Measure 3: Savings potentials, Normalization, Proportionalization and Creation of Plots and Tables

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Code for the calculation of the savings potential using the results of the LCA-studies. Normalization and Proportionalization is performed as well as the creation of plots and tables. The code needs to be adjusted to the specific measure in the parameter section. This is the example for measure 2.

To execute, change:
- Login data for Nextcloud
- Adjust download location
- Adjust upload location
- Adjust URLs for uploading

Load Packages:

```
# install.packages("httr")
# install.packages("readxl")
# install.packages("dplyr")
# install.packages("writexl")
# install.packages("ggplot2")
# install.packages("tidyr")
# install.packages("openxlsx")
# install.packages("flextable")
# install.packages("officer")

library(readxl)
library(httr)
library(dplyr)
library(writexl)
library(ggplot2)
library(tidyr)
library(openxlsx)
library(flextable)
library(officer)
```

Parameters

Parameters to be adjusted:

```r
measure <- "03" # "02", "03" or "04"
sheet <- 4 # 3,4 or 5
# name for columns
name_with <- "with RF"
name_without <- "without RF"
name_SP <- "SP RF"
name_SP_prop <- "prop. SP RF"
name_with_prop <- "prop. with RF"
name_without_prop <- "prop. without RF"
name_with_norm <- "norm. with RF"
name_without_norm <- "norm. without RF"
name_SP_norm <- "norm. SP RF"
# vector with excluded categories due to missing normalization factor
excluded_categories_nf <- c("Climate change: biogenic",
                            "Climate change: fossil",
                            "Climate change: land use and land use change",
                            "Ecotoxicity: freshwater, inorganics",
                            "Ecotoxicity: freshwater, organics",
                            "Human toxicity: carcinogenic, inorganics",
                            "Human toxicity: carcinogenic, organics",
                            "Human toxicity: non-carcinogenic, inorganics",
                            "Human toxicity: non-carcinogenic, organics")
# vector with excluded toxicity categories for Pareto rule
excluded_categories_pr <- c("Human toxicity: carcinogenic",
                            "Human toxicity: non-carcinogenic",
                            "Ecotoxicity: freshwater")

# storage location
location_download <- "C:/Users/Klene/Documents/Uni_Bremen/WS24_25/Masterarbeit/R/Daten/"
location_upload <- "C:/Users/Klene/Documents/Uni_Bremen/WS24_25/Masterarbeit/R/Results/"
# Login data for NextCloud
username <- "mkindler@uni-bremen.de" # username
password <- "xxxxxxx" # password
# WebDAV-URL to file
nextcloud_url <- "https://nc.uni-bremen.de/remote.php/dav/files/mkindler%40uni-bremen.de/Masterarbeit/Masterarbeit_II/R/Daten/Ergebnisse_LCA_basic.xlsx"
nextcloud_url_2 <- "https://nc.uni-bremen.de/remote.php/dav/files/mkindler%40uni-bremen.de/Masterarbeit/Masterarbeit_II/R/Results/"
```

Data preparation

Load data from NextCloud:

```r
# download file
response <- GET(nextcloud_url, authenticate(username, password, type = "basic"))
# Check successful downloading
if (status_code(response) == 200) {
  # Save file
```

```
  writeBin(content(response, "raw"), paste0(location_download, "Ergebnisse_LC
A_basic.xlsx"))
  cat("The file was successfully downloaded and saved locally.\n")
} else {
  cat("Error downloading the file. Status code: ", status_code(response), "\n
")
}
```

```
## The file was successfully downloaded and saved locally.
```

```
# Load results data from Excel file
results <- read_excel(paste0(location_download, "Ergebnisse_LCA_basic.xlsx"),
sheet = sheet)
# Check data type: DataFrame
if (is.data.frame(results)) {
  results <- results
} else {
  results <- as.data.frame(results)
}
# Rename columns
results <- results %>%
  rename(
    `impact category` = `Wirkungskategorien`,
    unit = Einheit
    )
```

```
# Load normalization factors from Excel file
NF <- read_excel(paste0(location_download, "Ergebnisse_LCA_basic.xlsx"), shee
t = 1)
```

```
## New names:
## • `` -> `...2`
## • `` -> `...3`
```

```
# Check data type: DataFrame
if (is.data.frame(NF)) {
  NF <- NF
} else {
  NF <- as.data.frame(NF)
}
# Set column names right
NF <- NF[-1, ]
colnames(NF) <- as.character(NF[1, ])
NF <- NF[-1, ]
# Select relevant columns
NF <- NF %>%
  select(`impact category`,
         NF = `normalization factor\r\n(Matuštík 2024)`)
```

