Uncertainty in global irrigation water use persists after 50 years of research

R code of the multiverse analysis

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Contents

1 Preliminary functions

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

sensobol::load_packages(c("openxlsx", "data.table", "tidyverse","cowplot",
                          "benchmarkme", "parallel", "wesanderson", "scales", "ncdf4",
                          "countrycode", "rworldmap", "sp", "doParallel", "here", "lme4",
                          "microbenchmark", "mgcv", "brms", "randomForest", "here",
                          "igraph", "ggraph", "gganimate", "magick",
                          "randomForestExplainer", "ggrepel"))

# Create custom theme -----------------------------------------------------------

theme_AP <- function() {
  theme_bw() +
    theme(panel.grid.major = element_blank(),
          panel.grid.minor = element_blank(),
          legend.background = element_rect(fill = "transparent",
                                           color = NA),
          legend.key = element_rect(fill = "transparent",
                                    color = NA),
          strip.background = element_rect(fill = "white"),
          legend.text = element_text(size = 7.3),
          axis.title = element_text(size = 10),
          legend.key.width = unit(0.4, "cm"),
          legend.key.height = unit(0.4, "cm"),
          legend.key.spacing.y = unit(0, "lines"),
          legend.box.spacing = unit(0, "pt"),
          legend.title = element_text(size = 7.3),
          axis.text.x = element_text(size = 7),
          axis.text.y = element_text(size = 7),
          axis.title.x = element_text(size = 7.3),
          axis.title.y = element_text(size = 7.3),
          plot.title = element_text(size = 8),
          strip.text.x = element_text(size = 7.4),
          strip.text.y = element_text(size = 7.4))
}

# Select color palette ----------------------------------------------------------

selected.palette <- "Darjeeling1"
```

```
# SOURCE ALL R FUNCTIONS NEEDED FOR THE STUDY ####################################

# Source all .R files in the "functions" folder ----------------------------------

r_functions <- list.files(path = here("functions"), pattern = "\\.R$", full.names = TRUE)
lapply(r_functions, source)
```

2 The Multiverse Analysis

2.1 The dataset

```r
# NAOMI DATASET ################################################################

references.projected <- data.table(read.xlsx("./data/references_projection.xlsx")) %>%
  .[, focus:= "projected"]

references.current <- data.table(read.xlsx("./data/references_current.xlsx")) %>%
  .[, focus:= "current"]

references.full.dt <- rbind(references.projected, references.current) %>%
  .[, study:= paste(author, model, climate.scenario, sep = ".")]

# CLEAN THE DATASET ############################################################

colnames_vector <- c("title", "author", "region")

# Remove leading and trailing spaces -------------------------------------------

references.full.dt[, (colnames_vector):= lapply(.SD, trimws), .SDcols = (colnames_vector)]
references.full.dt[, (colnames_vector):= lapply(.SD, str_squish), .SDcols = (colnames_vector)]

# Lowercaps --------------------------------------------------------------------

references.full.dt[, (colnames_vector):= lapply(.SD, tolower), .SDcols = (colnames_vector)]

# Remove multiple spaces -------------------------------------------------------

references.full.dt[, (colnames_vector):= lapply(.SD, function(x)
  gsub("\\s+", " ", x)), .SDcols = (colnames_vector)]

# Correct America --------------------------------------------------------------

references.full.dt[, region:= ifelse(region == "america", "americas", region)]

# Extract the publication year -------------------------------------------------

references.full.dt[, publication.date:= str_extract(author, "\\d{4}")] %>%
  .[, publication.date:= as.numeric(publication.date)]
```

```r
# FEATURES OF THE DATASET ######################################################

# Definition of target years ---------------------------------------------------
```

```r
target_year <- c(2000, 2010, 2050, 2070, 2100)

# Name of different studies ----------------------------------------------------

sort(unique(references.full.dt[variable == "iww" & region == "global", title]))
```

```
##  [1] "a global water scarcity assessment under shared socio-economic pathways - part 2: wate
##  [2] "a pathway of global food supply adaptation in a world with increasingly constrained g
##  [3] "a reservoir operation scheme for global river routing models"
##  [4] "agricultural green and blue water consumption and its influence on the global water s
##  [5] "an integrated assessment of global and regional water demands for electricity generat
##  [6] "an integrated model for the assessment of global water resources - part 2: applicatio
##  [7] "appraisal and assessment of world water resources"
##  [8] "aquastat: fao's global information system on water and agriculture"
##  [9] "bending the curve: toward global sustainability"
## [10] "cited in world resources 1990-1991, p. 172"
## [11] "climate change impacts on irrigation water requirements: effects of mitigation, 1990-
## [12] "climate impacts on global irrigation requirements under 19 gcms, simulated with a veg
## [13] "climate mitigation policy implications for global irrigation water demand"
## [14] "climate policy implications for agricultural water demand"
## [15] "future long-term changes in global water resources driven by socio-economic and clima
## [16] "global and regional evaluation of energy for water"
## [17] "global hydrological cycles and world water resources,"
## [18] "global impacts of conversions from natural to agricultural ecosystems on water resour
## [19] "global irrigation characteristics and effects simulated by fully coupled land surface
## [20] "global irrigation water demand: variability and uncertainties arising from agricultur
## [21] "global modeling of irrigation water requirements"
## [22] "global modeling of withdrawal, allocation and consumptive use of surface water and gr
## [23] "global monthly sectoral water use for 2010-2100 at 0.5° resolution across alternative
## [24] "global water demand and supply projections"
## [25] "globwat - a global water balance model to assess water use in irrigated agriculture"
## [26] "green and blue water accounting in the ganges and nile basins: implications for food
## [27] "high-resolution modeling of human and climate impacts on global water resources"
## [28] "how can we cope with the water resources situation by the year 2050?"
## [29] "human appropriation of renewable fresh water"
## [30] "impact of climate forcing uncertainty and human water use on global and continental w
## [31] "implementation and evaluation of irrigation techniques in the community land model"
## [32] "incorporating anthropogenic water regulation modules into a land surface model"
## [33] "incorporation of groundwater pumping in a global land surface model with the represen
## [34] "integrated crop water management might sustainably halve the global food gap"
## [35] "isimip database"
## [36] "long-term global water projections using six socioeconomic scenarios in an intgrated
## [37] "lpjml4 - a dynamic global vegetation model with managed land - part 2: model evaluati
## [38] "modelling global water stress of the recent past: on the relative importance of trend
## [39] "multimodel projections and uncertainties of irrigation water demand under climate cha
## [40] "pcr-globwb 2: a 5 arcmin global hydrological and water resources model"
## [41] "physical impacts of climate change on water resources"
```

```
## [42] "present-day irrigation mitigares heat extremes"
## [43] "projecting irrigation water requirements across multiple socio-economic development fu
## [44] "projection of future world water resources under sres scenarios: water withdrawal"
## [45] "quantifying global agricultural water appropriation with data derived from earth obse
## [46] "recent global cropland water consumption constrained by observations"
## [47] "reconciling irrigated food production with environmental flows for sustainable develo
## [48] "reconstructing 20th century global hydrography: a contribution to the global terrestr
## [49] "sustainability of global water use: past reconstruction and future projections"
## [50] "the land-water-energy-nexus: biophysical and economic consequences"
## [51] "the state of the world's land and water resources for food and agriculture"
## [52] "the united nations world water development report 2014: water and energy"
## [53] "the world’s water, 2000-2001: the biennial report on freshwater resources"
## [54] "united nations world water development report 2020: water and climate change"
## [55] "water 2050. moving toward a sustainable vision fot the earth's fresh water"
## [56] "water and sustainability. global pattern and long-range problems"
## [57] "water savings potentials of irrigation systems: global simulation of processes and li
## [58] "water scarcity in the twenty-first century"
## [59] "water sector assumptions for the shared socioeconomic pathways in an integrated model
## [60] "world agriculture towards 2030/2050: the 2012 revision"
## [61] "world agriculture towards 2030/2055"
## [62] "world resources 1992-93. a guide to the global environment"
## [63] "world water demand and supply, 1990 to 2025: scenarios and issues"
## [64] "world water in 2025 - global modeling and scenario analysis for the world commission 
## [65] "world water resources and their future"
```

```r
# Number of data points -------------------------------------------------------

nrow(references.full.dt[variable == "iww" & region == "global"])
```

```
## [1] 1408
```

```r
# Number of different studies per variable ------------------------------------------

references.full.dt[region == "global", unique(title), variable] %>%
  .[, .N, variable]
```

```
##    variable     N
##      <char> <int>
## 1:      iww    65
## 2:      tww    20
## 3:      iwc    20
## 4:      twc     4
## 5:      iwr     2
```

```r
# Number of data points for each target year ------------------------------------

references.full.dt[variable == "iww" & region == "global" &
                     estimation.year %in% target_year, .N, estimation.year]
```

```
##    estimation.year     N
```

```
##                <num> <int>
## 1:              2000    65
## 2:              2070   124
## 3:              2100   121
## 4:              2010   111
## 5:              2050   128
```

```r
# Number of unique studies estimating for each target year ---------------------

references.full.dt[variable == "iww" & region == "global" &
                     estimation.year %in% target_year, unique(title), estimation.year] %>%
  .[, .N, estimation.year]
```

```
##    estimation.year     N
##                <num> <int>
## 1:              2000    24
## 2:              2070     5
## 3:              2100     5
## 4:              2010    11
## 5:              2050    16
```

```r
# Number of data points for every targeted year --------------------------------

references.full.dt[variable == "iww" & region == "global", .N, estimation.year] %>%
  .[order(estimation.year)]
```

```
##     estimation.year     N
##                 <num> <int>
##  1:            1900     3
##  2:            1910     2
##  3:            1920     2
##  4:            1930     2
##  5:            1940     4
##  6:            1950     4
##  7:            1960     7
##  8:            1970     5
##  9:            1975    22
## 10:            1980    29
## 11:            1983     1
## 12:            1985    33
## 13:            1986     1
## 14:            1988     1
## 15:            1990    29
## 16:            1993     2
## 17:            1994     3
## 18:            1995    40
## 19:            1996     2
## 20:            2000    65
## 21:            2002     1
```

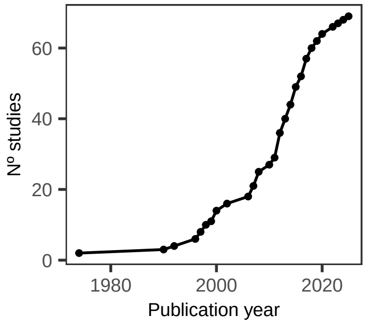
```
## 22:             2003     1
## 23:             2004     1
## 24:             2005    34
## 25:             2006     2
## 26:             2007     1
## 27:             2008     1
## 28:             2010   111
## 29:             2015     9
## 30:             2020    97
## 31:             2021     1
## 32:             2025    16
## 33:             2030    88
## 34:             2035     7
## 35:             2040    99
## 36:             2050   128
## 37:             2055     6
## 38:             2060    88
## 39:             2065     7
## 40:             2070   124
## 41:             2075     6
## 42:             2080   103
## 43:             2090    85
## 44:             2095    14
## 45:             2100   121
##     estimation.year     N
```

