

Untitled

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Import dataset and restructure.

```
# import dataset and restructure

Abstraction_master <- read.csv(file = url("https://raw.githubusercontent.com/meghanrforrest/SPBG-meta-r
  filter(eligibility == "Yes") |>
  mutate(
    spbg_count = case_when(
      spbg_present == "No" ~ 0,
      spbg_present == "Yes" & additional_spbg_1 == "No" ~ 1,
      spbg_present == "Yes" & additional_spbg_1 == "Yes" & additional_spbg_2 == "No" ~ 2,
      spbg_present == "Yes" & additional_spbg_1 == "Yes" & additional_spbg_2 == "Yes" & additional_spbg_3 == "No" ~ 3,
      spbg_present == "Yes" & additional_spbg_1 == "Yes" & additional_spbg_2 == "Yes" & additional_spbg_3 == "Yes" & additional_spbg_4 == "No" ~ 4,
      spbg_present == "Yes" & additional_spbg_1 == "Yes" & additional_spbg_2 == "Yes" & additional_spbg_3 == "Yes" & additional_spbg_4 == "Yes" ~ 5
    )

    # create variable for records which contain an adjusted bar graph
    contains_adj_spbg = case_when(
      spbg_present == "Yes" & c(adjusted_1 == "Yes" | adjusted_2 == "Yes" | adjusted_3 == "Yes" | adjusted_4 == "Yes") ~ TRUE,
      spbg_present == "No" ~ FALSE,
      spbg_count == 1 & adjusted_1 == "No" ~ 0,
      spbg_count == 2 & c(adjusted_1 == "No" & adjusted_2 == "No") ~ 0,
      spbg_count == 3 & c(adjusted_1 == "No" & adjusted_2 == "No" & adjusted_3 == "No") ~ 0,
      spbg_count == 4 & c(adjusted_1 == "No" & adjusted_2 == "No" & adjusted_3 == "No" & adjusted_4 == "No") ~ 0,
      spbg_count == 5 & c(adjusted_1 == "No" & adjusted_2 == "No" & adjusted_3 == "No" & adjusted_4 == "No") ~ 0
    ) |>

    # create a variable for whether the study contains an ADJUSTED stacked bar graph
    mutate(
      contains_adj_spbg = case_when(
        adjusted_1 == "Yes" | adjusted_2 == "Yes" | adjusted_3 == "Yes" | adjusted_4 == "Yes" | adjusted_5 == "Yes" ~ TRUE,
        TRUE ~ "No"
      )
    ) |>

    # separate out neurological conditions
    separate(neurological_condition, into = c("condition1", "condition2"),
      sep = ";",
      fill = "right",
      remove = TRUE) |>

    # remove unneeded variables
    select(c("doi",
```

```

    "condition1",
    "condition2",
    "figure_other",
    "spbg_present",
    "contains_adj_spbg")
)

```

Warning: Expected 2 pieces. Additional pieces discarded in 2 rows [34, 101].

Prepare a dataset for barplots

```

dat <- Abstraction_master |>
  mutate(
    any_figure_contains = case_when(
      spbg_present == "Yes" & contains_adj_spbg == "No" ~ "Unadjusted SPBG",
      contains_adj_spbg == "Yes" ~ "Adjusted SPBG",
      figure_other == "Yes" & spbg_present == "No" ~ "Other figure (No SPBG)",
      figure_other == "No" & spbg_present == "No" ~ "No figure"),

    # brush up the names of the neurological conditions
    condition1 = recode(
      condition1,
      "Ischemic stroke" = "Stroke",
      "Hemorrhagic stroke" = "Stroke",
      "Stroke (all)" = "Stroke"
    ) |>

    # make the records with two populations into their own observation
    pivot_longer(
      names_to = "which_condition",
      values_to = "neuropathology",
      cols = condition1:condition2) %>%
    filter(neuropathology != "") |>
    select(!"which_condition") |>

    # clean up names of neuropathologies
    mutate(neuropathology = recode(neuropathology,
      "Stroke (all)" = "Stroke (all)",
      "encephalitis" = "Encephalitis",
      "GBS" = "Guillain-Barré",
      "Huntington disease" = "Huntington's disease",
      "Huntington Disease" = "Huntington's disease")
    ) |>

    # releve the any_figure_contains variable
    mutate(
      any_figure_contains = fct_relevel(any_figure_contains,
        "No figure",
        "Other figure (No SPBG)",
        "Unadjusted SPBG",
        "Adjusted SPBG"),

