

# Assumptions in global irrigation models

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## 1 Number of assumptions

```
data_countA <- read_excel("nature.xlsx", sheet = "total")

p_countA <- ggplot(data_countA, aes(y = fct_reorder(factor(Model), Total, .desc = FALSE), x = Total, fill = factor(Model))) +
  geom_bar(stat = "identity") +
  labs(title = "a",
       x = "number of assumptions",
       y = "") +
  theme_bw() +
  theme(
    plot.title = element_text(size = 16, face = "bold", hjust = 0, vjust = 1),
    axis.title.x = element_text(size = 14),
    axis.text.x = element_text(size = 12),
    axis.text.y = element_text(size = 14),
    legend.position = "none",
    panel.grid = element_blank()
  ) +
  scale_fill_manual(values = "grey50")

data_countB <- read_excel("timecount.xlsx") %>%
  mutate(Year = as.numeric(sub(".*(\\d{4}).*", "\\1", Study))) %>%
  filter(!is.na(Year))

model_order <- c("MPI-HM", "MATSIRO", "CLM4.5", "VIC", "WaterGAP", "WBMplus", "PCR-GLOBWB", "H08", "LPJmL")

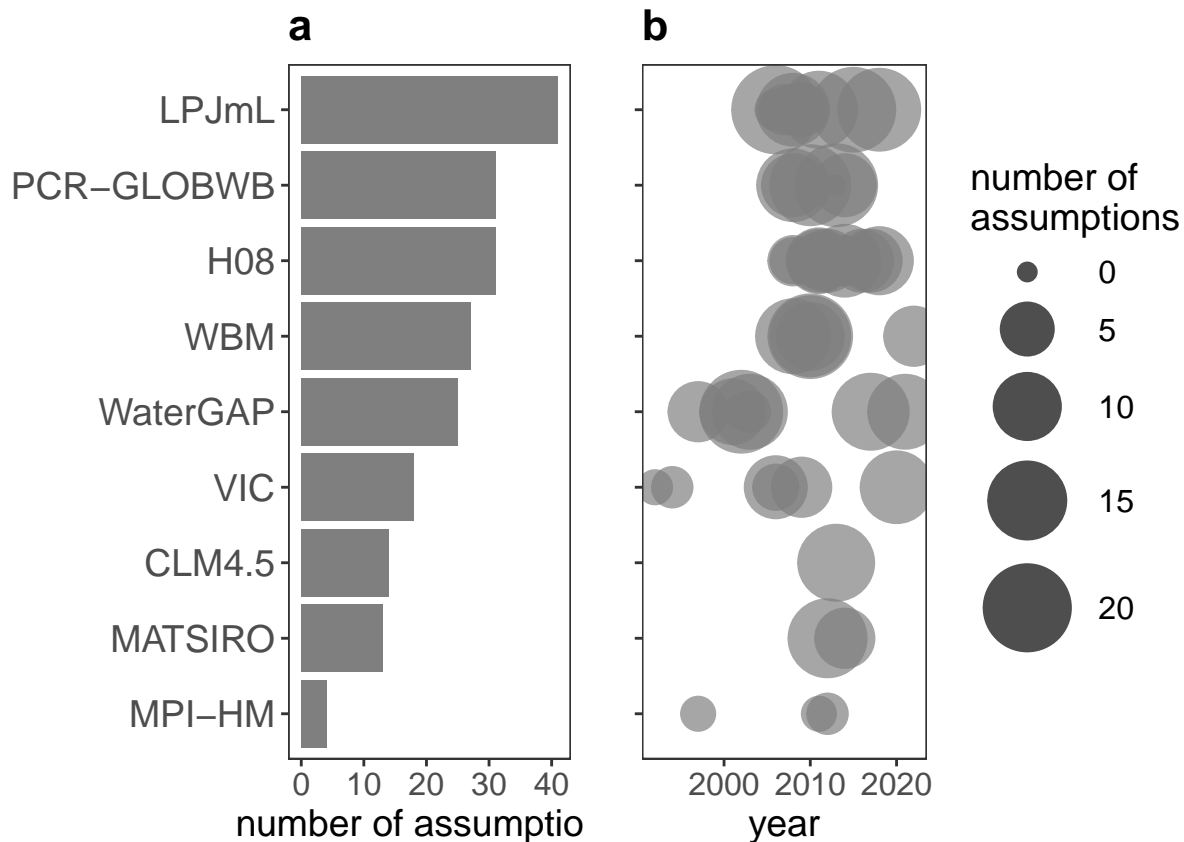
data_countB <- data_countB %>%
  mutate(Model = factor(Model, levels = model_order))
```

```

p_countB <- ggplot(data_countB, aes(x = Year, y = Model, size = `Count of assumptions`, color = "grey50")) +
  geom_point(alpha = 0.7) +
  theme_bw() +
  labs(title = "b", x = "year", y = "", size = "number of assumptions") +
  theme(
    plot.title = element_text(size = 16, face = "bold", hjust = 0, vjust = 1),
    axis.title.x = element_text(size = 14),
    axis.text.x = element_text(size = 12),
    axis.text.y = element_blank(),
    legend.title = element_text(size = 14),
    legend.text = element_text(size = 12),
    panel.grid = element_blank()
  ) +
  guides(color = "none") +
  scale_size_continuous(range = c(3, 15)) +
  scale_color_manual(values = "grey50")

combined_count <- grid.arrange(p_countA, p_countB, ncol = 2, nrow = 1)