```r
# Number of data points for year 2000 or later years ---------------------------

references.full.dt[variable == "iww" & region == "global", .N, estimation.year] %>%
  .[estimation.year >= 2000] %>%
  .[, N] %>%
  sum(.)
```

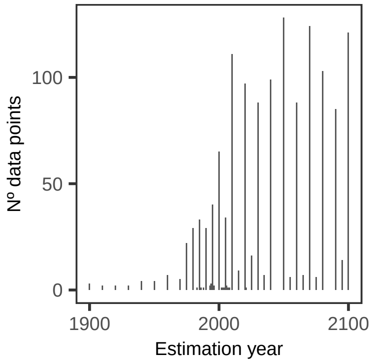
```
## [1] 1216
```

```r
# Cumulative sum of published studies ------------------------------------------

cumulative.iww <- references.full.dt[, .(title, publication.date, variable)] %>%
  .[variable == "iww"] %>%
  .[!duplicated(.)] %>%
  setorder(., publication.date) %>%
  .[, .N, publication.date] %>%
  .[, cumulative_sum := cumsum(N)] %>%
  ggplot(., aes(publication.date, cumulative_sum)) +
  geom_line() +
  scale_x_continuous(breaks = breaks_pretty(n = 3)) +
  geom_point(size = 0.7) +
  theme_AP() +
  labs(x = "Publication year", y = "Nº studies")
```

```
cumulative.iww
```

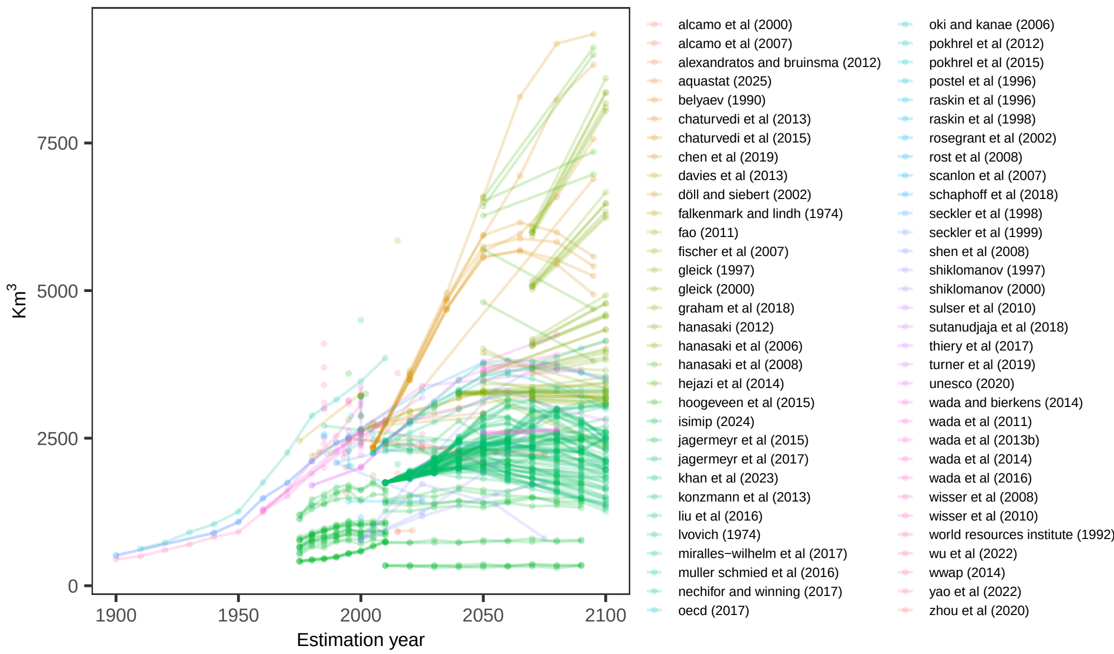



```
# DISTRIBUTION OF DATA POINTS THROUGH YEARS @####################################

plot.bar <- references.full.dt[variable == "iww" & region == "global", .N, estimation.year] %>%
  ggplot(., aes(estimation.year, N)) +
  geom_bar(stat = "identity") +
  scale_x_continuous(breaks = breaks_pretty(n = 3)) +
  labs(x = "Estimation year", y = "Nº data points") +
  theme_AP()

plot.bar
```

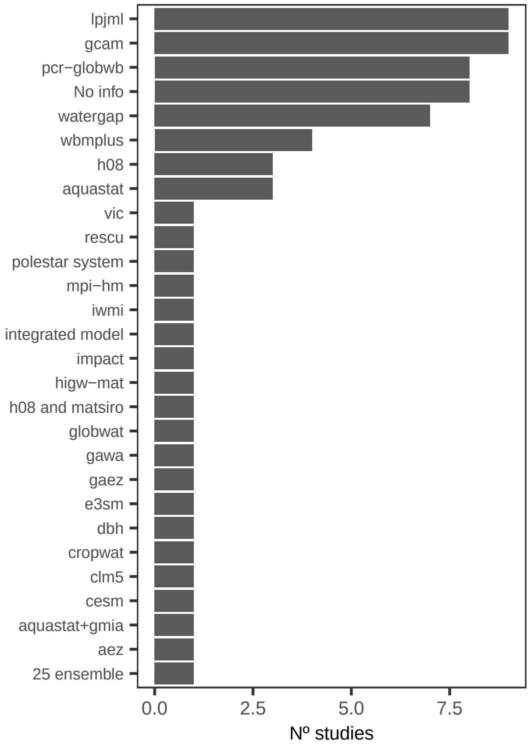



```
# PLOT ALL ESTIMATIONS ##############################################################

def.alpha <- 0.2

plot.iww <- references.full.dt[variable == "iww" & region == "global"] %>%
  .[, .(author, study, estimation.year, value)] %>%
  na.omit() %>%
  ggplot(., aes(estimation.year, value, color = author, group = study)) +
  geom_point(alpha = def.alpha, size = 0.5) +
  labs(x = "Estimation year", y = bquote("Km"^3)) +
  scale_color_discrete(name = "") +
  geom_line(alpha = def.alpha) +
  theme_AP() +
  guides(color = guide_legend(ncol = 2)) +
```

```
  theme(legend.text = element_text(size = 5.2),
        legend.key.width = unit(0.25, "cm"),
          legend.key.height = unit(0.25, "cm"))

plot.iww
```



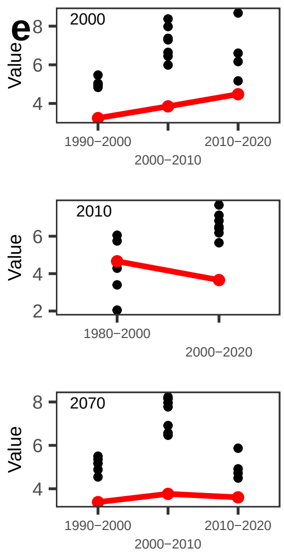

```
# PLOT NUMBER OF UNIQUE STUDIES PER MODEL ######################################

plot.models <- references.full.dt[variable == "iww" & region == "global"] %>%
  .[, .(title, doi, model)] %>%
  .[, model:= tolower(model)] %>%
  .[, unique(doi), model] %>%
  .[, model := gsub("(?i)watergap\\s*\\d*\\.?\\d*", "watergap", model, perl = TRUE)] %>%
  .[, .N, model]  %>%
  .[, model:= ifelse(is.na(model), "No info", model)] %>%
  ggplot(., aes(reorder(model, N), N)) +
  geom_bar(stat = "identity") +
  labs(x = "", y = "Nº studies") +
  coord_flip() +
  theme_AP() +
  theme(axis.text.y = element_text(size = 5.5))

plot.models
```



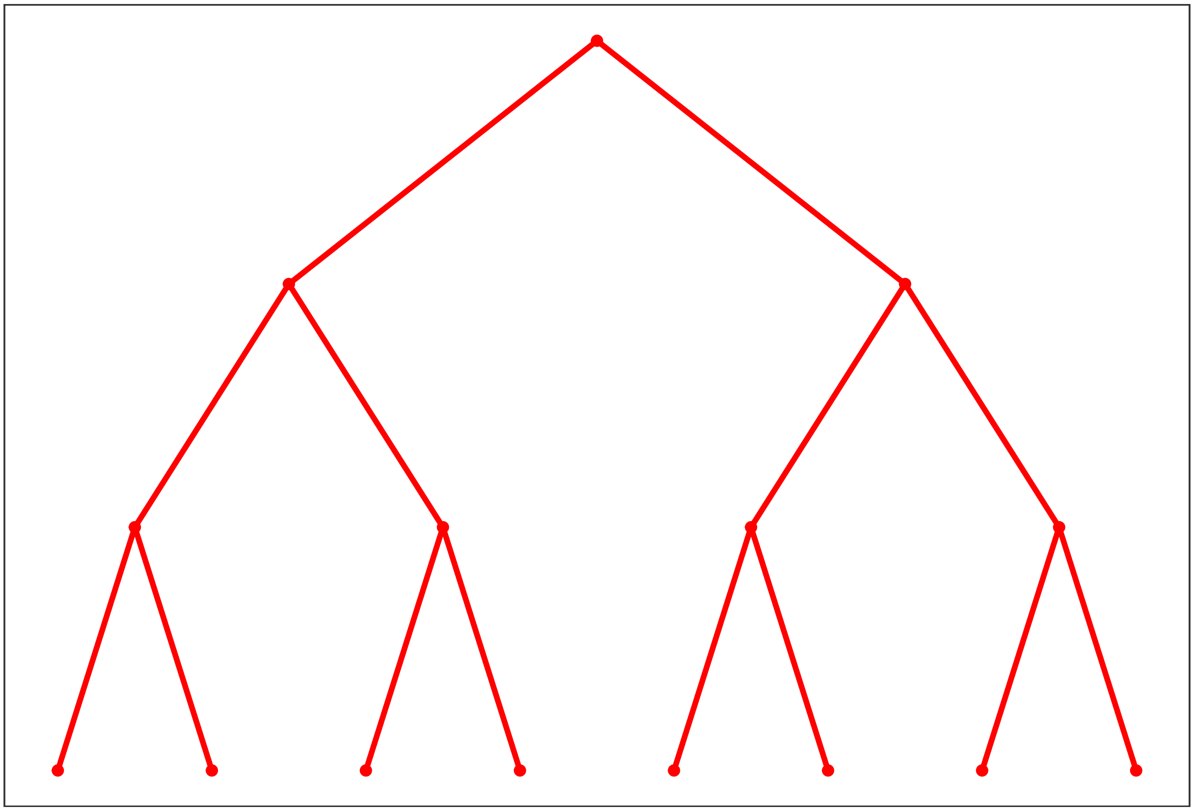
2.2 Graphical representation of the multiverse

