Abrupt transformation of West Greenland lakes following compound climate extremes associated with atmospheric rivers - Supplementary Information

VH

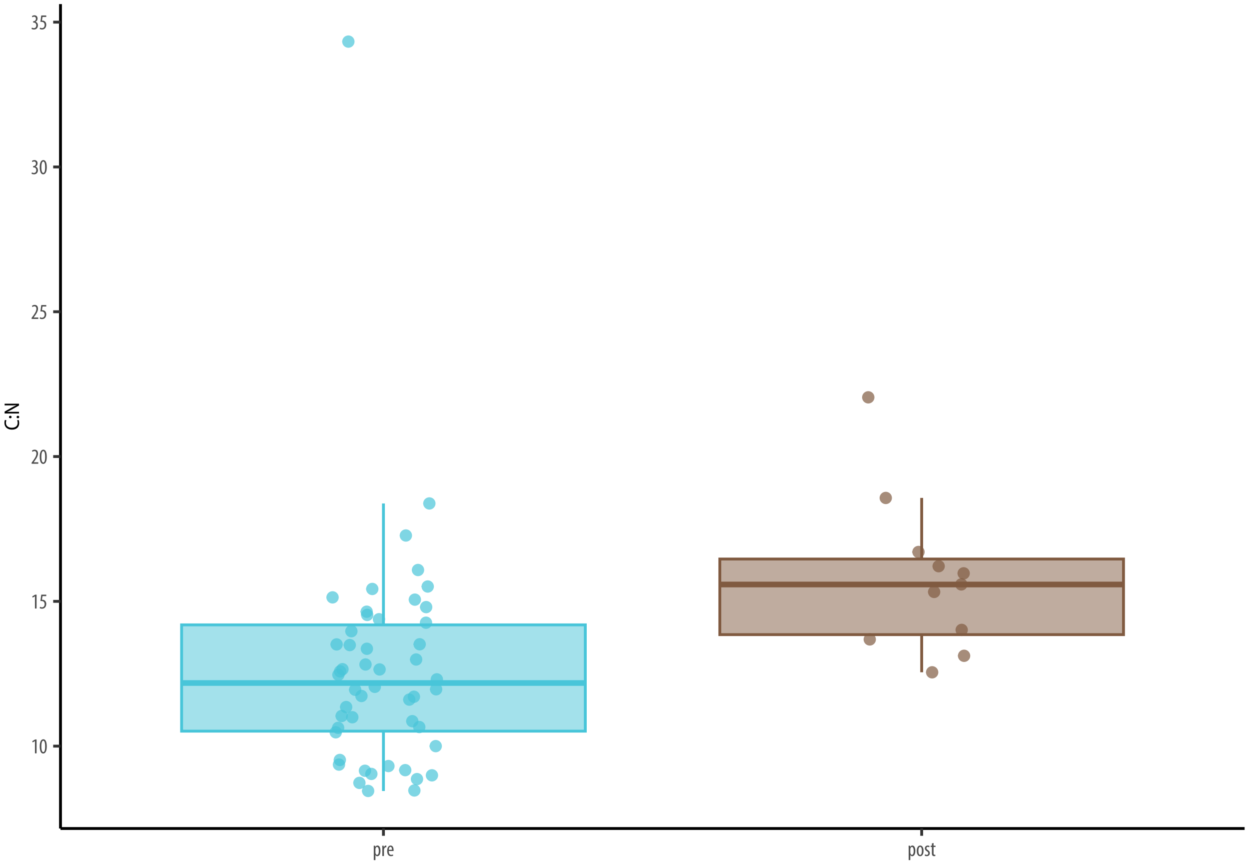
2024-10-28

```r
library(ggforce); library(showtext); library(ggdist); library(ggtext);
library(patchwork); library(prismatic); library(tidyverse)
library(zoo); library(rLakeAnalyzer); library(LakeMetabolizer); library(tidymodels)



library(showtext)
showtext_auto()



showtext_opts(dpi = 300)
showtext_auto()

import_myriad <- function(family = "Myriad Pro", silent = TRUE) {
  font_specs <- systemfonts::system_fonts() %>%
    dplyr::filter(family == .env[["family"]]) %>%
    dplyr::mutate(family = paste(.data[["family"]], .data[["style"]])) %>%
    dplyr::select(plain = .data[["path"]], name = .data[["family"]])

  purrr::pwalk(as.list(font_specs), systemfonts::register_font)

  if (!silent)  message(paste0("Hoisted ", nrow(font_specs), " variants:\n",
                               paste(font_specs$name, collapse = "\n")))
}

import_myriad()

import_myriad_semi <- function() {
  myriad_font_dir <- system.file("fonts", "myriad-pro", package = "myriad")
  sysfonts::font_add("Myriad Pro SemiCondensed",
                     regular = paste0(myriad_font_dir, "/", "MyriadPro-SemiCn.otf"),
                     bold = paste0(myriad_font_dir, "/", "MyriadPro-BoldSemiCn.otf"),
                     italic = paste0(myriad_font_dir, "/", "MyriadPro-SemiboldSemiCnIt.otf"),
                     bolditalic = paste0(myriad_font_dir, "/", "MyriadPro-SemiboldCondIt.otf"))
}

import_myriad_semi()
```

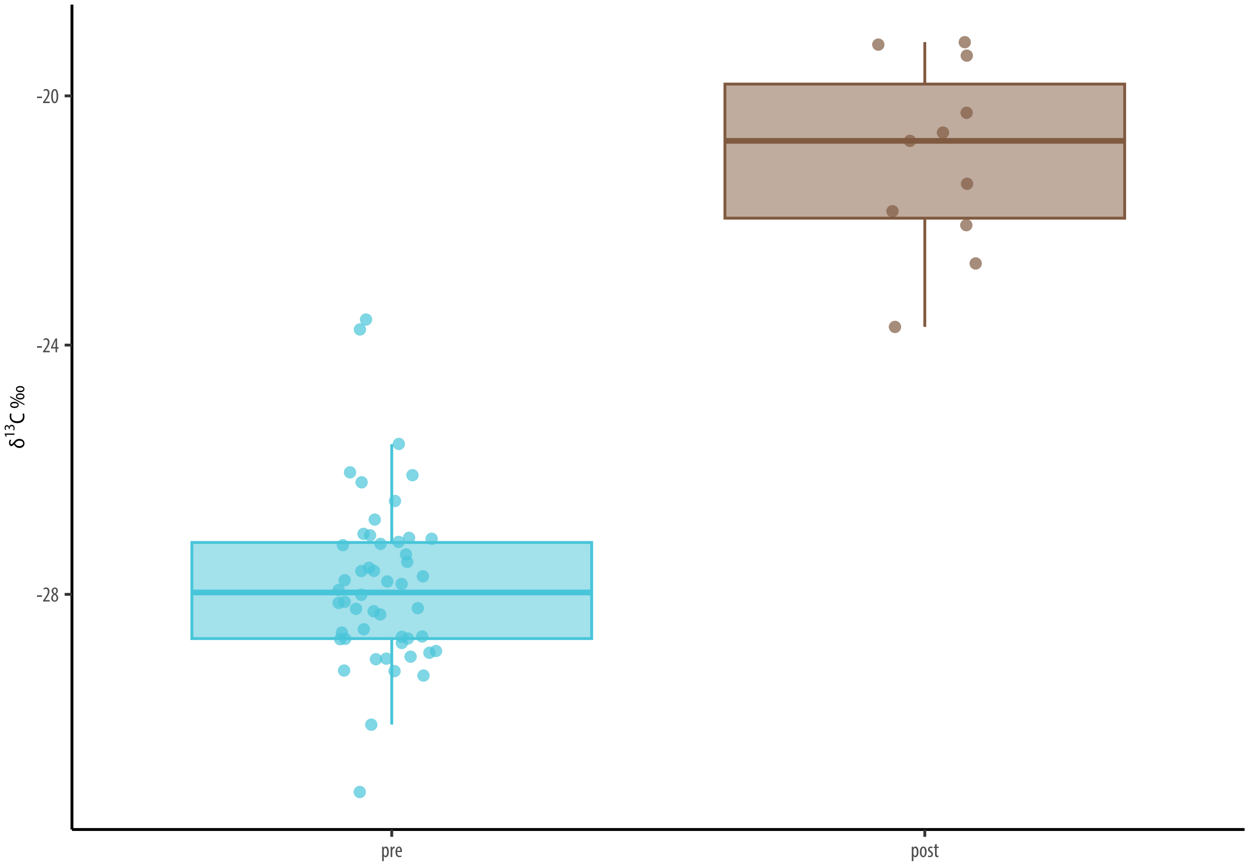
```
import_myriad_condensed <- function() {
  myriad_font_dir <- system.file("fonts", "myriad-pro", package = "myriad")
  sysfonts::font_add("Myriad Pro Condensed",
                     regular = paste0(myriad_font_dir, "/", "MyriadPro-Cond.otf"),
                     bold = paste0(myriad_font_dir, "/", "MyriadPro-BoldCond.otf"),
                     italic = paste0(myriad_font_dir, "/", "MyriadPro-CondIt.otf"),
                     bolditalic = paste0(myriad_font_dir, "/", "MyriadPro-BoldCondIt.otf"))
}

import_myriad_condensed()


theme_set(
  theme_classic() +
    theme(axis.text.x = element_text(size = 8, family = "Myriad Pro Condensed"),
          axis.text.y = element_text(size = 8, family = "Myriad Pro Condensed"),
          axis.title.x = element_text(size = 8, family = "Myriad Pro SemiCondensed"),
          axis.title.y = element_text(size = 8, family = "Myriad Pro SemiCondensed"),
          legend.text = element_text(size = 8, family = "Myriad Pro Condensed"),
          panel.grid.major.x = element_blank(),
          panel.grid.minor.x = element_blank(),
          panel.grid.minor.y = element_blank(),
          panel.grid.major.y = element_blank(),
          plot.margin = unit(c(0.05,0.05,0.05,0.05), "cm"))
)
```

```
# C:N ---------------------------------------------------------------------

cn <-
  read_csv('combined_files/combined_CNP_delC13.csv') %>%
  pivot_longer(
    cols = del13C_DOM:CN_Soil,
    names_to = 'variable',
    values_to = 'value') %>%
  mutate(main_var = if_else(str_detect(variable, "^CN_"),
                            'CN',
                            'delC13'
  ),
  pre_post = factor(pre_post,
                    levels = c('pre', 'post')))

(CN <- cn %>%
  filter(variable %in% c('CN_POM')  & Layer == 'epi') %>%
  mutate(variable = factor(variable,
                           levels = c('CN_POM'),
                           labels = c('POM'))) %>%
  ggplot(aes(x = pre_post, y = value, group = pre_post)) +
  geom_boxplot(aes(color = pre_post, fill = after_scale(clr_alpha(color, 0.5))),
               outlier.color = 'transparent') +
  geom_jitter(aes(color = pre_post), alpha = 0.7, width = 0.1, shape = 19) +
  scale_color_manual(values = c('#48C5D9', "#805A40")) +
  #scale_y_log10() +
  labs(x = NULL, y = 'C:N') +
  theme(strip.placement = 'outside',
```

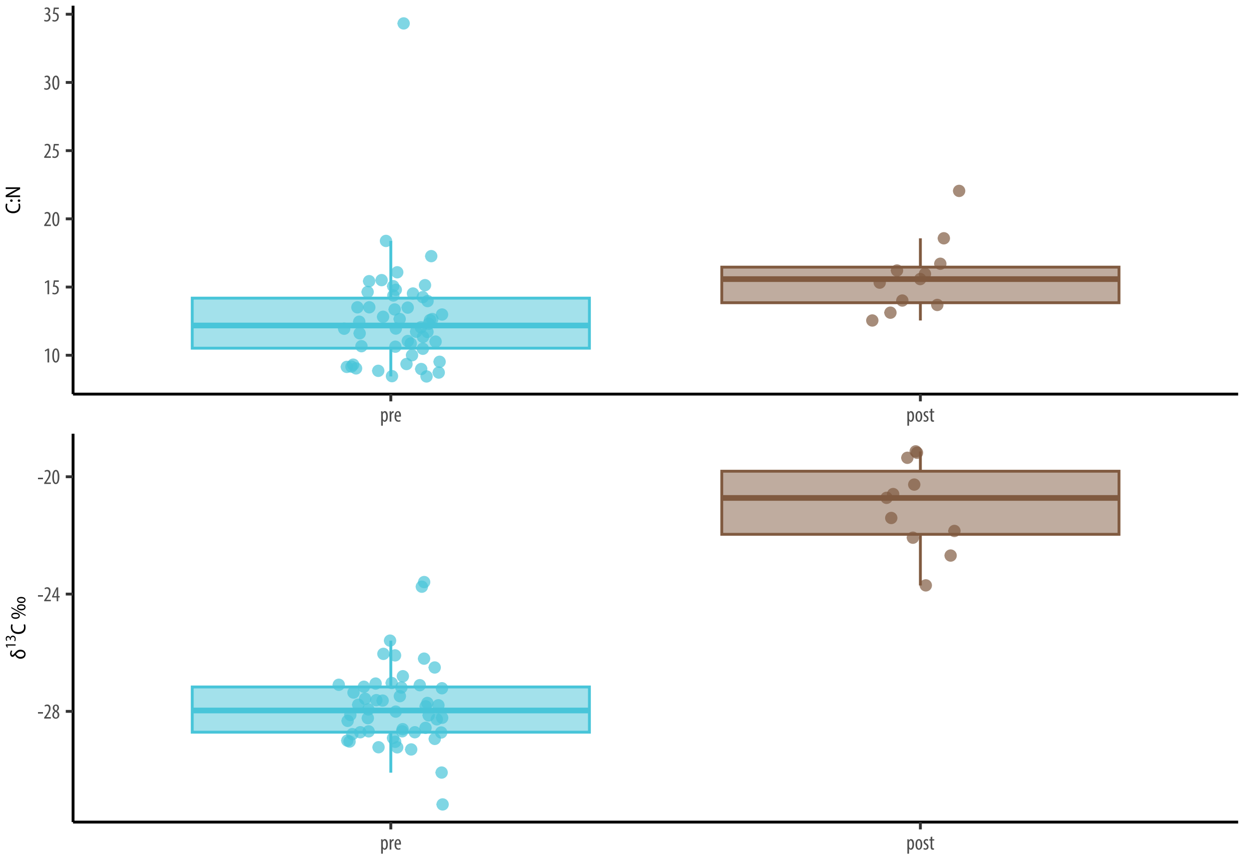
```
        strip.text = element_text(size = 8),
        strip.background = element_blank(),
        legend.position = 'none',
        axis.title.x = element_text(size = 10)))
```



```
(delC13 <- cn %>%
  filter(variable %in% c('del13C_POM')  & Layer == 'epi') %>%
  mutate(variable = factor(variable,