```



```

#ggsave("count.png", plot = combined_count, width = 10, height = 5, dpi = 600)

```

```

combined_count

```

```

## TableGrob (1 x 2) "arrange": 2 grobs
##   z      cells  name      grob
## 1 1 (1-1,1-1) arrange gtable[layout]
## 2 2 (1-1,2-2) arrange gtable[layout]

```

## 2 Nature of assumptions

```
data_aspectA <- read_excel("nature.xlsx", sheet = "count")

model_order_aspectA <- c("CLM4.5", "VIC", "MATSIRO", "PCR-GLOBWB", "LPJmL", "WaterGAP", "HO8", "WBM",

data_aspectA <- data_aspectA %>%
  mutate(Total = Pragmatic + Empirical,
         Pragmatic_ratio = Pragmatic / Total,
         Empirical_ratio = Empirical / Total)

data_aspectA_long <- data_aspectA %>%
  pivot_longer(cols = c(Pragmatic, Empirical),
               names_to = "Nature", values_to = "Count") %>%
  mutate(
    Model = factor(Model, levels = model_order_aspectA),
    Ratio = Count / Total
  )

custom_colors <- c("Pragmatic" = "#1ac6c6", "Empirical" = "#f07167")

p_aspectA <- ggplot(data_aspectA_long, aes(x = Model, y = Ratio, fill = Nature)) +
  geom_bar(stat = "identity", position = "fill") +
  geom_text(aes(label = paste0(Count, "/", Total),
                  position = position_stack(vjust = 0.5), size = 3.5, color = "black")) +
  labs(title = "a", x = "", y = "fraction") +
  scale_fill_manual(values = custom_colors, labels = c("Empirical", "Pragmatic")) +
  theme_bw() +
  theme(
    plot.title = element_text(size = 16, face = "bold", hjust = 0, vjust = 1),
    axis.text.x = element_text(size = 12, angle = 45, hjust = 1),