```r
# PLOT EXAMPLES TO ILLUSTRATE APPROACH #########################################

# Set seed for reproducibility ---------------------------------------------------

set.seed(123)

# Create datasets for different SD trends ---------------------------------------

data_increasing <- data.frame(
  period = rep(c("1990-2000", "2000-2010", "2010-2020"), times = c(5, 7, 4)),
  value = c(rnorm(5, mean = 5, sd = 0.3),  # Low SD
            rnorm(7, mean = 7, sd = 0.8),  # Medium SD
            rnorm(4, mean = 6, sd = 1.5)),  # High SD
  target_year = 2000
)

data_decreasing <- data.frame(
  period = rep(c("1980-2000", "2000-2020"), times = c(5, 7)),
  value = c(rnorm(5, mean = 5, sd = 1.5),  # High SD
            rnorm(7, mean = 7, sd = 0.8)), # Medium
  target_year = 2010
)

data_invertedV <- data.frame(
```

```r
  period = rep(c("1990-2000", "2000-2010", "2010-2020"), times = c(5, 7, 4)),
  value = c(rnorm(5, mean = 5, sd = 0.4),  # Low SD
            rnorm(7, mean = 7, sd = 1.4),  # High SD (peak in the middle)
            rnorm(4, mean = 5, sd = 0.4)),  # Low SD again
  target_year = 2070
)

# Function to compute SD and create a ggplot -----------------------------------

create_plot <- function(data, title) {
  sd_values <- data %>%
    group_by(period) %>%
    summarize(sd_value = sd(value) + 3)

  ggplot(data, aes(x = period, y = value)) +
    geom_point(size = 1) +
    geom_point(data = sd_values, aes(x = period, y = sd_value), color = "red", size = 1.5) +  #
    geom_line(data = sd_values, aes(x = period, y = sd_value, group = 1), color = "red", linewi
    theme_AP() +
    theme(axis.text.x = element_text(size = 5.35),
          plot.margin = unit(c(0.1, 0.1, 0, 0.1), "cm")) +
    scale_y_continuous(breaks = breaks_pretty(n = 3)) +
    scale_x_discrete(guide = guide_axis(n.dodge = 2)) +
    labs(x = "", y = "Value") +
    annotate("text", x = 0.1 + 0.5, y = max(data$value),
             label = unique(data$target_year), hjust = 0, vjust = 1,
             size = 2)
}


# Generate the three plots -----------------------------------------------------

p1 <- create_plot(data_increasing)
p2 <- create_plot(data_decreasing)
p3 <- create_plot(data_invertedV)

# Merge using plot_grid --------------------------------------------------------

plot.examples.trends.data <- plot_grid(p1, p2, p3, ncol = 1, labels = c("e", "", ""))
plot.examples.trends.data
```



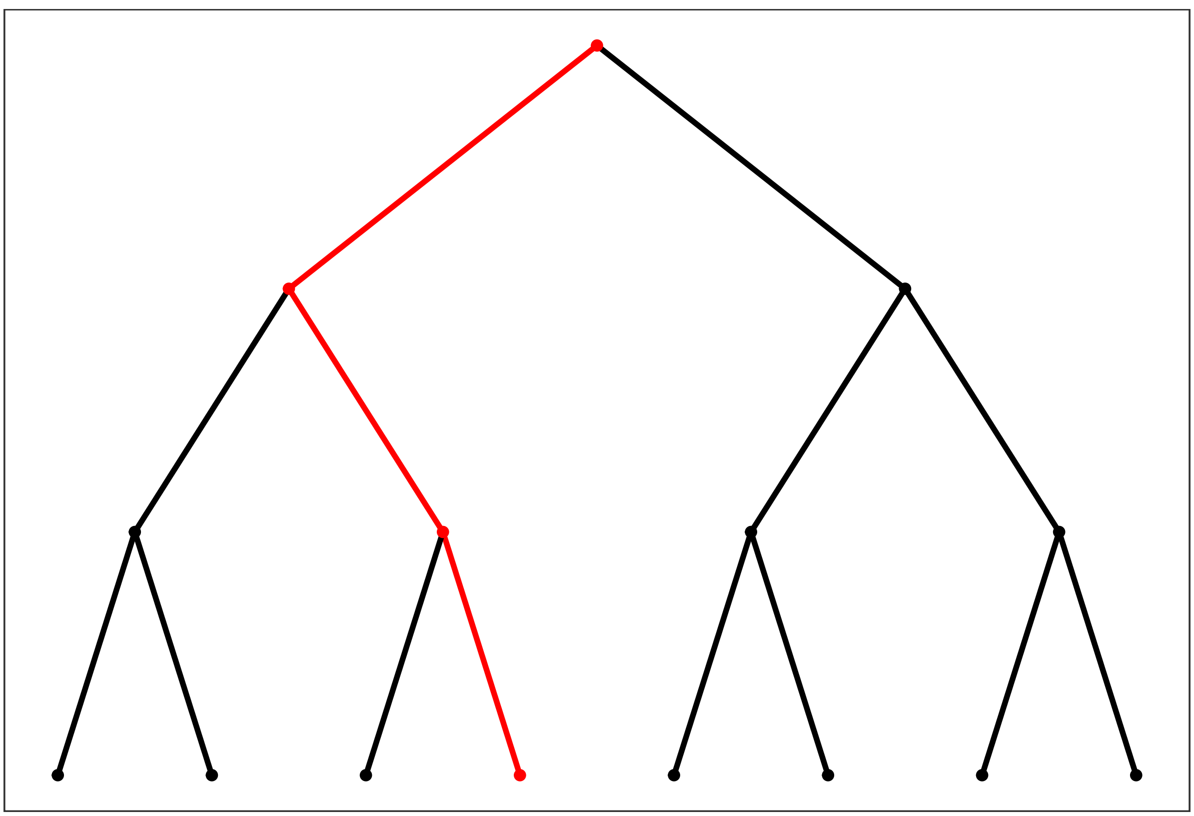

```r
# GRAPHICAL REPRESENTATION OF THE GARDEN OF FORKING PATHS #####################

# Define size of nodes ---------------------------------------------------------

size.nodes <- 1.5

# Create a balanced binary tree with height 3 ----------------------------------

tree <- make_tree(15, children = 2, mode = "out")

# Create a tree plot with all edges highlighted in red -------------------------

all.paths <- ggraph(tree, layout = "dendrogram") +
  geom_edge_link(color = "red", width = 1) +
  geom_node_point(size = size.nodes, color = "red") +
  theme_AP() +
  labs(x = "", y = "") +
  theme(legend.position = "none",
        axis.ticks = element_blank(),
        axis.text.x = element_blank(),
        axis.text.y = element_blank())

all.paths
```



```r
# Create a tree plot with only one analytical path highlighted -----------------

# Define the path to highlight (from root to a specific node) ------------------

highlight_nodes <- c(1, 2, 5, 11)  # Path: 1 → 2 → 5 → 11

highlight_edges <- apply(cbind(head(highlight_nodes, -1),
                               tail(highlight_nodes, -1)), 1, function(x)
                                 paste(x, collapse = "-"))

# Assign default colors (black) to all edges and nodes -------------------------

E(tree)$edge_color <- "black"
V(tree)$node_color <- "black"

# Extract edges from the tree and match with highlight_edges -------------------

edge_list <- apply(get.edgelist(tree), 1, function(x) paste(x, collapse = "-"))
```

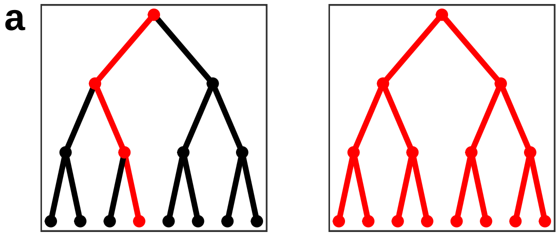
```
## Warning: `get.edgelist()` was deprecated in igraph 2.0.0.
## i Please use `as_edgelist()` instead.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```

```r
E(tree)$edge_color[edge_list %in% highlight_edges] <- "red"

# Highlight the selected nodes in red -___--------------------------------------

V(tree)$node_color[highlight_nodes] <- "red"

# Plot the tree with explicitly defined colors for both edges and nodes --------

one.path <- ggraph(tree, layout = "dendrogram") +
  geom_edge_link(aes(edge_color = edge_color), width = 1) +  # Correct edge colors
  geom_node_point(aes(color = node_color), size = size.nodes) +  # Correct node colors
  scale_edge_color_manual(values = c("black" = "black", "red" = "red")) +  # Fix for edges
  scale_color_manual(values = c("black" = "black", "red" = "red")) +  # Fix for nodes
  theme_AP() +
  labs(x = "", y = "") +
  theme(legend.position = "none",
        axis.ticks = element_blank(),
        axis.text.x = element_blank(),
        axis.text.y = element_blank())

one.path
```