                           levels = c('del13C_POM'),
                           labels = c('POM'))) %>%
  ggplot(aes(x = pre_post, y = value)) +
  geom_boxplot(aes(color = pre_post, fill = after_scale(clr_alpha(color, 0.5))),
             outlier.color = 'transparent') +
  geom_jitter(aes(color = pre_post), alpha = 0.7, width = 0.1, shape = 19) +
  scale_color_manual(values = c('#48C5D9', "#805A40")) +
  labs(x = NULL, y = expression(delta^{13}*C~"%")) +
  theme(strip.placement = 'outside',
        strip.text = element_text(size = 8),
        strip.background = element_blank(),
        legend.position = 'none',
        axis.title.x = element_text(size = 10)))
```

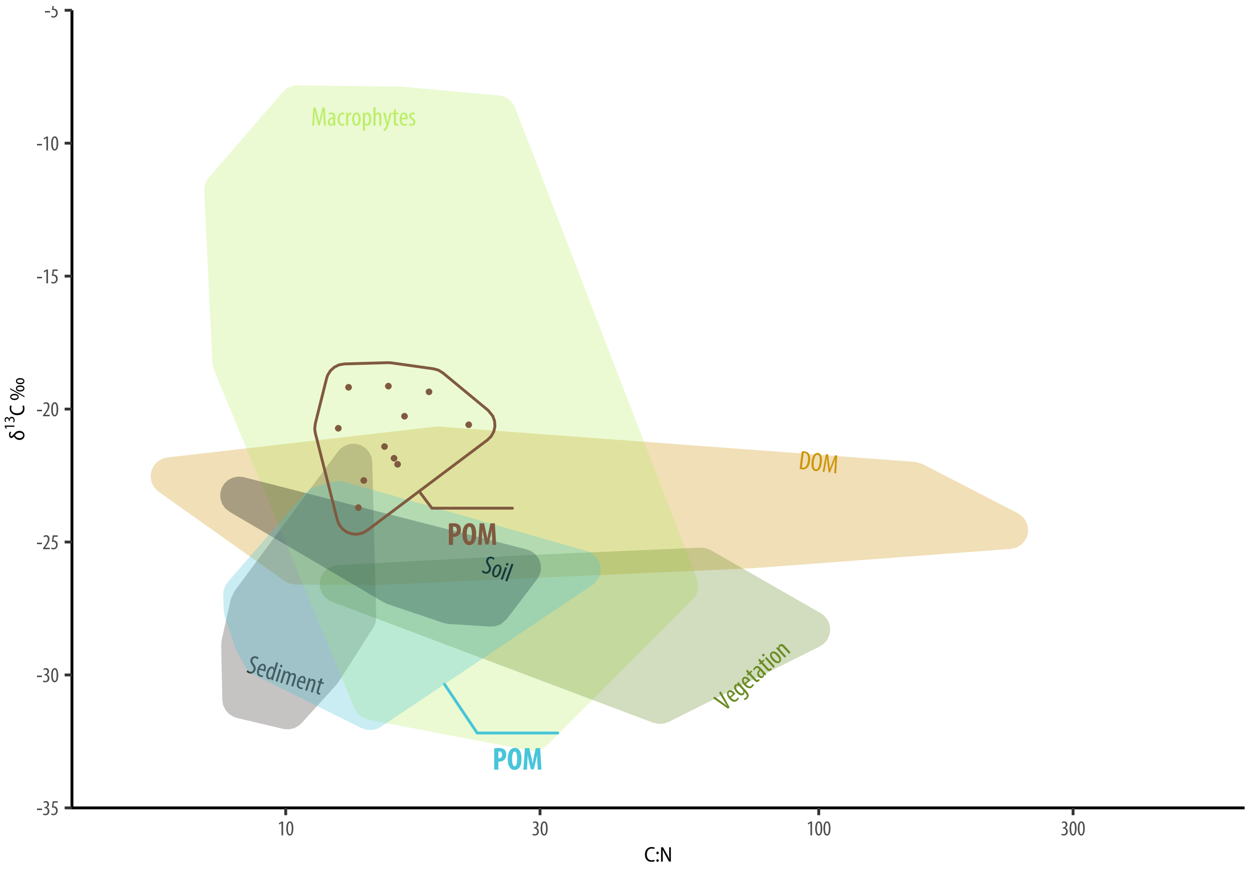


```
CN / delC13
```



```
# biplot -------------------------------------------------------------------


biplot <-
  read_csv('combined_files/combined_CNP_delC13.csv') %>%
  filter(Layer == 'epi') %>%
  pivot_longer(
    cols = del13C_DOM:del13C_Soil,
    names_to = 'del13C_source',
    values_to = 'del13C_value',
    names_prefix = 'del13C_') %>%
  pivot_longer(
    cols = CN_DOM:CN_Soil,
    names_to = 'CN_source',
    values_to = 'CN_value',
    names_prefix = 'CN_') %>%
  mutate(
         del13C_source = factor(del13C_source,
                                levels = c('DOM', 'POM', 'Sed', 'Mac', 'Veg', 'Soil'),
                                labels = c('DOM', 'POM', 'Sediment', 'Macrophytes', 'Vegetation', 'Soil
         CN_source = factor(CN_source,
                            levels = c('DOM', 'POM', 'Sed', 'Mac', 'Veg', 'Soil'),
                            labels = c('DOM', 'POM', 'Sediment', 'Macrophytes', 'Vegetation', 'Soil'))) %>%
  filter(del13C_source == CN_source)
```

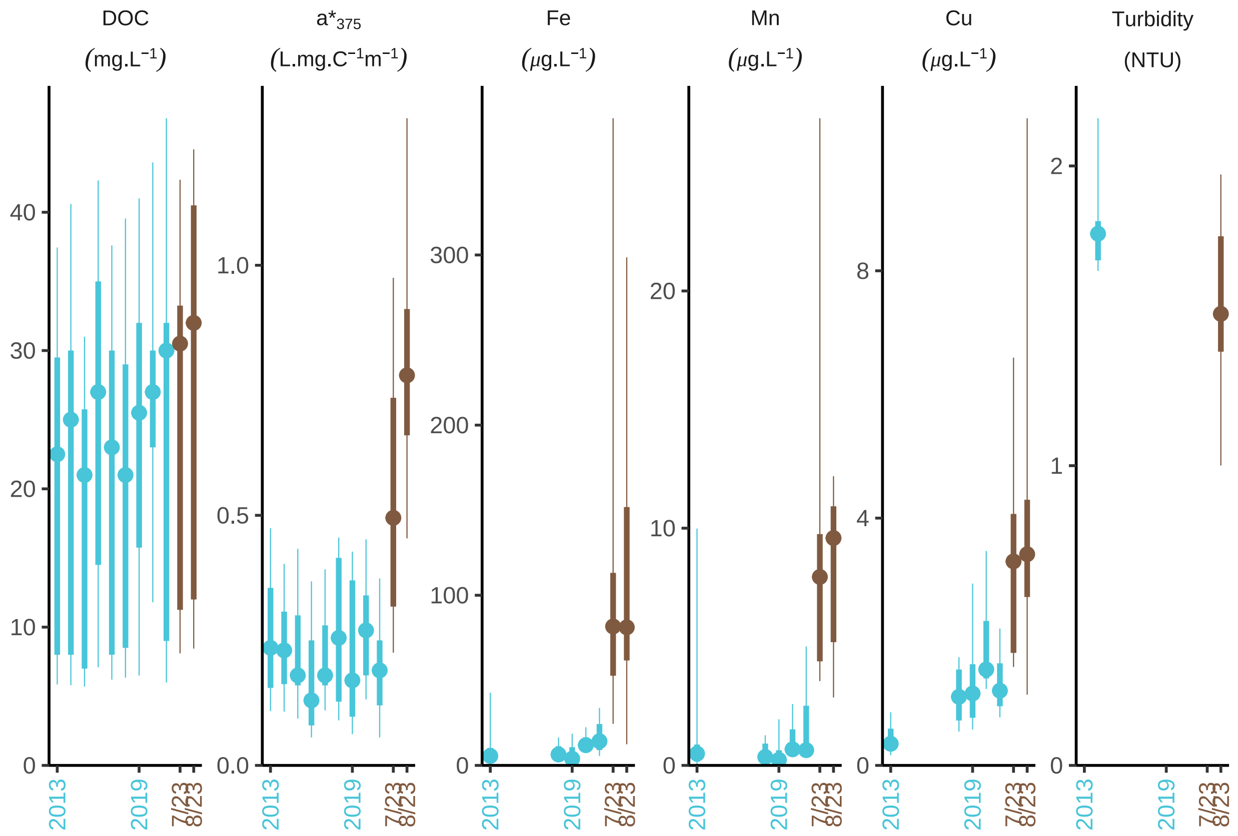
```r
# bioplot different labels

(cn_bp <- biplot %>%
    ggplot(aes(x = (CN_value), y = del13C_value)) +
    # everything pre, expect for POM
    geom_mark_hull(data = biplot %>%
                     filter(pre_post != 'post' &
                              del13C_source %in% c('Macrophytes', 'Sediment', 'DOM', 'Soil', 'Vegetatio
                   aes(fill = del13C_source),
                   label.fill = 'transparent',
                   color = 'transparent', concavity = 25, con.type = 'straight',
                   label.buffer = unit(15, 'mm'), con.cap = 0, label.fontsize = 8) +
    annotate("text", x = 14, y = -9, label = "Macrophytes",
             family = 'Myriad Pro Condensed', color = "#BCEE68", size = 3.5) +
    annotate("text", x = 10, y = -30, label = "Sediment", angle = -17,
             family = 'Myriad Pro Condensed', color = "#403434", size = 3.5) +
    annotate("text", x = 100, y = -22, label = "DOM",
             family = 'Myriad Pro Condensed', angle = -7, color = "#CD950C", size = 3.5) +
    annotate("text", x = 25, y = -26, label = "Soil",
             family = 'Myriad Pro Condensed', angle = -20, size = 3.5) +
    annotate("text", x = 75, y = -30, label = "Vegetation",
             family = 'Myriad Pro Condensed', angle = 42, color = "#698B22", size = 3.5) +
    # hulls for POM
    geom_mark_hull(data = biplot %>% filter(del13C_source == 'POM' & pre_post == 'pre'),
                   aes(label = del13C_source), expand = 0.02,
                   label.family = 'Myriad Pro Condensed',
                   label.colour = '#48C5D9', con.colour = '#48C5D9',
                   label.fill = 'transparent', fill = '#48C5D9', color = 'transparent',
                   concavity = 20, con.type = 'straight',
                   label.buffer = unit(5, "mm"), con.cap = 0) +
    geom_mark_hull(data = biplot %>% filter(del13C_source == 'POM' & pre_post == 'post'),
                   aes(label = del13C_source), expand = 0.02,
                   label.family = 'Myriad Pro Condensed',
                   label.colour = '#805A40', con.colour = '#805A40', color = '#805A40',
                   concavity = 20, con.type = 'straight', label.fill = 'transparent',
                   label.buffer = unit(0, "mm"), con.cap = 0) +
    geom_point(data = biplot %>% filter(del13C_source == 'POM' & pre_post == 'post'),
               color = '#805A40', size = 0.5) +
    labs(x = 'C:N', y = expression(delta^{13}*C~"\U2030")) +
    scale_fill_manual(values = c(DOM = "#CD950C",
                                 Macrophytes = "#BCEE68" ,