    axis.ticks.x = element_blank(),
    axis.text.y = element_text(size = 12),
    axis.title.y = element_text(size = 12),
    panel.grid = element_blank(),
    legend.position = "none"
  )

data_aspectB <- read_excel("nature.xlsx", sheet = "aspect")

data_aspectB_df <- data_aspectB %>%
  group_by(Model, Aspect) %>%
  mutate(Proportion = Count / sum(Count))

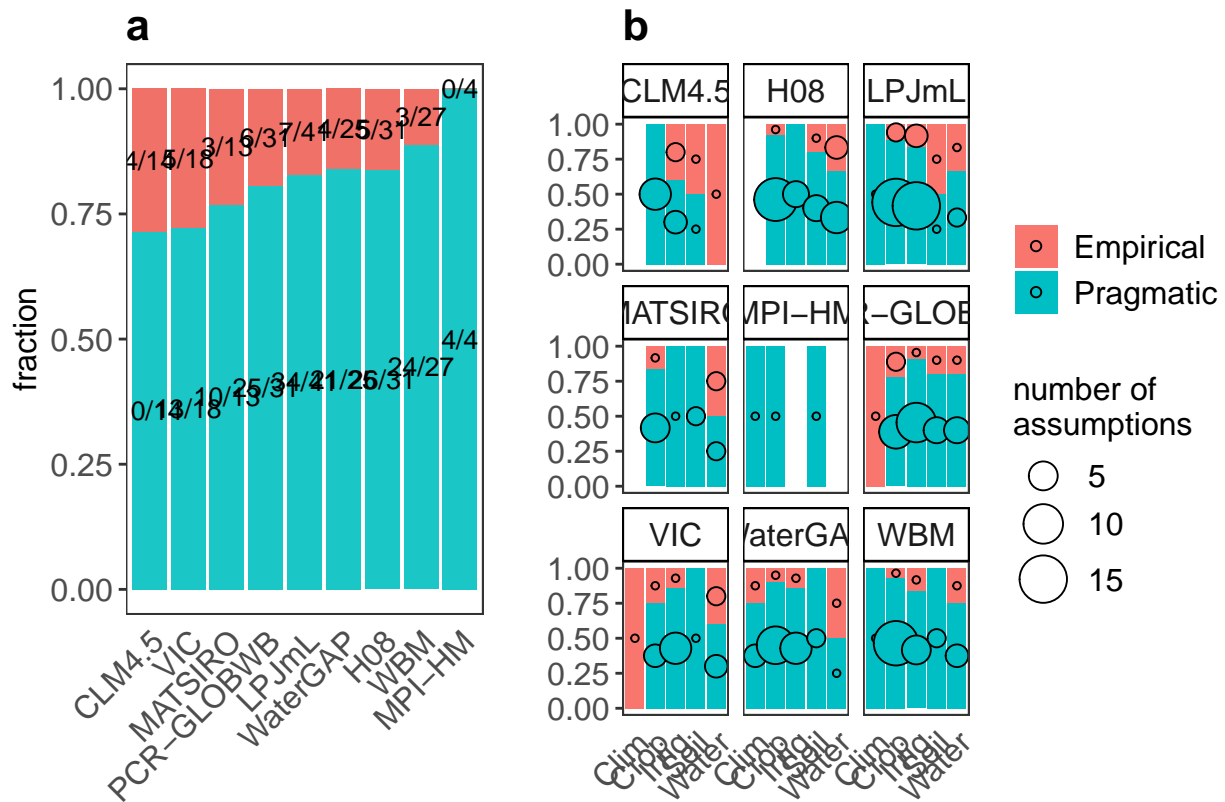
p_aspectB <- ggplot(data_aspectB_df, aes(x = Aspect, y = Proportion, fill = Nature)) +
  geom_bar(stat = "identity", position = "fill") +
  geom_point(aes(size = Count, fill = Nature,
                 position = position_fill(vjust = 0.5),
                 color = "black", shape = 21)) +
  scale_size_continuous(name = "count", range = c(1, 8)) +
  labs(title = "b", x = "", y = "", fill = "Nature of Assumption") +
  facet_wrap(~ Model) +
  theme_bw() +
```

```

theme(
  plot.title = element_text(size = 16, face = "bold", hjust = 0, vjust = 1),
  axis.text.x = element_text(size = 12, angle = 45, hjust = 1),
  axis.ticks.x = element_blank(),
  axis.text.y = element_text(size = 12),
  legend.title = element_text(size = 12),
  legend.text = element_text(size = 12),
  panel.grid = element_blank(),
  strip.background = element_rect(fill = "white", color = "black"),
  strip.text = element_text(size = 12)
) +
guides(fill = guide_legend(title = NULL),
       size = guide_legend(title = "number of\nassumptions"))

combined_aspect <- grid.arrange(p_aspectA, p_aspectB, ncol = 2, nrow = 1, widths = c(2, 3))

