## Warning in boot.ci(x, type = "all"): bootstrap variances needed for studentized
## intervals
```

```
names(ci_plot2) <- c("USA states", "Colorado counties", "Australian irrigation systems")

ci.dt <- data.table(Scale = c("USA states", "Colorado counties", "Australian irrigation systems
                    low.ci = c(ci_plot2$`USA states`$bca[[4]],
                               ci_plot2$`Colorado counties`$bca[[4]],
                               ci_plot2$`Australian irrigation systems`$bca[[4]]),
                    high.ci = c(ci_plot2$`USA states`$bca[[5]],
                                ci_plot2$`Colorado counties`$bca[[5]],
                                ci_plot2$`Australian irrigation systems`$bca[[5]])) %>%
  melt(., measure.vars = c("low.ci", "high.ci"))

tmp <- rbind(data.table(foo.states$t)[, Scale:= "USA states"],
             data.table(foo.counties$t)[, Scale:= "Colorado counties"],
             data.table(foo.beta$t)[, Scale:= "Australian irrigation systems"])
```

```
# PLOT BETA ------------------------------------------------------------------

# Plot
  ggplot(tmp, aes(V1)) +
  geom_histogram(color = "black", fill = "white") +
  geom_vline(data = ci.dt, aes(xintercept = value), color = "blue") +
  geom_vline(xintercept = 1, lty = 2) +
  labs(x = "$\\beta$", y = "Count") +
  facet_wrap(~Scale) +
  scale_x_continuous(breaks = pretty_breaks(n = 3)) +
  theme_AP() +
  theme(strip.background = element_rect(fill = "white"))
```

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



12 Irrigated area at the cell level

```
# PIXEL LEVEL ------------------------------------------------------------------

ncin <- nc_open("histsoc_landuse-totals_annual_1861_2005.nc")
lon <- ncvar_get(ncin, "lon")
lat <- ncvar_get(ncin, "lat")
tmp_array <- ncvar_get(ncin, "cropland_irrigated")
m <- (dim(tmp_array)[3] - 11):dim(tmp_array)[3]
tmp_slice <- lapply(m, function(m) tmp_array[, , m])
lonlat <- as.matrix(expand.grid(lon,lat))
tmp_vec <- lapply(tmp_slice, function(x) as.vector(x))
tmp_df01 <- lapply(tmp_vec, function(x) data.frame(cbind(lonlat, x)))
names(tmp_df01) <- m
da <- lapply(tmp_df01, data.table) %>%
  rbindlist(., idcol = "month") %>%
  na.omit() %>%
  .[!x == 0]
Country <- coords2country(da[1:nrow(da), 2:3])
df <- cbind(Country, da)
setDT(df)
df <- setnames(df, c("Var1", "Var2"), c("lon", "lat"))
mirca <- na.omit(df)[, .(area = mean(x)), .(Country, lon, lat)] %>%
  .[order(Country)]

# Function to open the Huang datasets
open_nc_mirca <- function(file, dname) {
  nc <- nc_open(file)
  ww <- ncvar_get(nc, dname)
  lon <- ncvar_get(nc, "lon")
  lat <- ncvar_get(nc, "lat")
  water <- rowSums(ww[, 469:ncol(ww)])
  ww.df <- data.frame(cbind(lon, lat, water))
```

```
  setDT(ww.df)
  ww.df <- ww.df[!water == 0]
  Country <- coords2country(ww.df[1:nrow(ww.df), 1:2])
  dt <- cbind(Country, ww.df) %>%
    na.omit() %>%
    .[, water:= water / 1000]
  return(dt)
}

# Function to open ISIMIP datasets
open_nc_mirca_isimip <- function(file, dname) {
  ncin <- nc_open(file)
  # get longitude, latitude, time
  lon <- ncvar_get(ncin, "lon")
  lat <- ncvar_get(ncin, "lat")
  # Get variable
  tmp_array <- ncvar_get(ncin, dname)
  # Retrieve last 12 months
  # get last year
  m <- (dim(tmp_array)[3] - 11):dim(tmp_array)[3]
  tmp_slice <- lapply(m, function(m) tmp_array[, , m])
  # create dataframe -- reshape data
  # matrix (nlon*nlat rows by 2 cols) of lons and lats
  lonlat <- as.matrix(expand.grid(lon,lat))
  # vector of `tmp` values
  tmp_vec <- lapply(tmp_slice, function(x) as.vector(x))
  # create dataframe and add names
  tmp_df01 <- lapply(tmp_vec, function(x) data.frame(cbind(lonlat, x)))
  names(tmp_df01) <- m
  da <- lapply(tmp_df01, data.table) %>%
    rbindlist(., idcol = "month") %>%
    na.omit()
  # Convert coordinates to country
  Country <- coords2country(da[1:nrow(da), 2:3])
  df <- cbind(Country, da)
  setDT(df)
  out <- na.omit(df)[, .(water = sum(x)), .(Country, Var1, Var2)] %>%
    .[, water:= water * 10000]
  out <- out[order(Country)] %>%
    .[!water == 0] %>%
    setnames(., c("Var1", "Var2"), c("lon", "lat"))
  return(out)
}

# HUANG ET AL DATASETS
names_nc_files <- c("withd_irr_lpjml.nc", "withd_irr_pcrglobwb.nc",
                    "withd_irr_h08.nc", "withd_irr_watergap.nc")
```

```
out.nc.mirca <- mclapply(names_nc_files, function(x)
  open_nc_mirca(x, "withd_irr"), mc.cores = detectCores() * 0.75)
names(out.nc.mirca) <- c("LPJmL", "PCR-GLOBWB", "H08", "WaterGap")
out.final.mirca <- rbindlist(out.nc.mirca, idcol = "Water.Dataset")

# ISIMIP DATASETS
files <- list("dbh_wfdei_nobc_hist_varsoc_co2_airrww_global_monthly_1971_2010.nc",
              "mpi-hm_miroc5_ewembi_picontrol_histsoc_co2_airrww_global_monthly_1861_2005.nc",
              "vic_wfdei_nobc_hist_pressoc_co2_airrww_global_monthly_1971_2010.nc")
dname <- "airrww"

isimip.dt.mirca <- mclapply(files, function(x)
  open_nc_mirca_isimip(file = x, dname = dname), mc.cores = detectCores() * 0.75)

names(isimip.dt.mirca) <- c("DBHM", "MPI-HM", "VIC")

# ADD CLM45
CLM45.mirca <- open_nc_mirca_isimip(file = "clm45_gfdl-esm2m_ewembi_historical_2005soc_co2_pir
                                    dname = "pirrww")

CLM45.mirca <- CLM45.mirca[, Water.Dataset:= "CLM45"] %>%
  setcolorder(., c("Water.Dataset", "Country", "lon", "lat", "water"))

final.isimip.mirca <- rbindlist(isimip.dt.mirca, idcol = "Water.Dataset") %>%
  rbind(CLM45.mirca) %>%
  rbind(out.final.mirca) %>%
  na.omit()

full.isimip <- merge(final.isimip.mirca, mirca, by = c("Country", "lon", "lat"), all.y = TRUE)

full.isimip[, `:=` (Code = countrycode(full.isimip[, Country],
                                       origin = "country.name",
                                       destination = "un"),
                    Continent = countrycode(full.isimip[, Country],
                                            origin = "country.name",
                                            destination = "continent"))]
```

```
## Warning in countrycode(full.isimip[, Country], origin = "country.name", : Some values were r
```

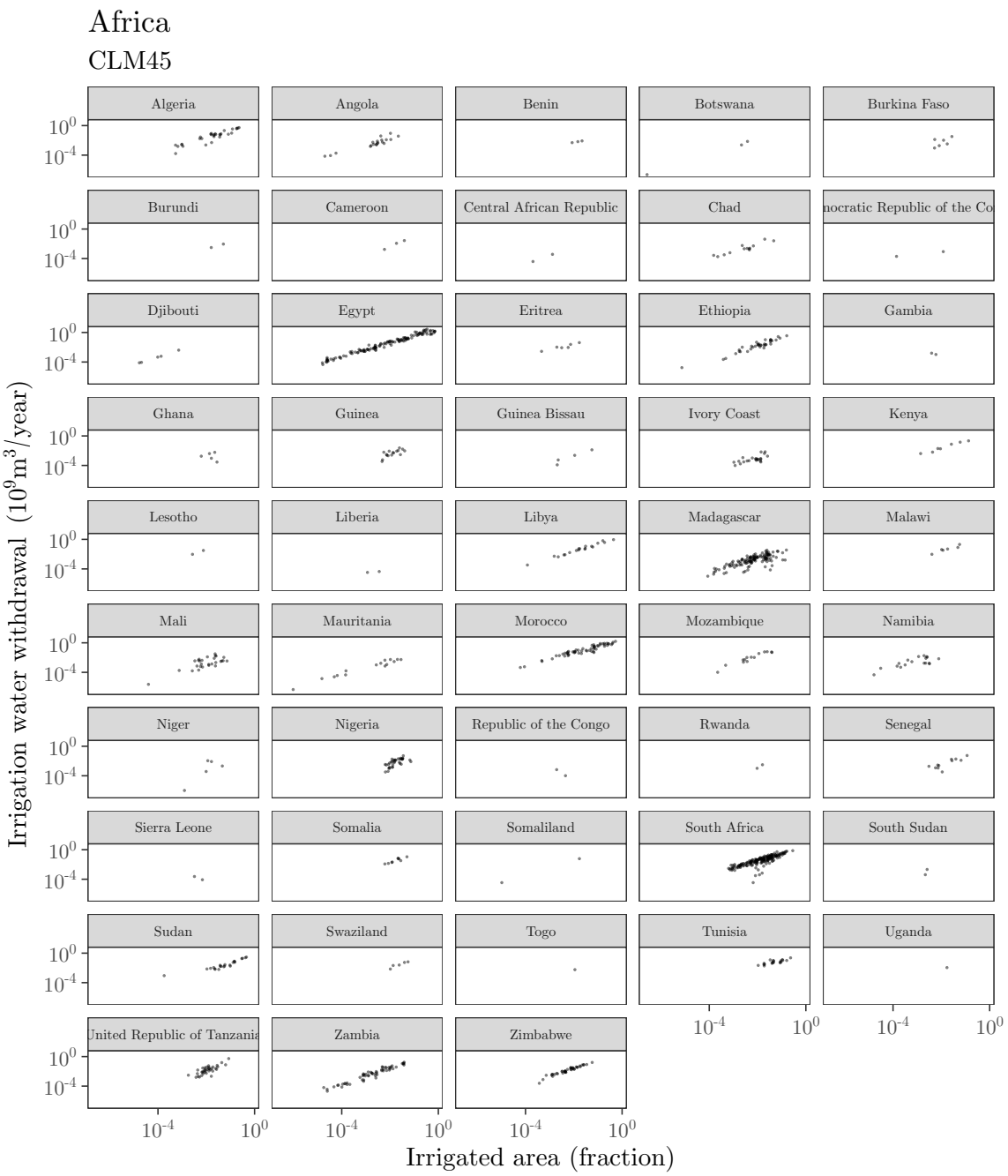
```
## Warning in countrycode(full.isimip[, Country], origin = "country.name", : Some values were r
```

```
full.isimip <- full.isimip[!Continent == "Oceania"]
```

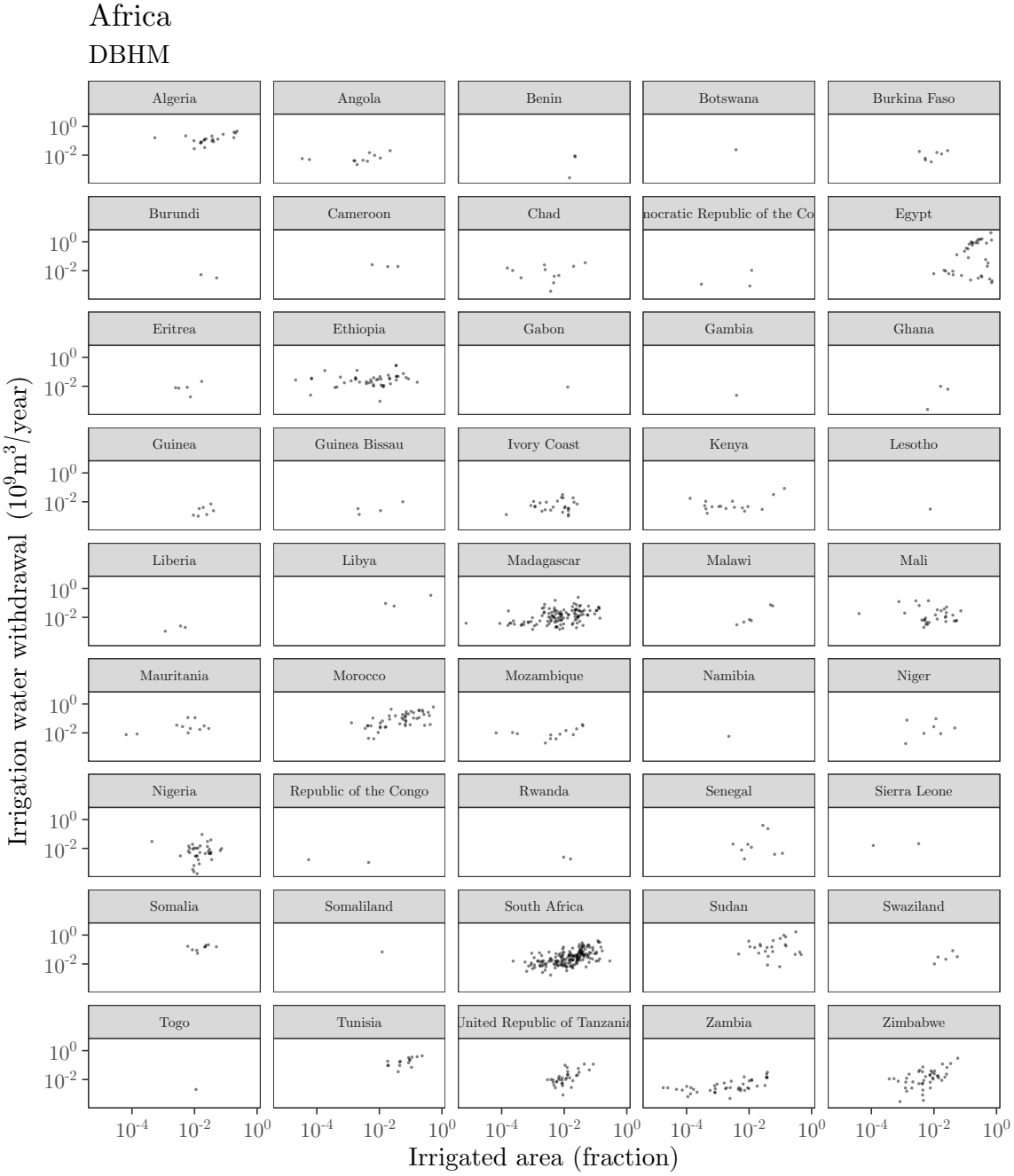
```
# PLOT ------------------------------------------------------------------------

full.isimip.split <- split(full.isimip, full.isimip$Continent) %>%
  lapply(., function(x) split(x, x$Water.Dataset))

gg <- list()
```

```
for(i in names(full.isimip.split)) {
  for(j in names(full.isimip.split[[i]])) {
    gg[[i]][[j]] <- ggplot(full.isimip.split[[i]][[j]], aes(area, water)) +
      geom_point(size = 0.1, alpha = 0.5) +
      scale_x_log10(breaks = trans_breaks("log10", function(x) 10 ^ (2 * x)),
                    labels = trans_format("log10", math_format(10 ^ .x))) +
      scale_y_log10(breaks = trans_breaks("log10", function(x) 10 ^ (2 * x)),
                    labels = trans_format("log10", math_format(10 ^ .x))) +
      facet_wrap(~Country,
                 ncol = 5) +
      labs(x = "Irrigated area (fraction)",
           y = expression(paste("Irrigation water withdrawal ", " ", "(", 10^9, m^3/year, "", "
      theme_AP() +
      theme(strip.text.x = element_text(size = 6)) +
      ggtitle(label = names(full.isimip.split[i]),
              subtitle = names(full.isimip.split[[i]][j]))
  }
}