                                 Vegetation = "#698B22",
                                 Soil = "black",
                                 Sediment = "#403434")) +
    scale_color_manual(values = c(pre = '#48C5D9', post = "#805A40")) +
    scale_x_log10(limits = c(5, 500)) +
    scale_y_continuous(limits = c(-35,-5), expand = c(0,0)) +
    theme(legend.position = 'none'))
```



```
# nutrients and metals ------------------------------------------------------------------


# A) contributing factors: DOC, a375, Fe, Mn, Cu
# B) nutrients
# C) % difference


env <-
  read_csv('combined_files/Greenland_2013-2023_env_MASTER_september_23.csv') %>%
  rename(lake = Lake,
         layer = Layer,
         date = Date,
         depth = Depth) %>%
  mutate(DIN = NO3 + NH4,
         DINTP = DIN/TP,
         a380spec = a380/DOC, # add carbon-normalized a380 (~degree of color per C)
         a375spec = a375/DOC, # add carbon-normalized a380 (~degree of color per C)
         SUVA254 = a254/DOC,
         across(c(DOC, NO3, NH4), round, 0), # correct rounding of variables
         across(c(DINTP, a254, a380, a375, SR, a375spec, a380spec, SUVA254), round, 2),
         year = year(date)) %>% # correct rounding of variables)
  filter(lake %in% c('SS8', 'SS85', 'SS901', 'SS903', 'SS906', 'SS909', 'SS2',
                     'SS18', 'SS1590', 'SS1381')) %>%
  mutate(pre_post =
           case_when(year(date) < 2023 ~ 'pre',
```

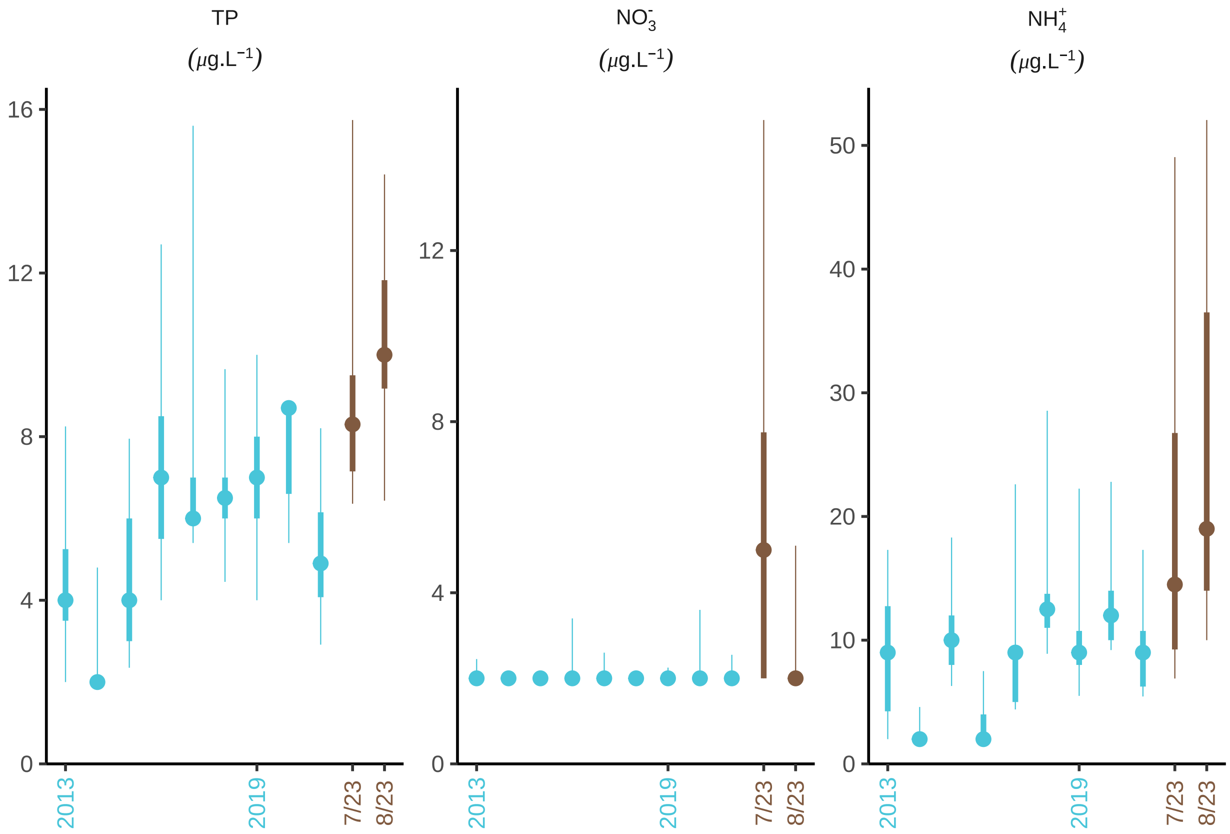
```r
                     year(date) == 2023 ~ 'post'),
         pre_post = factor(pre_post,
                           levels = c('pre', 'post')),
         month = month(date)) %>%
  filter(month %in% c(6,7,8) &
        layer %in% c('epi') &
          year > 2012) %>%
  select(lake, date, layer, year, pre_post, DOC, a375spec, TP, NO3, NH4, turbidity)


metal <-
  read_csv('combined_files/metals_comb.csv') %>%
  filter(element %in% c('Fe', 'Mn', 'Cu') &
           layer == 'epi' &
           lake %in% c('SS8', 'SS85', 'SS901', 'SS903', 'SS906', 'SS909', 'SS2',
                       'SS18', 'SS1590', 'SS1381') &
           month %in% c(6,7,8)) %>%
  select(date, lake, element, conc) %>%
  pivot_wider(names_from = 'element',
              values_from = 'conc') %>%
  mutate(Mn = Mn/1000,
         Cu = Cu/1000)

# combine

env_comb <-
  env %>%
  left_join(metal,
            by = c('date', 'lake')) %>%
  pivot_longer(cols = DOC:Cu,
               names_to = 'variable',
               values_to = 'value')

diff_comb <-
  env_comb %>%
  group_by(variable, pre_post) %>%
  summarise(mean = mean(value, na.rm = T),
            min = min(value, na.rm = T),
            max = max(value, na.rm = T)) %>%
  pivot_wider(names_from = pre_post,
              values_from = c(mean, min, max)) %>%
  summarise(diff = ((mean_post-mean_pre)/mean_pre)*100)

# color

pre = c("#48C5D9","#48C5D9","#805A40", "#805A40")


# figure 2a ---------------------------------------------------------------


(panel_A <- env_comb %>%
  filter(variable %in% c('DOC', 'a375spec', 'Fe', 'Mn', 'Cu', 'turbidity')) %>%
```

```
mutate(variable = factor(variable,
                         levels = c('DOC', 'a375spec', 'Fe', 'Mn', 'Cu', 'turbidity'),
                         labels = c(
                           expression(atop("DOC", (mg.L^{-1}))),
                           expression(atop("a*"["375"], (L.mg.C^{-1}*m^{-1}))),
                           expression(atop("Fe", (mu*g.L^{-1}))),
                           expression(atop("Mn", (mu*g.L^{-1}))),
                           expression(atop("Cu", (mu*g.L^{-1}))),
                           expression(atop("Turbidity", "(NTU)"))
                         ))) %>%
mutate(
  year = factor(year),
  year = case_when(year == 2023 & month(date) == 7 ~ '7/23',
                   year == 2023 & month(date) == 8 ~ '8/23',
                   T ~ year)) %>%
ggplot(aes(x = year, y = value, color = pre_post)) +
stat_pointinterval(point_interval = 'median_qi', .width = c(0.5, 0.9),
                   interval_size_range = c(0.2,1)) +

scale_color_manual(NULL, values = c(pre = '#48C5D9', post = "#805A40")) +
scale_y_continuous(limits = c(0,NA),
                   expand = expansion(mult = c(0,.05)),
                   n.breaks = 4) +