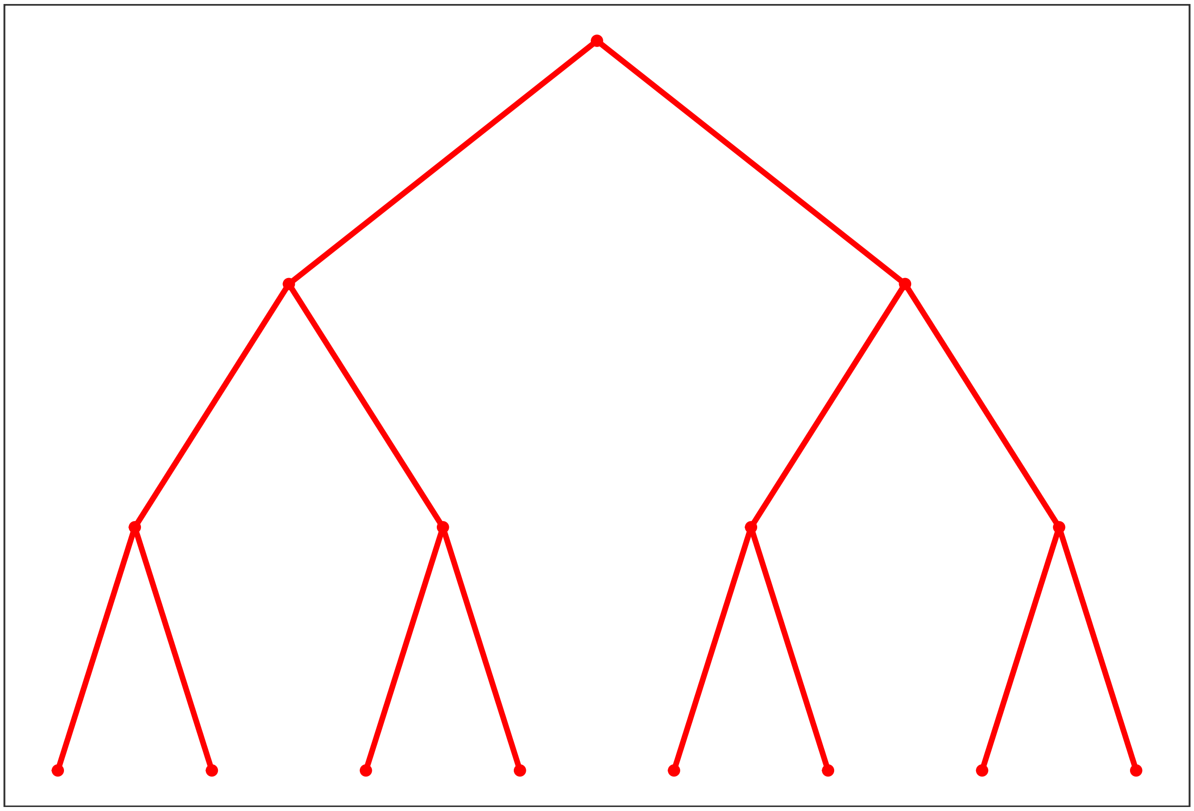


```r
# MERGE FORKING PATHS ##########################################################
```

```r
plot_grid(one.path, all.paths, ncol = 2, labels = c("a", ""))
```

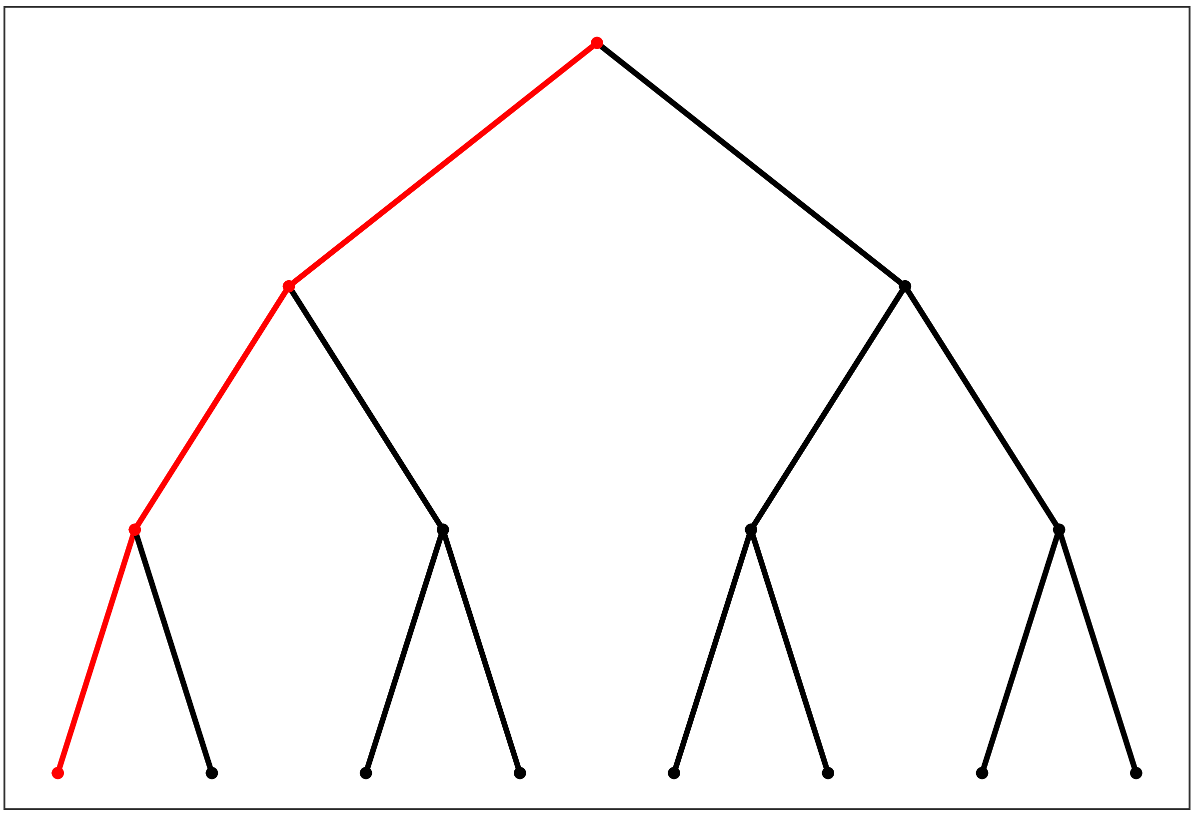



```r
# GRAPHICAL REPRESENTATION OF THE GARDEN OF FORKING PATHS #####################

# Define size of nodes ---------------------------------------------------------

size.nodes <- 1.5

# Create a balanced binary tree with height 3 ----------------------------------

tree <- make_tree(15, children = 2, mode = "out")

# Create a tree plot with all edges highlighted in red -------------------------

all.paths <- ggraph(tree, layout = "dendrogram") +
  geom_edge_link(color = "red", width = 1) +
  geom_node_point(size = size.nodes, color = "red") +
  theme_AP() +
  labs(x = "", y = "") +
  theme(legend.position = "none",
        axis.ticks = element_blank(),
        axis.text.x = element_blank(),
        axis.text.y = element_blank())

all.paths
```



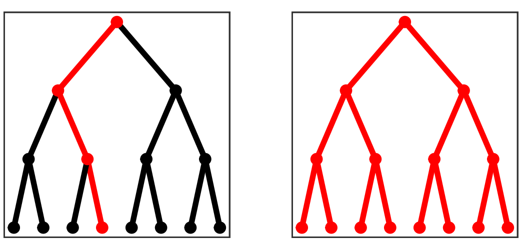
```r
# Create a tree plot with only one analytical path highlighted -----------------

# Define the path to highlight (from root to a specific node) ------------------

highlight_nodes <- c(1, 2, 4, 8)  # Path: 1 → 2 → 5 → 11

highlight_edges <- apply(cbind(head(highlight_nodes, -1),
                               tail(highlight_nodes, -1)), 1, function(x)
                                 paste(x, collapse = "-"))

# Assign default colors (black) to all edges and nodes -------------------------

E(tree)$edge_color <- "black"
V(tree)$node_color <- "black"

# Extract edges from the tree and match with highlight_edges -------------------

edge_list <- apply(get.edgelist(tree), 1, function(x) paste(x, collapse = "-"))
E(tree)$edge_color[edge_list %in% highlight_edges] <- "red"

# Highlight the selected nodes in red -___--------------------------------------

V(tree)$node_color[highlight_nodes] <- "red"

# Plot the tree with explicitly defined colors for both edges and nodes --------
```

```
one.path2 <- ggraph(tree, layout = "dendrogram") +
  geom_edge_link(aes(edge_color = edge_color), width = 1) +  # Correct edge colors
  geom_node_point(aes(color = node_color), size = size.nodes) +  # Correct node colors
  scale_edge_color_manual(values = c("black" = "black", "red" = "red")) +  # Fix for edges
  scale_color_manual(values = c("black" = "black", "red" = "red")) +  # Fix for nodes
  theme_AP() +
  labs(x = "", y = "") +
  theme(legend.position = "none",
        axis.ticks = element_blank(),
        axis.text.x = element_blank(),
        axis.text.y = element_blank())

one.path2
```



```
# MERGE FORKING PATHS ##############################################################

plot_grid(one.path, all.paths, ncol = 2, labels = c("a", ""))
```

a



2.3 The garden of forking paths

```r
# DEFINE THE UNCERTAINTY SPACE #################################################

# Target year ------------------------------------------------------------------

## Defined above

# Target year interval ---------------------------------------------------------

target_year_interval <- c("yes", "no")

# Interval publication ---------------------------------------------------------

interval <- c(10, 15, 20)

# Metrics of study -------------------------------------------------------------

metrics <- c("cv", "range", "sd", "var", "entropy", "iqr")

# Rolling windows --------------------------------------------------------------

rolling_window_factor <- c(1, 0.5)

# Define the forking paths -----------------------------------------------------

forking_paths <- expand.grid(target_year = target_year,
                             target_year_interval = target_year_interval,
                             interval = interval,
                             rolling_window_factor = rolling_window_factor,
                             metric = c(metrics, paste(metrics, "_normalized", sep = ""))) %>%
  data.table()

# Number of simulations --------------------------------------------------------

nrow(forking_paths)
```

```
## [1] 720
```

```r
# RUN MODEL ####################################################################

# Select only simulations at the global level of iww ---------------------------

dt <- references.full.dt[variable == "iww" & region == "global"]

# Run simulations --------------------------------------------------------------

trend <- list()
```

```r
for (i in 1:nrow(forking_paths)) {

  trend[[i]] <- forking_paths_fun(dt = dt,
                                  target_year = forking_paths[[i, "target_year"]],
                                  target_year_interval = forking_paths[[i, "target_year_interva
                                  interval = forking_paths[[i, "interval"]],
                                  rolling_window_factor = forking_paths[[i, "rolling_window_fac
                                  metric = forking_paths[[i, "metric"]])
}
```

```r
# ARRANGE DATA ##################################################################

output.dt <- lapply(trend, function(x) x[["results"]]) %>%
  do.call(rbind, .) %>%
  data.table() %>%
  setnames(., "V1", "trend") %>%
  .[, row:= .I]

final.dt <- cbind(forking_paths, output.dt)

# Export simulations ------------------------------------------------------------

fwrite(final.dt, "forking.paths.dataset.csv")
write.xlsx(final.dt, "forking.paths.dataset.xlsx")

# Print the fraction of simulations in each classification ---------------------

final.dt %>%
  .[, .(total = .N), trend] %>%
  .[, fraction:= total / nrow(output.dt)] %>%
  print()
```