gg
```

```
## $Africa
## $Africa$CLM45
```

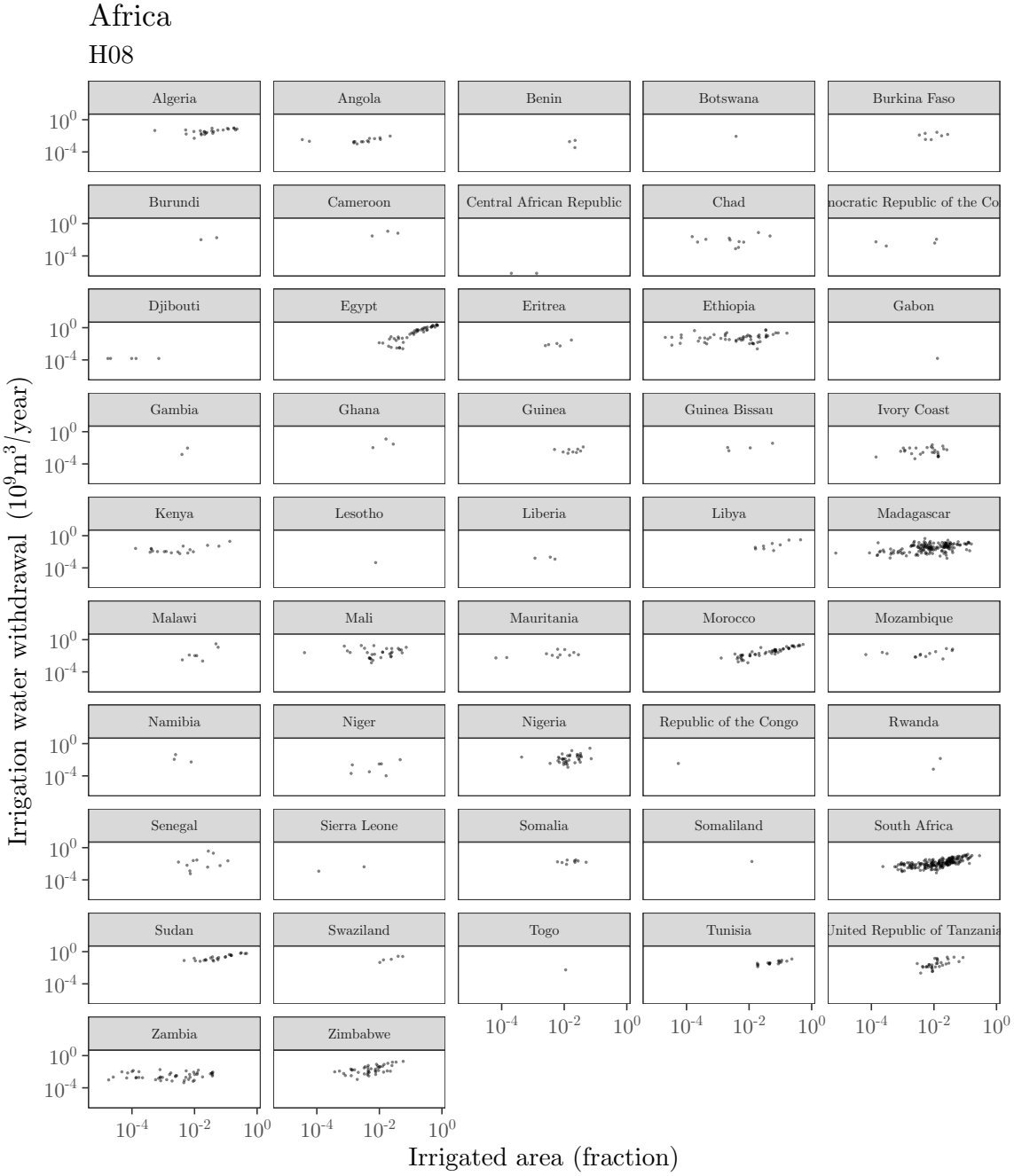

Africa
CLM45
Algeria
Angola
Benin
Botswana
Burkina Faso
Burundi
Cameroon
Central African Republic
Chad
nocratic Republic of the Co
Djibouti
Egypt
Eritrea
Ethiopia
Gambia
Ghana
Guinea
Guinea Bissau
Ivory Coast
Kenya
Lesotho
Liberia
Libya
Madagascar
Malawi
Mali
Mauritania
Morocco
Mozambique
Namibia
Niger
Nigeria
Republic of the Congo
Rwanda
Senegal
Sierra Leone
Somalia
Somaliland
South Africa
South Sudan
Sudan
Swaziland
Togo
Tunisia
Uganda
United Republic of Tanzania
Zambia
Zimbabwe
Irrigation water withdrawal (10^9m^3/year)
Irrigated area (fraction)
10^0
10^{-4}

```
##
## $Africa$DBHM
```


Africa
DBHM
Algeria
Angola
Benin
Botswana
Burkina Faso
Burundi
Cameroon
Chad
nocratic Republic of the Co
Egypt
Eritrea
Ethiopia
Gabon
Gambia
Ghana
Guinea
Guinea Bissau
Ivory Coast
Kenya
Lesotho
Liberia
Libya
Madagascar
Malawi
Mali
Mauritania
Morocco
Mozambique
Namibia
Niger
Nigeria
Republic of the Congo
Rwanda
Senegal
Sierra Leone
Somalia
Somaliland
South Africa
Sudan
Swaziland
Togo
Tunisia
United Republic of Tanzania
Zambia
Zimbabwe
Irrigation water withdrawal ($10^9 m^3$/year)
Irrigated area (fraction)

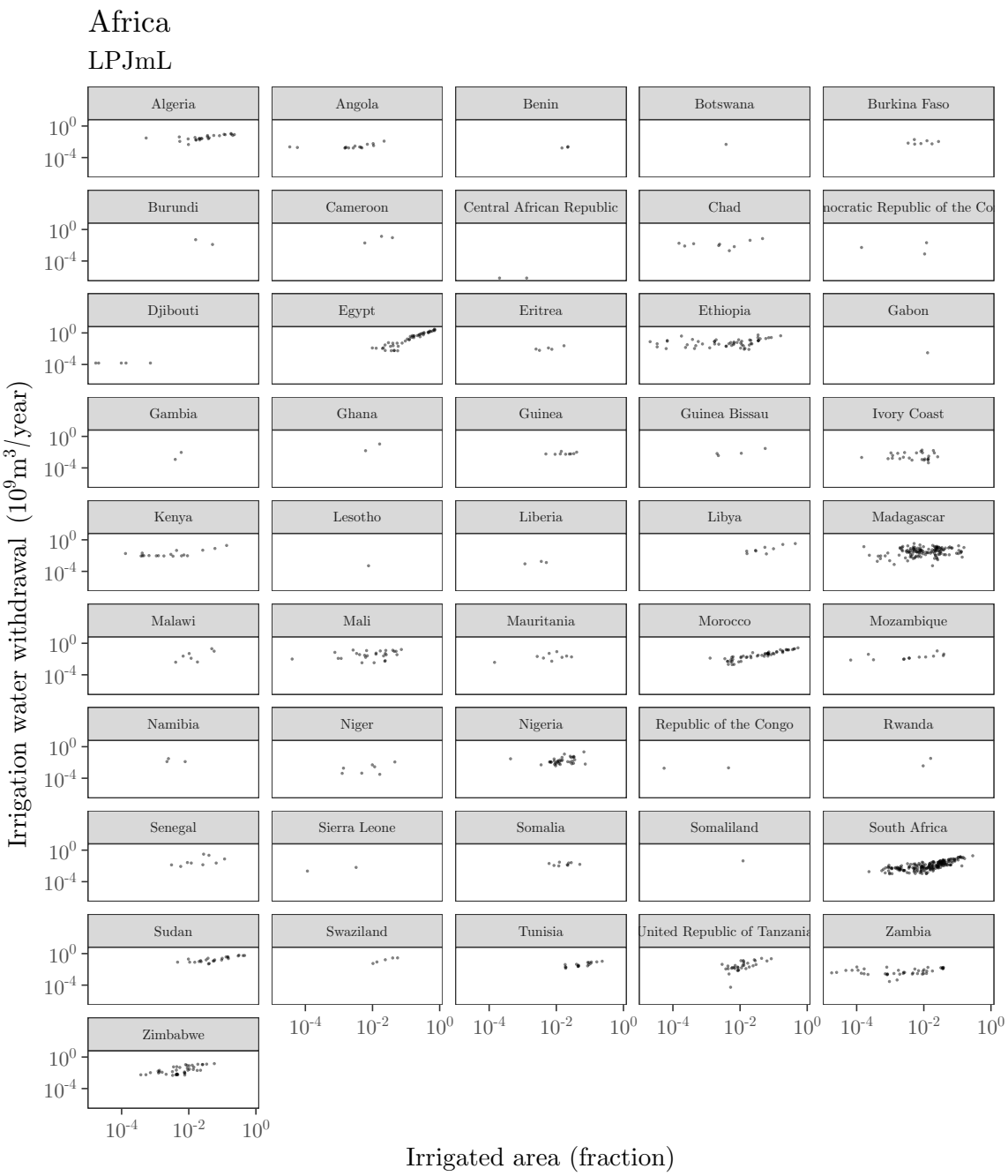
##

$Africa$H08

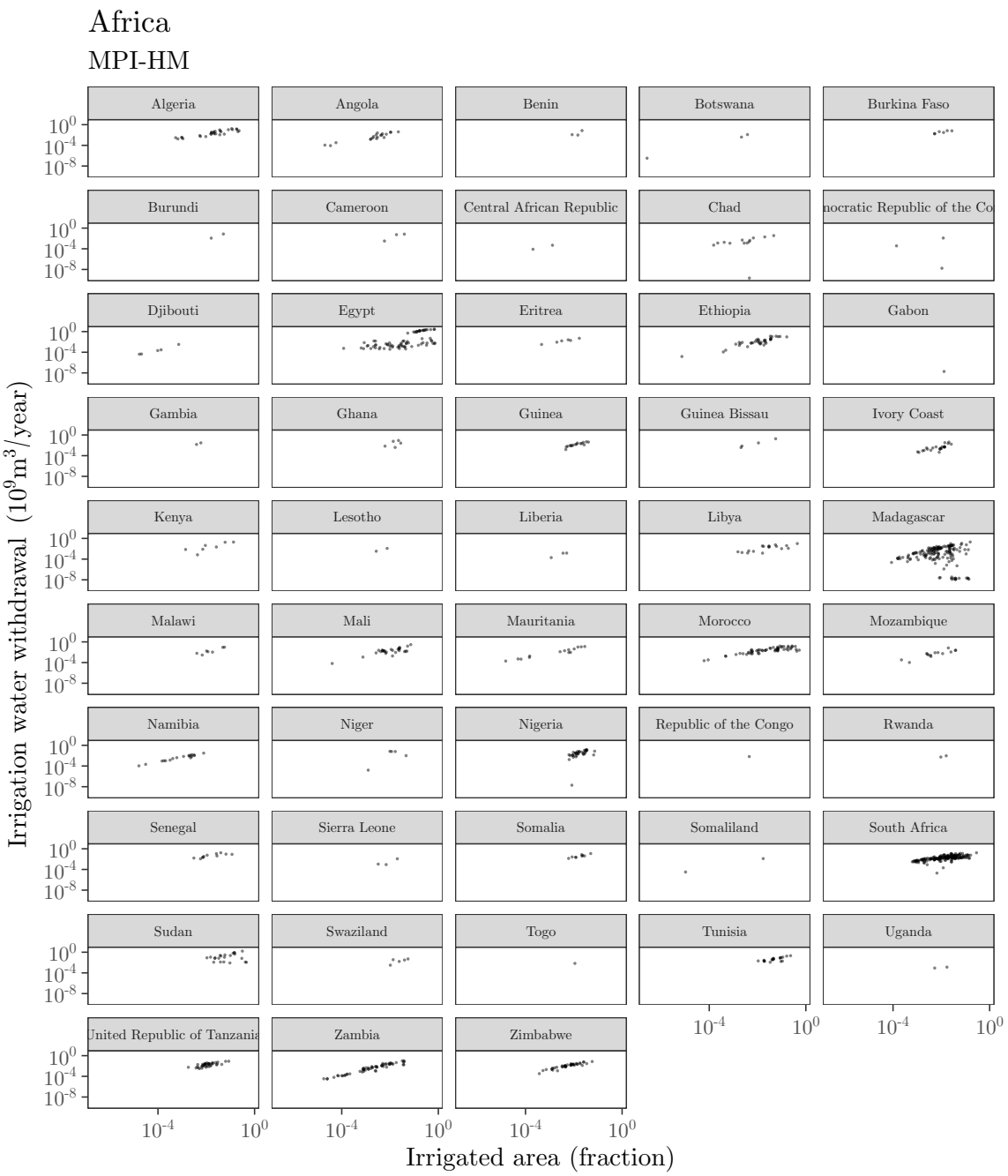


##

$Africa$LPJmL

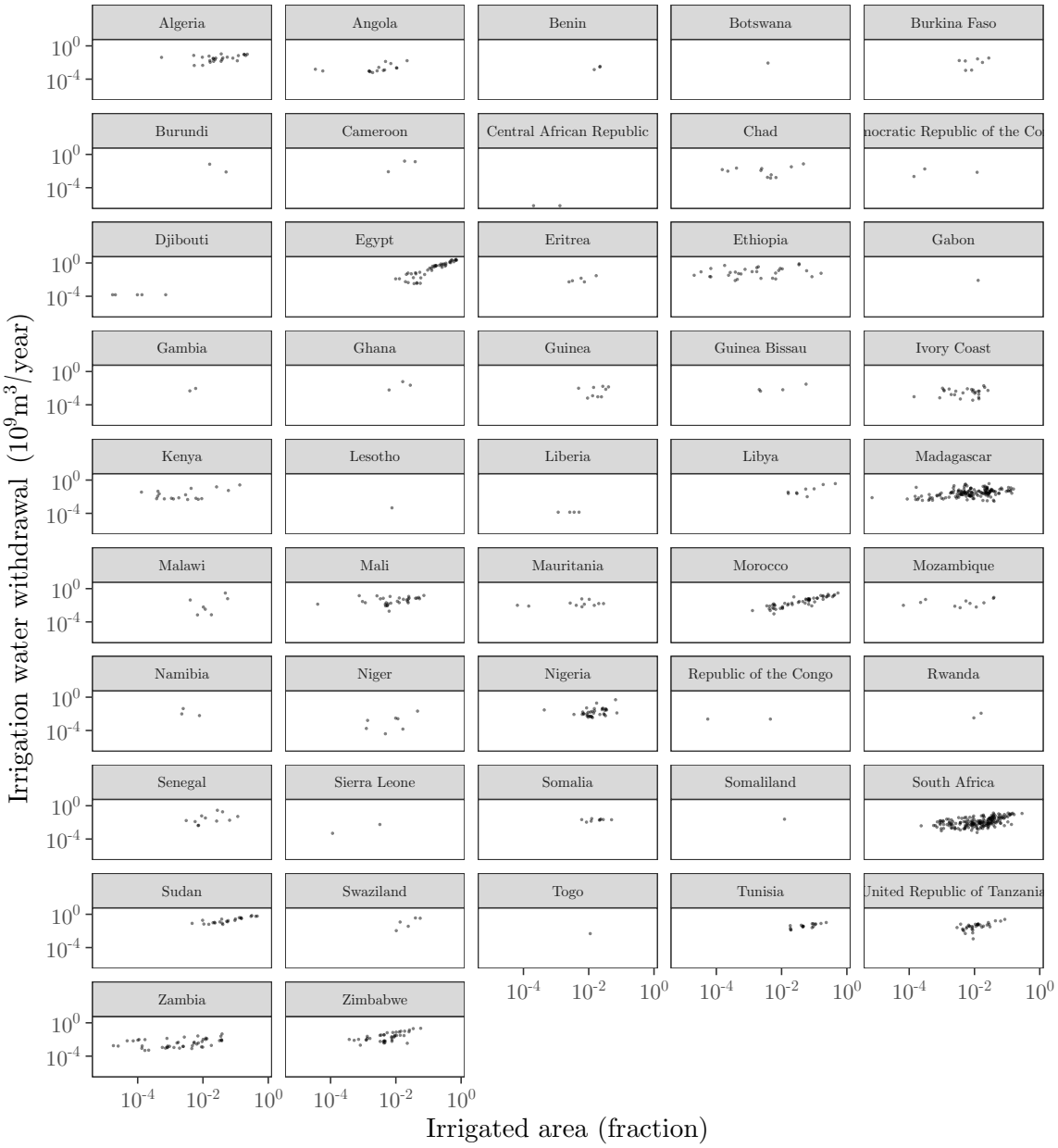