scale_x_discrete(breaks = c('2013', '2019', '7/23', '8/23')) +
facet_wrap(~variable, labeller = label_parsed, nrow = 1, scales = 'free_y') +
theme_classic() +
theme(strip.placement = 'outside',
      strip.text = element_text(size = 8),
      strip.background = element_blank(),
      legend.position = 'none',
      axis.text.x = element_text(color = pre, angle = 90, vjust = 0.5),
      axis.title.x = element_text(size = 10)) +
labs(y = NULL, x = NULL))
```



```
# figure 2b ----------------------------------------------------------------


(panel_B <- env_comb %>%
    filter(variable %in% c('TP', 'NO3', 'NH4')) %>%
    mutate(value = if_else(variable == 'NO3' & value < 2,
                           2,
                           value)) %>%
    mutate(variable = factor(variable,
                             levels = c('TP', 'NO3', 'NH4'),
                             labels = c(
                               expression(atop("TP", (mu*g.L^{-1}))),
                               expression(atop("NO"['3']^{'-'}, (mu*g.L^{-1}))),
                               expression(atop("NH"['4']^{'+'}, (mu*g.L^{-1})))

                             ))) %>%
   mutate(
     year = factor(year),
     year = case_when(year == 2023 & month(date) == 7 ~ '7/23',
                      year == 2023 & month(date) == 8 ~ '8/23',
                      T ~ year)) %>%
    ggplot(aes(x = year, y = value, color = pre_post)) +
    stat_pointinterval(point_interval = 'median_qi', .width = c(0.5, 0.9), interval_size_range = c(0.2,
    scale_color_manual(NULL, values = c(pre = '#48C5D9', post = "#805A40")) +
    scale_y_continuous(limits = c(0,NA),
                       expand = expansion(mult = c(0,.05))) +
   scale_x_discrete(breaks = c('2013', '2019', '7/23', '8/23')) +
```

```
    facet_wrap(~variable, labeller = label_parsed, nrow = 1, scales = 'free_y') +
    theme_classic() +
    theme(strip.placement = 'outside',
          strip.text = element_text(size = 8),
          strip.background = element_blank(),
          legend.position = 'none',
          axis.text.x = element_text(color = pre, angle = 90, vjust = 0.5),
          axis.title.x = element_text(size = 10)) +
    labs(y = NULL, x = NULL))
```



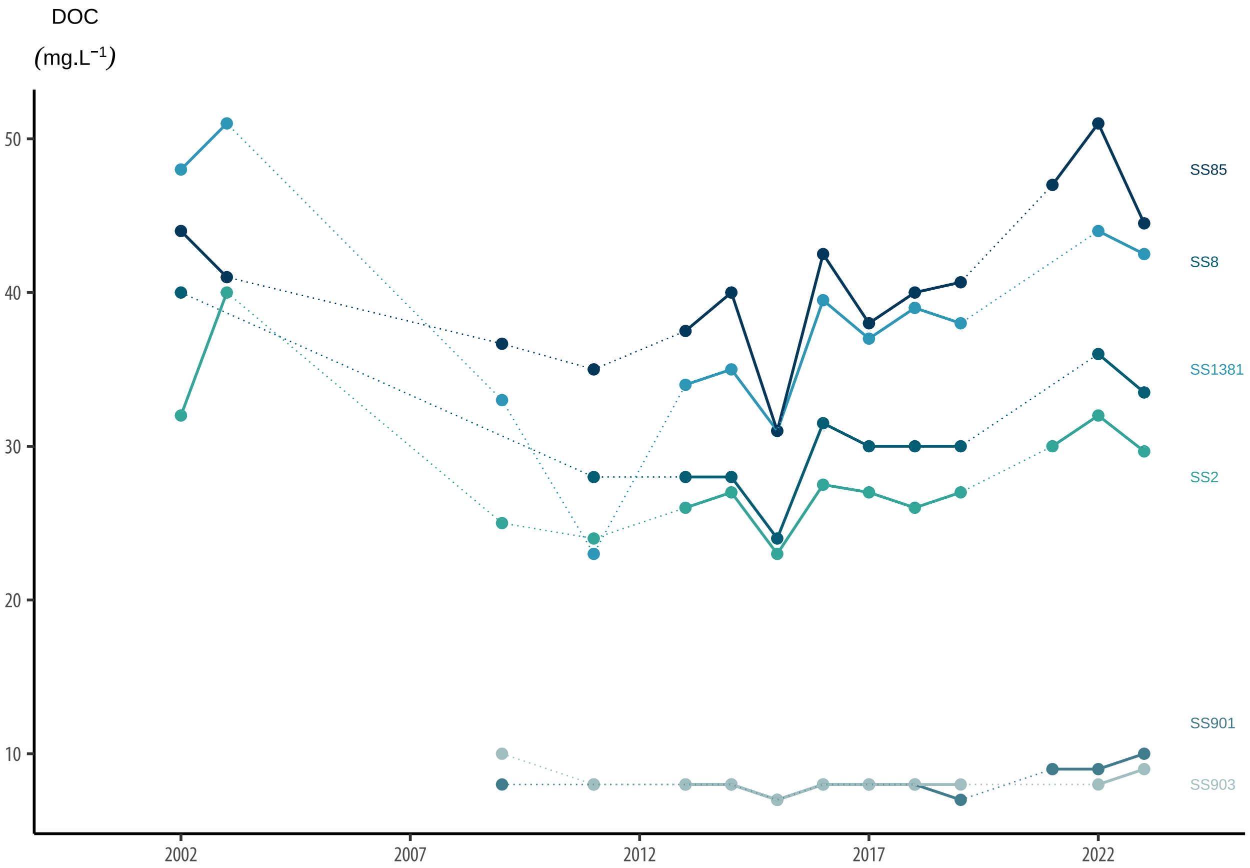
```
env_comb %>%
  select(variable, value, pre_post) %>%
  nest(data = c(value, pre_post)) %>%
  mutate(
    t_test = purrr::map(.x = data, .f = \(x){
      t.test(x$value ~ x$pre_post)  %>%
        broom::tidy()
    })) %>%
  dplyr::select(-data)  %>%
  tidyr::unnest(cols = t_test)
```

```
## # A tibble: 9 x 11
##   variable  estimate estimate1 estimate2 statistic    p.value parameter conf.low
##   <chr>        <dbl>     <dbl>     <dbl>     <dbl>      <dbl>     <dbl>    <dbl>
## 1 DOC         -4.00      22.6      26.6       -1.26 0.216           28.3 -1.05e+1
## 2 a375spec    -0.435      0.23      0.665     -6.33 0.00000206      22.5 -5.78e-1
## 3 TP          -4.15       5.72      9.88      -5.48 0.00000870      26.7 -5.71e+0
```

```
## 4 NO3          -1.95       2.1      4.05      -1.90 0.0725          19.1 -4.10e+0
## 5 NH4         -14.0        8.93    23.0       -3.70 0.00141         20.2 -2.19e+1
## 6 turbidity    0.287       1.81     1.53       2.17 0.0459          15.5  5.89e-3
## 7 Mn           -8.17       1.23     9.40      -5.17 0.0000408       21.0 -1.15e+1
## 8 Fe         -115.        10.5    125.        -4.37 0.000325        19.1 -1.70e+2
## 9 Cu           -2.70       1.16     3.86      -3.78 0.00117         20.1 -4.18e+0
## # i 3 more variables: conf.high <dbl>, method <chr>, alternative <chr>
```

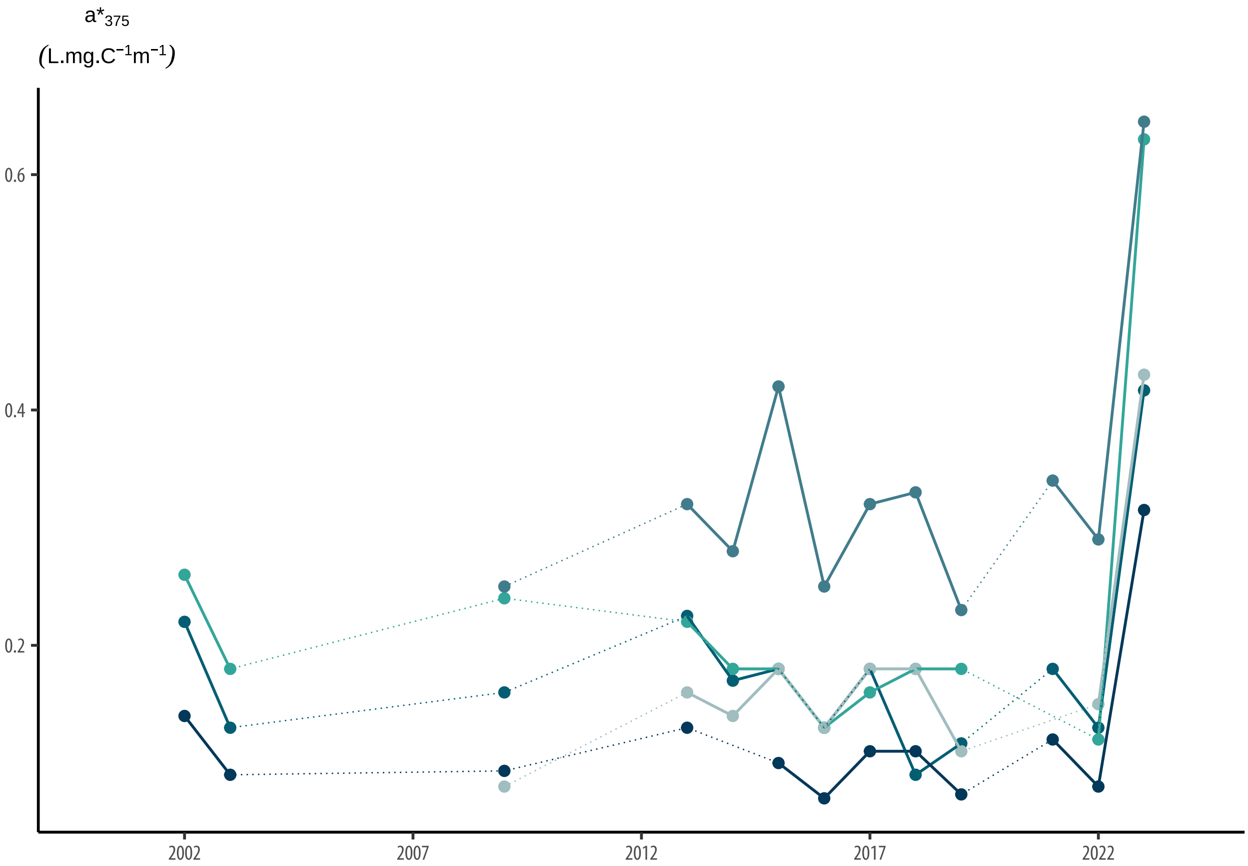
```
# panel D -----------------------------------------------------------------

# show all data for SS2, SS85, and SS8

old <-
  read_csv('combined_files/Greenland_2013-2023_env_MASTER_september_23.csv') %>%
  rename(lake = Lake,
         layer = Layer,
         date = Date,
         depth = Depth) %>%
  mutate(DIN = NO3 + NH4,
         DINTP = DIN/TP,
         a380spec = a380/DOC, # add carbon-normalized a380 (~degree of color per C)
         a375spec = a375/DOC, # add carbon-normalized a380 (~degree of color per C)
         SUVA254 = a254/DOC,
         across(c(DOC, NO3, NH4), round, 0), # correct rounding of variables
         across(c(DINTP, a254, a380, a375, SR, a375spec, a380spec, SUVA254), round, 2),