Calculations

Savings potential

Calculation of Savings Potentials:

```
results <- results %>%
  mutate(!!sym(name_SP) := !!sym(name_without) - !!sym(name_with))
```

Normalization

Calculation of normalized values (to the planetary boudaries (Matuštík 2024)):

```
# Join of results and NF according to the impact categories
results <- left_join(results, NF, by = c("impact category" = "impact category
"))
# Convert all columns except the first two into numerical values
results <- results %>%
  mutate_at(vars(-1, -2), as.numeric)

# Remove categories without normalization factors
results_norm <- results %>%
  filter(!`impact category` %in% excluded_categories_nf)

# Calculation of the normalised values by dividing the column values by the n
ormalization factors
results_norm <- results_norm %>%
  mutate(
    across(!c(`impact category`, unit, NF), ~ .x / NF, .names = "norm. {.col}
")
    )
```

Determine relevant impact categories

Calculation of proportion of total savings potential of each measure:

```
# Removing the toxicity categories
results_prop <- results_norm %>%
  filter(!`impact category` %in% excluded_categories_pr)

# Calculate the sum of each normalized column and divide the values by this s
um
results_prop <- results_prop %>%
  mutate(
    !!sym(name_without_prop) := !!sym(name_without_norm) / sum(abs(!!sym(name
_without_norm)), na.rm = TRUE),
    !!sym(name_with_prop) := !!sym(name_with_norm) / sum(abs(!!sym(name_with_
norm)), na.rm = TRUE),
    !!sym(name_SP_prop) := !!sym(name_SP_norm) / sum(abs(!!sym(name_SP_norm))
, na.rm = TRUE)
  )
norm_sum <- sum(abs(results_prop[[name_SP_norm]]))
```

Determine relevant impact categories:

```
# Sort categories by proportion of total savings potential
results_prop <- results_prop %>%
  arrange(desc(abs(!!sym(name_SP_prop))))
# Calculation of the cumulative total and mark categories that contribute to
the sum of 0.8
results_prop <- results_prop %>%
  mutate(
    `cum. sum` = cumsum(abs(!!sym(name_SP_prop))),
    relevant = (`cum. sum` < 0.8) | lag(`cum. sum` < 0.8, default = FALSE)
  )
# Mark at least the highest three impact categories
results_prop$relevant[1:3] <- TRUE
```

Save as csv-file

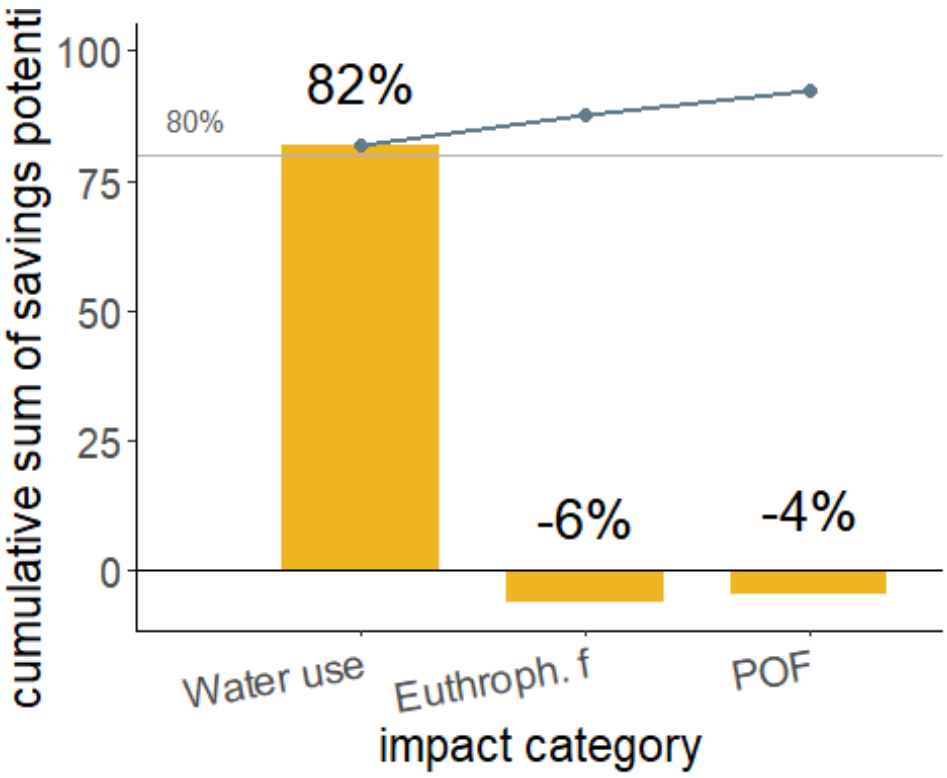
```
write.csv(results_prop, paste0(location_upload, measure, "_data.csv"), row.na
mes = FALSE)
```