```
##
## $Africa$`MPI-HM`
```

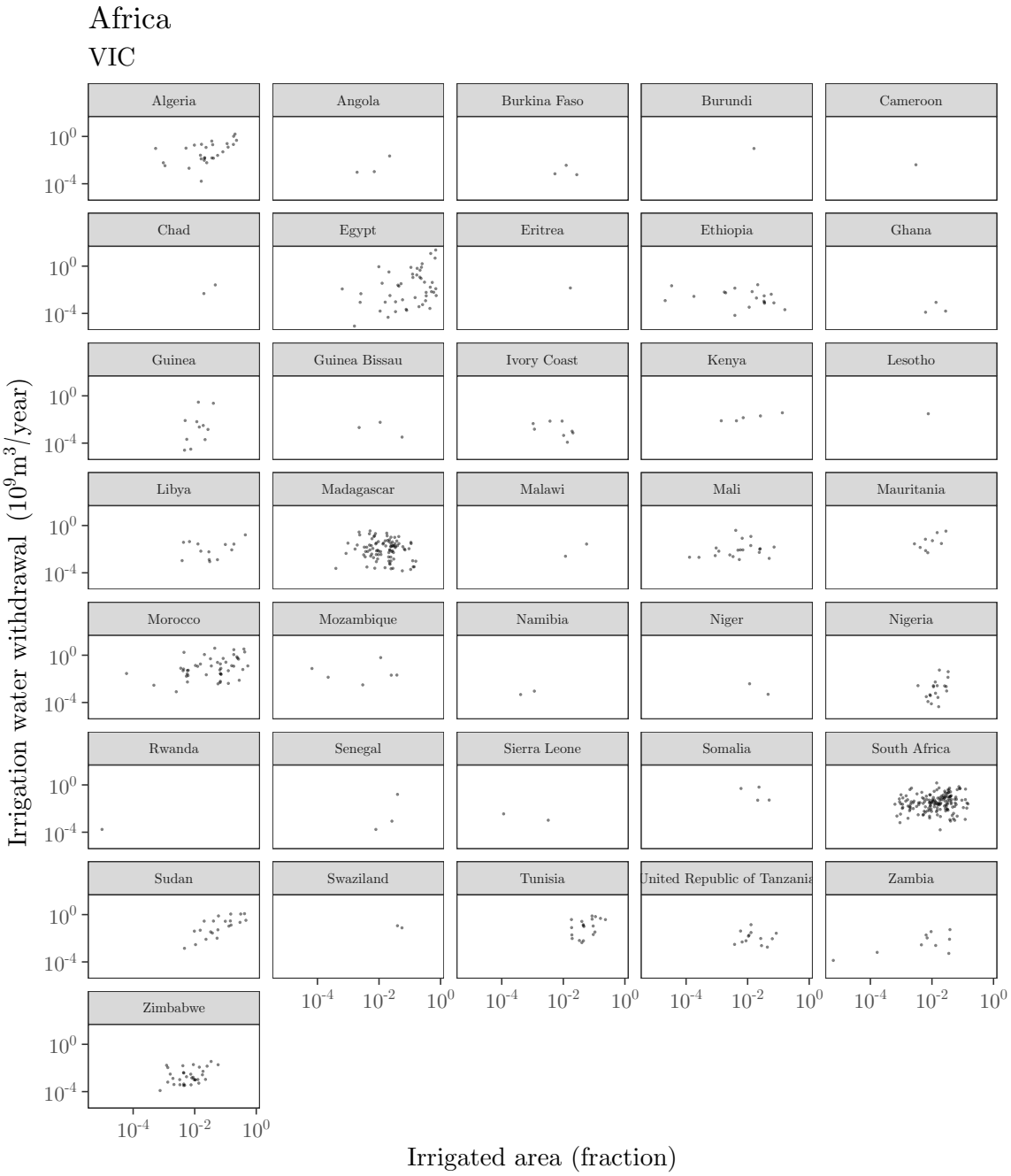


##

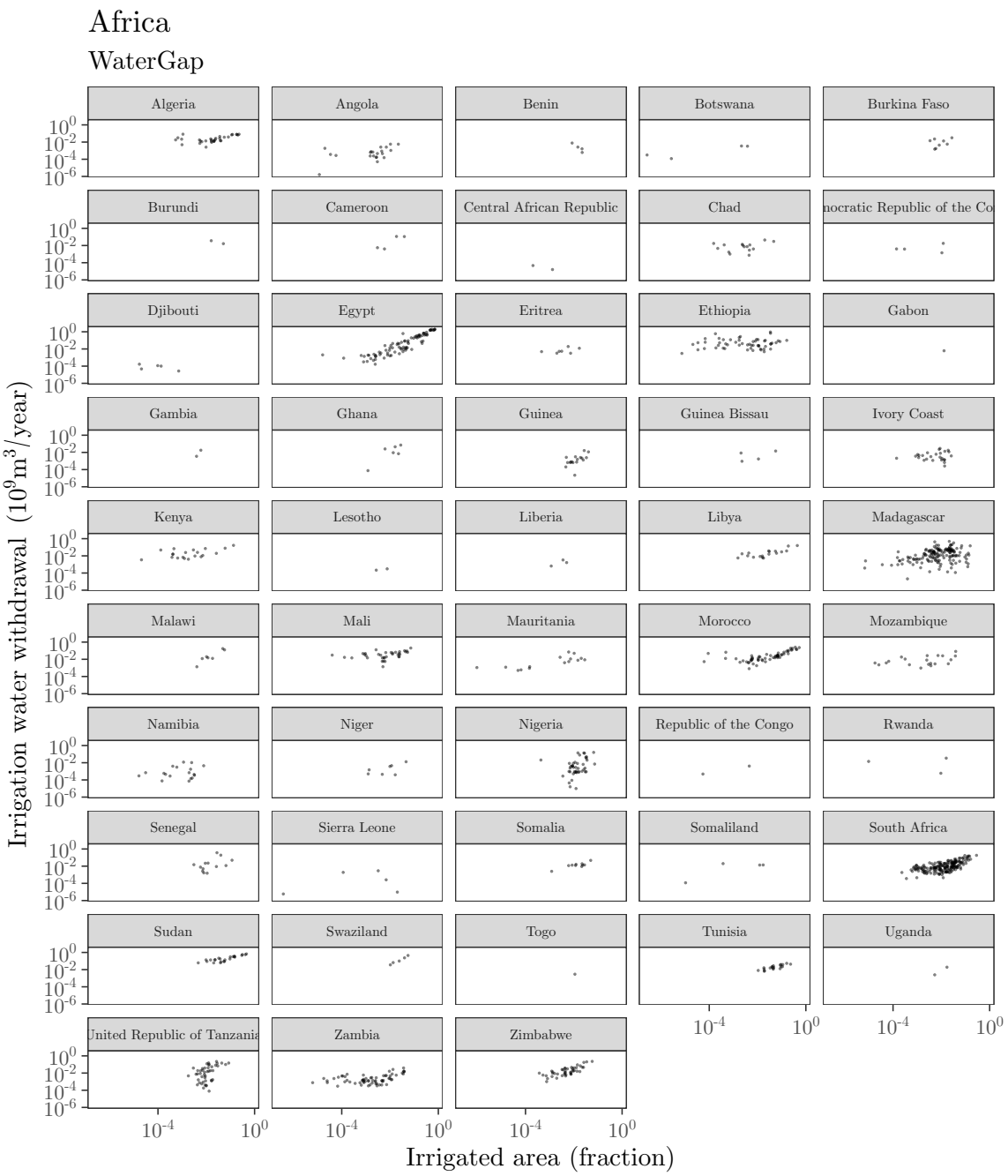
$Africa$`PCR-GLOBWB`


Africa
PCR-GLOBWB
Algeria
Angola
Benin
Botswana
Burkina Faso
Burundi
Cameroon
Central African Republic
Chad
nocratic Republic of the Co
Djibouti
Egypt
Eritrea
Ethiopia
Gabon
Gambia
Ghana
Guinea
Guinea Bissau
Ivory Coast
Kenya
Lesotho
Liberia
Libya
Madagascar
Malawi
Mali
Mauritania
Morocco
Mozambique
Namibia
Niger
Nigeria
Republic of the Congo
Rwanda
Senegal
Sierra Leone
Somalia
Somaliland
South Africa
Sudan
Swaziland
Togo
Tunisia
United Republic of Tanzania
Zambia
Zimbabwe
Irrigation water withdrawal (10^9m^3/year)
Irrigated area (fraction)