         year = year(date)) %>% # correct rounding of variables)
  filter(lake %in% c('SS8', 'SS85', 'SS901', 'SS903', 'SS906', 'SS909', 'SS2',
                     'SS18', 'SS1590', 'SS1381')) %>%
  mutate(pre_post =
           case_when(year(date) < 2023 ~ 'pre',
                     year(date) == 2023 ~ 'post'),
         pre_post = factor(pre_post,
                           levels = c('pre', 'post')),
         month = month(date)) %>%
  filter(month %in% c(6,7,8) &
           layer %in% c('epi')) %>%
  select(lake, date, layer, year, pre_post, DOC, a375spec, TP)

(doc_old <- expand_grid(
  year = seq(from = 2000, to = 2023),
  lake = c('SS1381', 'SS2', 'SS8', 'SS85', 'SS901', 'SS903')) %>%
  left_join(old,
            by = c('year', 'lake')) %>%
  arrange(date) %>%
    group_by(year, lake) %>%
    summarise(DOC = mean(DOC, na.rm = T)) %>%
  ggplot(aes(x = year, y = DOC)) +
  annotate('text', x = 2024, y = 48, label = 'SS85', color = '#023859', hjust = 0, size = 2) +
  annotate('text', x = 2024, y = 42, label = 'SS8', color = '#035E73', hjust = 0, size = 2) +
  annotate('text', x = 2024, y = 35, label = 'SS1381', color = '#2D97B7', hjust = 0, size = 2) +
  annotate('text', x = 2024, y = 28, label = 'SS2', color = '#33A69A', hjust = 0, size = 2) +
    annotate('text', x = 2024, y = 12, label = 'SS901', color = '#417C8C', hjust = 0, size = 2) +
    annotate('text', x = 2024, y = 8, label = 'SS903', color = '#A0BDBF', hjust = 0, size = 2) +
  geom_point(aes(color = lake)) +
```

```
 geom_line(aes(color = lake)) +
 geom_line(data = old %>%
       group_by(year, lake) %>%
       summarise(DOC = mean(DOC, na.rm = T)) %>%
       filter(!is.na(DOC) & lake %in% c('SS1381', 'SS2', 'SS8', 'SS85', 'SS901', 'SS903')),
      aes(color = lake), linetype = 'dotted', linewidth = 0.25) +
 scale_color_manual(values = c('#035E73', '#33A69A', '#2D97B7', '#023859', '#417C8C', '#A0BDBF')) +
 scale_x_continuous(limits = c(2000,2024), breaks = seq(from = 2002, to = 2024, by = 5)) +
 coord_cartesian(clip = 'off') +
 theme(legend.position = 'none',
    plot.subtitle = element_text(size = 8)) +
 labs(x = NULL, y = NULL, subtitle = expression(atop("DOC", (mg.L^{-1})))))
```

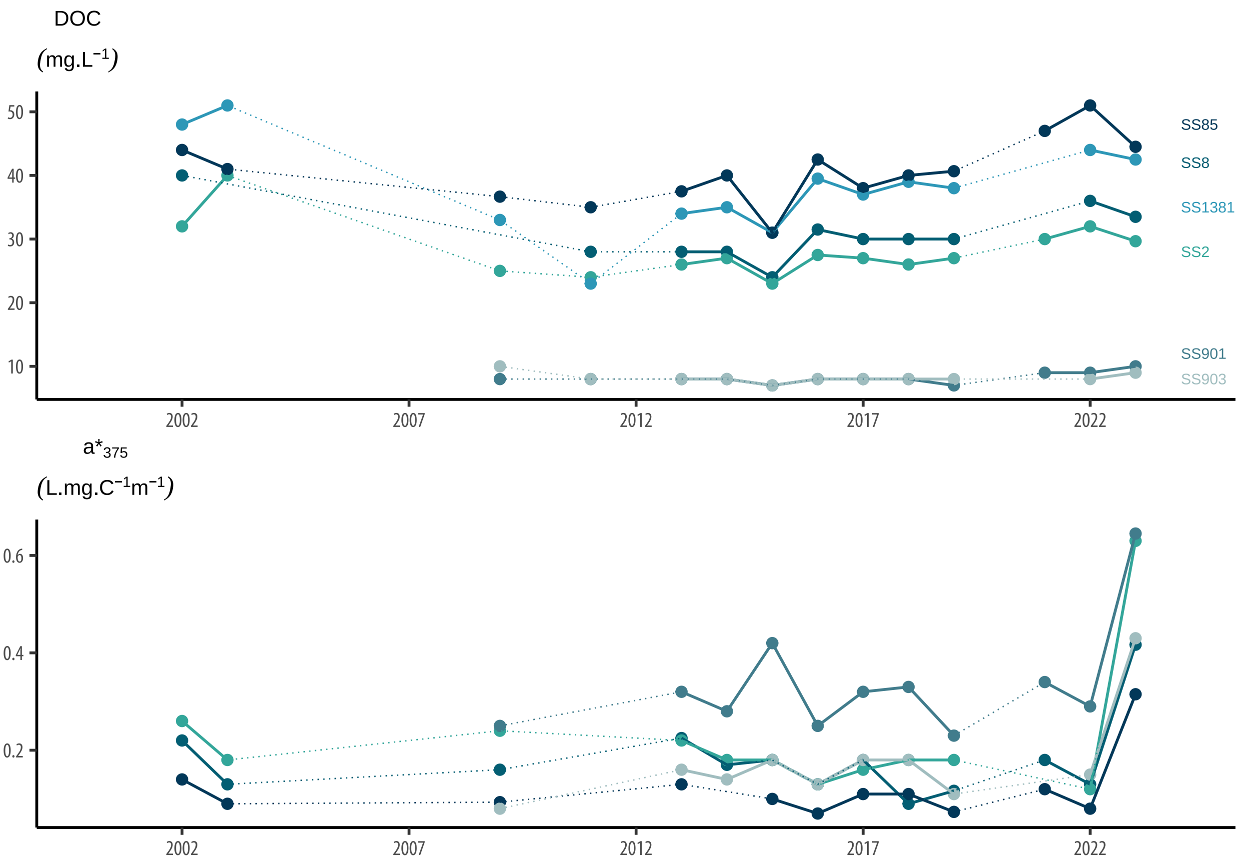


```
(a375_old <- expand_grid(
 year = seq(from = 2000, to = 2023),
 lake = c('SS2', 'SS8', 'SS85', 'SS901', 'SS903')) %>%
  left_join(old,
      by = c('year', 'lake')) %>%
 arrange(date) %>%
 group_by(year, lake) %>%
 summarise(a375spec = mean(a375spec, na.rm = T)) %>%
 ggplot(aes(x = year, y = a375spec)) +
 geom_point(aes(color = lake)) +
 geom_line(aes(color = lake)) +
 geom_line(data = old %>%
       group_by(year, lake) %>%
```

```
              summarise(a375spec = mean(a375spec, na.rm = T)) %>%
              filter(!is.na(a375spec) & lake %in% c('SS2', 'SS8', 'SS85', 'SS901', 'SS903')),
            aes(color = lake), linetype = 'dotted', linewidth = 0.25) +
    scale_color_manual(values = c('#035E73', '#33A69A', '#023859', '#417C8C', '#A0BDBF')) +
  scale_x_continuous(limits = c(2000,2024), breaks = seq(from = 2002, to = 2024, by = 5)) +
  theme(legend.position = 'none',
        plot.subtitle = element_text(size = 8)) +
  labs(x = NULL, y = NULL, subtitle = expression(atop("a*"["375"], (L.mg.C^{-1}*m^{-1}))))
```



```
# ggsave("output/plots/Fig2_lines_with_old_375.pdf", width = 15, height = 10, units = "cm")

doc_old / a375_old
```



```
# difference ---------------------------------------------------------------

env_comb %>%
  mutate(pre_post =
           case_when(
             year(date) == 2023 & month(date) == 8 ~ 'aug_23',
             year(date) == 2023 & month(date) == 7 ~ 'jul_23',
             T ~ 'pre'),
         pre_post = factor(pre_post, levels = c('pre', 'jul_23', 'aug_23'), labels = c('pre', 'jul_23',
  group_by(lake, variable, pre_post) %>%
  summarise(mean = mean(value, na.rm = T)) %>%
  pivot_wider(names_from = pre_post,
              values_from = mean) %>%
  summarise(
    diff_jul = ((jul_23-pre)/pre)*100,
    diff_aug = ((aug_23-pre)/pre)*100) %>%
  group_by(variable) %>%
  summarise(mean_jul = mean(diff_jul, na.rm = T),
            med_jul = median(diff_jul, na.rm = T),
            mean_aug = mean(diff_aug, na.rm = T),
            med_aug = median(diff_aug, na.rm = T))
```