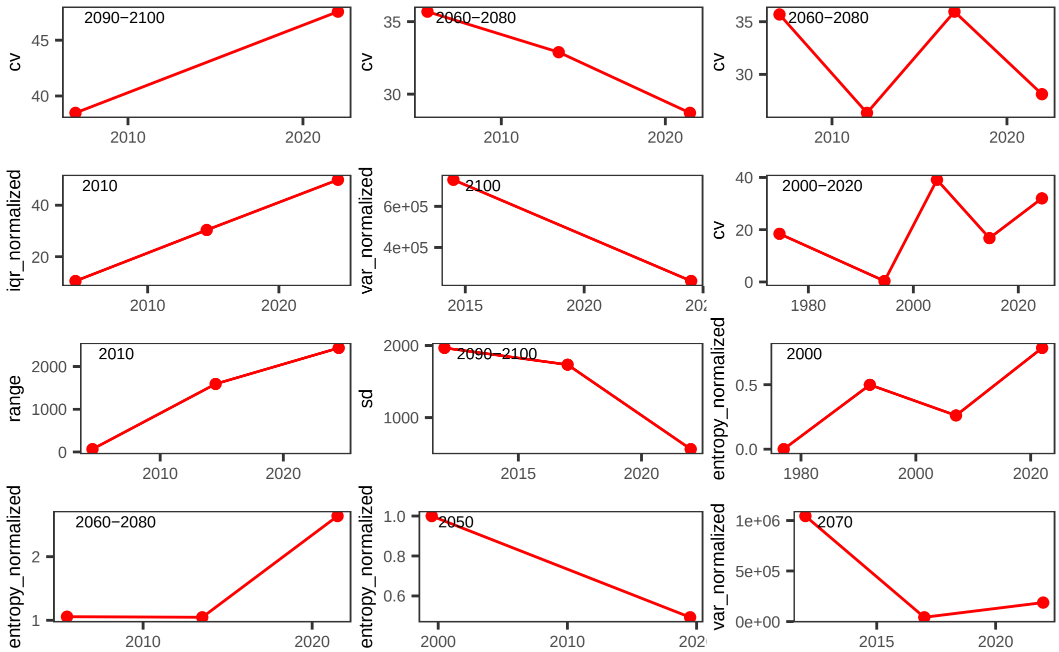
```
##           trend total   fraction
##          <char> <int>      <num>
## 1:       Random   345 0.47916667
## 2:     Decrease   149 0.20694444
## 3:     Increase   196 0.27222222
## 4: single point    30 0.04166667
```

```r
# Now remove all simulations that produced just one single point ---------------

final.dt <- final.dt[!trend == "single point"]

# Simulations that did not lead to a reduction in uncertainty ------------------

final.dt %>%
  .[, .(total = .N), trend] %>%
  .[, fraction:= total / nrow(output.dt)] %>%
```

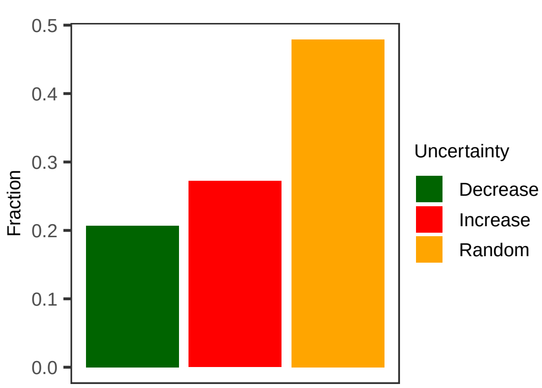
```r
  .[!trend == "Decrease"] %>%
  .[, sum(fraction)]
```

```
## [1] 0.7513889
```

```r
# PLOTS FORKING PATHS EXAMPLES ################################################

plots.dt <- lapply(trend, function(x) x[["plot"]])

# Increasing trends -----------------------------------------------------------

plots.increasing <- plot_grid(plots.dt[[15]], plots.dt[[667]], plots.dt[[117]],
                              plots.dt[[644]], ncol = 1)

# Decreasing trend ------------------------------------------------------------

plots.decreasing <- plot_grid(plots.dt[[44]], plots.dt[[600]], plots.dt[[155]],
                              plots.dt[[628]], ncol = 1)

# Random trend ----------------------------------------------------------------

plots.random <- plot_grid(plots.dt[[34]], plots.dt[[2]], plots.dt[[616]],
                          plots.dt[[579]], ncol = 1)

# Merge -----------------------------------------------------------------------

plots.examples.trends <- plot_grid(plots.increasing, plots.decreasing,
                                   plots.random, ncol = 3)

plots.examples.trends
```




```
# PLOT RESULTS ################################################################

selected_colors <- c("Increase" = "red", "Decrease" = "darkgreen", "Random" = "orange")

plot.fraction <- final.dt[, .(total = .N), trend] %>%
  .[, fraction:= total / nrow(output.dt)] %>%
  ggplot(., aes(trend, fraction, fill = trend)) +
  geom_bar(stat = "identity") +
  labs(x = "", y = "Fraction") +
  scale_fill_manual(values = selected_colors, name = "Uncertainty") +
  scale_x_discrete(guide = guide_axis(n.dodge = 2)) +
  theme_AP() +
  theme(axis.ticks.x = element_blank(),
        axis.text.x = element_blank(),
        legend.position = "right")

plot.fraction
```



2.4 Random forest model

```
# RANDOM FOREST ##################################################################

# Convert categorical variables to factors ------------------------------------

df <- data.frame(final.dt[trend != "single point"]) # Remove 5% observations
df$metric <- as.factor(df$metric)
df$trend <- as.factor(df$trend)
df$target_year_interval <- as.factor(df$target_year_interval)

# Train the model with weights on 2,000 random trees ----------------------------

rf_model <- randomForest(trend ~ target_year + target_year_interval + interval +
                           rolling_window_factor + metric,
                         data = df, importance = TRUE, ntree = 5000,
                         classwt = c(1.5, 2, 1), mtry = 3)

# Check model summary ----------------------------------------------------------

print(rf_model)
```

```
##
## Call:
##  randomForest(formula = trend ~ target_year + target_year_interval +      interval + rolling
##                Type of random forest: classification
##                      Number of trees: 5000
## No. of variables tried at each split: 3
##
##         OOB estimate of  error rate: 18.84%
## Confusion matrix:
##          Decrease Increase Random class.error
## Decrease      109       26     14   0.2684564
## Increase       21      147     28   0.2500000
## Random         19       22    304   0.1188406
```

```
# View variable importance -----------------------------------------------------

dt_rf_model <- data.frame(importance(rf_model))
dt_rf_model
```

```
##                       Decrease  Increase    Random MeanDecreaseAccuracy
## target_year          233.33675 127.67405 235.39101            313.15103
## target_year_interval   2.49685  80.37727  73.15638             91.51887
## interval             122.21030  73.59620 158.73968            192.26397
## rolling_window_factor  93.60813 128.16285 227.48552            256.35584
## metric                97.93797 120.70981  37.83513            135.03712
##                      MeanDecreaseGini
## target_year                 110.60836
```

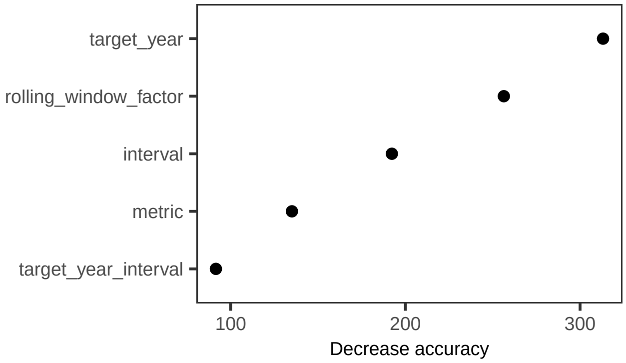
```
## target_year_interval          38.66901
## interval                      64.52131
## rolling_window_factor         40.38888
## metric                       150.02786
```

```
# Compute importance -----------------------------------------------------------

importance_frame <- measure_importance(rf_model)
data <- importance_frame[importance_frame$no_of_trees > 0, ]

# Retrieve data ----------------------------------------------------------------

data_for_labels <- importance_frame[importance_frame$variable %in%
                                      important_variables(importance_frame, k = 10,
                                                          measures = c("mean_min_depth",
                                                                       "times_a_root",
                                                                       "no_of_nodes")),]

data_for_labels
```

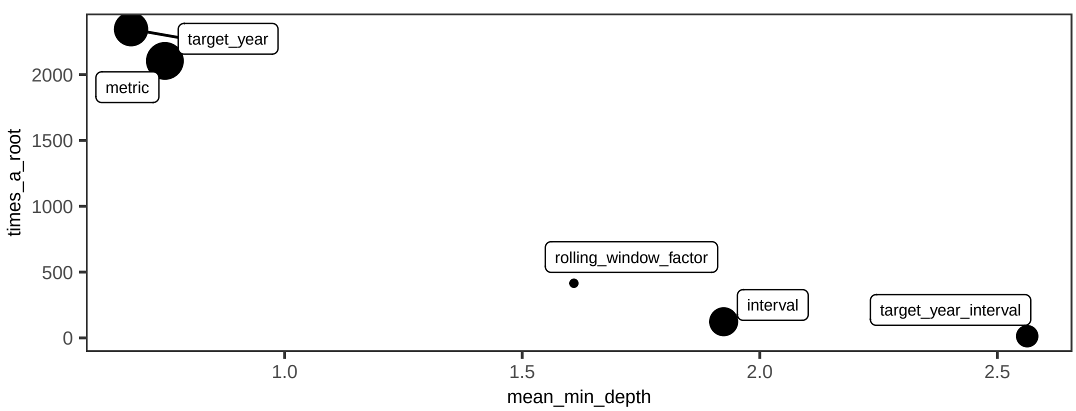
```
##                variable mean_min_depth no_of_nodes accuracy_decrease
## 1              interval         1.9240      130132        0.07868340
## 2                metric         0.7480      219195        0.06873110
## 3 rolling_window_factor         1.6088       48391        0.09902980
## 4           target_year         0.6768      179300        0.16078828
## 5  target_year_interval         2.5628       84286        0.03069028
##   gini_decrease no_of_trees times_a_root p_value
## 1      64.52131        5000          123       1
## 2     150.02786        5000         2104       0
## 3      40.38888        5000          415       1
## 4     110.60836        5000         2345       0
## 5      38.66901        5000           13       1
```

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

plot.rf <- data.frame(importance(rf_model)) %>%
  rownames_to_column(., var = "factors") %>%
  data.table() %>%
  setnames(., c("MeanDecreaseAccuracy", "MeanDecreaseGini"),
           c("Accuracy", "Gini")) %>%
  melt(., measure.vars = c("Accuracy", "Gini")) %>%
  .[variable == "Accuracy"] %>%
  ggplot(., aes(reorder(factors, value), value)) +
  geom_point() +
  coord_flip() +
  scale_y_continuous(breaks = breaks_pretty(n = 3)) +
  labs(x = "", y = "Decrease accuracy") +
  theme_AP()
```