```
##
## $Africa$VIC
```



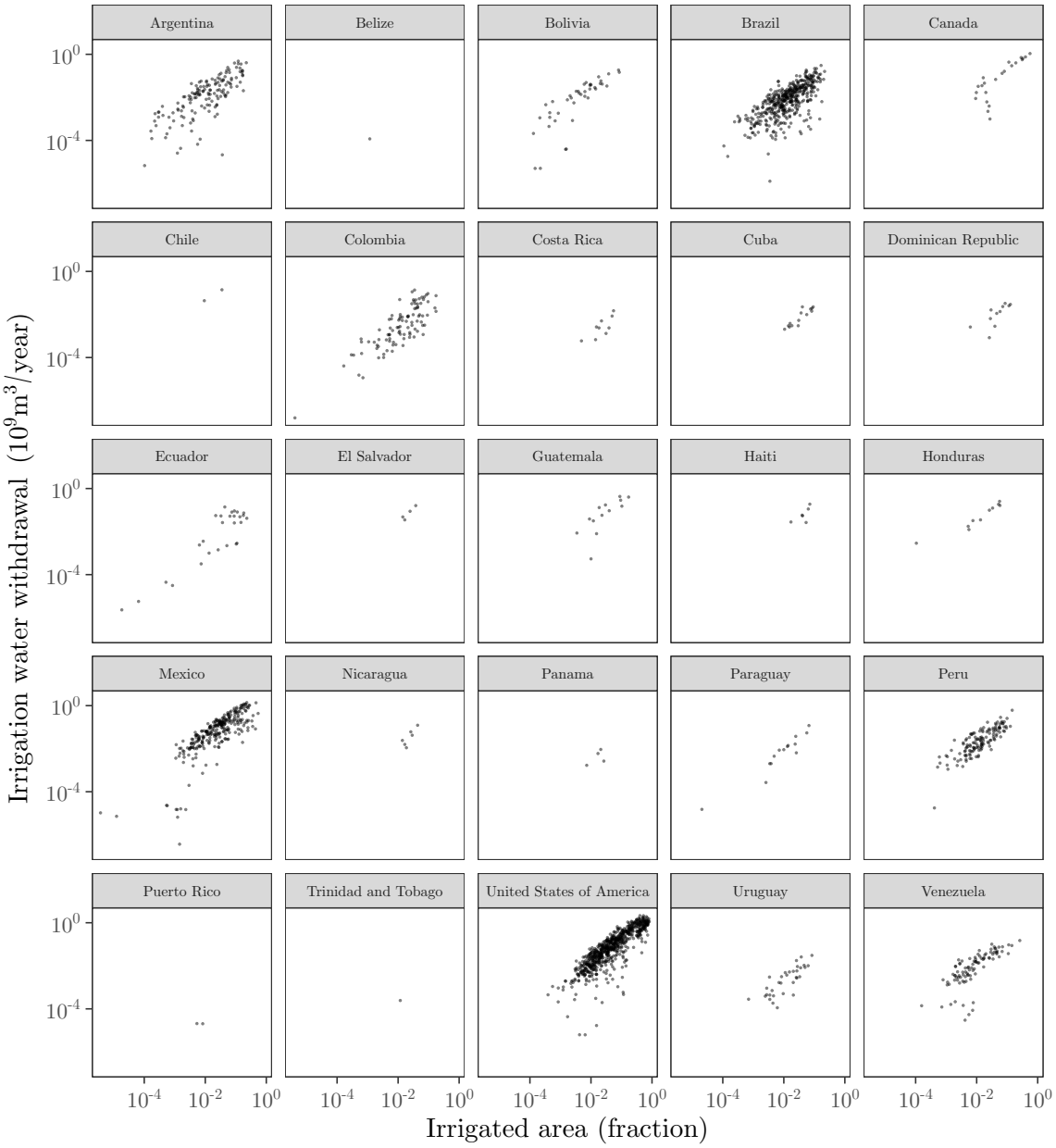

```
##
## $Africa$WaterGap
```



##
##
$Americas
$Americas$CLM45

Americas

CLM45

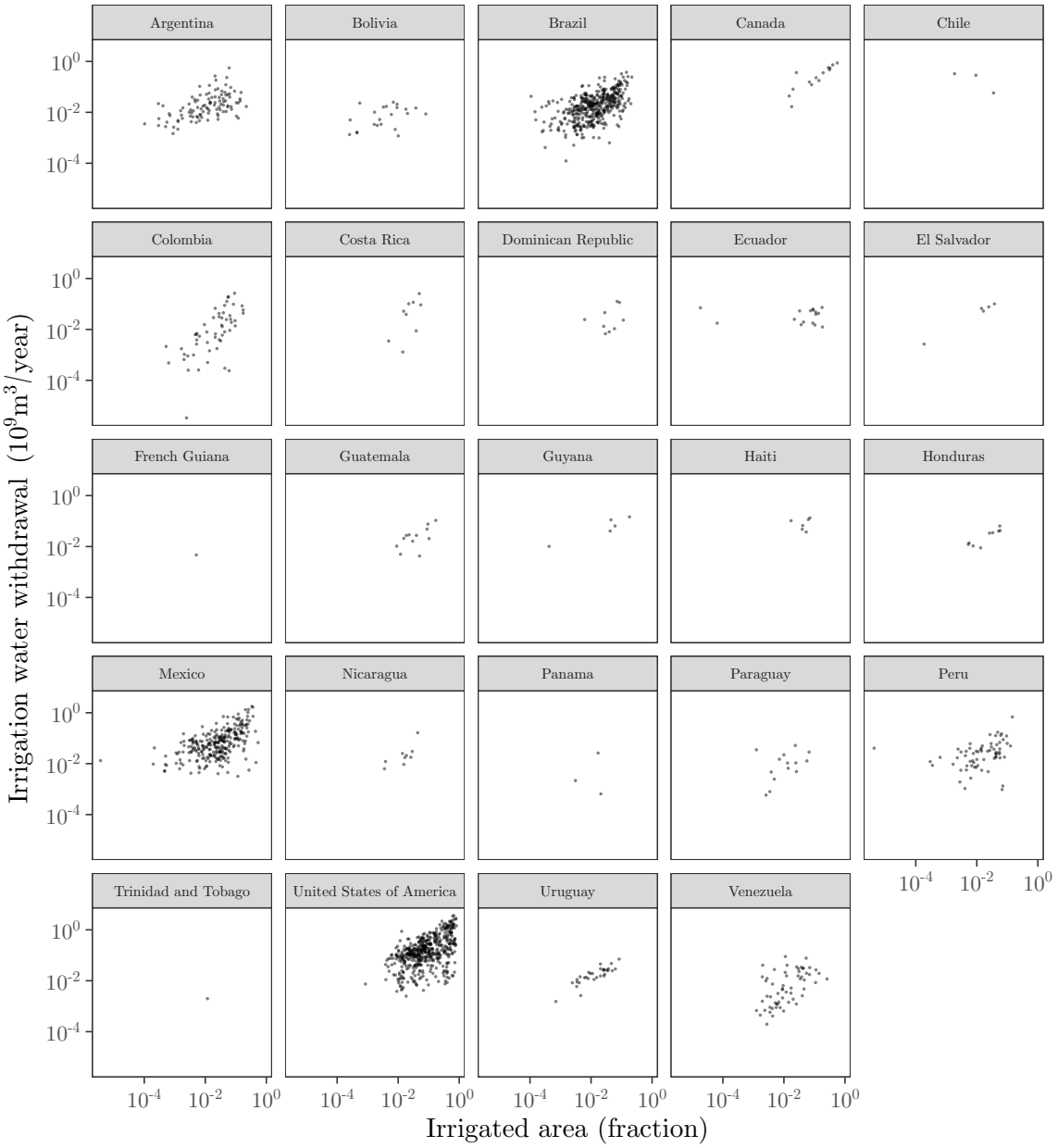


##

$Americas$DBHM

Americas

DBHM

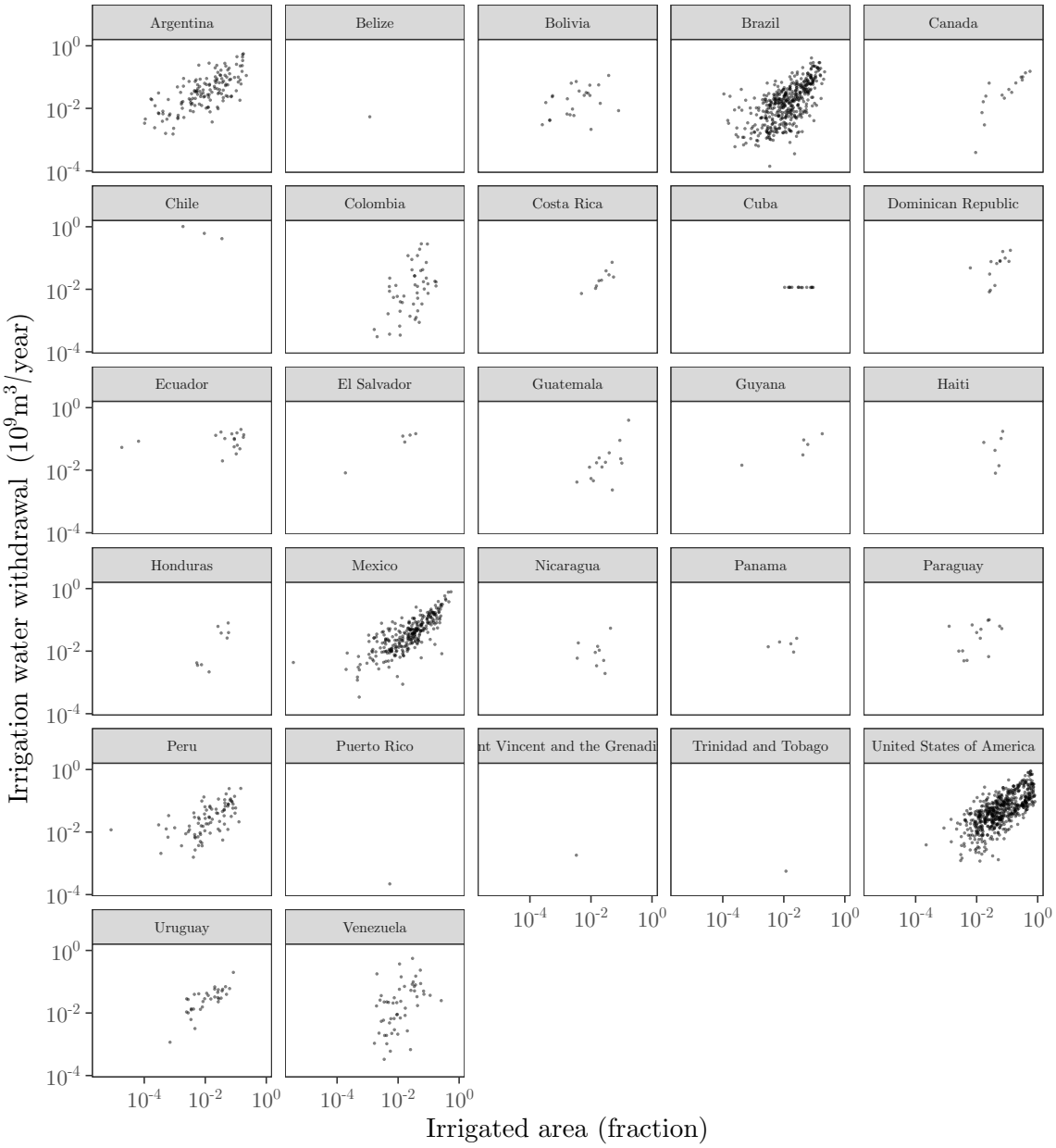


##

$Americas$H08

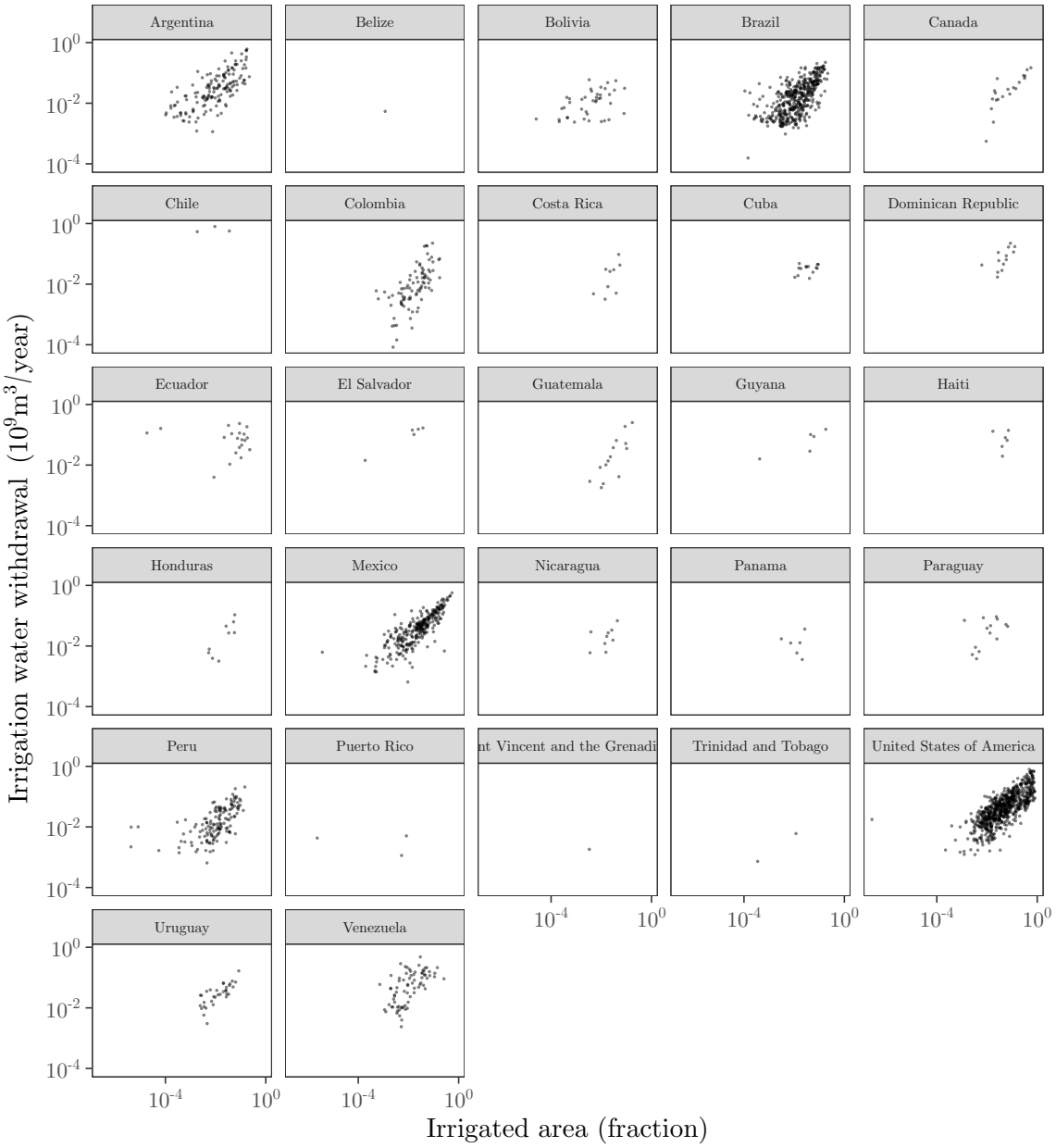
Americas

H08

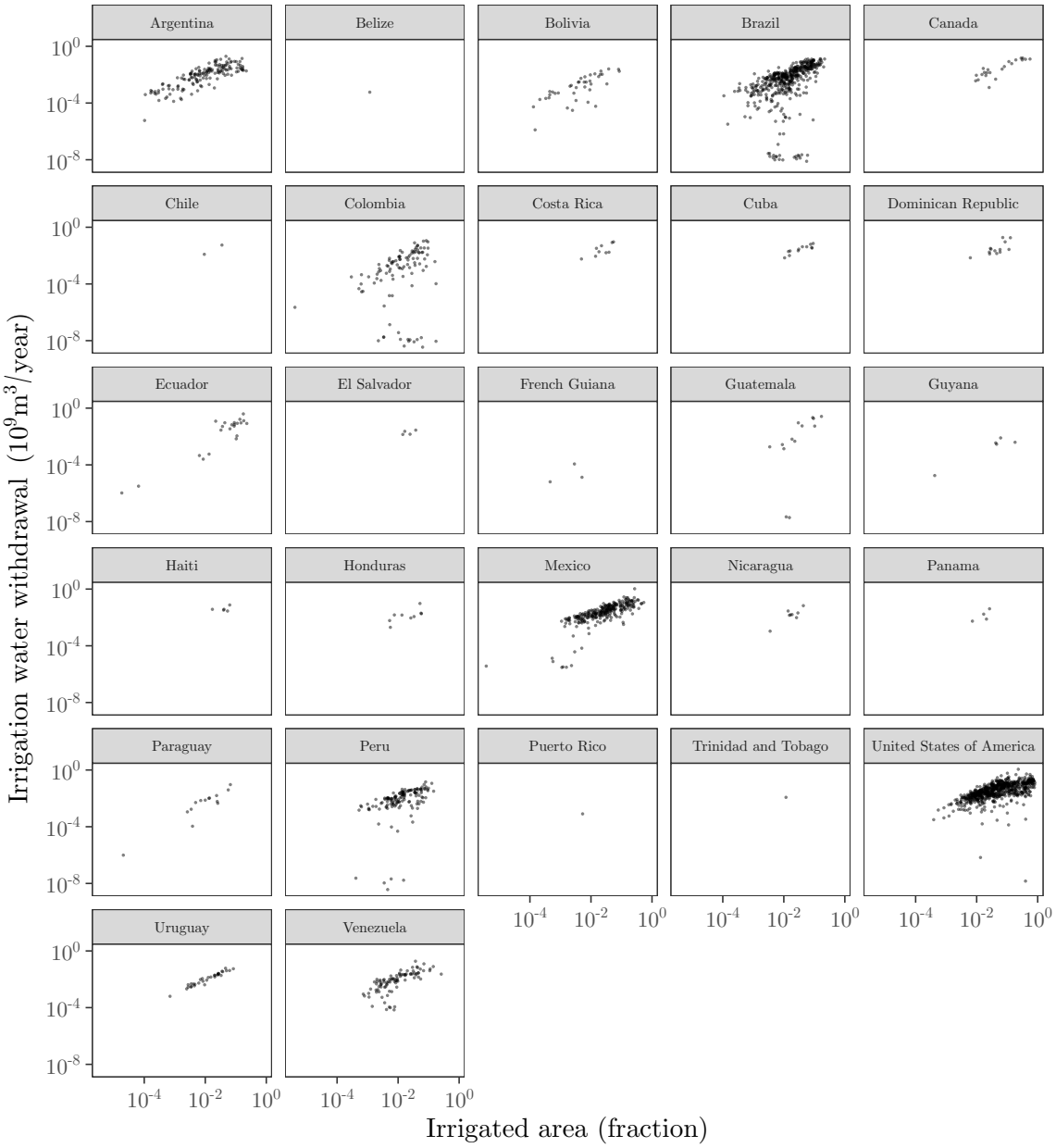


##

$Americas$LPJmL

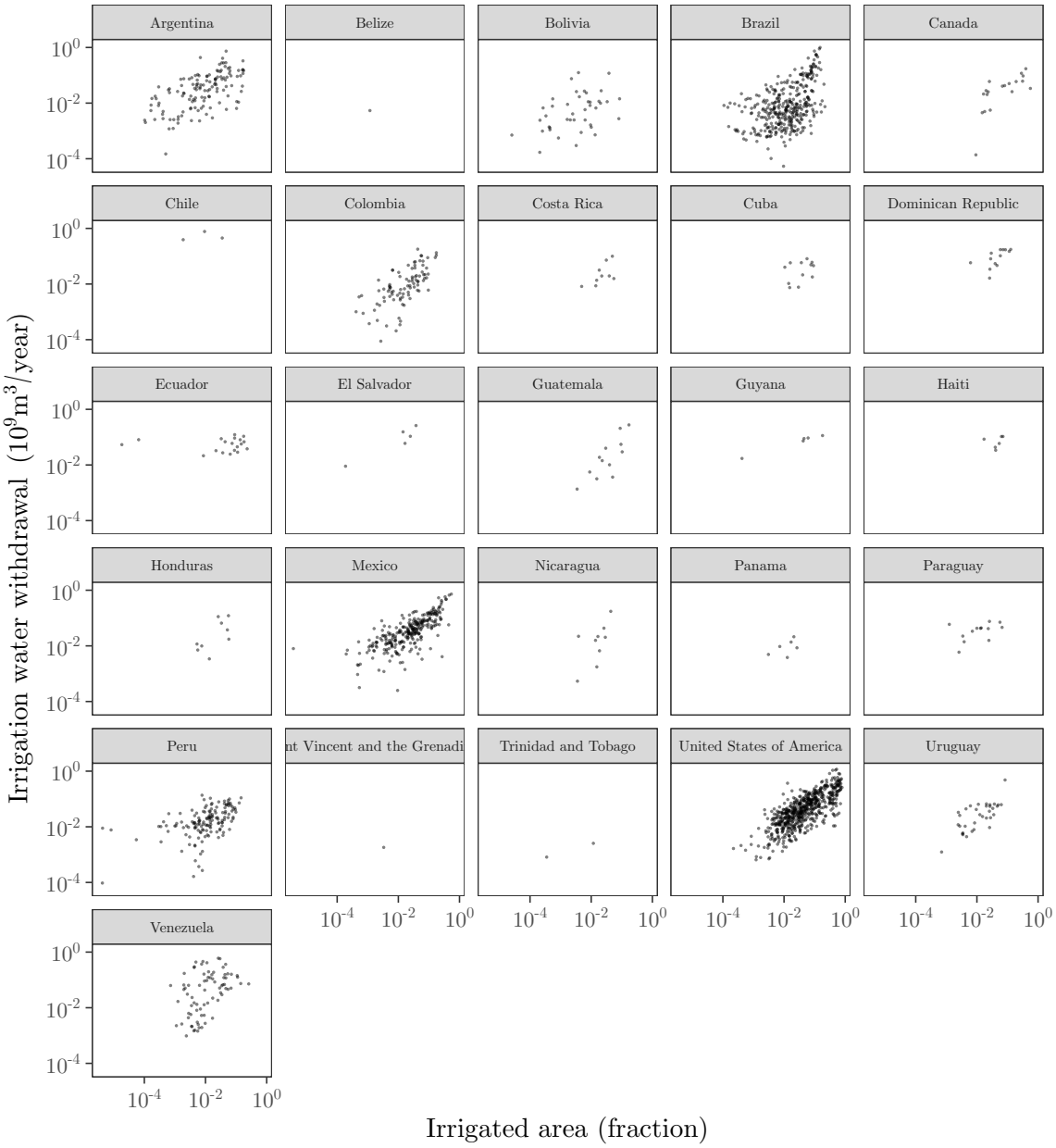



```
##
## $Americas$`MPI-HM`
```



##

$Americas$`PCR-GLOBWB`

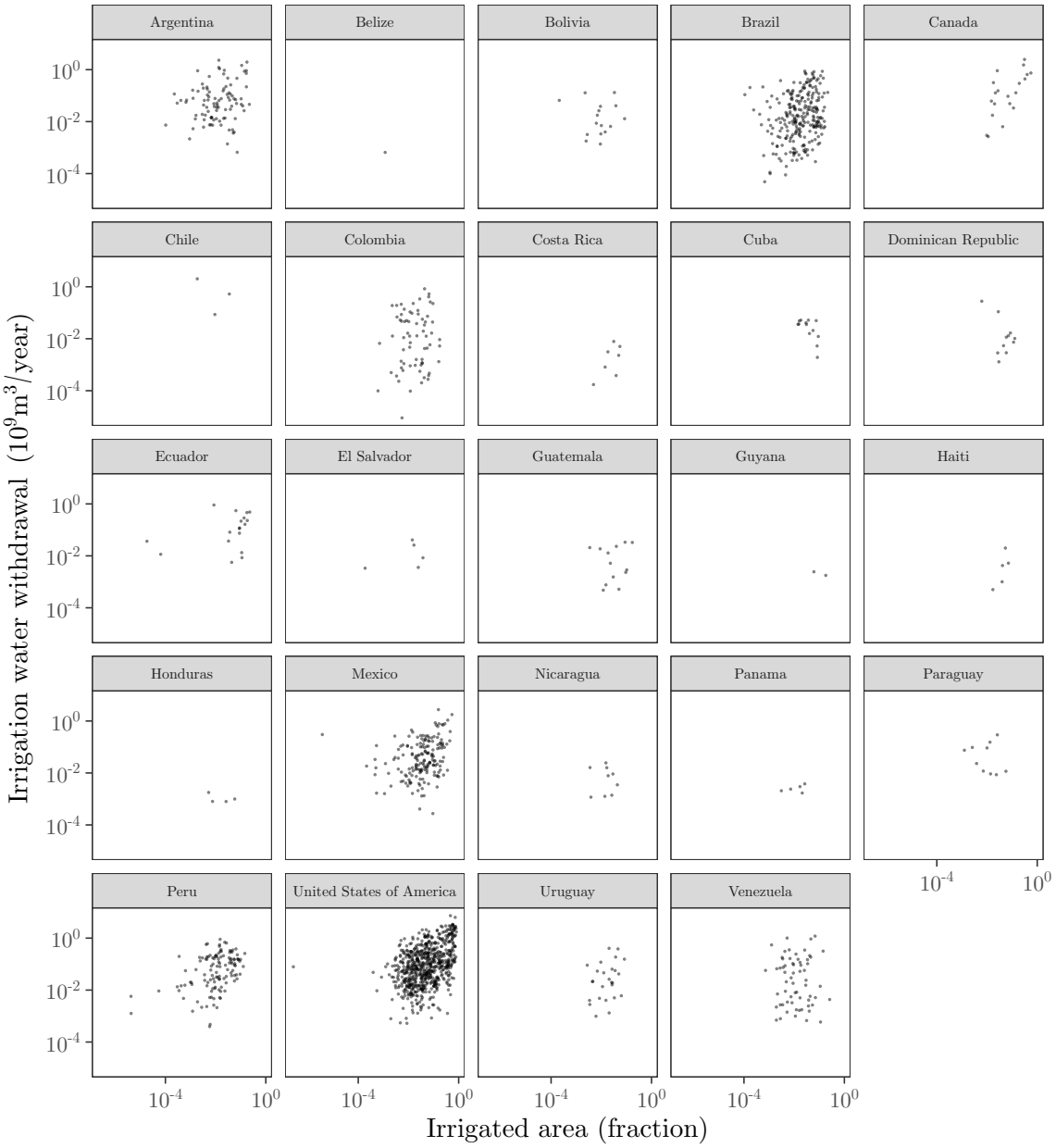


##

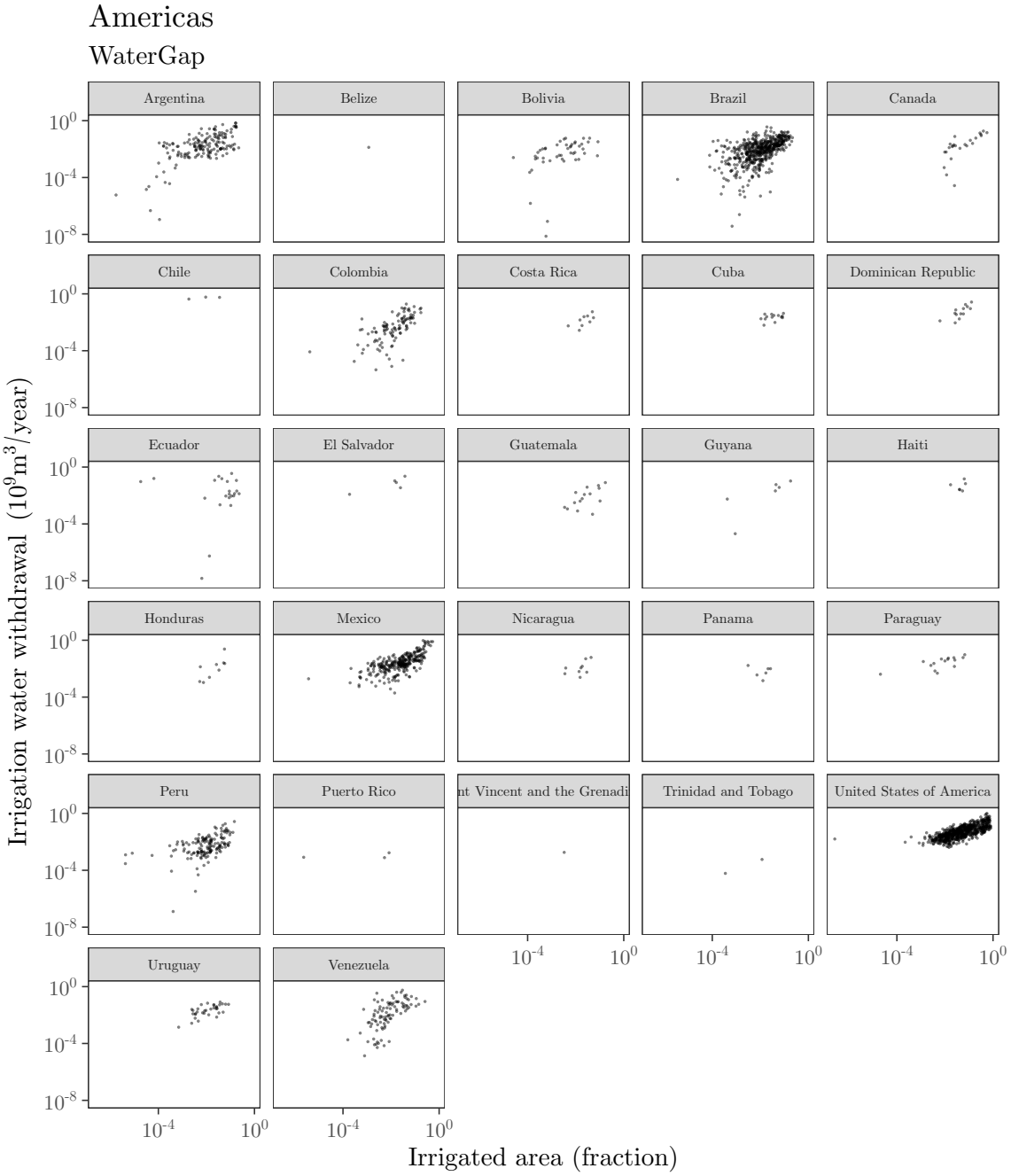
$Americas$VIC

Americas

VIC



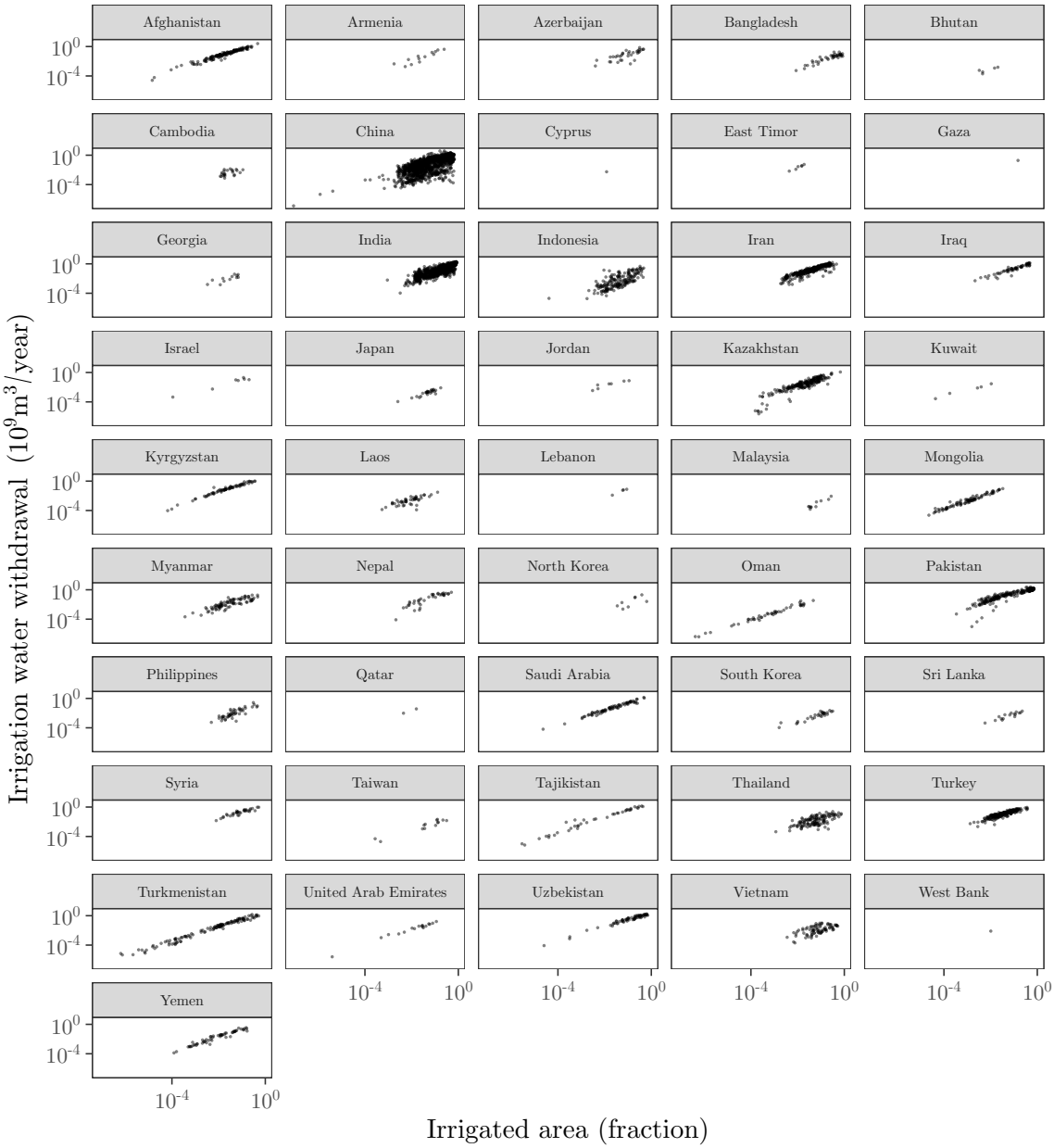