```
## # A tibble: 9 x 5
##   variable  mean_jul med_jul mean_aug med_aug
##   <chr>        <dbl>   <dbl>    <dbl>   <dbl>
## 1 Cu           208.    219.     261.     186.
## 2 DOC           21.5    13.2     36.1     28.4
```

```
## 3 Fe          1008.    788.    929.     874.
## 4 Mn          1603.   1315.   1410.     815.
## 5 NH4          123.     73.2   191.     123.
## 6 NO3          200.    133.     -9.35   -50
## 7 TP            65.7    48.7    80.2     76.4
## 8 a375spec     131.    132.    302.     237.
## 9 turbidity    NaN      NA     -13.1    -16.1
```

```r
# param t-test

# average
env_comb %>%
  filter(variable != 'turbidity') %>%
  group_by(variable, lake, pre_post) %>%
  summarise(mean = mean(value, na.rm = T)) %>%
  nest(data = c(mean, lake, pre_post)) %>%
  mutate(
    t_test = purrr::map(.x = data, .f = \(x){
      t.test(x$mean ~ x$pre_post, paired = T)  %>%
        broom::tidy()
    })) %>%
  dplyr::select(-data)  %>%
  tidyr::unnest(cols = t_test)
```

```
## # A tibble: 8 x 9
## # Groups:   variable [8]
##   variable estimate statistic   p.value parameter conf.low conf.high method
##   <chr>       <dbl>     <dbl>     <dbl>     <dbl>    <dbl>     <dbl> <chr>
## 1 Cu          -2.70     -3.59 0.00588           9    -4.41    -0.998 Paired t-t~
## 2 DOC         -5.13     -3.18 0.0112            9    -8.78    -1.48  Paired t-t~
## 3 Fe       -115.        -3.23 0.0103            9 -195.      -34.5   Paired t-t~
## 4 Mn          -8.22     -4.89 0.000860          9  -12.0      -4.42  Paired t-t~
## 5 NH4        -14.3      -3.72 0.00480           9  -23.0      -5.60  Paired t-t~
## 6 NO3         -1.97     -2.10 0.0652            9    -4.09     0.152 Paired t-t~
## 7 TP          -4.09     -6.35 0.000133          9    -5.54    -2.63  Paired t-t~
## 8 a375spec    -0.433    -7.08 0.0000581         9    -0.571   -0.295 Paired t-t~
## # i 1 more variable: alternative <chr>
```

```r
# just july
env_comb %>%
  mutate(pre_post =
           case_when(
             year(date) == 2023 & month(date) == 8 ~ 'aug_23',
             year(date) == 2023 & month(date) == 7 ~ 'jul_23',
             T ~ 'pre')) %>%
  filter(pre_post != 'aug_23' & variable != 'turbidity') %>%
  group_by(variable, lake, pre_post) %>%
  summarise(mean = mean(value, na.rm = T)) %>%
  nest(data = c(mean, lake, pre_post)) %>%
  mutate(
    t_test = purrr::map(.x = data, .f = \(x){
      t.test(x$mean ~ x$pre_post, paired = T)  %>%
        broom::tidy()
    })) %>%
  dplyr::select(-data)  %>%
```

```r
  tidyr::unnest(cols = t_test)
```

```
## # A tibble: 8 x 9
## # Groups:   variable [8]
##   variable estimate statistic  p.value parameter conf.low conf.high method
##   <chr>       <dbl>     <dbl>    <dbl>     <dbl>    <dbl>     <dbl> <chr> 
## 1 Cu          2.29       4.94 0.000805         9    1.24       3.34 Paired t-te~
## 2 DOC         4.03       3.13 0.0120           9    1.12       6.94 Paired t-te~
## 3 Fe        119.         2.90 0.0175           9   26.3      212.   Paired t-te~
## 4 Mn          9.34       3.27 0.00972          9    2.87      15.8  Paired t-te~
## 5 NH4        12.0        2.56 0.0308           9    1.38      22.5  Paired t-te~
## 6 NO3         4.12       2.34 0.0441           9    0.136      8.10 Paired t-te~
## 7 TP          3.65       4.23 0.00221          9    1.70       5.60 Paired t-te~
## 8 a375spec    0.306      5.08 0.000664         9    0.169      0.442 Paired t-te~
## # i 1 more variable: alternative <chr>
```

```r
# just august
env_comb %>%
  mutate(pre_post =
           case_when(
             year(date) == 2023 & month(date) == 8 ~ 'aug_23',
             year(date) == 2023 & month(date) == 7 ~ 'jul_23',
             T ~ 'pre')) %>%
  filter(pre_post != 'jul_23' & variable != 'turbidity') %>%
  group_by(variable, lake, pre_post) %>%
  summarise(mean = mean(value, na.rm = T)) %>%
  nest(data = c(mean, lake, pre_post)) %>%
  mutate(
    t_test = purrr::map(.x = data, .f = \(x){
      t.test(x$mean ~ x$pre_post, paired = T)  %>%
        broom::tidy()
    })) %>%
  dplyr::select(-data)  %>%
  tidyr::unnest(cols = t_test)
```

```
## # A tibble: 8 x 9
## # Groups:   variable [8]
##   variable estimate statistic   p.value parameter conf.low conf.high method
##   <chr>       <dbl>     <dbl>     <dbl>     <dbl>    <dbl>     <dbl> <chr> 
## 1 Cu          3.11      2.82  0.0201            9    0.614      5.61 Paired t-t~
## 2 DOC         6.38      3.21  0.0106            9    1.89      10.9  Paired t-t~
## 3 Fe        111.        3.57  0.00602           9   40.6      181.   Paired t-t~
## 4 Mn          7.10      6.75  0.0000837         9    4.72       9.48 Paired t-t~
## 5 NH4        16.7       3.42  0.00765           9    5.63      27.7  Paired t-t~
## 6 NO3        -0.182    -0.324 0.753             9   -1.45       1.09 Paired t-t~
## 7 TP          4.52      7.76  0.0000281         9    3.20       5.84 Paired t-t~
## 8 a375spec    0.581     8.72  0.0000111         9    0.430      0.731 Paired t-t~
## # i 1 more variable: alternative <chr>
```

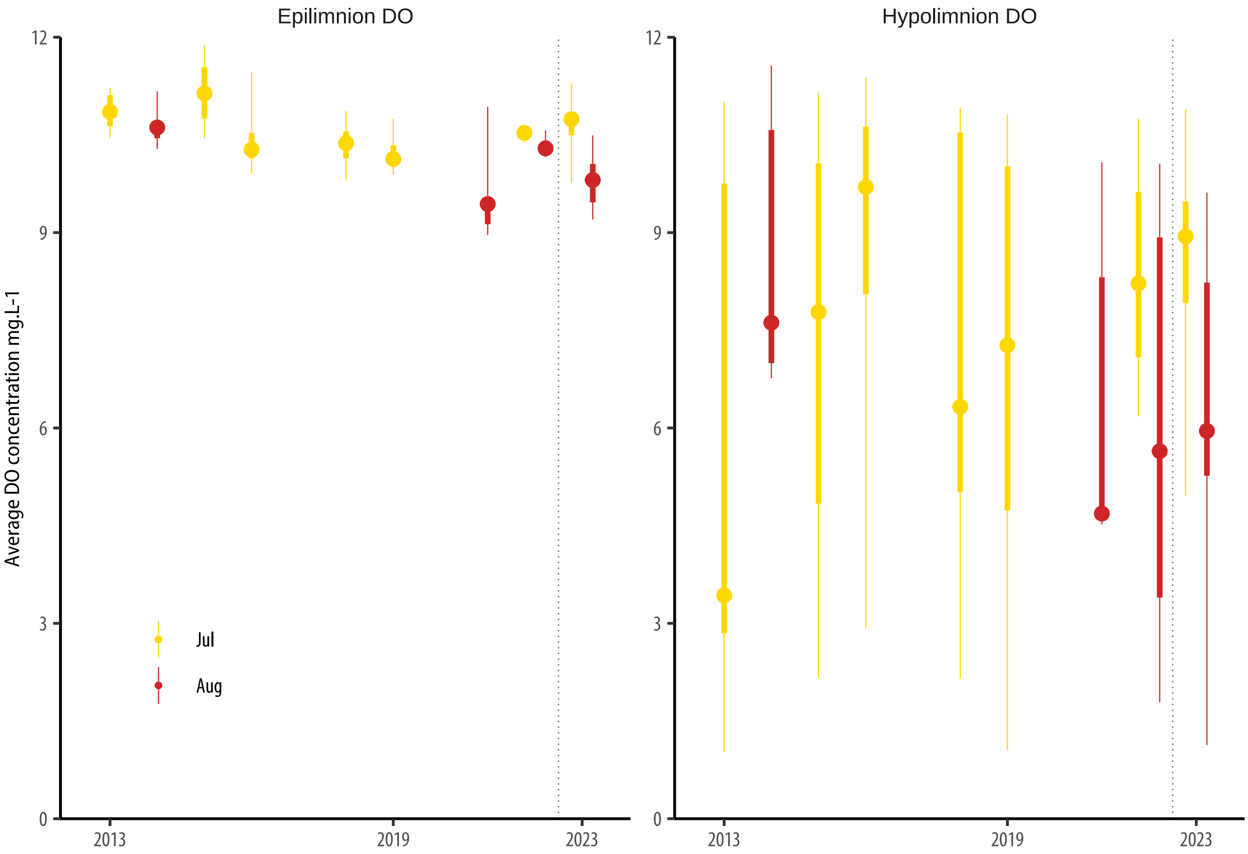
```r
# just turbidity
env_comb %>%
  mutate(pre_post =
           case_when(
             year(date) == 2023 ~ 'post',
             T ~ 'pre')) %>%
```

```r
  filter(variable == 'turbidity' & lake != 'SS909') %>%
  group_by(variable, lake, pre_post) %>%
  summarise(mean = mean(value, na.rm = T)) %>%
  nest(data = c(mean, lake, pre_post)) %>%
  mutate(
    t_test = purrr::map(.x = data, .f = \(x){
      t.test(x$mean ~ x$pre_post, paired = T)  %>%