```

```
any_figure_contains = recode(any_figure_contains,
                             "SPBG" = "Stacked proportional bar graph"))
```

```
mutate( any_figure_contains = recode( any_figure_contains, "SPBG" = "Stacked proportional bar
graph"))
```

```
#set up a dataframe for the "Stroke v. Other" barplot
dat_barplot_stroke <- dat |>
  mutate(
    neuropathology = fct_other(neuropathology, keep = "Stroke",
                              other_level = "Other *"),
    neuropathology = fct_relevel(neuropathology, "Other *", "Stroke"))
```

```
barplot_stroke <- ggplot(dat_barplot_stroke,
                         aes(x= neuropathology,
                             fill = any_figure_contains)) +
  geom_bar(width = 0.5,
           color = "white") +
```

```
  coord_flip() +
```

```
  scale_fill_manual(values = c("#533E57",
                                "#8b738e",
                                "#d2b3d6",
                                "#d9f4e6"),
                    limits = c("Adjusted SPBG",
                                "Unadjusted SPBG",
                                "Other figure (No SPBG)",
                                "No figure")) +
```

```
  theme_minimal() +
  theme(
    panel.grid.major.y = element_blank(),
    panel.grid.minor.y = element_blank(),
    panel.grid.minor = element_blank(),
    axis.text.y = element_blank(),

    legend.title=element_blank(),
    legend.key.size = unit(1, 'cm'),
    legend.key.height = unit(.3, 'cm'),
    legend.key.width = unit(.35, 'cm'),
    legend.text = element_text(size = 9),
    legend.position = c(0.5, 1.0),
    legend.direction="horizontal",

    axis.ticks = element_blank(),

    axis.title.y=element_blank(),
    axis.title.x=element_blank(),
```

```

plot.margin = unit(c(0.8,3,0,0), "cm")) +
geom_text(
  stat= 'count' , aes(label=..count..),
  position = position_stack(vjust = .5),
  size = 3,
  color = 'black') +
annotate("text", x = 2, y = 215, label = "Total = 192", size = 3, fontface = "bold"
) +
annotate("text", x = 1, y = 83, label = "Total = 60", size = 3, fontface = "bold") +
annotate("text", x = 2.35, y = 106, label = "Studies in the sample with a stroke population", size = 4,
fontface = "bold", color = "green") +
annotate("text", x = 1.35, y = 116, label = "Studies in the sample with a non-stroke population", size = 4,
fontface = "bold", color = "green") +
scale_y_continuous(limits = c(0, 250))

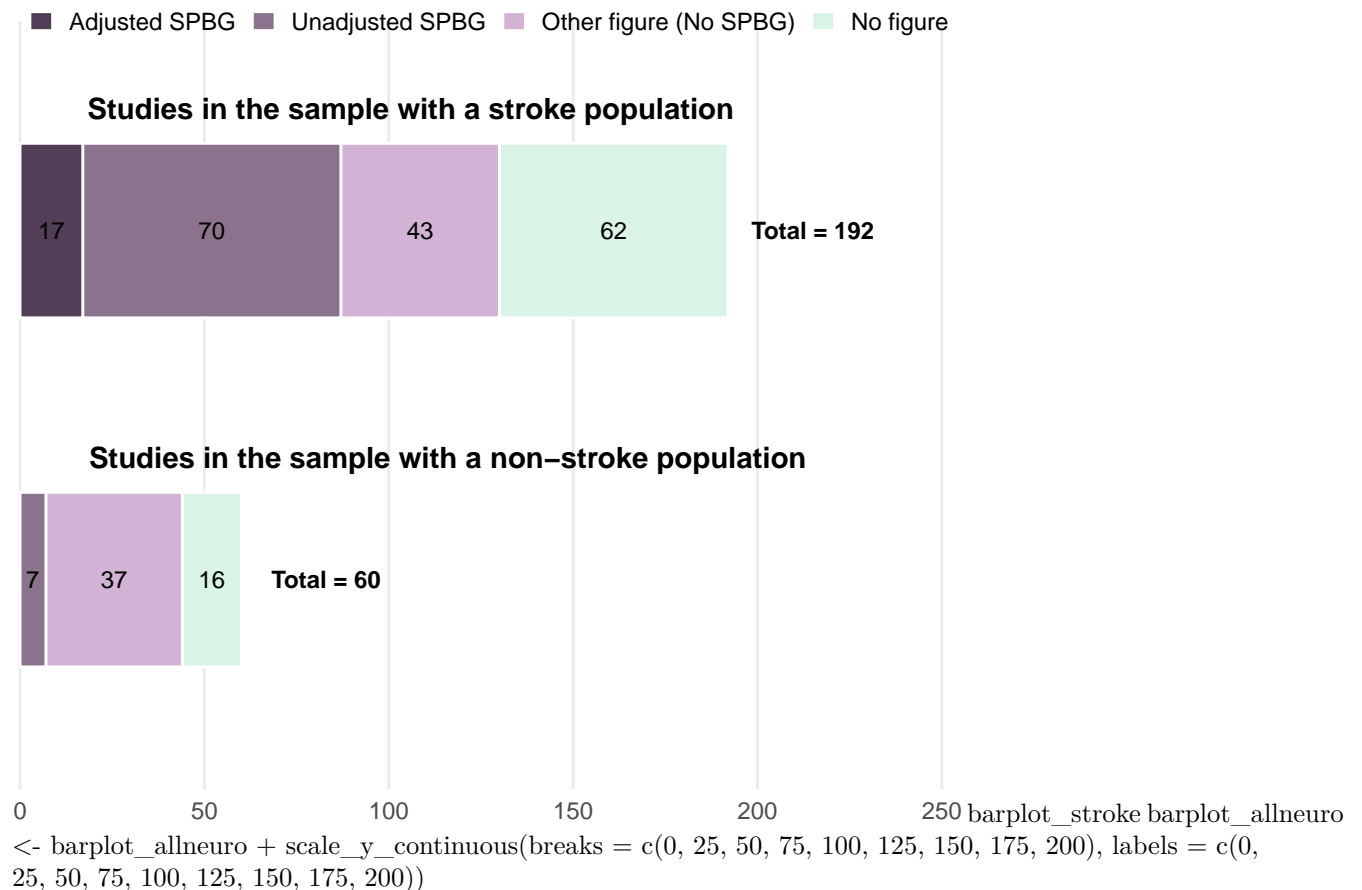
```