```
##
## $Americas$WaterGap
```




```
##
##
## $Asia
## $Asia$CLM45
```

Asia

CLM45

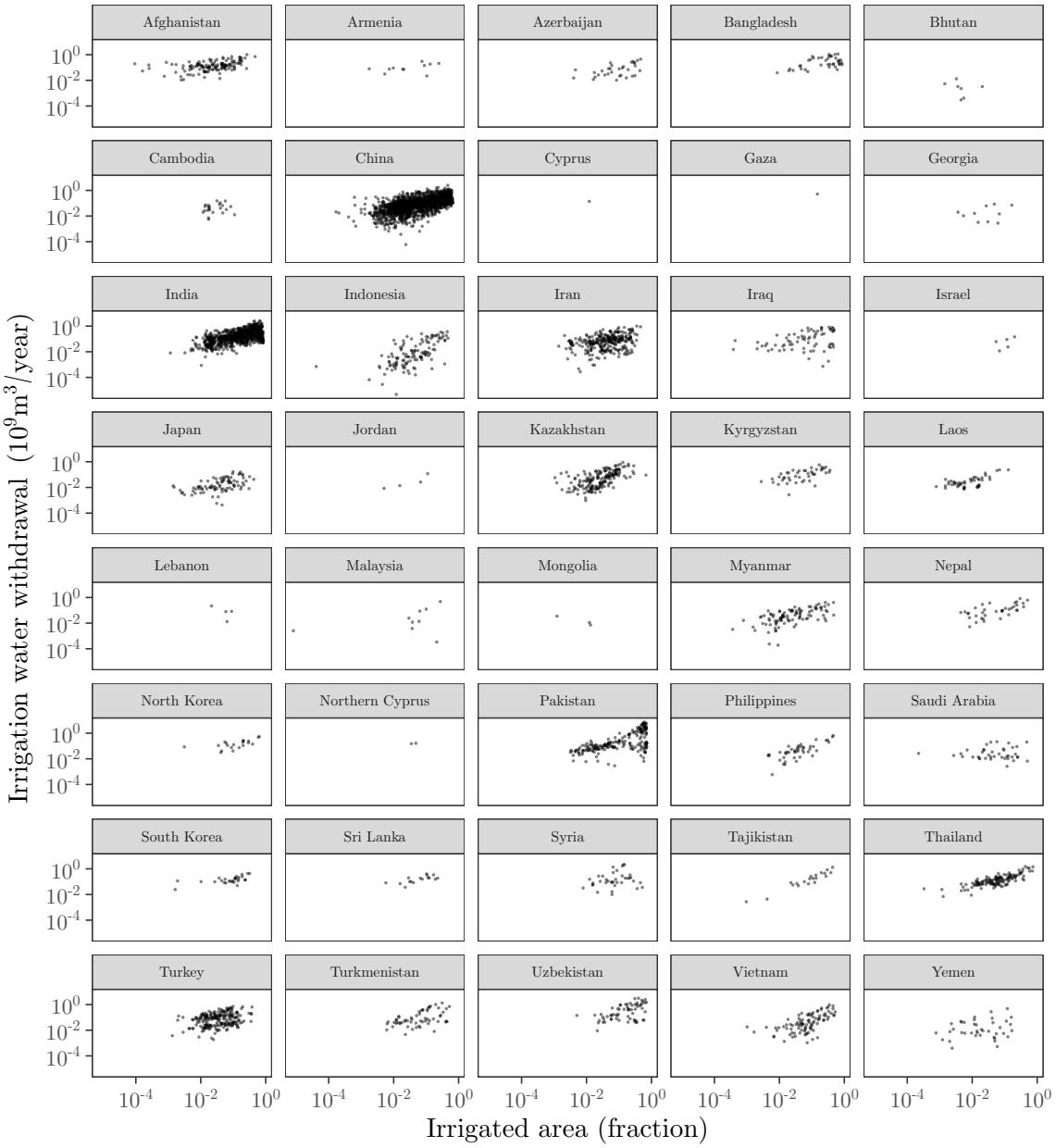


##

$Asia$DBHM

Asia

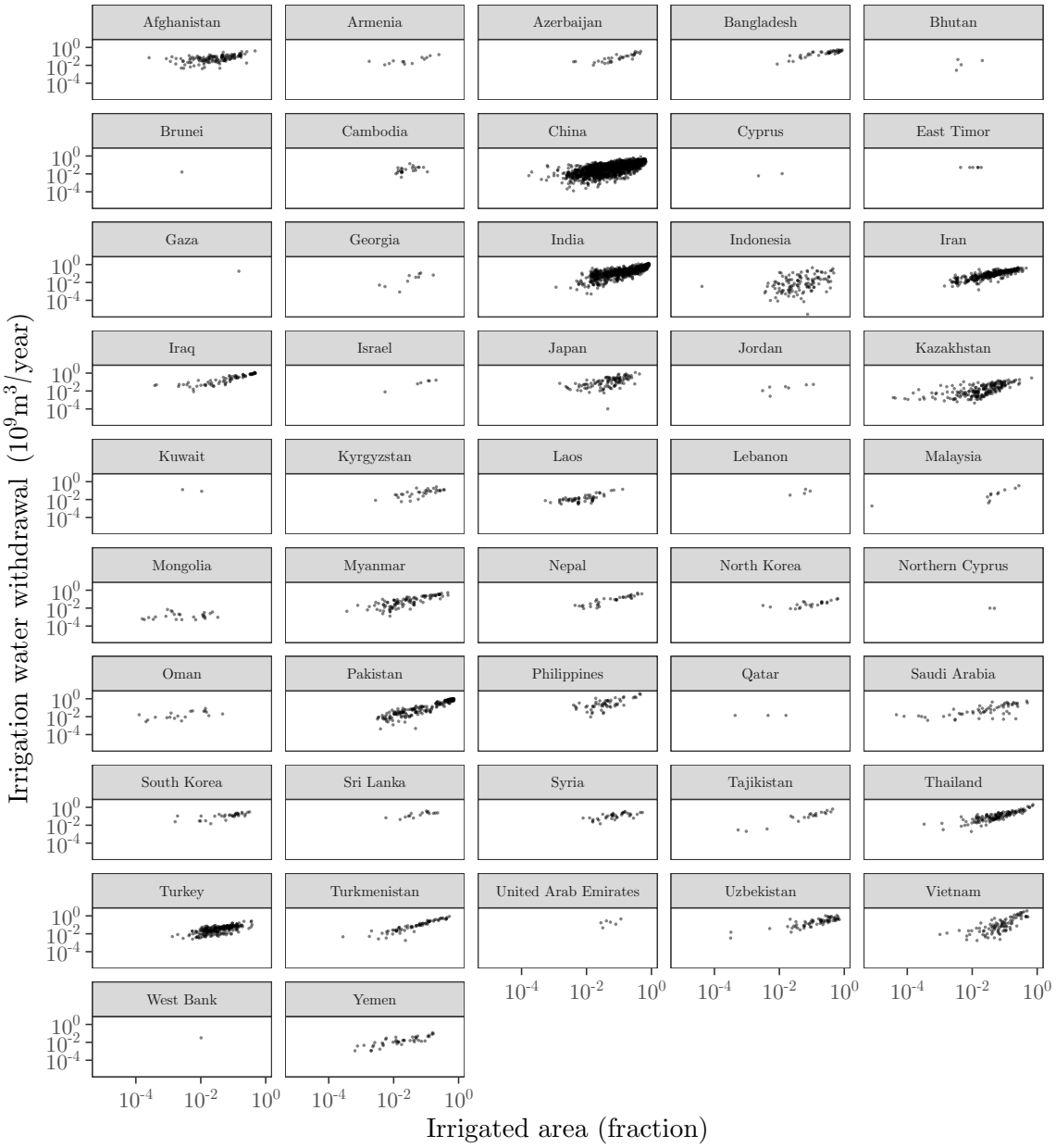
DBHM




```
##
## $Asia$H08
```

Asia

H08

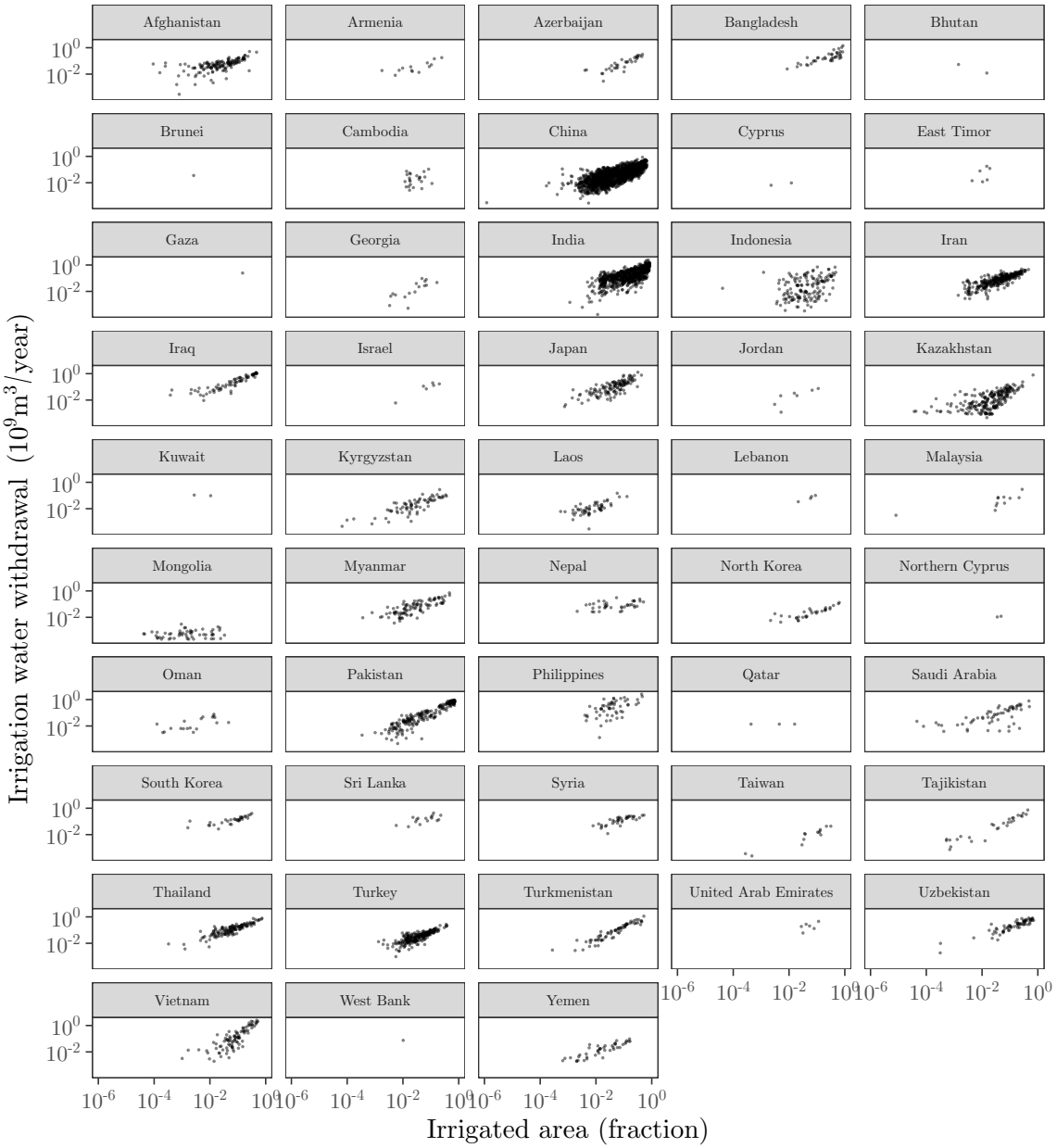


##

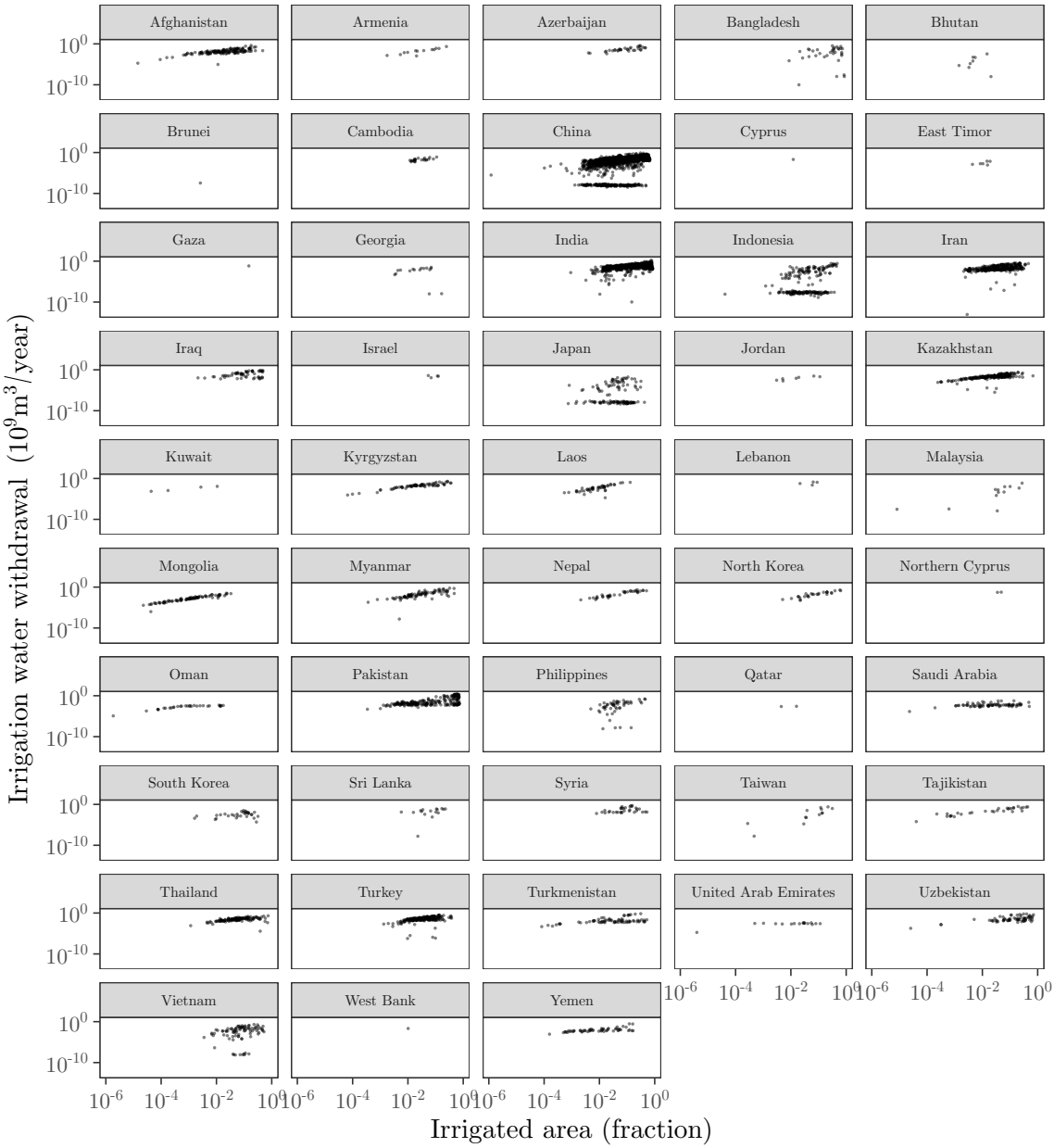
$Asia$LPJmL

Asia

LPJmL