```



```

#ggsave("aspectratio.png", plot = combined_aspect, width = 12, height = 5, dpi = 600)

```

```

combined_aspect

```

```

## TableGrob (1 x 2) "arrange": 2 grobs
##   z      cells      name      grob
## 1 1 (1-1,1-1) arrange gtable[layout]
## 2 2 (1-1,2-2) arrange gtable[layout]

```

### 3 Evolution of assumptions (LPJmL)

```
data_code <- read_excel("code.xlsx") %>%
  filter(Model == "LPJmL") %>%
  mutate(UniqueID = paste(Code, Author, sep = "_")) %>%
  arrange(Code, Year) %>%
  group_by(Code) %>%
  mutate(NextAuthor = lead(Author),
         NextYear = lead(Year),
         NextCode = lead(Code)) %>%
  ungroup()

edges_code <- data_code %>%
  filter(!is.na(NextAuthor) & Code == NextCode) %>%
  mutate(to = paste(NextCode, NextAuthor, sep = "_")) %>%
  select(from = UniqueID, to)

vertices_code <- data_code %>%
  distinct(UniqueID, Code, Author, Year)

facet_rects_code <- data.frame(
  xmin = c(1, 37, 73, 91, 95),
  xmax = c(36, 72, 90, 94, 105),
  facet = c("Crop", "Irrigation", "Soil", "Climate", "Water"),
  fill_color = c("lightgreen", "lavender", "peachpuff", "lightcoral", "lightblue"),
  label_x = c(18.5, 54.5, 81.5, 92.5, 100)
)

ellipse_data_code <- data.frame(
  x0 = c(17, 64),
  y0 = c(2011, 2015),
  a = c(12, 36),
  b = c(0.8, 0.8),
  angle = c(0, 0)
)

graph_code <- graph_from_data_frame(d = edges_code, vertices = vertices_code, directed = FALSE)
V(graph_code)$degree <- degree(graph_code, mode = "all")

custom_layout_code <- as.data.frame(vertices_code %>% select(Code, Year))
colnames(custom_layout_code) <- c("x", "y")

ggraph(graph_code, layout = custom_layout_code) +