barplot_stroke

```

## Warning: The dot-dot notation ('..count..') was deprecated in ggplot2 3.4.0.
## i Please use 'after_stat(count)' instead.
## This warning is displayed once every 8 hours.
## Call 'lifecycle::last_lifecycle_warnings()' to see where this warning was
## generated.

```



Make barplot of all conditions except stroke

```

barplot_data_notstroke <-
  dat %>%
  mutate(
    any_figure_contains = case_when(
      spbg_present == "Yes" ~ "SPBG",
      figure_other == "Yes" & spbg_present == "No" ~ "Other figure (No SPBG)",
      figure_other == "No" & spbg_present == "No" ~ "No figure")) |>
  filter(neuropathology!= "Stroke") |>
  mutate(
    neuropathology = recode(neuropathology,
      "TBI" = "Traumatic brain injury"
    )
  )

barplot_data_notstroke$neuropathology[barplot_data_notstroke$neuropathology%in% names(which(table(barplot_data_notstroke$neuropathology) > 1))] = "Other"

positions_notstroke <- c("Other †",
  "Traumatic brain injury",
  "Guillain-Barré",
  "Encephalitis",
  "Huntington's disease",
  "Parkinson's disease",
  "Multiple sclerosis")

barplot_notstroke <- ggplot(barplot_data_notstroke, aes(x = neuropathology, fill = any_figure_contains)) +
  geom_bar(width = 0.9, color = "white") +
  scale_fill_manual(values = c("#d9f4e6",
    "#d2b3d6",
    "#8b738e")) +

  scale_x_discrete(limits = positions_notstroke) +
  coord_flip() +
  theme_minimal() +
  theme(
    panel.grid.major.y = element_blank(),
    panel.grid.minor.y = element_blank(),
    panel.grid.minor.x = element_blank(),
    panel.background = element_blank(),
    axis.text.y = element_text(size= 9, colour = "black"),
    axis.title.y=element_blank(),
    legend.title=element_blank(),
    legend.position = "none",
    axis.ticks = element_blank(),
    axis.title.x = element_text(size = 10),
    plot.margin = unit(c(1.0,0,0,0), "cm")) +

  ylab("Number of Papers") +
  geom_text(stat= 'count' , aes(label=..count..),
    position = position_stack(vjust = .5),