```
##
## $Asia$`MPI-HM`
```

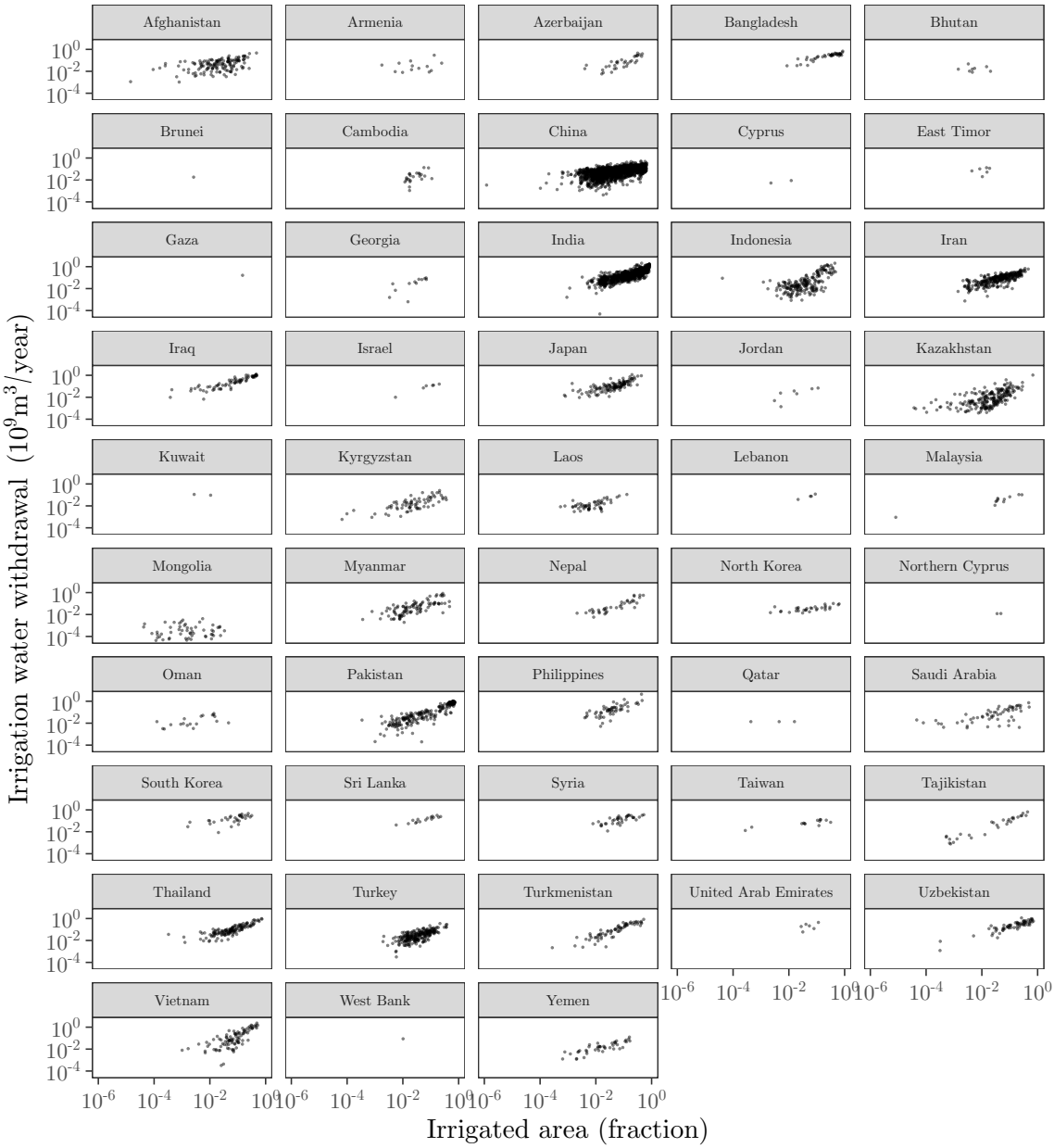


##

$Asia$`PCR-GLOBWB`

Asia

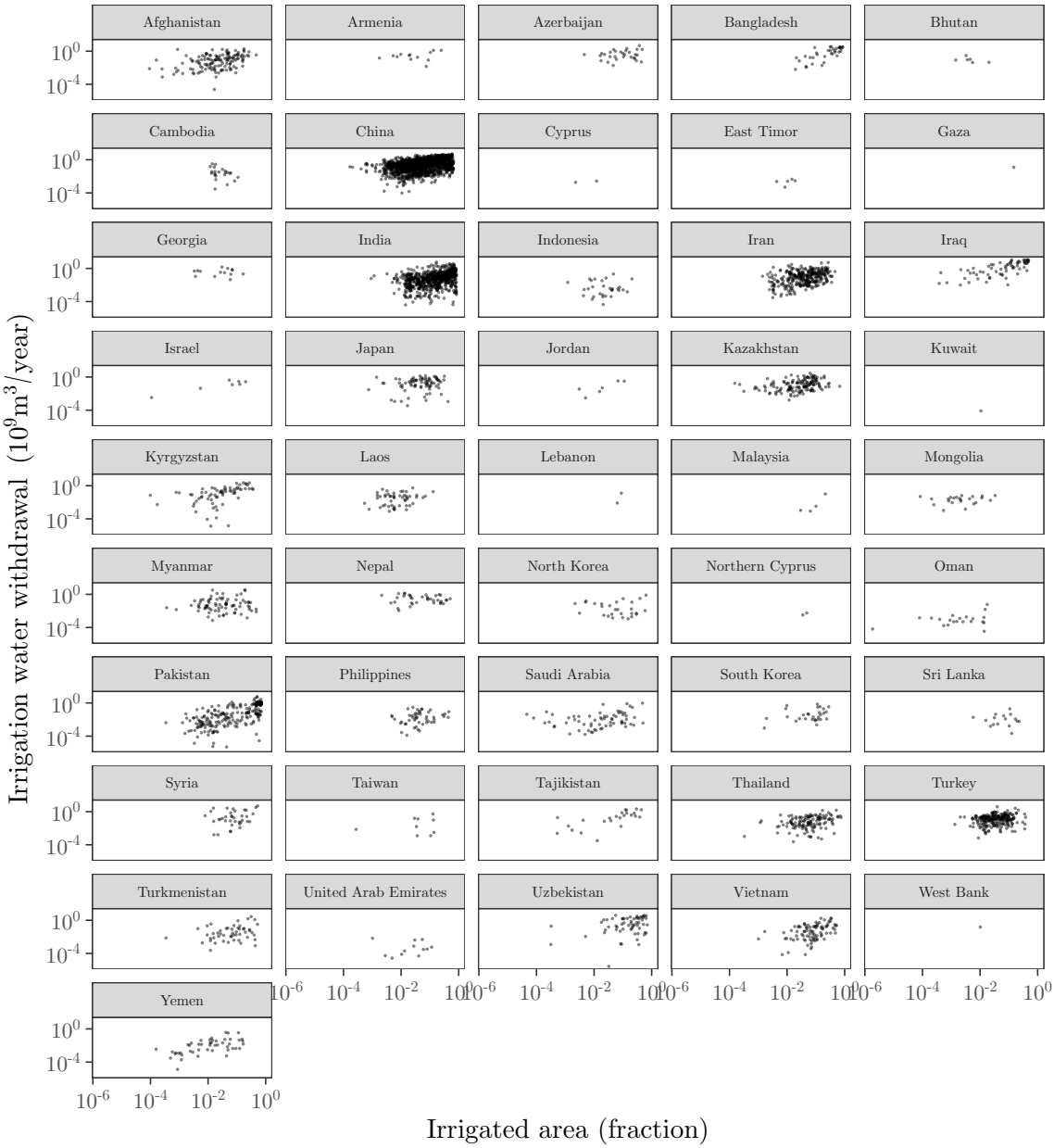
PCR-GLOBWB




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

Asia

VIC

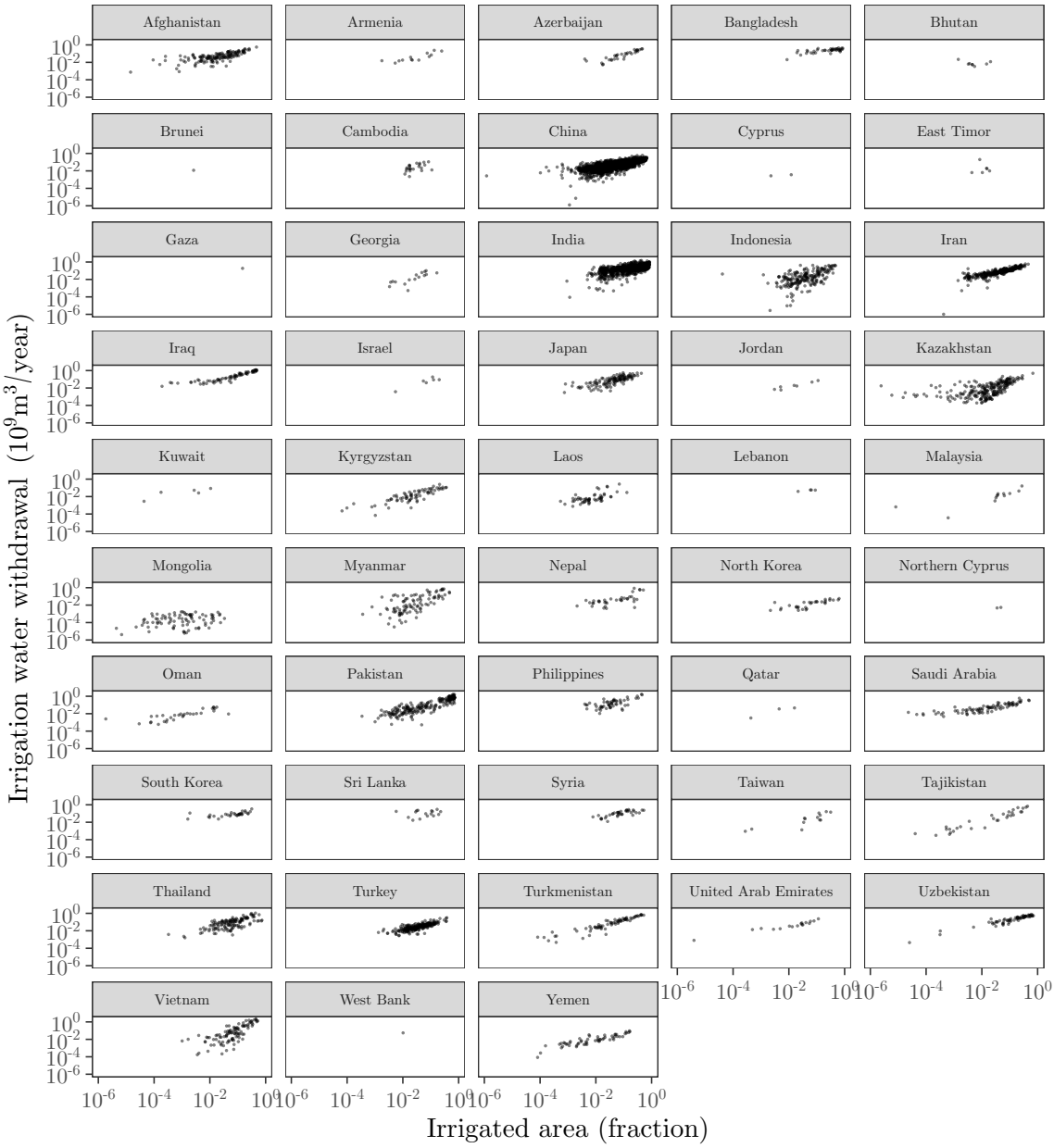


##

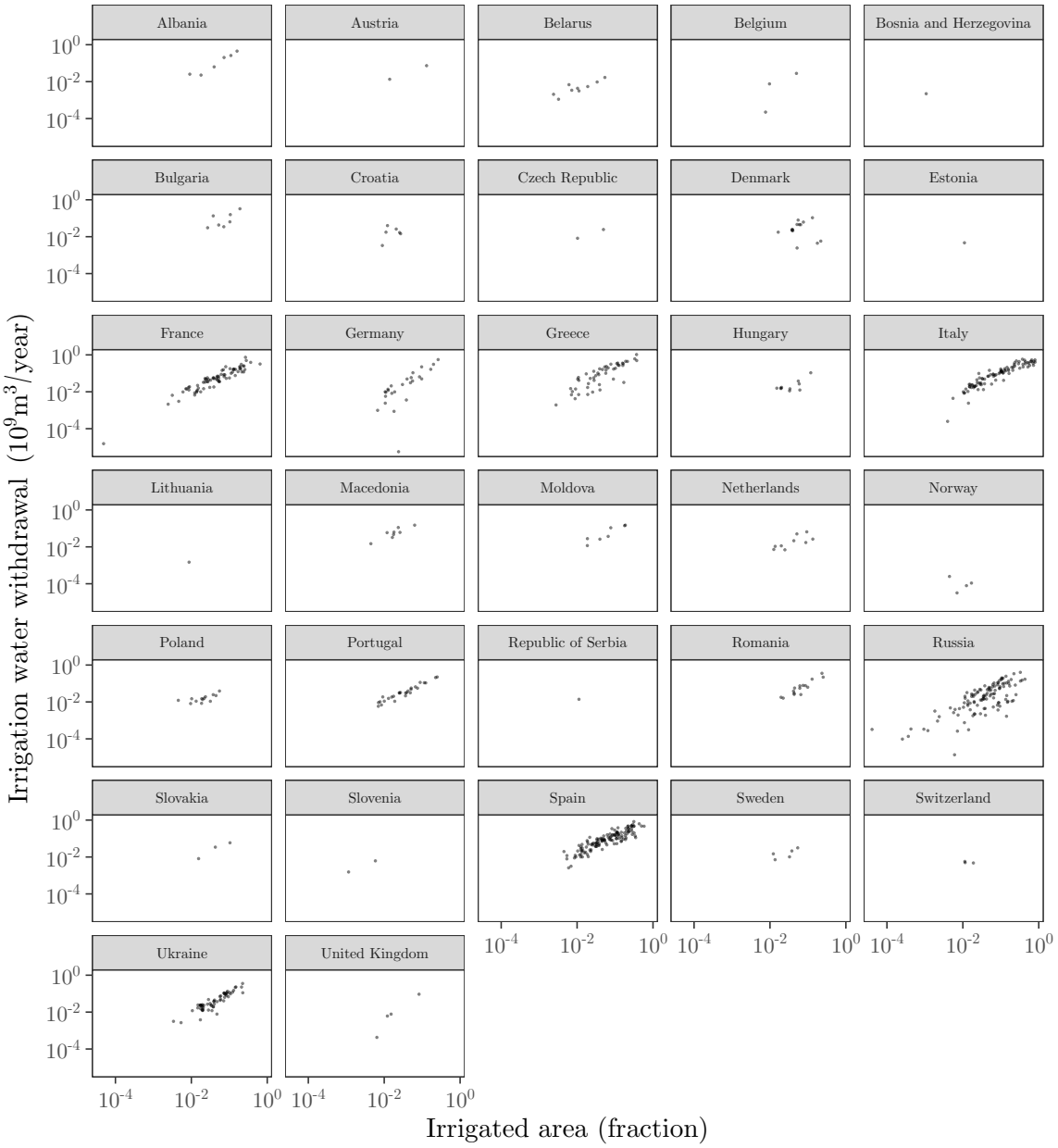
$Asia$WaterGap

Asia

WaterGap

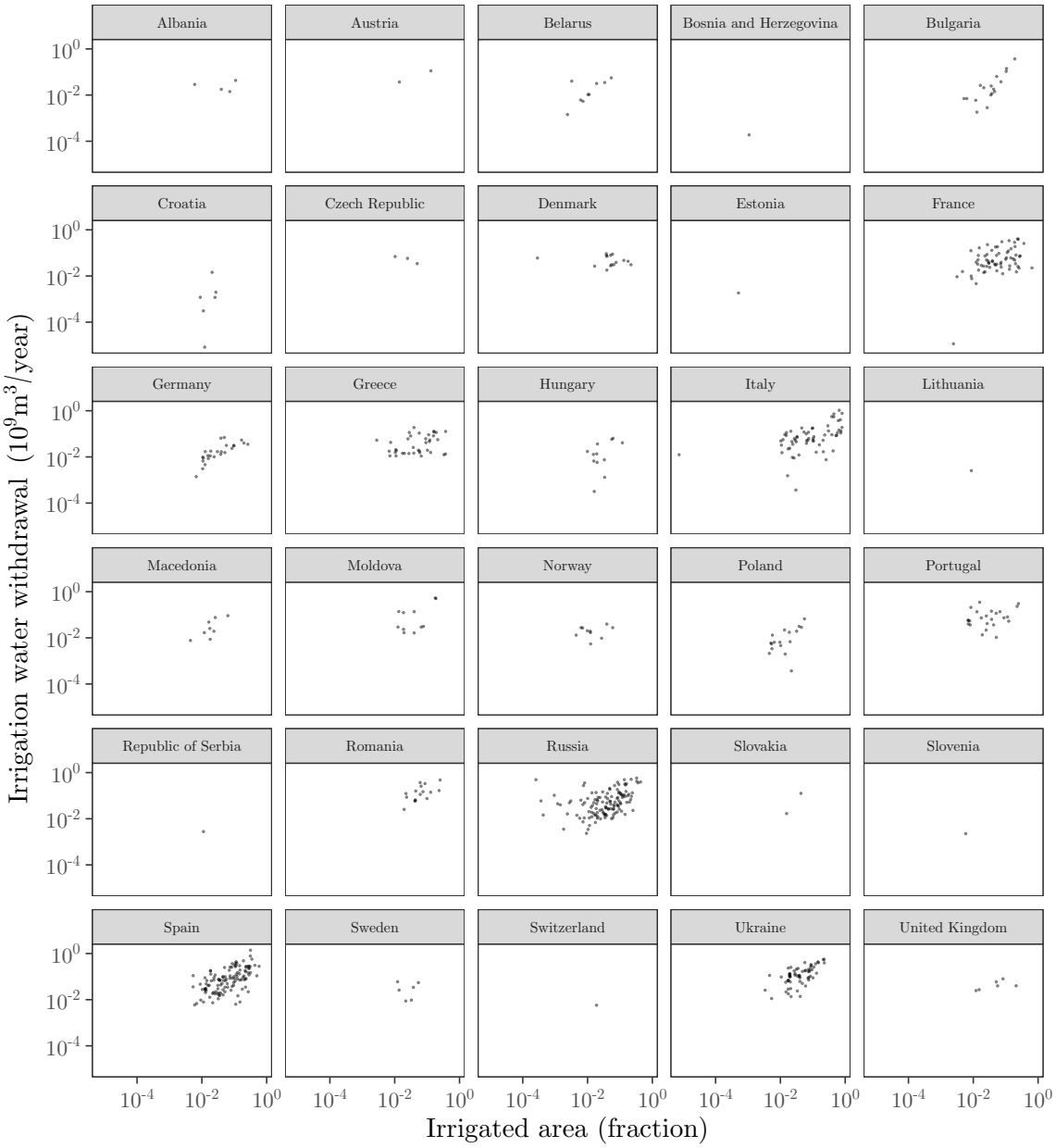