```
plot.rf
```




```
# MULTIWAY IMPORTANCE PLOT ##################################################

plot.multiway <- ggplot(data, aes(x = mean_min_depth, y = times_a_root)) +
  geom_point(data = data_for_labels, aes(size = no_of_nodes)) +
  geom_label_repel(data = data_for_labels, aes(label = variable),
                   show.legend = FALSE, size = 2) +
  scale_size_continuous(breaks = c(min(data$no_of_nodes),
                                   median(data$no_of_nodes),
                                   max(data$no_of_nodes)),
                        label = label_number(accuracy = 10000)) +
  theme_AP() +
  theme(legend.position = "none")

plot.multiway
```

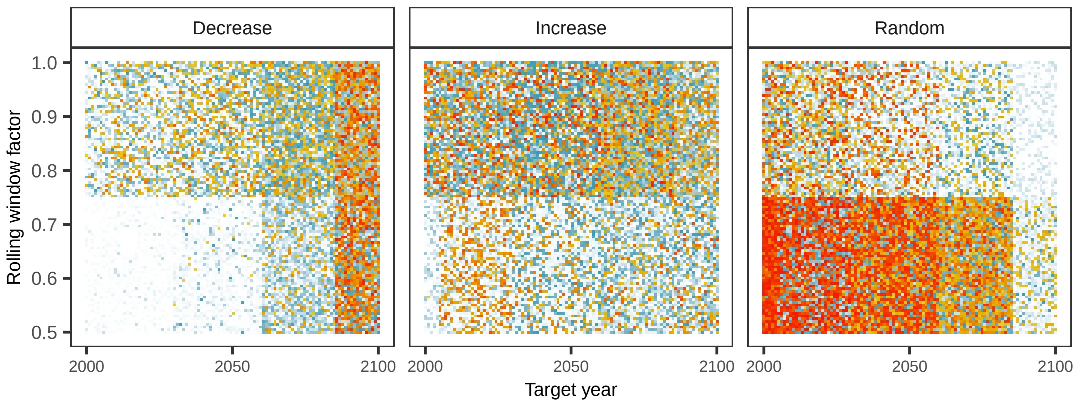



```
# # INTERACTIONS PLOT ##########################################################

# Redefine facet labels ------------------------------------------------------

supp.labs <- c("Decrease", "Increase", "Random")
names(supp.labs) <- paste("probability_", supp.labs, sep = "")

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

```
plot.predict <- plot_predict_interaction(rf_model, df, "target_year", "rolling_window_factor")
  theme_AP() +
  scale_fill_gradientn(colours = c("white", wes_palette("Zissou1")),
                       name = "probability",
                       breaks = c(0, 0.5, 1)) +
  theme(plot.title = element_blank()) +
  labs(x = "Target year", y = "Rolling window factor") +
  scale_x_continuous(breaks = pretty_breaks(n = 3)) +
  facet_grid(~variable,  labeller = labeller(variable = supp.labs)) +
  theme(legend.position = "none",
        axis.text.x = element_text(size = 6.1))
```

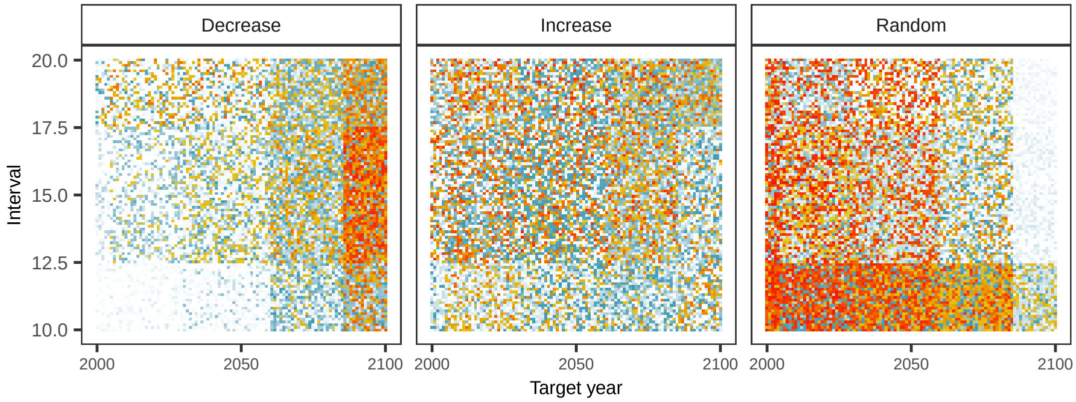
```
## Scale for fill is already present.
## Adding another scale for fill, which will replace the existing scale.
```

```
plot.predict
```

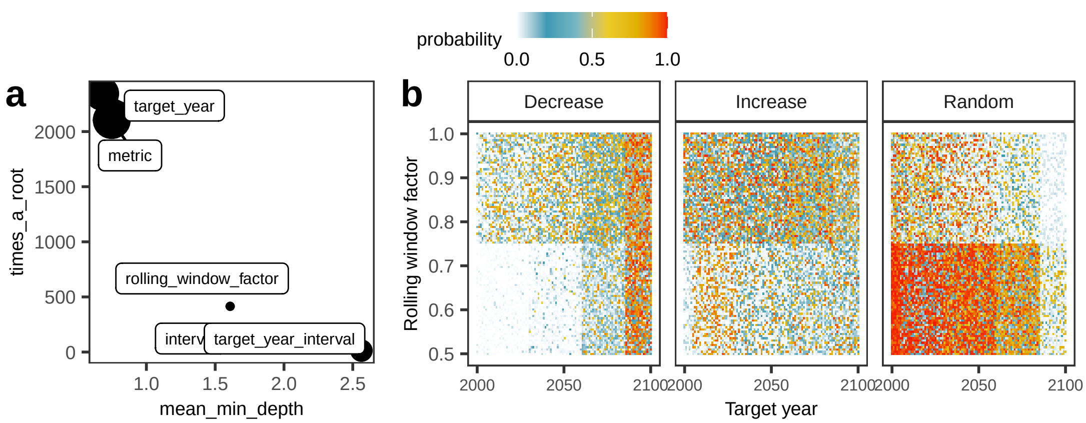



```
# Now on different combinations

plot_predict_interaction(rf_model, df, "target_year", "interval") +
  theme_AP() +
  scale_fill_gradientn(colours = c("white", wes_palette("Zissou1")),
                       name = "probability",
                       breaks = c(0, 0.5, 1)) +
  theme(plot.title = element_blank()) +
  labs(x = "Target year", y = "Interval") +
  scale_x_continuous(breaks = pretty_breaks(n = 3)) +
  facet_grid(~variable,  labeller = labeller(variable = supp.labs)) +
  theme(legend.position = "none",
        axis.text.x = element_text(size = 6.1))
```

```
## Scale for fill is already present.
## Adding another scale for fill, which will replace the existing scale.
```




```
# MERGE RANDOM FOREST PLOTS ##################################################

legend <- get_legend_fun(plot.predict + theme(legend.position = "top"))
bottom <- plot_grid(plot.multiway, plot.predict, ncol = 2, rel_widths = c(0.36, 0.64),
                    labels = "auto")
plot_grid(legend, bottom, rel_heights = c(0.13, 0.87), ncol = 1)
```




```
library(rpart)
```

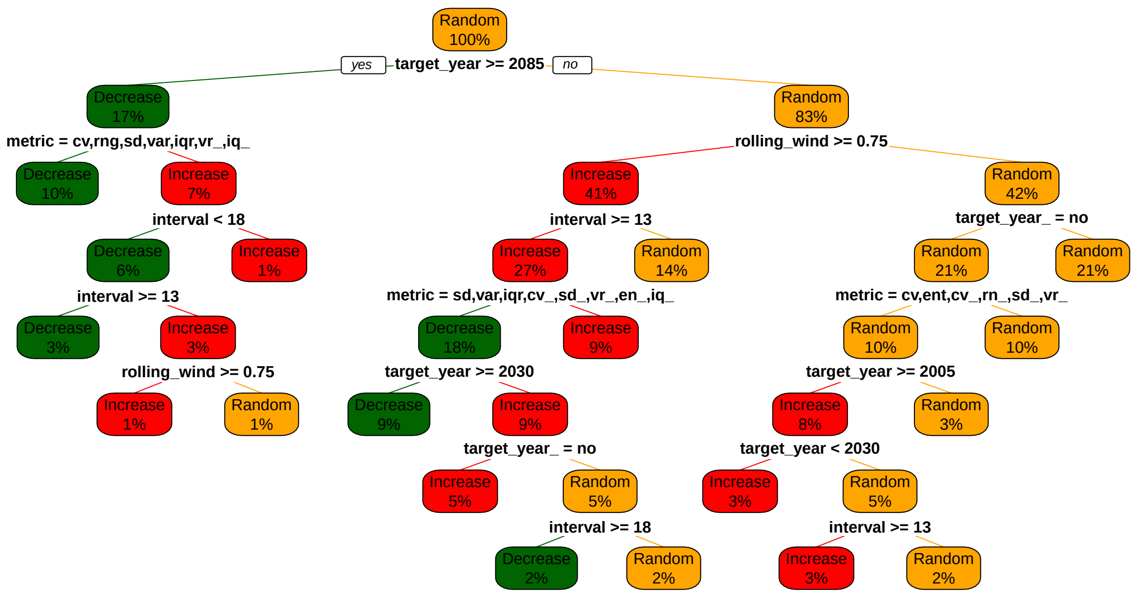
```
## Warning: package 'rpart' was built under R version 4.3.3
```

```
library(rpart.plot)
```