  geom_rect(data = facet_rects_code, aes(xmin = xmin, xmax = xmax, ymin = -Inf, ymax = Inf, fill = facet_rects_code$fill_color,
    alpha = 0.2, color = NA) +
  scale_fill_manual(values = setNames(facet_rects_code$fill_color, facet_rects_code$facet)) +
  geom_edge_link(arrow = arrow(length = unit(2, 'mm')),
    end_cap = circle(2, 'mm'),
    color = 'gray60') +
  geom_node_point(color = "gray40", size = 3) +
  scale_x_continuous(breaks = seq(min(vertices_code$Code), max(vertices_code$Code), by = 1), expand = c(0.05, 0.05)) +
  scale_y_reverse(breaks = seq(min(vertices_code$Year), max(vertices_code$Year), by = 2), expand = c(0.05, 0.05)) +
  labs(x = "", y = "year") +
```

```

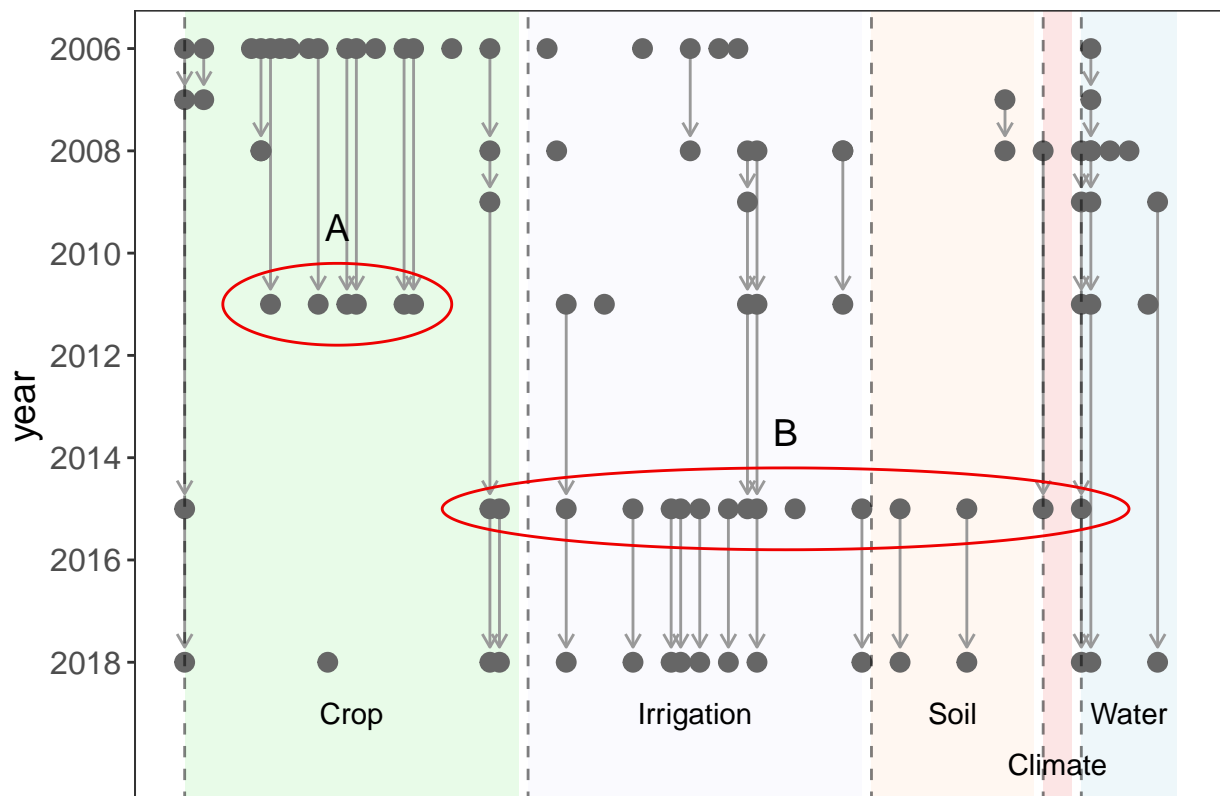
theme_bw() +
theme(
  plot.title = element_text(size = 16, face = "bold", hjust = 0, vjust = 1),
  axis.text.y = element_text(size = 12),
  panel.grid = element_blank(),
  axis.text.x = element_blank(),
  axis.ticks.x = element_blank(),
  axis.title.y = element_text(size = 14),
  legend.position = "none"
) +
geom_vline(data = facet_rects_code, aes(xintercept = xmin), color = "black", linetype = "dashed", size = 1) +
geom_text(data = facet_rects_code, aes(x = label_x,
  y = ifelse(facet == "Climate", max(vertices_code$Year) + 2.0, max(vertices_code$Year) - 2.0),
  label = facet), vjust = 0.5, color = "black", size = 4) +
ggforce::geom_ellipse(data = ellipse_data_code,
  aes(x0 = x0, y0 = y0, a = a, b = b, angle = angle),
  color = "red2", fill = NA, size = 0.5) +
annotate("text", x = 17, y = 2009.5, label = "A", size = 5, color = "black") +
annotate("text", x = 64, y = 2013.5, label = "B", size = 5, color = "black")