Plot

Plot the relevant impact categories

```
# Ensure that the impact category retains the order in which it appears in th
e data
results_prop$`impact category` <- factor(results_prop$`impact category`, leve
ls = results_prop$`impact category`)

# Prepare data
data_plot <- results_prop %>%
  filter(relevant == TRUE) %>%
  mutate(
    across(.cols = starts_with("prop."), .fns = ~ . * 100),
    `cum. sum` = `cum. sum`*100) %>%
  select(`impact category`, name_SP_prop, `cum. sum`)

# Rename long impact categories
data_plot <- data_plot %>%
  mutate(`impact category` = case_when(
    `impact category` == "Photochemical oxidant formation: human health" ~ "P
OF",
    `impact category` == "Eutrophication: freshwater" ~ "Euthroph. f",
    TRUE ~ `impact category`
  ))

# Ensure that the impact category retains the order in which it appears in th
e data
data_plot$`impact category` <- factor(data_plot$`impact category`, levels = d
ata_plot$`impact category`)
```

```r
# Plot relvant impact categories with their proportion of the total savings p
otential, kumulative sum
ggplot(data_plot, aes(x = `impact category`, y = !!sym(name_SP_prop))) +
  geom_bar(stat = "identity", width = 0.7, fill = "goldenrod2", show.legend =
FALSE) +
  geom_line(aes(y = `cum. sum`, group = 1), color = "lightskyblue4", size = 1
) +
  geom_point(aes(y = `cum. sum`), color = "lightskyblue4", size = 2) +
  geom_hline(yintercept = 80, color = "grey70", linetype = "solid") +
  geom_hline(yintercept = 0, color = "black", linetype = "solid") +
  annotate("text", x = 0, y = 80, label = "80%", color = "grey35", size = 4,
hjust = -0.5, vjust = -1) +
  geom_text(aes(
    y = !!sym(name_SP_prop),
    label = paste0(format(round(!!sym(name_SP_prop), 0), nsmall = 0), "%")),
    vjust = ifelse(data_plot$`impact category` != "Water use", -1.5, -1), siz
e = 7) +
  labs(
    x = "impact category",
    y = "cumulative sum of savings potentials"
  ) +
  theme_classic() +
  theme(
    axis.text.x = element_text(angle = 10, hjust = 1, size = 15),
    axis.text.y = element_text(size = 15),
    axis.title.x = element_text(size = 17),
    axis.title.y = element_text(size = 17)
  ) +
  coord_cartesian(ylim = c(NA, 100))
```