        broom::tidy()
    })) %>%
  dplyr::select(-data)  %>%
  tidyr::unnest(cols = t_test)
```

```
## # A tibble: 1 x 9
## # Groups:   variable [1]
##   variable  estimate statistic p.value parameter conf.low conf.high method
##   <chr>        <dbl>     <dbl>   <dbl>     <dbl>    <dbl>     <dbl> <chr>
## 1 turbidity   -0.276     -1.56   0.156         8   -0.683     0.131 Paired t-te~
## # i 1 more variable: alternative <chr>
```

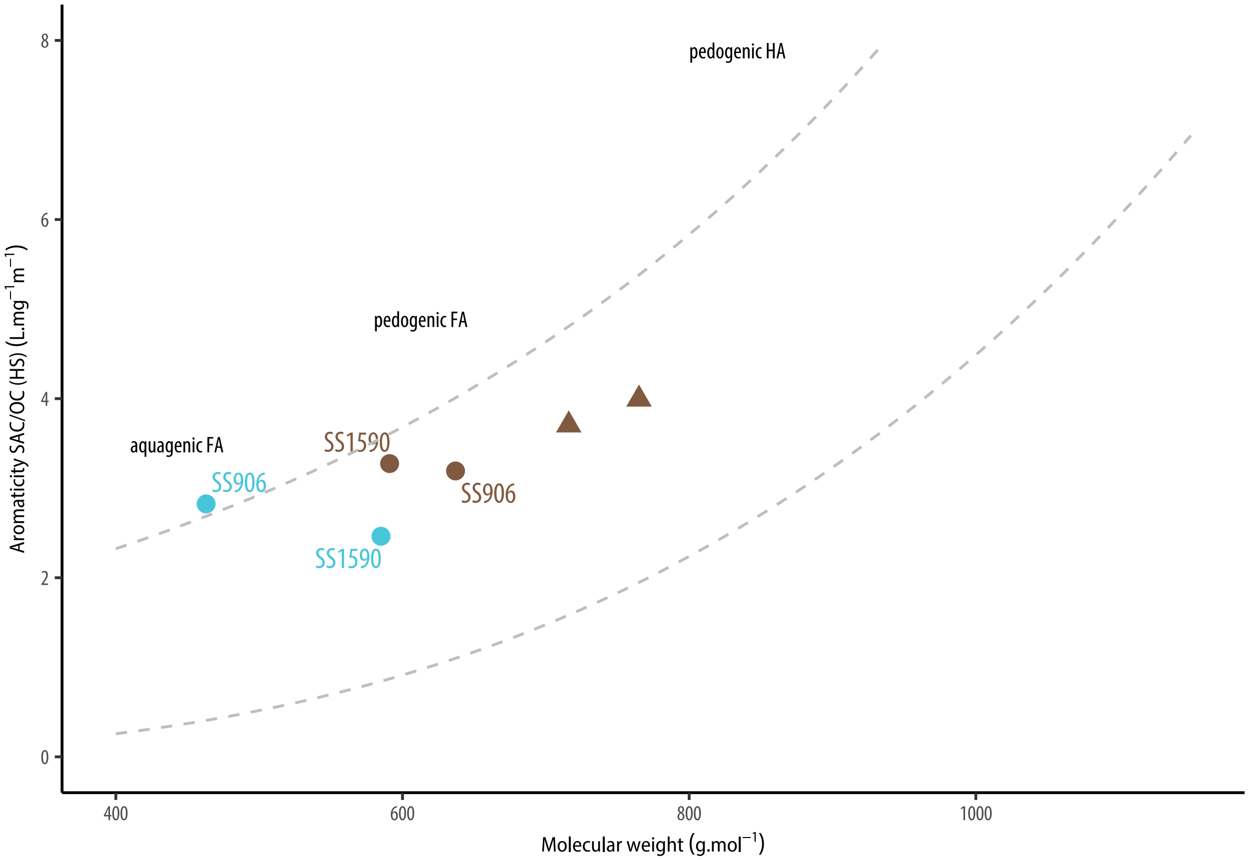
```r
# OXYGEN ---------------------------------------------------------------


do_water <- read_csv('combined_files/do_water_2013_2023.csv')


names_vars <- as_labeller(
  c(avg_DO_epi = 'Epilimnion DO',
    avg_DO_hypo = 'Hypolimnion DO'
  ))


(do <- do_water %>%
  mutate(year = year(date),
         month = lubridate::month(date, label = T),
         jul = yday(date)) %>%
  filter(month %in% c('Jul', 'Aug'),
         year > 2010 &
         lake %in% c('SS8', 'SS85', 'SS901', 'SS903', 'SS906', 'SS909', 'SS2',
                     'SS18', 'SS1590', 'SS1381')) %>%
  # epi_DO:hypo_DO,
    pivot_longer(cols = avg_DO_epi:avg_DO_hypo,
                 values_to = 'value',
                 names_to = 'variable') %>%
  mutate(pre_post =
           case_when(year < 2023 ~ 'pre',
                     year == 2023 ~ 'post'),
         pre_post = factor(pre_post,
                           levels = c('pre', 'post'))) %>%
  ggplot(aes(x = year, y = value, color = month)) +
  stat_pointinterval(point_interval = 'median_qi', .width = c(0.5, 0.9), position = position_dodge(widt
  scale_color_manual(NULL, values = c("#FFD700", "#CD2626")) +
  geom_vline(aes(xintercept = 2022.5), linetype = 3, linewidth = 0.25, color = 'grey45') +
  scale_y_continuous(limits = c(0,12),
                     expand = expansion(mult = c(0,0))) +
```

```
  scale_x_continuous(breaks = c(2013, 2019, 2023)) +
  labs(x = NULL, y = 'Average DO concentration mg.L-1') +
  facet_wrap(~variable, ncol = 5, labeller = names_vars, scales = 'free_y') +
  theme(strip.placement = 'outside',
        strip.text = element_text(size = 8),
        strip.background = element_blank(),
        legend.position = c(0.1, 0.2),
        axis.title.x = element_text(size = 10)))
```



```
# DOM ---------------------------------------------------------------


# humification pathway ---------------------------------------------------
# devtools::install_github("liamgilbey/ggwaffle")

library(ggwaffle)

dom <- read_csv('combined_files/DOM_comparison.csv') %>%
  mutate(pre_post =
           case_when(year < 2023 ~ 'pre',
                     year == 2023 ~ 'post'),
         pre_post = factor(pre_post,
                           levels = c('pre', 'post'))) %>%
  filter(layer %in% c('epi', 'watershed'))

(D <- dom %>%
  ggplot(
```

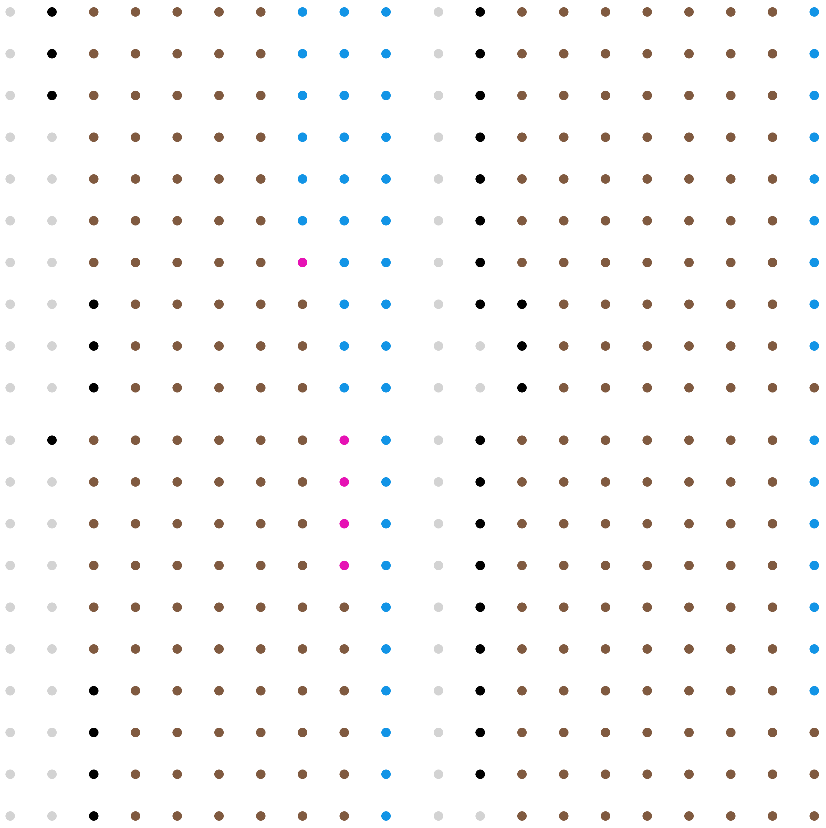
```
  aes(x = mol_weights, y = aromaticity)) +
# geom_point(aes(color = pre_post, shape = layer), alpha = 0.5) +
geom_point(
  data = dom %>% filter(lake %in% c('SS1590', 'SS906')),
  aes(color = pre_post, shape = layer),
  size = 3) +
  geom_point(
    data = dom %>% filter(layer == 'watershed'),
    aes(color = pre_post, shape = layer),
    size = 3) +
ggrepel::geom_text_repel(
  data = dom %>% filter(lake %in% c('SS1590', 'SS906')),
    aes(label = lake, color = pre_post),
    family = "Myriad Pro Condensed") +
annotate('text', x = 410, y = 3.4, vjust = 0, hjust = 0, size = 3,
           family = "Myriad Pro Condensed",
           label = 'aquagenic FA') +
annotate('text', x = 580, y = 4.8, vjust = 0, hjust = 0, size = 3,
           family = "Myriad Pro Condensed",
           label = 'pedogenic FA') +
  annotate('text', x = 800, y = 7.8, vjust = 0, hjust = 0, size = 3,
           family = "Myriad Pro Condensed",
           label = 'pedogenic HA') +
scale_x_continuous(limits = c(400, 1150)) +
scale_y_continuous(limits = c(0, 8)) +
scale_color_manual(NULL, values = c(pre = '#48C5D9', post = "#805A40")) +
stat_function(fun = function(x) 0.9263*exp(0.0023*x), colour = "gray", linetype = 2) +
stat_function(fun = function(x) 2e-09*x^(3.117), colour = "gray", linetype = 2) +
labs(x = expression("Molecular weight"~(g.mol^{-1})),
     y = expression("Aromaticity SAC/OC (HS)"~(L.mg^{-1}*m^{-1}))) +
theme(legend.position = 'none'))
```



```
dom_comp <-
  dom %>%
  filter(lake %in% c('SS1590', 'SS906')) %>%
  pivot_longer(cols = c('BP', 'HS', 'BB', 'LMWN', 'LMWA'),
               names_to = 'comp',
               values_to = 'value') %>%
  dplyr::select(lake, pre_post, comp, value) %>%
  group_by(lake, pre_post) %>%
  mutate(sum = sum(value),
         prop = round((value/sum)*100, 1))

# waffles
pre_906 <- dom_comp %>%
  filter(lake == 'SS906' & pre_post == 'pre') %>%
  mutate(prop = round(prop, 0)) %>%
  uncount(prop) %>%
  waffle_iron(aes_d(group = comp),
              rows = 10) %>%
  ggplot(aes(x = x, y = y, colour = group)) +
  geom_waffle(tile_shape = 'circle', size = 1) +
  coord_fixed() +
  scale_colour_manual(values = c('BP' = "black",
                                 'HS' = "#805A40",
                                 'BB' = "lightgrey",
                                 'LMWN' = '#1294E6',
                                 'LMWA' = '#E612B4')) +
```

```
  labs(y = NULL, x = NULL) +
  theme(legend.position = 'none',
        axis.line = element_blank(),
        axis.text.x = element_blank(),
        axis.text.y = element_blank(),
        axis.ticks = element_blank(),
        axis.title = element_blank())

post_906 <- dom_comp %>%
  filter(lake == 'SS906' & pre_post == 'post') %>%
