WK8

2025-08-21

```r
library(tidyverse)
```

```
## -- Attaching core tidyverse packages ------------------------ tidyverse 2.0.0 --
## v dplyr     1.1.4     v readr     2.1.5
## v forcats   1.0.0     v stringr   1.5.1
## v ggplot2   3.5.2     v tibble    3.2.1
## v lubridate 1.9.4     v tidyr     1.3.1
## v purrr     1.0.4
## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become error
```

```r
library(readxl)
library(lubridate)
library(janitor)
```

```
##
## Attaching package: 'janitor'
##
## The following objects are masked from 'package:stats':
##
##     chisq.test, fisher.test
```

```r
library(purrr)
library(readr)
library(ggthemes)
library(ggeffects)
library(lme4)
```

```
## Loading required package: Matrix
##
## Attaching package: 'Matrix'
##
## The following objects are masked from 'package:tidyr':
##
##     expand, pack, unpack
```

```r
library(dplyr)
library(ggplot2)
#install.packages("emmeans")
library(emmeans)
```

```
## Welcome to emmeans.
## Caution: You lose important information if you filter this package's results.
## See '? untidy'
```

```r
#install.packages("broom.mixed")
library(broom.mixed)
library(viridis)
```

```
## Loading required package: viridisLite
```

```r
library(nlme)
```

```
##
## Attaching package: 'nlme'
##
## The following object is masked from 'package:lme4':
##
##     lmList
##
## The following object is masked from 'package:dplyr':
##
##     collapse
```

```r
library(mgcv)
```

```
## This is mgcv 1.9-3. For overview type 'help("mgcv-package")'.
```

```r
#setwd("C:/Users/Tobyz/Desktop/S.tort-light-growth/Data")
```

import plant data

```r
plant <- read.csv("Data/WL2-2023_Size_Combined.csv") %>%
  clean_names() %>%
  mutate(survey_date = as.Date(survey_date, format = "%m/%d/%Y"))
summary(plant)
```

```
##   survey_date            block              genotype            pop_mf
##  Min.   :2023-07-03   Length:17336       Length:17336       Length:17336
##  1st Qu.:2023-08-02   Class :character   Class :character   Class :character
##  Median :2023-08-30   Mode  :character   Mode  :character   Mode  :character
##  Mean   :2023-08-28
##  3rd Qu.:2023-09-20
##  Max.   :2023-10-20
##
##   parent_pop              mf              rep           height_cm
##  Length:17336       Min.   : 1.000   Min.   : 1.000   Min.   : 0.100
##  Class :character   1st Qu.: 2.000   1st Qu.: 4.000   1st Qu.: 1.700
##  Mode  :character   Median : 5.000   Median : 8.000   Median : 3.100
##                     Mean   : 4.584   Mean   : 7.932   Mean   : 4.491
##                     3rd Qu.: 6.000   3rd Qu.:11.000   3rd Qu.: 5.700
##                      Max.   :14.000   Max.   :27.000   Max.   :39.400
##                                                        NA’s   :8762
##   long_leaf_cm   survey_notes
##  Min.   :0.100   Length:17336
##  1st Qu.:1.600   Class :character
##  Median :2.500   Mode  :character
##  Mean   :2.599
##  3rd Qu.:3.500
##  Max.   :9.000
##  NA’s   :9350
```