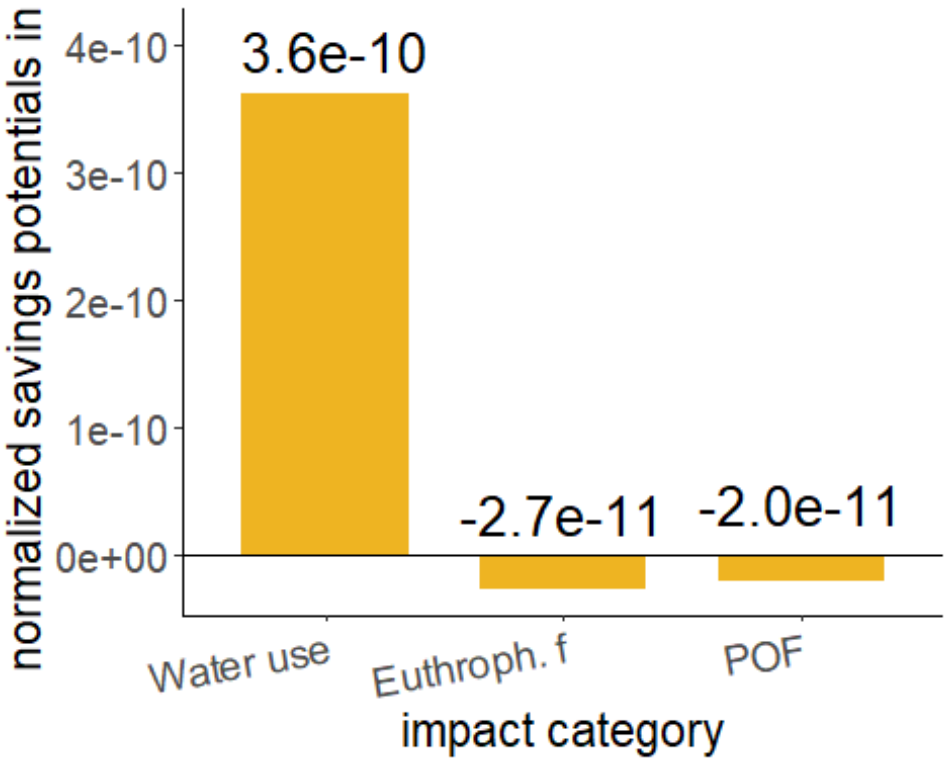



```
# Save plot
ggsave(paste0(location_upload, measure, "_relevant_SP_prop.png"), dpi = 600)

## Saving 5 x 4 in image
```

Plot relevant categories with their norm. savings potential:

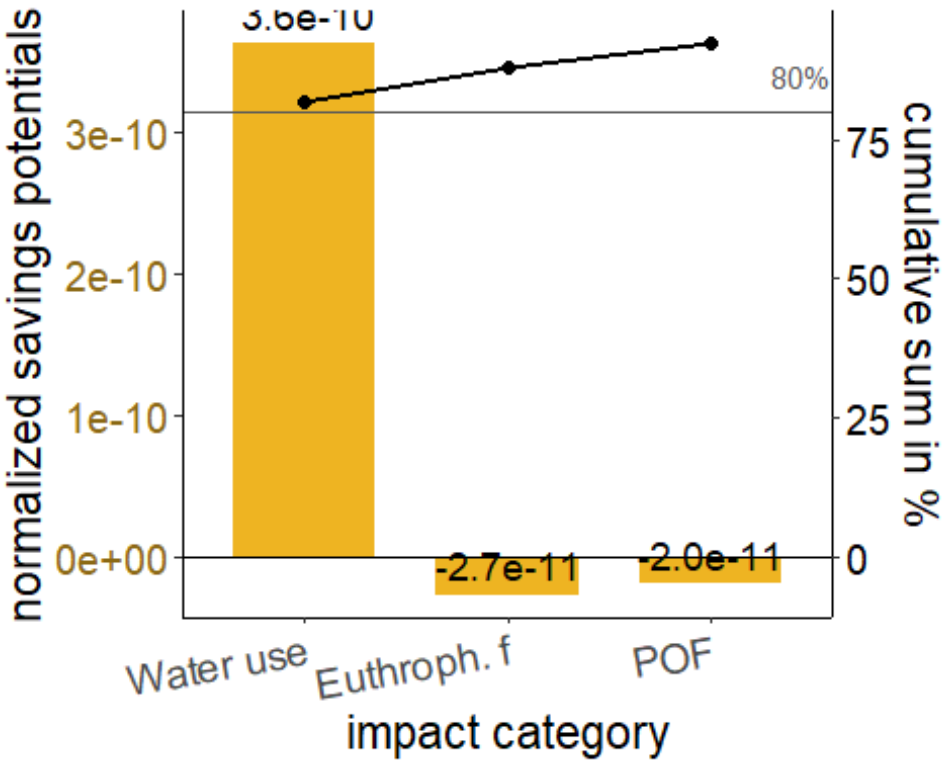
```
# Ensure that the impact category retains the order in which it appears in th
e data
results_norm$`impact category` <- factor(results_norm$`impact category`, leve
ls = results_norm$`impact category`)

results_relevant <- results_prop %>%
  select(`impact category`, relevant)

results_norm <- left_join(results_norm, results_relevant, by = c("impact cate
gory" = "impact category"))

# Prepare data
data_plot <- results_norm %>%
  filter(relevant == TRUE) %>%
  select(`impact category`, name_SP_norm) %>%
  arrange(desc(abs(!!sym(name_SP_norm))))

## Warning: Using an external vector in selections was deprecated in tidysele
ct 1.1.0.
## i Please use `all_of()` or `any_of()` instead.
##   # Was:
```

```
##   data %>% select(name_SP_norm)
##
##   # Now:
##   data %>% select(all_of(name_SP_norm))
##
## See <https://tidyselect.r-lib.org/reference/faq-external-vector.html>.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.

# Rename long impact categories
data_plot <- data_plot %>%
  mutate(`impact category` = case_when(
    `impact category` == "Photochemical oxidant formation: human health" ~ "P
OF",
    `impact category` == "Eutrophication: freshwater" ~ "Euthroph. f",
    TRUE ~ `impact category`
  ))

# Ensure that the impact category retains the order in which it appears in th
e data
data_plot$`impact category` <- factor(data_plot$`impact category`, levels = d
ata_plot$`impact category`)

ggplot(data_plot, aes(x = `impact category`, y = !!sym(name_SP_norm))) +
  geom_bar(stat = "identity", width = 0.7, fill = "goldenrod2", show.legend =
FALSE) +
  geom_hline(yintercept = 0, color = "black", linetype = "solid") +
  geom_text(aes(
    y = !!sym(name_SP_norm),
    label = format(!!sym(name_SP_norm), scientific = TRUE, digits = 2)),
    vjust = ifelse(data_plot$`impact category` != "Water use", -1.3, -0.5),
    size = 7) +
  labs(
    x = "impact category",
    y = "normalized savings potentials in %"
  ) +
  theme_classic() +
  theme(
    axis.text.x = element_text(angle = 10, hjust = 1, size = 15),
    axis.text.y = element_text(size = 15),
    axis.title.x = element_text(size = 17),
    axis.title.y = element_text(size = 17)
  ) +
  scale_y_continuous(expand = expansion(mult = c(0.05, 0.17)))
```




```r
# Save plot
ggsave(paste0(location_upload, measure, "_relevant_SP_norm.png"), dpi = 600)

## Saving 5 x 4 in image

# create cumsum and arrange descending
data_plot <- data_plot %>%
  arrange(desc(abs(!!sym(name_SP_norm)))) %>%
  mutate(
    cumsum = cumsum(abs(!!sym(name_SP_norm) / norm_sum)) * 100
  )

# max. values for scaling
max_norm <- max(data_plot[[name_SP_norm]])
max_cumsum <- max(data_plot$cumsum)

# Conversion factor
factor <- max_norm / max_cumsum

ggplot(data_plot, aes(x = `impact category`)) +
  geom_bar(aes(y = !!sym(name_SP_norm)), stat = "identity",
           width = 0.7, fill = "goldenrod2", show.legend = FALSE) +
  geom_line(aes(y = cumsum * factor, group = 1), color = "black", size = 1) +
  geom_point(aes(y = cumsum * factor), color = "black", size = 2) +
  geom_hline(yintercept = 0, color = "black", linetype = "solid") +
  geom_hline(yintercept = 80 * factor, color = "grey35", linetype = "solid")
+
  annotate("text", x = 3.3, y = 80 * factor, label = "80%", color = "grey35",
```

```
size = 4, hjust = 0, vjust = -1) +
  geom_text(aes(
    y = !!sym(name_SP_norm),
    label = format(!!sym(name_SP_norm), scientific = TRUE, digits = 2)),
    vjust = -0.5, size = 5) +
  scale_y_continuous(
    name = "normalized savings potentials",
    sec.axis = sec_axis(~ . / factor, name = "cumulative sum in %"),
  expand = expansion(mult = c(0.04, 0.06))
  ) +
  labs(x = "impact category") +
  theme_classic() +
  theme(
    axis.text.x = element_text(angle = 10, hjust = 1, size = 15),
    axis.text.y.left = element_text(color = "goldenrod4", size = 15),
    axis.text.y.right = element_text(color = "black", size = 15),
    axis.title.x = element_text(size = 17),
    axis.title.y.left = element_text(size = 17),
    axis.title.y.right = element_text(size = 17)
  )
```




```
# Save plot
ggsave(paste0(location_upload, measure, "_relevant_SP_norm_allin1.png"), dpi
= 600)

## Saving 5 x 4 in image
```