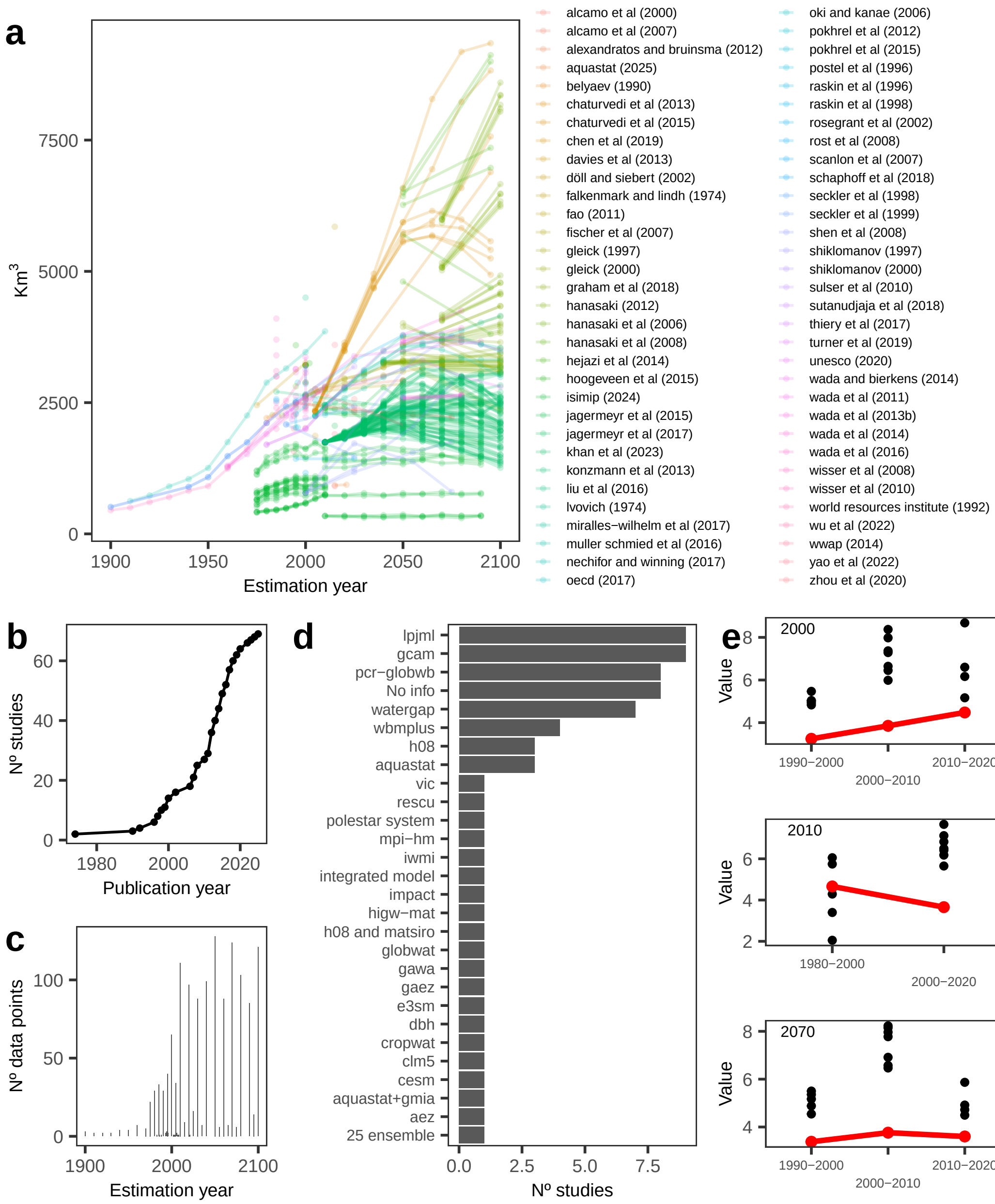
```
## Warning: package 'rpart.plot' was built under R version 4.3.3
```

```
# Fit a decision tree model-
tree_model <- rpart(trend ~ target_year + target_year_interval + interval
                    + rolling_window_factor + metric,
                    data = final.dt, method = "class")

# Plot the tree
# Fit a decision tree model
tree_model <- rpart(trend ~ target_year + target_year_interval + interval +
                      rolling_window_factor + metric,
                    data = final.dt, method = "class")
```

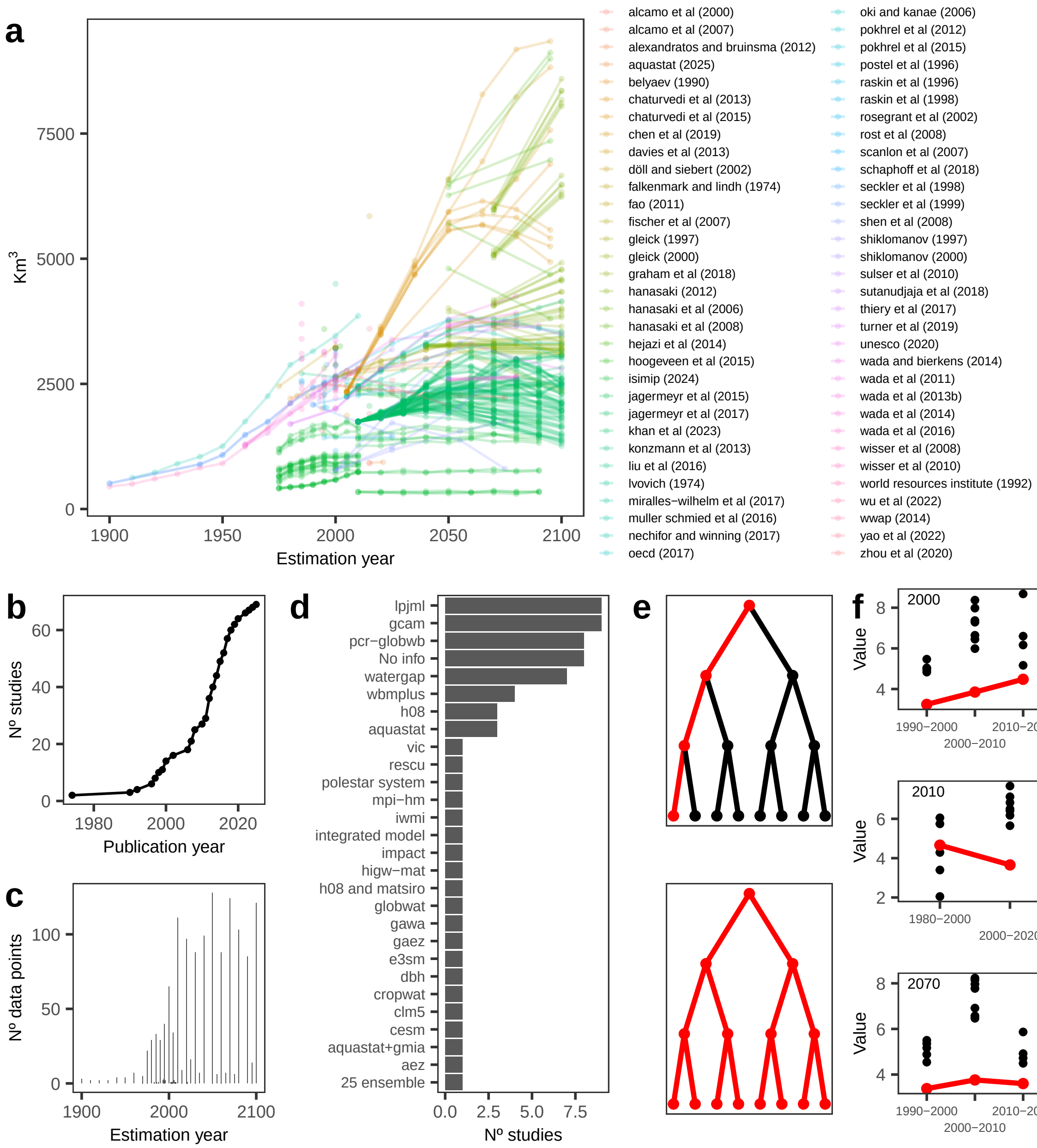
```r
heat.tree <- function(tree, low.is.green = FALSE, ...) { # dots args passed to prp
  y <- tree$frame$yval
  cols <- ifelse(y == 1, "darkgreen", ifelse(y == 2, "red", "orange"))
  prp(tree, branch.col = cols, box.col = cols, ...)
}

heat.tree(tree_model, type = 2, extra = 100, gap = 0, fallen.leaves = FALSE,
          tweak = 1.4, clip.right.labs = FALSE)
```




```r
left <- plot_grid(cumulative.iww, plot.bar, ncol = 1, labels = c("b", "c"))
bottom <- plot_grid(left, plot.models, ncol = 2, labels = c("", "d"), rel_widths = c(0.4, 0.6)
bottom.right <- plot_grid(bottom, plot.examples.trends.data, ncol = 2, rel_widths = c(0.7, 0.3
plot_grid(plot.iww, bottom.right, ncol = 1, rel_heights = c(0.5, 0.5), labels = c("a", ""))
```




```r
# MERGE SA ######################################################################

plot.examples.trends.data <-plot_grid(p1, p2, p3, ncol = 1)
left <- plot_grid(cumulative.iww, plot.bar, ncol = 1, labels = c("b", "c"))
forking.paths <- plot_grid(one.path, all.paths, ncol = 1)
bottom <- plot_grid(left, plot.models, forking.paths, ncol = 3, labels = c("", "d", "e"),
                    rel_widths = c(0.33, 0.4, 0.26))
bottom.right <- plot_grid(bottom, plot.examples.trends.data, ncol = 2, rel_widths = c(0.8, 0.2
                          labels = c("", "f"))
plot_grid(plot.iww, bottom.right, ncol = 1, rel_heights = c(0.5, 0.5), labels = c("a", ""))
```

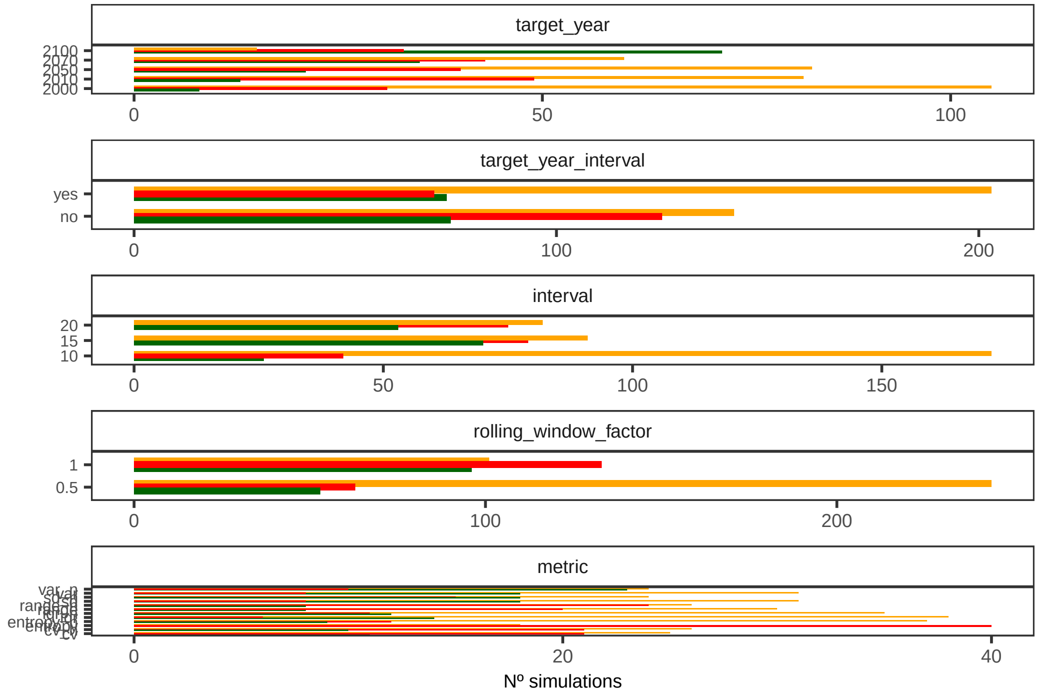



```r
# SENSITIVITY ANALYSIS PLOT BY FACET ############################################

plot.sa.facet <- final.dt %>%
  melt(., measure.vars = c("target_year", "target_year_interval", "interval",
                           "rolling_window_factor", "metric")) %>%
  .[, .N, .(variable, value, trend)] %>%
  .[ , value := gsub("_normalized", "_n", value)] %>%
  ggplot(., aes(value, N, fill = trend)) +
  scale_fill_manual(values = selected_colors, name = "Uncertainty") +
  geom_bar(stat = "identity", position = position_dodge(0.5)) +
  facet_wrap(~variable, scale = "free", ncol = 1) +
  labs(x = "", y = "Nº simulations") +
  scale_y_continuous(breaks = breaks_pretty(n = 3)) +
```