```

```

## Warning: Using `size` aesthetic for lines was deprecated in ggplot2 3.4.0.
## i Please use `linewidth` instead.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.

```



```
#ggsave("lpjml_assumptions.png", width = 5, height = 4, dpi = 600)
```

## 4 Sharing of assumptions

```
data_freq <- read_excel("freq.xlsx")

filtered_freq <- data_freq %>%
  filter(Frequency >= 2) %>%
  group_by(Nature) %>%
  summarise(Count = n()) %>%
  mutate(Percentage = Count / sum(Count) * 100)

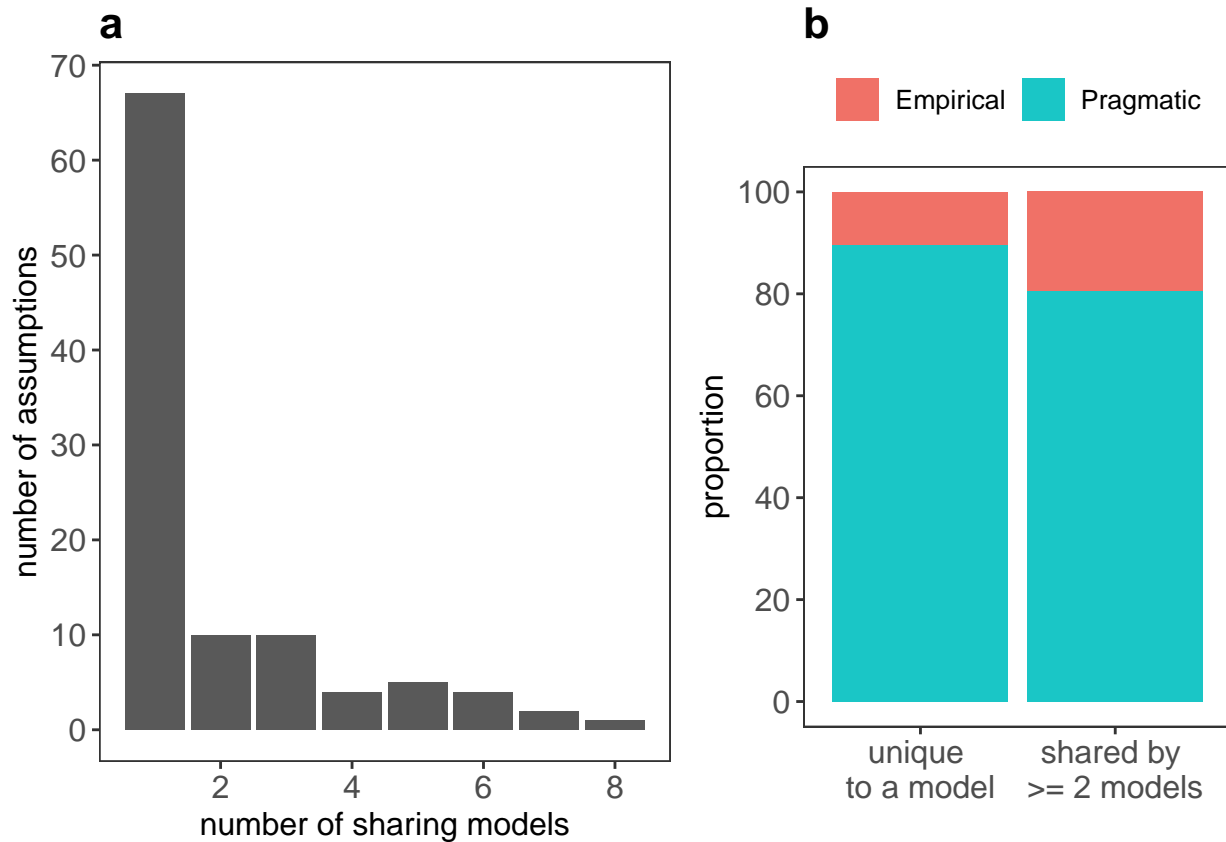
p_hist <- ggplot(data_freq, aes(x = Frequency)) +
  geom_bar() +
  scale_y_continuous(breaks = seq(0, 80, by = 10)) +
  labs(title = "a", x = "number of sharing models", y = "number of assumptions") +
  theme_bw() +
  theme(
    plot.title = element_text(size = 16, face = "bold", hjust = 0, vjust = 1),
    axis.text = element_text(size = 12),
    axis.title.x = element_text(size = 12),
    axis.title.y = element_text(size = 12),
    panel.grid = element_blank(),
    legend.position = "none"
  )

assumption_summary <- data_freq %>%
  mutate(Group = ifelse(Frequency == 1, "unique \nto a model", "shared by \n 2 models")) %>%
  group_by(Group, Nature) %>%
  summarise(Count = n()) %>%
  group_by(Group) %>%
  mutate(Percentage = Count / sum(Count) * 100) %>%
  mutate(Group = factor(Group, levels = c("unique \nto a model", "shared by \n 2 models")))

## `summarise()` has grouped output by 'Group'. You can override using the
## `.groups` argument.

p_normalized <- ggplot(assumption_summary, aes(x = Group, y = Percentage, fill = Nature)) +
  geom_bar(stat = "identity", position = "stack") +
  scale_fill_manual(values = c("Empirical" = "#f07167", "Pragmatic" = "#1ac6c6")) +
  scale_y_continuous(breaks = seq(0, 100, by = 20)) +
  labs(title = "b", x = "", y = "proportion") +
  theme_bw() +
  theme(
    plot.title = element_text(size = 16, face = "bold", hjust = 0, vjust = 1),
    axis.text = element_text(size = 12),
    axis.title.x = element_text(size = 12),
    axis.title.y = element_text(size = 12),
    panel.grid = element_blank(),
    legend.position = "top",
    legend.title = element_blank(),
    legend.text = element_text(size = 10)
  )
```

```
combined_freq <- grid.arrange(p_hist, p_normalized, ncol = 2, widths = c(0.55, 0.45))
```



```
#ggsave("freq.png", plot = combined_freq, width = 6, height = 4, dpi = 600)
```

```
combined_freq
```

```
## TableGrob (1 x 2) "arrange": 2 grobs
##   z      cells  name      grob
## 1 1 (1-1,1-1) arrange gtable[layout]
## 2 2 (1-1,2-2) arrange gtable[layout]
```

