

task7_3

2025-09-30

```
# Load required packages -----
library(ggplot2)    # plotting
library(dplyr)      # data manipulation
library(tidyr)      # reshape/summary helpers
library(stringr)    # title wrapping for small figures

# Bring the built-in CO2 dataset into a tibble -----
co2 <- as_tibble(CO2)                                # CO2 has columns: Plant, Type, Treatment,
conc, uptake

# Make sure 'conc' is numeric (some R versions may keep factor; this is safe) ----
co2 <- co2 %>% mutate(conc = as.numeric(as.character(conc)))

# Quick peek at structure and a few rows -----
str(co2)                                              # print structure to the knit log
```

```
## tibble [84 × 5] (S3: tbl_df/tbl/data.frame)
## $ Plant      : Ord.factor w/ 12 levels "Qn1"<"Qn2"<"Qn3"<...: 1 1 1 1 1 1 1 2 2 2 ...
## $ Type       : Factor w/ 2 levels "Quebec","Mississippi": 1 1 1 1 1 1 1 1 1 1 ...
## $ Treatment: Factor w/ 2 levels "nonchilled","chilled": 1 1 1 1 1 1 1 1 1 1 ...
## $ conc       : num [1:84] 95 175 250 350 500 675 1000 95 175 250 ...
## $ uptake     : num [1:84] 16 30.4 34.8 37.2 35.3 39.2 39.7 13.6 27.3 37.1 ...
## - attr(*, "formula")=Class 'formula' language uptake ~ conc | Plant
## .. ..- attr(*, ".Environment")=<environment: R_EmptyEnv>
## - attr(*, "outer")=Class 'formula' language ~Treatment * Type
## .. ..- attr(*, ".Environment")=<environment: R_EmptyEnv>
## - attr(*, "labels")=List of 2
## ..$ x: chr "Ambient carbon dioxide concentration"
## ..$ y: chr "CO2 uptake rate"
## - attr(*, "units")=List of 2
## ..$ x: chr "(uL/L)"
## ..$ y: chr "(umol/m^2 s)"
```

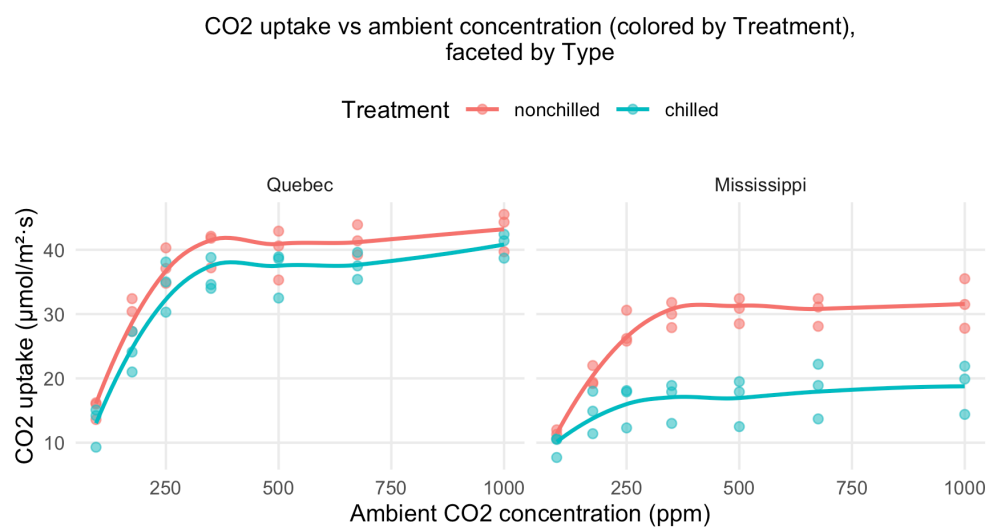
```
print(head(co2, 6))                                # show first six rows on the page
```

```
## # A tibble: 6 × 5
##   Plant Type   Treatment    conc uptake
##   <ord> <fct>   <fct>      <dbl> <dbl>
## 1 Qn1   Quebec nonchilled    95     16
## 2 Qn1   Quebec nonchilled   175    30.4
## 3 Qn1   Quebec nonchilled   250    34.8
## 4 Qn1   Quebec nonchilled   350    37.2
## 5 Qn1   Quebec nonchilled   500    35.3
## 6 Qn1   Quebec nonchilled   675    39.2
```