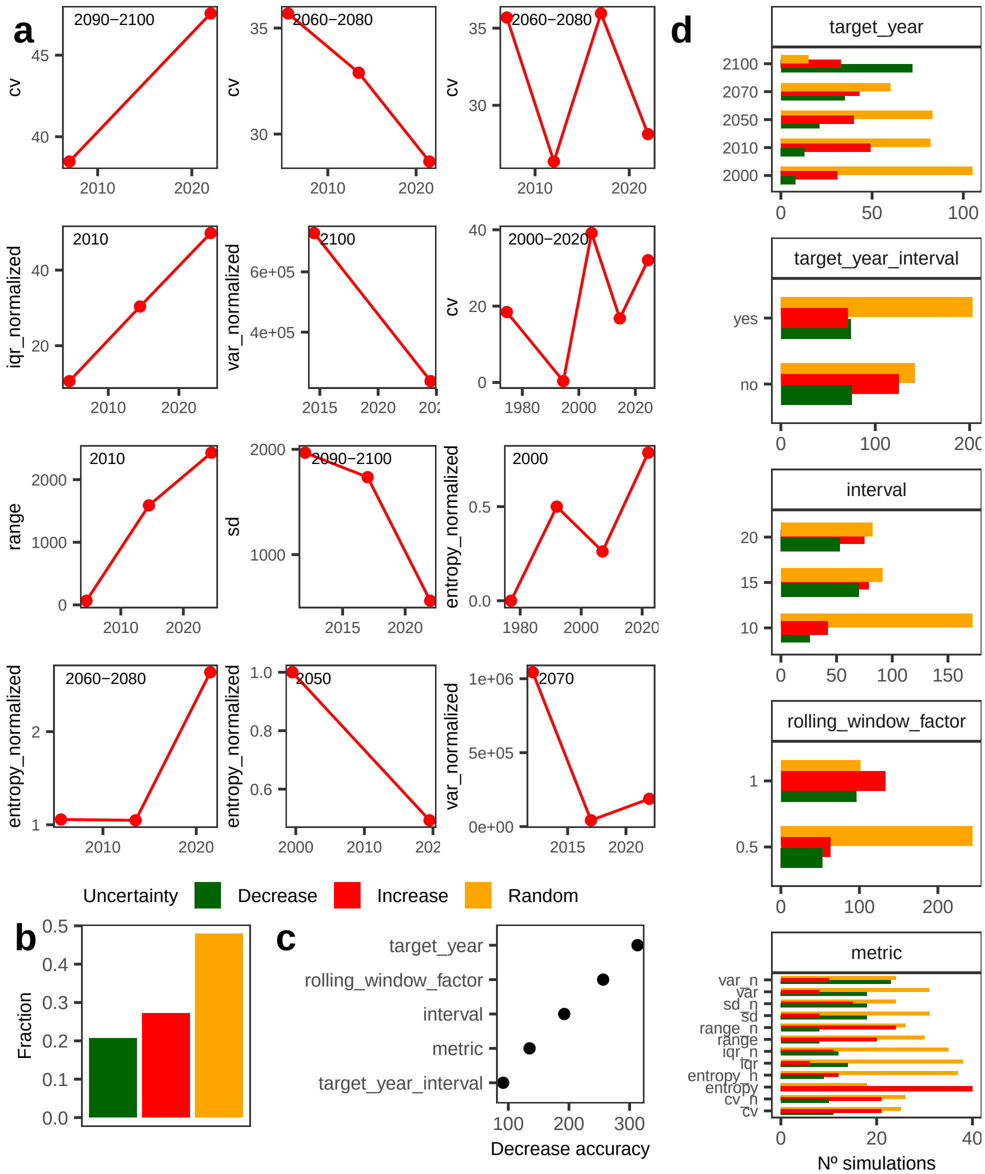
```r
  theme_AP() +
  coord_flip() +
  theme(legend.position = "none",
        axis.text.y = element_text(size = 5.5),
        plot.margin = unit(c(0.05, 0, 0, 0.05), "cm"))
```

```
## Warning in melt.data.table(., measure.vars = c("target_year",
## "target_year_interval", : 'measure.vars' [target_year, target_year_interval,
## interval, rolling_window_factor, ...] are not all of the same type. By order of
## hierarchy, the molten data value column will be of type 'character'. All
## measure variables not of type 'character' will be coerced too. Check DETAILS in
## ?melt.data.table for more on coercion.
```

```r
plot.sa.facet
```




```r
# MERGE SENSITIVITY ANALYSIS PLOTS ##############################################

legend <- get_legend_fun(plot.fraction + theme(legend.position = "top"))
top <- plot_grid(plot.fraction + theme(legend.position = "none"), plot.rf, ncol = 2,
                 rel_widths = c(0.4, 0.6), labels = c("b", "c"))
top.with.legend <- plot_grid(legend, top, rel_heights = c(0.1, 0.9), ncol = 1)

left <- plot_grid(plots.examples.trends, top.with.legend, ncol = 1,
          rel_heights = c(0.75, 0.25))
plot_grid(left, plot.sa.facet, ncol = 2, rel_widths = c(0.67, 0.33),
          labels = c("a", "d"))
```



a
b
c
d
Uncertainty
Decrease
Increase
Random
Fraction
Decrease accuracy
Nº simulations
target_year
target_year_interval
interval
rolling_window_factor
metric

3 Session information

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

sessionInfo()
```

```
## R version 4.3.3 (2024-02-29)
## Platform: aarch64-apple-darwin20 (64-bit)
## Running under: macOS Sonoma 14.2.1
##
## Matrix products: default
## BLAS:   /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/lib/libRblas.0.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/lib/libRlapack.dylib;
##
## locale:
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## time zone: Europe/London
## tzcode source: internal
##
## attached base packages:
## [1] parallel  stats     graphics  grDevices utils     datasets  methods
## [8] base
##
## other attached packages:
##  [1] randomForest_4.7-1.2 brms_2.22.0          Rcpp_1.0.13-1
##  [4] mgcv_1.9-1           nlme_3.1-166         microbenchmark_1.5.0
##  [7] lme4_1.1-35.5        Matrix_1.6-5         here_1.0.1
## [10] doParallel_1.0.17    iterators_1.0.14     foreach_1.5.2
## [13] rworldmap_1.3-8      sp_2.1-4             countrycode_1.6.0
## [16] ncdf4_1.23           scales_1.3.0         wesanderson_0.3.7
## [19] benchmarkme_1.0.8    cowplot_1.1.3        lubridate_1.9.3
## [22] forcats_1.0.0        stringr_1.5.1        dplyr_1.1.4
## [25] purrr_1.0.2          readr_2.1.5          tidyr_1.3.1
## [28] tibble_3.2.1         ggplot2_3.5.1        tidyverse_2.0.0
## [31] data.table_1.16.2    openxlsx_4.2.7.1
##
## loaded via a namespace (and not attached):
##  [1] Rdpack_2.6.2          rlang_1.1.4           magrittr_2.0.3
##  [4] matrixStats_1.4.1     compiler_4.3.3        loo_2.8.0
##  [7] vctrs_0.6.5           maps_3.4.2.1          crayon_1.5.3
## [10] pkgconfig_2.0.3       fastmap_1.2.0         backports_1.5.0
## [13] labeling_0.4.3        utf8_1.2.4            rmarkdown_2.29
## [16] tzdb_0.4.0            nloptr_2.1.1          tinytex_0.54
## [19] xfun_0.49             terra_1.7-78          R6_2.5.1
## [22] stringi_1.8.4         boot_1.3-31           estimability_1.5.1
## [25] knitr_1.49            fields_16.3           bayesplot_1.11.1
## [28] splines_4.3.3         timechange_0.3.0      tidyselect_1.2.1
```

```
## [31] rstudioapi_0.17.1     abind_1.4-8          yaml_2.3.10
## [34] codetools_0.2-20      lattice_0.22-6       withr_3.0.2
## [37] bridgesampling_1.1-2  benchmarkmeData_1.0.4 posterior_1.6.0
## [40] coda_0.19-4.1         evaluate_1.0.1       RcppParallel_5.1.9
## [43] zip_2.3.1             pillar_1.9.0         tensorA_0.36.2.1
## [46] checkmate_2.3.2       distributional_0.5.0 generics_0.1.3
## [49] rprojroot_2.0.4       hms_1.1.3            rstantools_2.4.0
## [52] munsell_0.5.1         minqa_1.2.8          sensobol_1.1.5
## [55] xtable_1.8-4          glue_1.8.0           emmeans_1.10.5
## [58] tools_4.3.3           mvtnorm_1.3-2        dotCall64_1.2
## [61] grid_4.3.3            rbibutils_2.3        colorspace_2.1-1
## [64] raster_3.6-30         cli_3.6.3            spam_2.11-0
## [67] fansi_1.0.6           viridisLite_0.4.2    Brobdingnag_1.2-9
## [70] gtable_0.3.6          digest_0.6.37        farver_2.1.2
## [73] htmltools_0.5.8.1     lifecycle_1.0.4      httr_1.4.7
## [76] MASS_7.3-60.0.1
```

```r
## Return the machine CPU ------------------------------------------------------

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

```
## Machine:
```

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

```r
## Return number of true cores ------------------------------------------------

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

```
## Num cores:
```

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

```r
## Return number of threads ---------------------------------------------------

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

```
## Num threads:
```

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