```

```

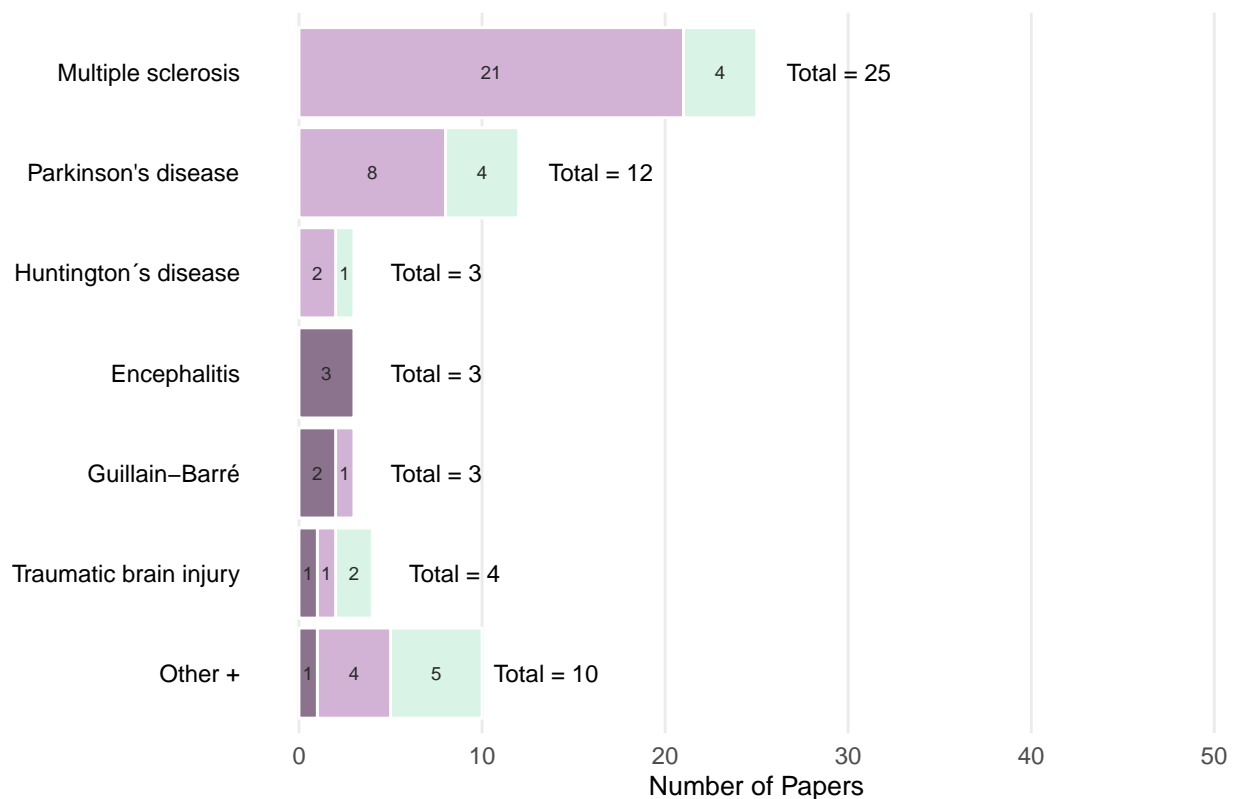
color = 'grey16',
size = 2.5) +

annotate("text", x = 1, y = 13.5, label = "Total = 10", size = 3) +
annotate("text", x = 2, y = 8.5, label = "Total = 4", size = 3) +
annotate("text", x = 3, y = 7.5, label = "Total = 3", size = 3) +
annotate("text", x = 4, y = 7.5, label = "Total = 3", size = 3) +
annotate("text", x = 5, y = 7.5, label = "Total = 3", size = 3) +
annotate("text", x = 6, y = 16.5, label = "Total = 12", size = 3) +
annotate("text", x = 7, y = 29.5, label = "Total = 25", size = 3) +

scale_y_continuous(limits = c(0, 50))