consolidate light measurement to a weekly measurement

```
#import light data
light_raw <- read_csv("Data/IntBioHalfHourTable_clean.txt")
```

```
## Rows: 4063 Columns: 139
## -- Column specification --------------------------------------------------------
## Delimiter: ","
## dbl  (138): RECORD, BattV_Max, PTemp_C_Max, SlrW_Avg, SlrW_Max, SlrW_Min, Sl...
## dttm   (1): TIMESTAMP
##
## i Use ‘spec()‘ to retrieve the full column specification for this data.
## i Specify the column types or set ‘show_col_types = FALSE‘ to quiet this message.
```

```
#weekly measurement
weekly_light <- light_raw %>%
  mutate(
    timestamp = ymd_hms(TIMESTAMP),
    SlrW_Avg = as.numeric(SlrW_Avg),  # turn into number format
    week = floor_date(timestamp, "week")
  ) %>%
  group_by(week) %>%
  summarise(
    weekly_avg_SlrW = mean(SlrW_Avg, na.rm = TRUE),
    .groups = "drop"
  )
```

```
## Warning: There was 1 warning in ‘mutate()‘.
## i In argument: ‘timestamp = ymd_hms(TIMESTAMP)‘.
## Caused by warning:
## !  84 failed to parse.
```

```
# result
print(weekly_light)
```

```
## # A tibble: 14 x 2
##    week                weekly_avg_SlrW
##    <dttm>                        <dbl>
##  1 2023-07-30 00:00:00            280.
##  2 2023-08-06 00:00:00            277.
##  3 2023-08-13 00:00:00            186.
##  4 2023-08-20 00:00:00         184.
##  5 2023-08-27 00:00:00         200.
##  6 2023-09-03 00:00:00         211.
##  7 2023-09-10 00:00:00         204.
##  8 2023-09-17 00:00:00         189.
##  9 2023-09-24 00:00:00         159.
## 10 2023-10-01 00:00:00         138.
## 11 2023-10-08 00:00:00         133.
## 12 2023-10-15 00:00:00         135.
## 13 2023-10-22 00:00:00         116.
## 14 NA                           -0.616
```

Investigate or filter out plants that show negative growth #Q: How could we deal with bad observations? #Solution: find out tolerance value and then filter out observance data lager than the tolerance value #Figure A: Histogram showing the frequency of decreases in plant height between consecutive surveys. Most negative growth values are close to zero, likely reflecting measurement noise, while a small number of extreme decreases (<=–5 cm) suggest errors and were removed from subsequent analyses.