1) Uptake vs CO₂ concentration — by Treatment,

faceted by Type

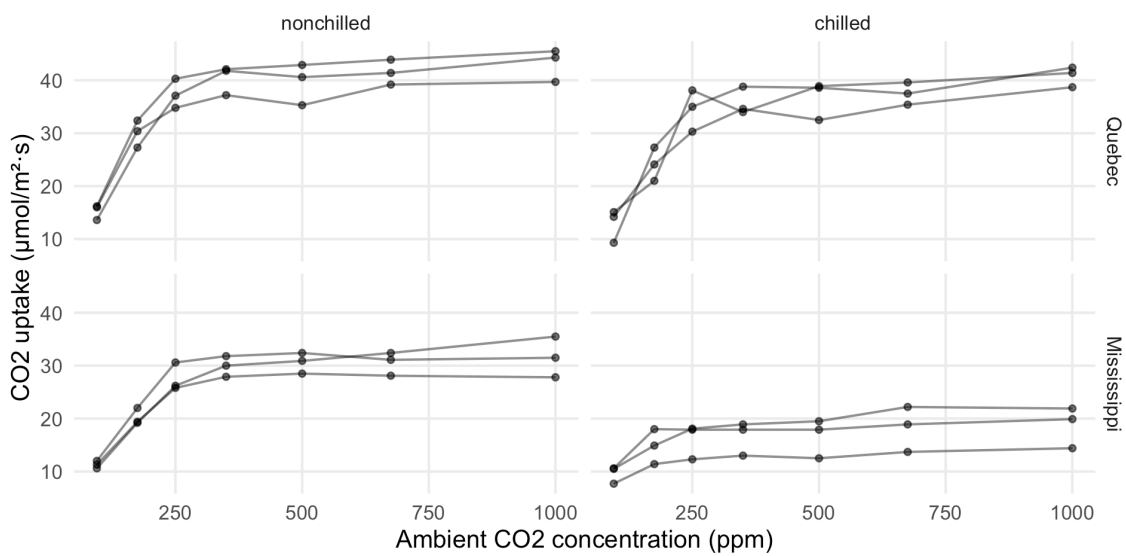
```
# Scatter with smoothed trendlines (loess) to see shape and treatment effect -----
ggplot(co2, aes(x = conc, y = uptake, color = Treatment)) +
  geom_point(alpha = 0.6, size = 1.6) + # raw points, slightly transparent
  geom_smooth(se = FALSE, method = "loess", span = 0.8, linewidth = 0.8) + # smooth trendline
  facet_wrap(~ Type, ncol = 2) + # one panel per plant origin (Quebec/Mississippi)
  labs(title = str_wrap("CO2 uptake vs ambient concentration (colored by Treatment), faceted by Type", 60),
        x = "Ambient CO2 concentration (ppm)", y = "CO2 uptake (μmol/m²·s)", color = "Treatment") +
  theme_minimal(base_size = 10) +
  theme(plot.title = element_text(size = 10, hjust = 0.5),
        legend.position = "top",
        panel.grid.minor = element_blank())
```



2) Plant-level profiles — small multiples (each line is a Plant)

```
# Show per-plant response curves to inspect variability within each group -----
ggplot(co2, aes(x = conc, y = uptake, group = Plant)) +
  geom_line(alpha = 0.5) + # one line per Plant across concentrations
  geom_point(alpha = 0.6, size = 1) +
  facet_grid(Type ~ Treatment) + # grid: rows=Type, cols=Treatment
  labs(title = "Per-plant uptake profiles across CO2 concentrations",
        x = "Ambient CO2 concentration (ppm)", y = "CO2 uptake (μmol/m²·s)") +
  theme_minimal(base_size = 10) +
  theme(plot.title = element_text(size = 10, hjust = 0.5),
        panel.grid.minor = element_blank())
```