  mutate(prop = round(prop, 0)) %>%
  uncount(prop) %>%
  waffle_iron(aes_d(group = comp),
              rows = 10) %>%
  ggplot(aes(x = x, y = y, colour = group)) +
  geom_waffle(tile_shape = 'circle', size = 1) +
  scale_colour_manual(values = c('BP' = "black",
                                 'HS' = "#805A40",
                                 'BB' = "lightgrey",
                                 'LMWN' = '#1294E6')) +
  coord_fixed() +
  labs(y = NULL, x = NULL) +
  theme(legend.position = 'none',
        axis.line = element_blank(),
        axis.text.x = element_blank(),
        axis.text.y = element_blank(),
        axis.ticks = element_blank(),
        axis.title = element_blank())

pre_15 <- dom_comp %>%
  filter(lake == 'SS1590' & pre_post == 'pre') %>%
  mutate(prop = round(prop, 0),
         prop = if_else(comp == 'LMWN',
                        10,
                        prop)) %>%
  uncount(prop) %>%
  waffle_iron(aes_d(group = comp),
              rows = 10) %>%
  ggplot(aes(x = x, y = y, colour = group)) +
  geom_waffle(tile_shape = 'circle', size = 1) +
  coord_fixed() +
  scale_colour_manual(values = c('BP' = "black",
                                 'HS' = "#805A40",
                                 'BB' = "lightgrey",
                                 'LMWN' = '#1294E6',
                                 'LMWA' = '#E612B4')) +
  labs(y = NULL, x = NULL) +
  theme(legend.position = 'none',
        axis.line = element_blank(),
        axis.text.x = element_blank(),
        axis.text.y = element_blank(),
        axis.ticks = element_blank(),
        axis.title = element_blank())
```

```r
post_15 <- dom_comp %>%
  filter(lake == 'SS1590' & pre_post == 'post') %>%
  mutate(prop = round(prop, 0)) %>%
  uncount(prop) %>%
  waffle_iron(aes_d(group = comp),
              rows = 10) %>%
  ggplot(aes(x = x, y = y, colour = group)) +
  geom_waffle(tile_shape = 'circle', size = 1) +
  scale_colour_manual(values = c('BP' = "black",
                                 'HS' = "#805A40",
                                 'BB' = "lightgrey",
                                 'LMWN' = '#1294E6')) +
  coord_fixed() +
  labs(y = NULL, x = NULL) +
  theme(legend.position = 'none',
        axis.line = element_blank(),
        axis.text.x = element_blank(),
        axis.text.y = element_blank(),
        axis.ticks = element_blank(),
        axis.title = element_blank())



(pre_906 + post_906) / (pre_15 + post_15)
```



```r
# subset of pigments in sediments -----------------------------------------
library(tidypaleo)
```

```
sed <-
  read_csv('combined_files/pigment_sediments_20240124.csv') %>%
  separate_wider_delim(Depth, ' - ', names = c('depth_start', 'depth_end')) %>%
  rename(lake = Lake) %>%
  mutate(
    Chlorophyll_a_plus = rowSums(select(., c('Pheophytin_a','Chlorophyllide a','Chlorophyll_a','Pheopho
    Carotenoids_sum = rowSums(select(., c('Fucoxanthin', 'Alloxanthin', 'Canthaxanthin'))),
    Chl_Phaeo_ratio = if_else(Pheophytin_a == 0,
                              Chlorophyll_a,
                              Chlorophyll_a/Pheophytin_a),
    depth_end = as.numeric(depth_end),
    depth_start = as.numeric(depth_start),
    mid_depth = (depth_start+depth_end)/2, .keep = 'unused') %>%
  select(lake, mid_depth, Chlorophyll_a_plus, Carotenoids_sum, Chl_Phaeo_ratio, Fucoxanthin, Alloxanthi
  pivot_longer(cols = Chlorophyll_a_plus:Canthaxanthin,
               names_to = 'pig',
               values_to = 'conc')

# average

average_sed_direction <-
  sed %>%
  pivot_wider(names_from = 'mid_depth',
              values_from = 'conc',
  ) %>%
  rowwise() %>%
  mutate(
    downcore_avg = mean(c(`0.375`, `0.625`, `0.875`)),
    downcore_sd = sd(c(`0.375`, `0.625`, `0.875`)),
    downcore_se = downcore_sd/sqrt(3),
    trend =
      case_when(
        `0.125` >= downcore_avg + downcore_se  ~ 'increase',
        `0.125` <= downcore_avg - downcore_se ~ 'decrease',
        T ~ 'no change' # no change just means 0 or data not available
      )) %>%
 # filter(trend != 'no change') %>%
  group_by(pig, lake) %>%
  pivot_longer(cols = 3:6,
               names_to = 'mid_depth',
               values_to = 'conc') %>%
  # scale all concentrations - grouped by pigment and lake
  mutate(mid_depth = as.numeric(mid_depth),
         conc_scaled = scale(conc)) %>%
  filter(downcore_avg != 0) %>%
  group_by(trend, pig, mid_depth) %>%
  # average across trends
  summarise(mean_conc = mean(conc_scaled, na.rm = T),
            sd_conc = sd(conc_scaled, na.rm = T),
            n = n())
```

```
order_fact <- c("Chlorophyll_a_plus", "Carotenoids_sum", "Chl_Phaeo_ratio", "Fucoxanthin", "Canthaxanth
                "Alloxanthin", "Myxoxanthophyll"  )


average_sed_direction %>%
  mutate(pig = factor(pig, levels = order_fact),
         trend = factor(trend, levels = c('no change', 'decrease', 'increase')))%>%
  ggplot(aes(x = mean_conc, y = mid_depth)) +
  # geom_point(aes(color = trend)) +
  geom_errorbarh(aes(xmin = mean_conc - sd_conc, xmax = mean_conc + sd_conc, color = trend),
                 height = 0.02) +
  geom_lineh(aes(group = trend, color = trend, linewidth = n), lineend = 'round') +
  geom_vline(aes(xintercept = 0), alpha = 0.2) +
  scale_y_reverse() +
  scale_x_continuous(breaks = c(-1,-0,1)) +
  scale_color_manual(values = c('grey45', "#BCEE68", "#228B22")) +
  facet_grid(~pig, scales = 'free_x') +
  labs(x = "z-scored pigment concentration (nmol pigment.g sediment)",
       y = 'Depth (cm)') +
  theme(
    strip.text = element_text(size = 6)
  )
```