## 5 Network citation of pragmatic assumptions

```
nodes_net <- read_excel("combined_citations.xlsx", sheet = "nodes")
edges_net <- read_excel("combined_citations.xlsx", sheet = "edges") %>%
  filter(!is.na(Source) & !is.na(Target))

nodes_net <- nodes_net %>% distinct(ID, .keep_all = TRUE)
model_colors_net <- setNames(scales::hue_pal()(length(unique(nodes_net$Model))), unique(nodes_net$Model))

size_range_net <- c(1, 10)
degree_limits_net <- range(nodes_net$degree, na.rm = TRUE)

titles_net <- c("a. Paddy vs nonpaddy", "b. Unlimited water supply")
plot_list_net <- list()
```



```

for (dataset in unique(nodes_net$Dataset)) {
  dataset_nodes <- nodes_net %>% filter(Dataset == dataset)
  dataset_edges <- edges_net %>% filter(Dataset == dataset & Source %in% dataset_nodes$ID & Target %in%

  graph_net <- graph_from_data_frame(dataset_edges, vertices = dataset_nodes, directed = TRUE)
  layout_net <- create_layout(graph_net, layout = 'mds')
  layout_net$x <- as.numeric(dataset_nodes$Year)
  layout_net$y <- runif(length(V(graph_net)), min = -10, max = 10)

  plot_net <- ggraph(layout_net) +
    geom_edge_link(arrow = arrow(length = unit(3, 'mm')), end_cap = circle(4, 'mm'), color = 'gray') +
    geom_node_point(aes(color = Model, size = degree), show.legend = FALSE) +
    geom_node_text(aes(label = Label), repel = TRUE, size = 3.5) +
    scale_color_manual(values = model_colors_net) +
    scale_size_continuous(limits = degree_limits_net, range = size_range_net) +
    scale_x_continuous(breaks = seq(min(dataset_nodes$Year), max(dataset_nodes$Year), by = 5), expand =
    labs(title = titles_net[which(unique(nodes_net$Dataset) == dataset)], x = "") +
    theme_bw() +