```
##
##
## $Europe
## $Europe$CLM45
```


Europe
CLM45
Albania
Austria
Belarus
Belgium
Bosnia and Herzegovina
Bulgaria
Croatia
Czech Republic
Denmark
Estonia
France
Germany
Greece
Hungary
Italy
Lithuania
Macedonia
Moldova
Netherlands
Norway
Poland
Portugal
Republic of Serbia
Romania
Russia
Slovakia
Slovenia
Spain
Sweden
Switzerland
Ukraine
United Kingdom
Irrigation water withdrawal (10^9m^3/year)
Irrigated area (fraction)

##

$Europe$DBHM

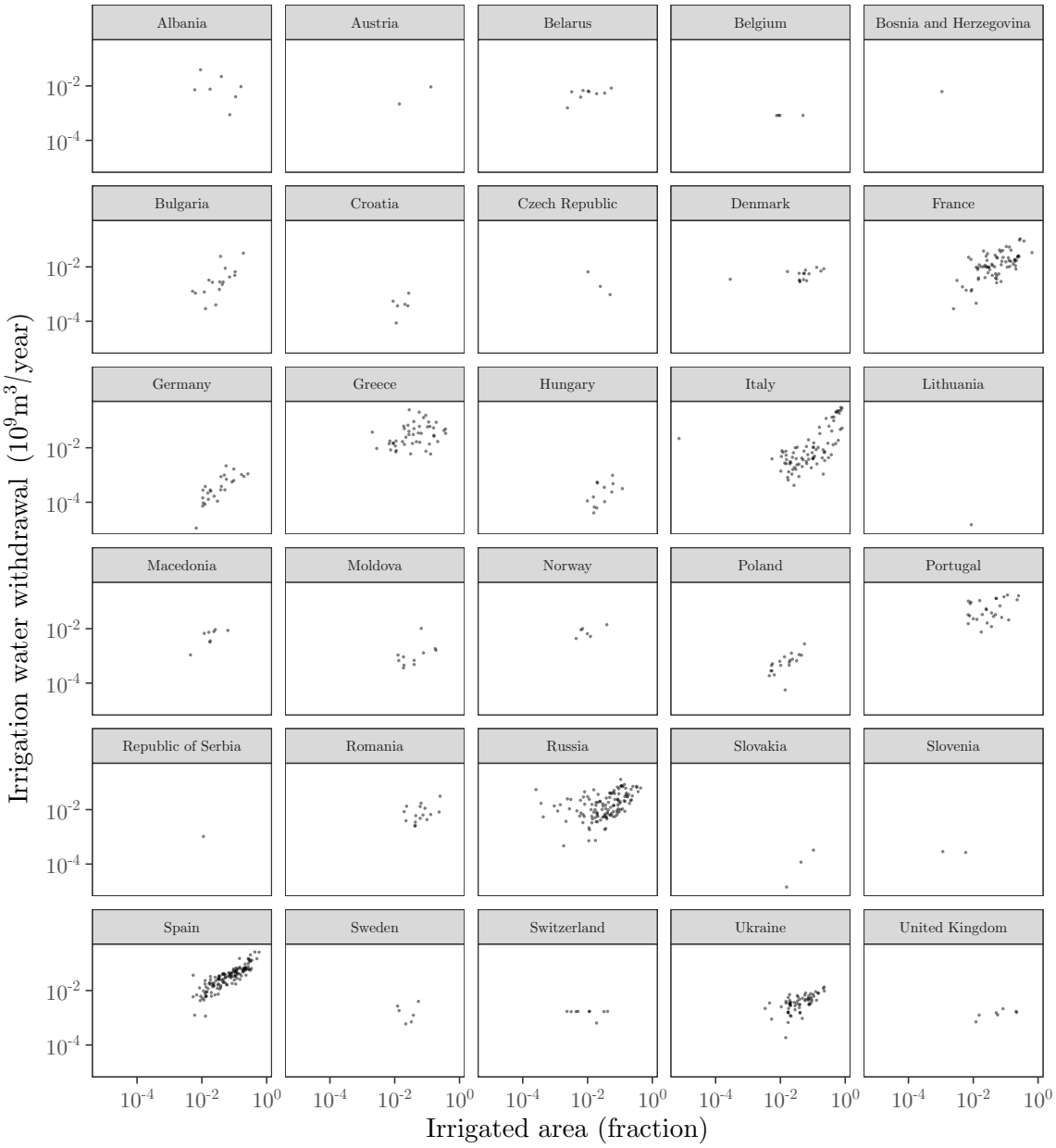

Europe
DBHM
Albania
Austria
Belarus
Bosnia and Herzegovina
Bulgaria
Croatia
Czech Republic
Denmark
Estonia
France
Germany
Greece
Hungary
Italy
Lithuania
Macedonia
Moldova
Norway
Poland
Portugal
Republic of Serbia
Romania
Russia
Slovakia
Slovenia
Spain
Sweden
Switzerland
Ukraine
United Kingdom
Irrigation water withdrawal ($10^9 m^3$/year)
Irrigated area (fraction)

##

$Europe$H08

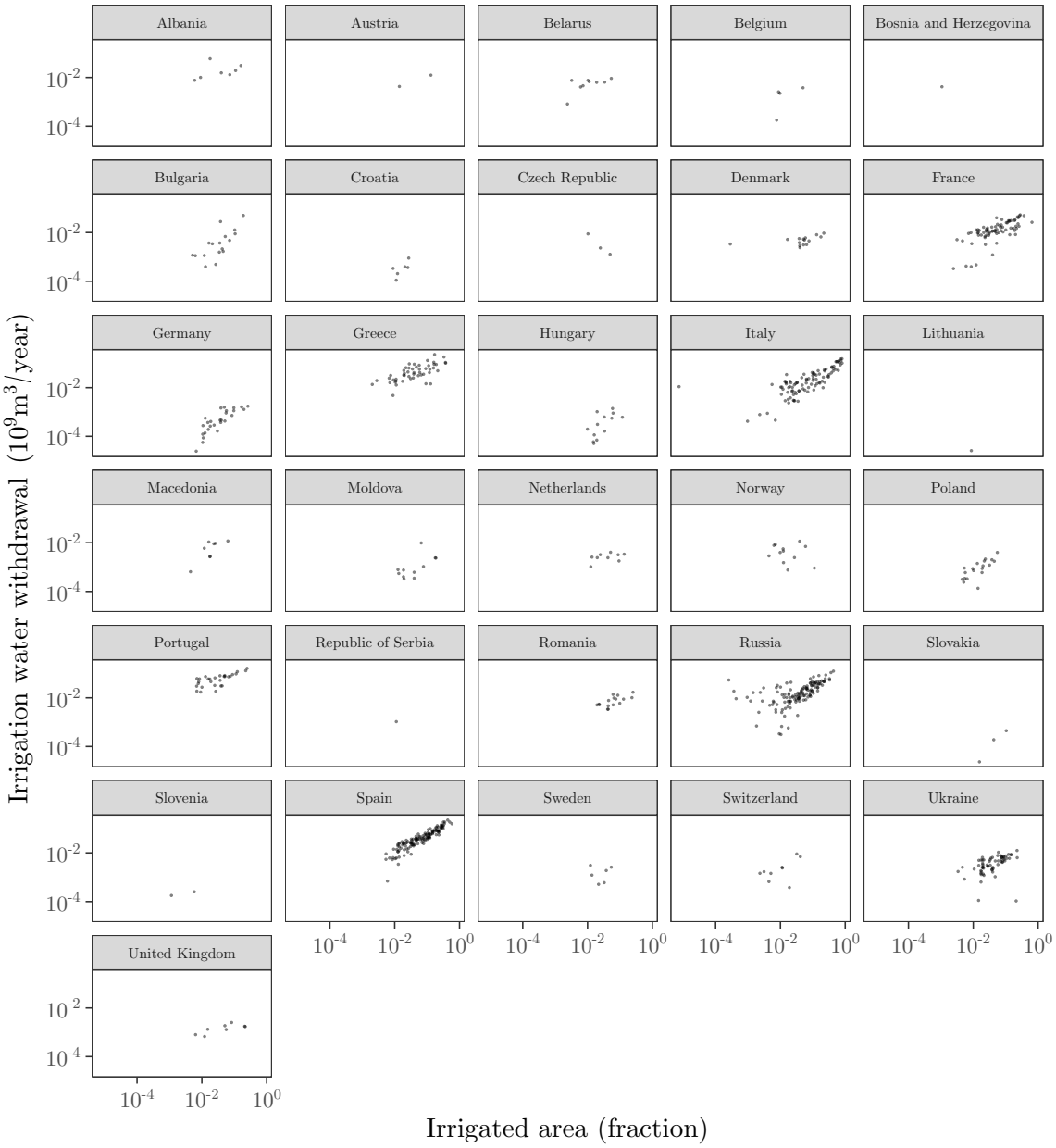
Europe

H08



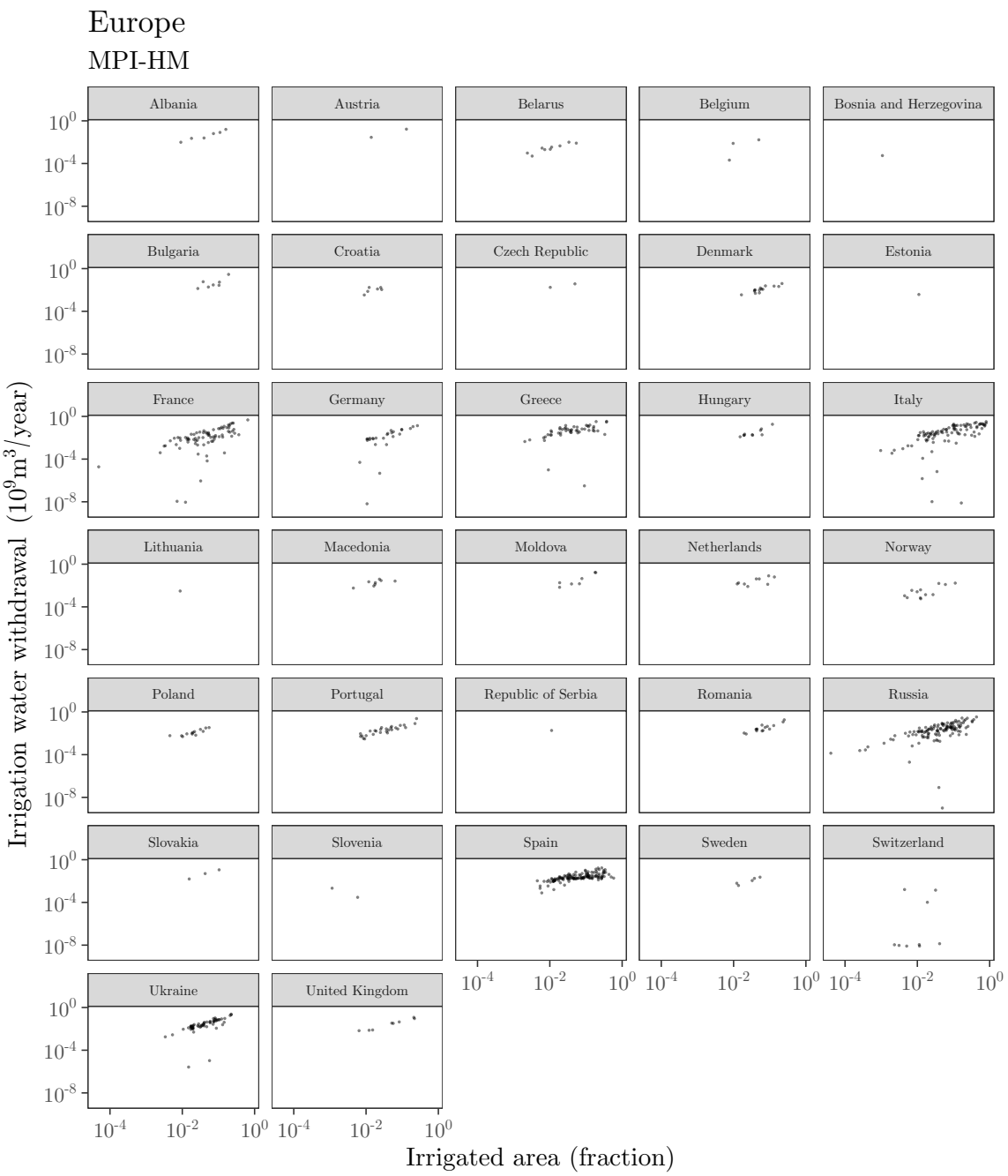
##

$Europe$LPJmL



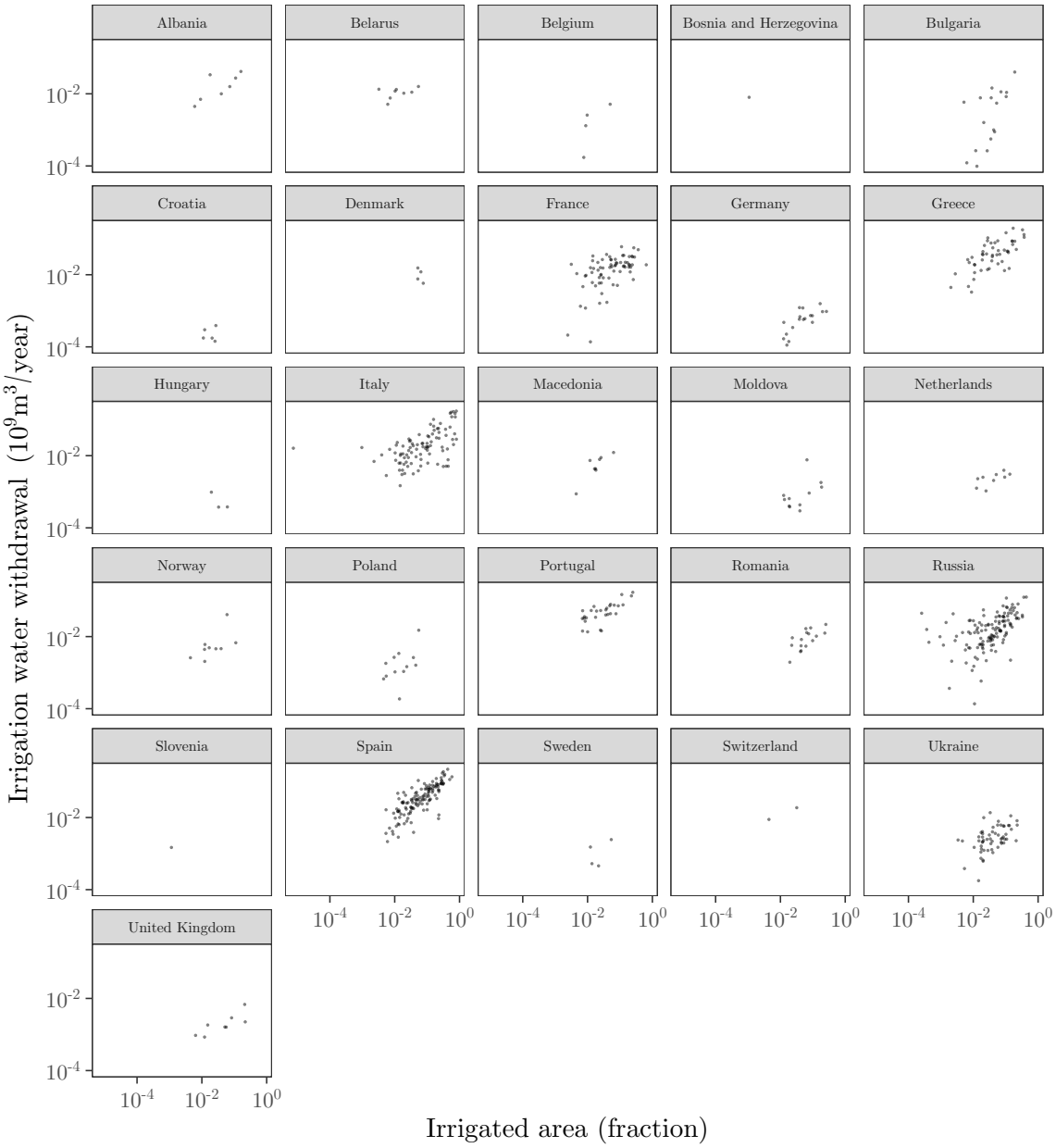
##

$Europe$`MPI-HM`



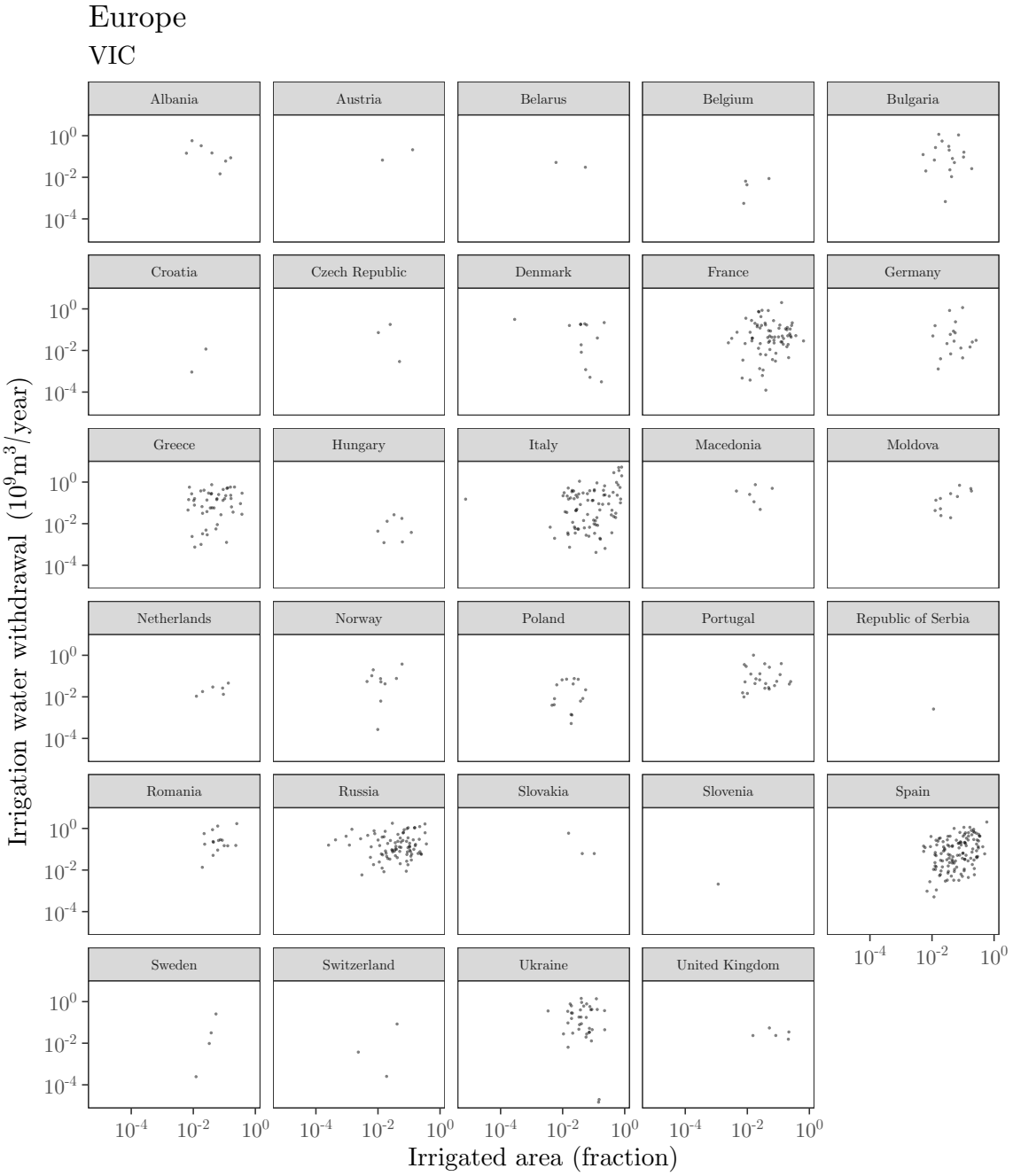
##

$Europe$`PCR-GLOBWB`


Europe
PCR-GLOBWB
Albania
Belarus
Belgium
Bosnia and Herzegovina
Bulgaria
Croatia
Denmark
France
Germany
Greece
Hungary
Italy
Macedonia
Moldova
Netherlands
Norway
Poland
Portugal
Romania
Russia
Slovenia
Spain
Sweden
Switzerland
Ukraine
United Kingdom
Irrigation water withdrawal ($10^9 m^3$/year)
Irrigated area (fraction)

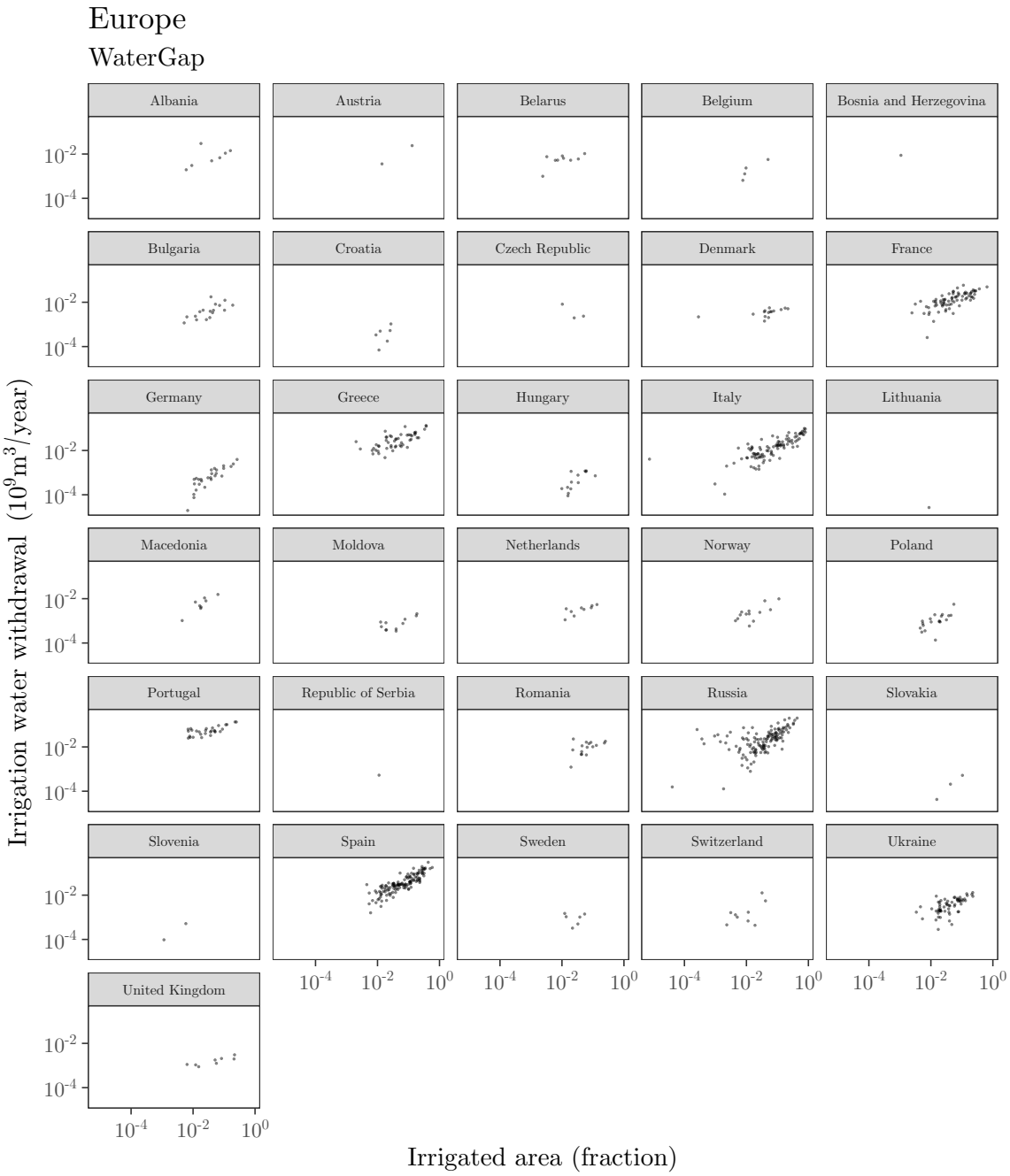
##

$Europe$VIC



##

$Europe$WaterGap



13 Session information

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

sessionInfo()
```

```
## R version 4.0.3 (2020-10-10)
## Platform: x86_64-apple-darwin17.0 (64-bit)
## Running under: macOS Catalina 10.15.7
```

```
##
## Matrix products: default
## BLAS:   /Library/Frameworks/R.framework/Versions/4.0/Resources/lib/libRblas.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/4.0/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
##
## attached base packages:
## [1] grid      parallel  stats     graphics  grDevices utils     datasets
## [8] methods   base
##
## other attached packages:
##  [1] iml_0.10.1          randomForest_4.6-14 checkpoint_0.4.10
##  [4] rsample_0.0.9       robustbase_0.93-7   gridExtra_2.3
##  [7] forcats_0.5.1       stringr_1.4.0       dplyr_1.0.5
## [10] purrr_0.3.4         readr_1.4.0         tidyr_1.1.3
## [13] tibble_3.1.0        ggplot2_3.3.3       tidyverse_1.3.0
## [16] benchmarkme_1.0.7   cowplot_1.1.1       naniar_0.6.0
## [19] broom_0.7.6         ggridges_0.5.3      mice_3.13.0
## [22] lmtest_0.9-38       zoo_1.8-9           sandwich_3.0-0
## [25] mvoutlier_2.0.9     sgeostat_1.0-27     complmrob_0.7.0
## [28] doParallel_1.0.16   iterators_1.0.13    foreach_1.5.1
## [31] MASS_7.3-53.1       scales_1.1.1        boot_1.3-27
## [34] IDPmisc_1.1.20      countrycode_1.2.0   rworldmap_1.3-6
## [37] sp_1.4-5            ncdf4_1.17          sensobol_1.0.1
## [40] data.table_1.14.0
##
## loaded via a namespace (and not attached):
##   [1] readxl_1.3.1          backports_1.2.1       spam_2.6-0
##   [4] plyr_1.8.6            splines_4.0.3         listenv_0.8.0
##   [7] fda_5.1.9             digest_0.6.27         htmltools_0.5.1.1
##  [10] fansi_0.4.2           checkmate_2.0.0       magrittr_2.0.1
##  [13] cluster_2.1.1         ks_1.12.0             Metrics_0.1.4
##  [16] hdrcde_3.4            openxlsx_4.2.3        globals_0.14.0
##  [19] modelr_0.1.8          tikzDevice_0.12.3.1   fds_1.8
##  [22] colorspace_2.0-0      rvest_1.0.0           rrcov_1.5-5
##  [25] haven_2.3.1           rbibutils_2.0         xfun_0.22
##  [28] crayon_1.4.1          RCurl_1.98-1.3        jsonlite_1.7.2
##  [31] survival_3.2-10       glue_1.4.2            gtable_0.3.0
##  [34] car_3.0-10            kernlab_0.9-29        prabclus_2.3-2
##  [37] DEoptimR_1.0-8        maps_3.3.0            abind_1.4-5
##  [40] VIM_6.1.0             mvtnorm_1.1-1         DBI_1.1.1
##  [43] GGally_2.1.1          Rcpp_1.0.6            sROC_0.1-2
##  [46] laeken_0.5.1          foreign_0.8-81        proxy_0.4-25
##  [49] mclust_5.4.7          dotCall64_1.0-1       prediction_0.3.14
##  [52] stats4_4.0.3          vcd_1.4-8             truncnorm_1.0-8
##  [55] httr_1.4.2            RColorBrewer_1.1-2    fpc_2.2-9
```

```
##  [58] modeltools_0.2-23     ellipsis_0.3.1        rainbow_3.6
##  [61] farver_2.1.0          pkgconfig_2.0.3       reshape_0.8.8
##  [64] NADA_1.6-1.1          flexmix_2.3-17        nnet_7.3-15
##  [67] dbplyr_2.1.1          utf8_1.2.1            tidyselect_1.1.0
##  [70] rlang_0.4.10          munsell_0.5.0         cellranger_1.1.0
##  [73] tools_4.0.3           cli_2.4.0             generics_0.1.0
##  [76] ranger_0.12.1         pls_2.7-3             evaluate_0.14
##  [79] cvTools_0.3.2         yaml_2.2.1            fs_1.5.0
##  [82] knitr_1.31            filehash_2.4-2        zip_2.1.1
##  [85] visdat_0.5.3          future_1.21.0         xml2_1.3.2
##  [88] rstudioapi_0.13       compiler_4.0.3        curl_4.3
##  [91] e1071_1.7-6           zCompositions_1.3.4   reprex_2.0.0
##  [94] robCompositions_2.3.0 pcaPP_1.9-73          stringi_1.5.3
##  [97] highr_0.8             fields_11.6           lattice_0.20-41
## [100] Matrix_1.3-2          vctrs_0.3.7           furrr_0.2.2
## [103] pillar_1.5.1          lifecycle_1.0.0       Rdpack_2.1.1
## [106] bitops_1.0-6          maptools_1.1-1        R6_2.5.0
## [109] KernSmooth_2.23-18    rio_0.5.26            parallelly_1.24.0
## [112] codetools_0.2-18      benchmarkmeData_1.0.4 assertthat_0.2.1
## [115] withr_2.4.1           diptest_0.75-7        hms_1.0.0
## [118] class_7.3-18          rmarkdown_2.7         carData_3.0-4
## [121] lubridate_1.7.10      tinytex_0.31
```