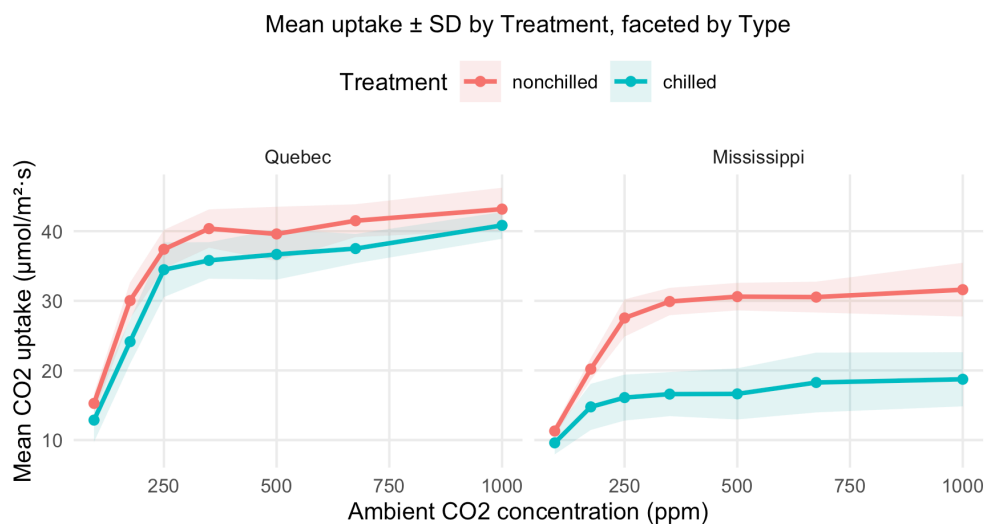
Per-plant uptake profiles across CO2 concentrations



3) Group summaries — mean \pm SD across plants at each concentration

```
# Compute summary stats per (Type, Treatment, conc) -----
sum_df <- co2 %>%
  group_by(Type, Treatment, conc) %>%
  summarise(mean_uptake = mean(uptake, na.rm = TRUE),
            sd_uptake   = sd(uptake,   na.rm = TRUE),
            .groups = "drop")

# Plot mean curves with SD ribbons to compare groups -----
ggplot(sum_df, aes(x = conc, y = mean_uptake, color = Treatment, fill = Treatment)) +
  geom_ribbon(aes(ymin = mean_uptake - sd_uptake, ymax = mean_uptake + sd_uptake),
            alpha = 0.15, linewidth = 0) +      # variability band
  geom_line(linewidth = 0.9) +                  # mean curve
  geom_point(size = 1.6) +                      # show means at each concentration
  facet_wrap(~ Type, ncol = 2) +
  labs(title = "Mean uptake  $\pm$  SD by Treatment, faceted by Type",
       x = "Ambient CO2 concentration (ppm)", y = "Mean CO2 uptake (μmol/m²·s)",
       color = "Treatment", fill = "Treatment") +
  theme_minimal(base_size = 10) +
  theme(plot.title = element_text(size = 10, hjust = 0.5),
        legend.position = "top",
        panel.grid.minor = element_blank())
```



4) Distribution view — uptake by Type & Treatment

```
# Compare overall distribution of uptake across Type × Treatment -----
ggplot(co2, aes(x = interaction(Type, Treatment), y = uptake, fill = Treatment)) +
  geom_violin(trim = FALSE, alpha = 0.5) + # shape of distribution
  geom_boxplot(width = 0.2, outlier.shape = 21, outlier.size = 1.3) + # robust summary
  stat_summary(fun = mean, geom = "point", shape = 23, size = 2.2, fill = "white") + # mean marker
  labs(title = "Distribution of CO2 uptake by Type × Treatment",
       x = "Group (Type × Treatment)", y = "CO2 uptake (μmol/m²·s)", fill = "Treatment") +
  theme_minimal(base_size = 10) +
  theme(plot.title = element_text(size = 10, hjust = 0.5),
       axis.text.x = element_text(angle = 15, hjust = 1),
       legend.position = "none")
```