Tables

Prepare data:

```
# Select relevant columns
results_prop <- results_prop %>%
  select(`impact category`, unit, !!sym(name_without_prop), !!sym(name_with_p
rop),
         !!sym(name_SP_prop))
results_norm <- results_norm %>%
  select(`impact category`, unit, !!sym(name_without_norm), !!sym(name_with_n
orm),
         !!sym(name_SP_norm))
# Join of 'results' and 'results_norm' according to the impact categories
results <- left_join(results, results_norm, by = c("impact category" = "impac
t category"))
results <- results %>%
  select(-unit.y) %>%
  rename(unit = unit.x)
# Join of 'results' and 'results_prop' according to the impact categories
results <- left_join(results, results_prop, by = c("impact category" = "impac
t category"))
results <- results %>%
  select(-unit.y) %>%
  rename(unit = unit.x)
# Sort descending according to normalized savings potential
results <- results %>%
  arrange(desc(abs(!!sym(name_SP_norm))))
```

Create tables:

```
# Only results
table_results <- results %>%
  select("impact category", "unit", !!sym(name_without), !!sym(name_with), !!
sym(name_SP)) %>%
  arrange(desc(abs(!!sym(name_SP)))) %>%
  mutate(
    across(-all_of(c("impact category", "unit")), ~ formatC(.x, format = "e",
digits = 2)))
# Create flextable
ft <- flextable(table_results) %>%
  theme_vanilla() %>%
  autofit() %>%
  bold(part = "header") %>%
  border_outer() %>%
  border_inner_h() %>%
  border_inner_v()
# Save as PNG
tf <- tempfile(fileext = ".png")
save_as_image(x = ft, path = paste0(location_upload, measure, "_results", ".p
ng"))
```

```
## [1] "C:/Users/Klene/Documents/Uni_Bremen/WS24_25/Masterarbeit/R/Results/03
_results.png"
```

```
# Saving potentials
table_results <- results %>%
  select(`impact category`, unit, !!sym(name_SP), !!sym(name_SP_norm),  !!sym
(name_SP_prop)) %>%
  arrange(desc(abs(!!sym(name_SP_norm)))) %>%
  mutate(
    across(-all_of(c("impact category", "unit")), ~ formatC(.x, format = "e",
digits = 2)))
# Create flextable
ft <- flextable(table_results) %>%
  theme_vanilla() %>%
  autofit() %>%
  bold(part = "header") %>%
  border_outer() %>%
  border_inner_h() %>%
  border_inner_v()
# Save as PNG
tf <- tempfile(fileext = ".png")
save_as_image(x = ft, path = paste0(location_upload, measure, "_results_SPs",
".png"))
```

```
## [1] "C:/Users/Klene/Documents/Uni_Bremen/WS24_25/Masterarbeit/R/Results/03
_results_SPs.png"
```

```
# Normalized results
table_results <- results %>%
  select("impact category", "unit", !!sym(name_without_norm), !!sym(name_with
_norm), !!sym(name_SP_norm)) %>%
  arrange(desc(abs(!!sym(name_SP_norm)))) %>%
  mutate(
    across(-all_of(c("impact category", "unit")), ~ formatC(.x, format = "e",
digits = 2)))
# Removing the categories without normalization factors
table_results <- table_results %>%
  filter(!`impact category` %in% excluded_categories_nf)
# Rename columns
table_results <- table_results %>%
  rename(!!sym(name_without) := !!sym(name_without_norm),
           !!sym(name_with) := !!sym(name_with_norm),
           !!sym(name_SP) := !!sym(name_SP_norm)
           )
# Create flextable
ft <- flextable(table_results) %>%
  theme_vanilla() %>%
  autofit() %>%
  bold(part = "header") %>%