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

```
## Machine:
```

```
## [1] "Intel(R) Core(TM) i9-9900K CPU @ 3.60GHz"
```

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

```
## Num cores:
```

```
## [1] 8
```

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

```
## Num threads:
```

```
## [1] 16
```

```
## Return the machine RAM
cat("RAM: "); print (get_ram()); cat("\n")
```

```
## RAM:
```

```
## 34.4 GB
```

References

Frenken, Karen, and Virginie Gillet. 2012. "Irrigation water requirement and water withdrawal by country." Food; Agriculture Organization of the United Nations. http://www.fao.org/3/a-bc824e.pdf.

Huang, Zhongwei, Mohamad Hejazi, Xinya Li, Qiuhong Tang, Chris Vernon, Guoyong Leng, Yaling Liu, et al. 2018. "Global gridded monthly sectoral water use dataset for 1971-2010: v2." https://doi.org/10.5281/ZENODO.1209296.

Liu, Yaling, Mohamad Hejazi, Page Kyle, Son H. Kim, Evan Davies, Diego G. Miralles, Adriaan J. Teuling, Yujie He, and Dev Niyogi. 2016. "Global and regional evaluation of energy for water." *Environmental Science and Technology* 50 (17): 9736–45. https://doi.org/10.1021/acs.est.6b01065.