    theme(
      plot.title = element_text(size = 16, face = "bold", hjust = 0, vjust = 1),
      axis.text.x = element_text(size = 12),
      panel.grid = element_blank(),
      axis.text.y = element_blank(),
      axis.ticks.y = element_blank(),
      axis.title.y = element_blank()
    )

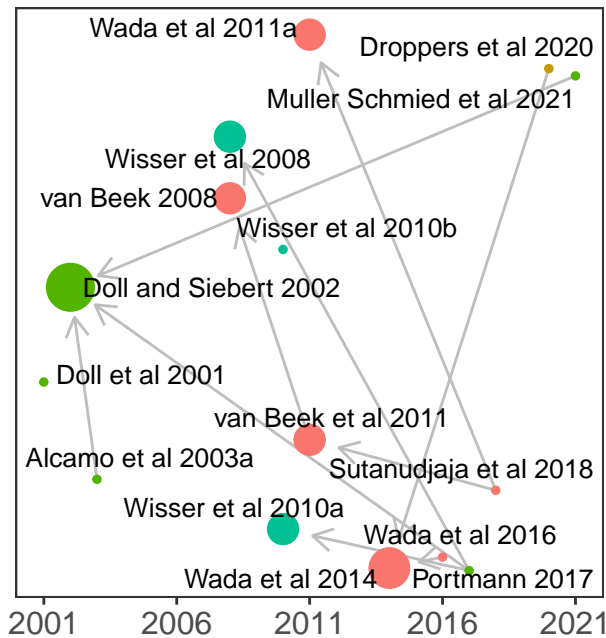
  plot_list_net[[dataset]] <- plot_net
}

legend_plot_net <- ggplot(nodes_net, aes(x = 1, y = 1, color = Model, size = degree)) +
  geom_point(show.legend = TRUE) +
  scale_color_manual(values = model_colors_net, guide = guide_legend(nrow = 1)) +
  scale_size_continuous(name = "citation", limits = degree_limits_net, range = size_range_net, guide =
  theme_void() +
  theme(legend.position = "bottom", legend.direction = "horizontal",
    legend.box = "vertical", legend.box.spacing = unit(0.25, "lines"),
    plot.title = element_text(size = 16, face = "bold", hjust = 0, vjust = 1),
    legend.title = element_text(size = 14), # Larger legend title
    legend.text = element_text(size = 12)) # Larger legend text

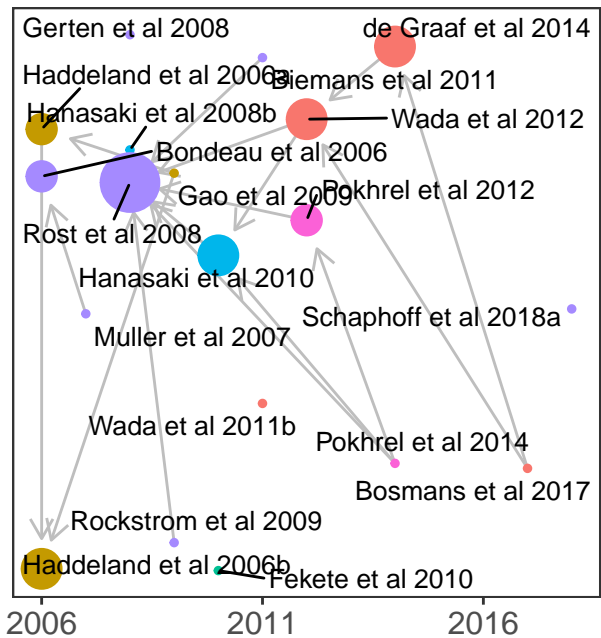
# Arrange plots with combined legend
final_plot <- grid.arrange(
  arrangeGrob(grobs = plot_list_net, nrow = 1),
  legend_plot_net,
  ncol = 1,
  heights = c(4, 0.6)
)

```

## a. Paddy vs nonpaddy



## b. Unlimited water supply



citation • 0 1 2 3 4 5

• H08 • IPIM • MATSIRO • PCR\_GLOBWB • VIC • WaterGAP • V

*# Save the final plot*

```
ggsave("combined_network.png", plot = final_plot, width = 12, height = 6, dpi = 600)
```

final\_plot

```
## TableGrob (2 x 1) "arrange": 2 grobs
##   z      cells   name      grob
## 1 1 (1-1,1-1) arrange gtable[arrange]
## 2 2 (2-2,1-1) arrange gtable[layout]
```