  border_outer() %>%
  border_inner_h() %>%
  border_inner_v()
```

```r
# Save as PNG
tf <- tempfile(fileext = ".png")
save_as_image(x = ft, path = paste0(location_upload, measure, "_results_norm"
, ".png"))
```

```
## [1] "C:/Users/Klene/Documents/Uni_Bremen/WS24_25/Masterarbeit/R/Results/03
_results_norm.png"
```

```r
# Proportion data
table_results <- results %>%
  select("impact category", "unit", !!sym(name_without_prop), !!sym(name_with
_prop), !!sym(name_SP_prop)) %>%
  arrange(desc(abs(!!sym(name_SP_prop)))) %>%
  mutate(
    across(-all_of(c("impact category", "unit")), ~ formatC(.x, format = "e",
digits = 2)))
# Removing the categories without normalization factor
table_results <- table_results %>%
  filter(!`impact category` %in% excluded_categories_nf)
# Removing the toxicity categories
table_results <- table_results %>%
  filter(!`impact category` %in% excluded_categories_pr)
# Rename columns
table_results <-table_results %>%
  rename(!!sym(name_without) := !!sym(name_without_prop),
         !!sym(name_with) := !!sym(name_with_prop),
         !!sym(name_SP) := !!sym(name_SP_prop),
         )
# Create flextable
ft <- flextable(table_results) %>%
  theme_vanilla() %>%
  autofit() %>%
  bold(part = "header") %>%
  border_outer() %>%
  border_inner_h() %>%
  border_inner_v()
# Save as PNG
tf <- tempfile(fileext = ".png")
save_as_image(x = ft, path = paste0(location_upload, measure, "_results_prop"
, ".png"))
```

```
## [1] "C:/Users/Klene/Documents/Uni_Bremen/WS24_25/Masterarbeit/R/Results/03
_results_prop.png"
```

Upload files

```r
# # List of Excel files to be uploaded
# files_to_upload <- list.files(path = location_upload, pattern = "\\.xlsx$",
full.names = TRUE)
# # Loop over all files and upload
# for (file_path in files_to_upload) {
#   # Creating the file name
```

```
#   file_name <- basename(file_path)
#   # Upload file
#   response <- PUT(
#     url = paste0(nextcloud_url_2, file_name),
#     authenticate(username, password),
#     body = upload_file(file_path)
#   )
#   # Check upload status
#   if (status_code(response) == 201) {
#     print(paste(file_name, "was successfully uploaded."))
#   } else if (status_code(response) == 204) {
#     print(paste(file_name, "was successfully replaced (no content returned)
."))
#   } else {
#     print(paste("Error uploading", file_name, ". Status-Code:", status_code
(response)))
#   }
# }
#
# # List of PNG files to be uploaded
# files_to_upload <- list.files(path = location_upload, pattern = "\\.png$",
full.names = TRUE)
# # Loop over all files and upload
# for (file_path in files_to_upload) {
#   # Create the file name
#   file_name <- basename(file_path)
#   # Upload file
#   response <- PUT(
#     url = paste0(nextcloud_url_2, file_name),
#     authenticate(username, password),
#     body = upload_file(file_path)
#   )
#   # Check upload status
#   if (status_code(response) == 201) {
#     print(paste(file_name, "was successfully uploaded."))
#   } else if (status_code(response) == 204) {
#     print(paste(file_name, "was successfully replaced (no content returned)
."))
#   } else {
#     print(paste("Error uploading", file_name, ". Status-Code:", status_code
(response)))
#   }
# }
```