```

barplot_notstroke



(“lightcyan2”, “#FFE082”, “darkorange2”)) device= “tiff”, dpi=700) ggsave(“figure3_draft4.png”) Combine both bargraphs into one figure

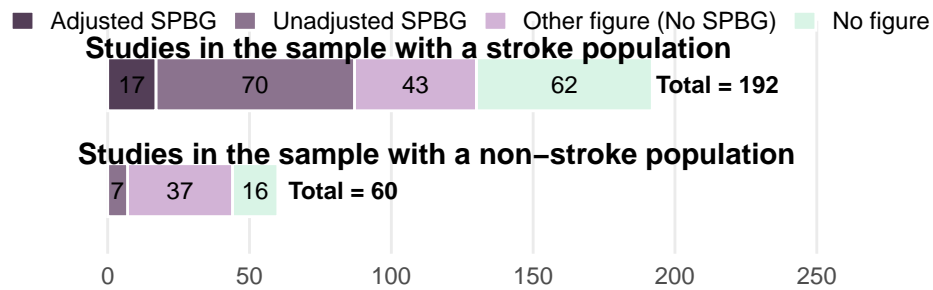
```

combined_barplot <- ggarrange(
  barplot_stroke,
  barplot_notstroke,
  labels = c("A", "B"),
  ncol = 1, nrow = 2,
  heights = c(1.23, 2),
  align = "v")

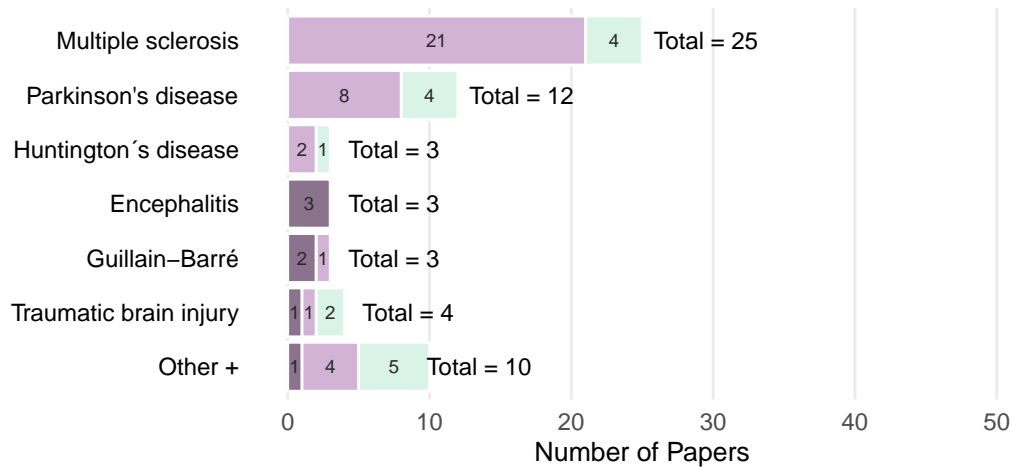
combined_barplot

```

A



B



```
#ggsave("figure3_draft5.png")
```

```
gA <- ggplotGrob(barplot_stroke)
gB <- ggplotGrob(barplot_notstroke)
gB$layout$clip[gB$layout$name == "panel1"] <- "off"
maxWidth = grid::unit.pmax(gA$widths[2:5], gB$widths[2:5])
gA$widths[2:5] <- as.list(maxWidth)
gB$widths[2:5] <- as.list(maxWidth)

gB$widths <- gA$widths

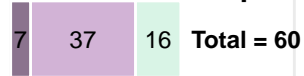
combined_plot1 <- grid.arrange(gA, gB, ncol=1)
grid.lines(x = unit(c(0.34, 0.8), "npc"), y = unit(c(0.51, 0.42), "npc"), gp = gpar(col = "darkgrey"))
grid.text("Breakdown of non-stroke populations in sample", x = unit(0.05, "npc"), y = unit(0.44, "npc"))
```

Adjusted SPBG Unadjusted SPBG Other figure (No SPBG) No figure

Studies in the sample with a stroke population



Studies in the sample with a non-stroke population



0 50 100 150 200 250

Breakdown of non-stroke populations in sample