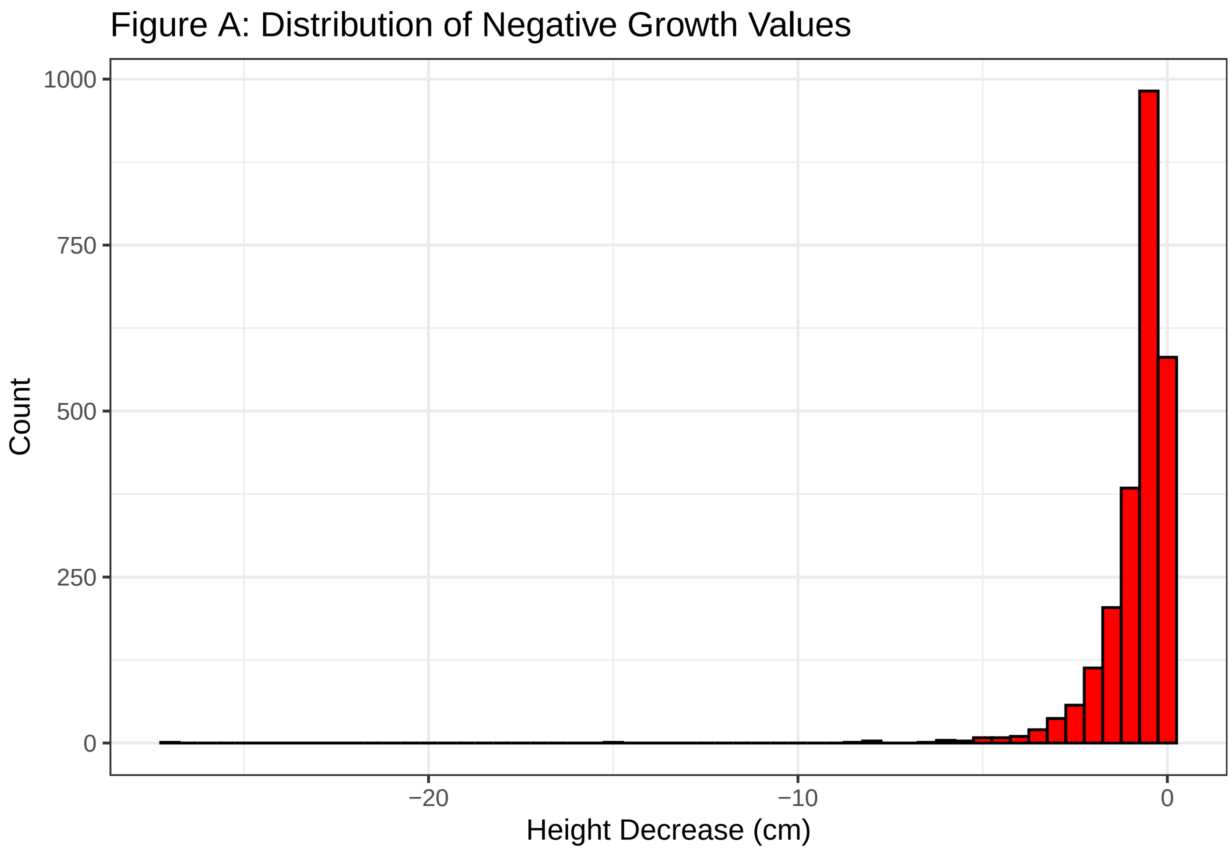
```r
#PID
plant_growth <- plant %>%
  unite("PID", genotype:rep, sep = "_", remove = FALSE) %>%
  mutate(survey_date = as.Date(survey_date))

#find out plants with negative growth
plant_growth %>%
  arrange(PID, survey_date) %>%  # arrange in time sequence
  group_by(PID) %>%
  mutate(growth = height_cm - lag(height_cm)) %>%  # find out the diff btw nearby dates
  summarise(has_negative_growth = any(growth < 0, na.rm = TRUE)) %>%
  filter(has_negative_growth) -> neg_growth_plants
neg_growth_plants
```

```
## # A tibble: 826 x 2
##    PID                  has_negative_growth
##    <chr>                <lgl>
##  1 BH_1_10_BH_1_BH_1_10 TRUE
##  2 BH_1_12_BH_1_BH_1_12 TRUE
##  3 BH_1_13_BH_1_BH_1_13 TRUE
##  4 BH_1_1_BH_1_BH_1_1   TRUE
##  5 BH_1_4_BH_1_BH_1_4   TRUE
##  6 BH_1_7_BH_1_BH_1_7   TRUE
##  7 BH_2_10_BH_2_BH_2_10 TRUE
##  8 BH_2_11_BH_2_BH_2_11 TRUE
##  9 BH_2_12_BH_2_BH_2_12 TRUE
## 10 BH_2_13_BH_2_BH_2_13 TRUE
## # i 816 more rows
```

```r
#find out tolerance value
neg_growth_values <- plant_growth %>%
  arrange(PID, survey_date) %>%
  group_by(PID) %>%
  mutate(growth = height_cm - lag(height_cm)) %>%
  ungroup() %>%
  filter(growth < 0)

ggplot(neg_growth_values, aes(x = growth)) +
  geom_histogram(binwidth = 0.5, fill = "red", color = "black") +
  labs(
    title = "Figure A: Distribution of Negative Growth Values",
    x = "Height Decrease (cm)",
    y = "Count"
  ) +
  theme_bw()
```



```r
#filter out plants with negative growth < -5
plant_growth_cleaned <- plant_growth

repeat {
  plant_growth_cleaned <- plant_growth_cleaned %>%
    arrange(PID, survey_date) %>%
    group_by(PID) %>%
    mutate(growth = height_cm - lag(height_cm)) %>%
    filter(is.na(growth) | growth >= -5) %>%
    select(-growth) %>%
    ungroup()

  check <- plant_growth_cleaned %>%
    arrange(PID, survey_date) %>%
    group_by(PID) %>%
    mutate(growth = height_cm - lag(height_cm)) %>%
    filter(growth < -5)

  if (nrow(check) == 0) break
}
```

Measure Growth via Daily Growth Rate

```
#define daily growth rate
plant_growth_daily <- plant_growth_cleaned %>%
  arrange(PID, survey_date) %>%
  group_by(PID) %>%
  mutate(
    prev_height = lag(height_cm),
    prev_date = lag(survey_date),
    days_elapsed = as.numeric(survey_date - prev_date),
    daily_growth = (height_cm - prev_height) / days_elapsed
  ) %>%
  ungroup()
```

Correlate Growth with Solar Radiation #Q: How does plant growth correlate with solar radiation? #Test: Find correlation value and plot correlation #Figure B: Scatter plot showing the relationship between weekly average solar radiation (SlrW, W/m^2) and daily growth rate (cm/day). Each point represents an observation, and the red line indicates the fitted linear regression.

```
#Align plant growth data to week
plant_weekly <- plant_growth_daily %>%
  filter(!is.na(daily_growth), days_elapsed > 0) %>%
  mutate(week = floor_date(survey_date, "week"))

#Adds `weekly_avg_SlrW` to plant data
plant_with_light <- plant_weekly %>%
  left_join(weekly_light, by = "week")

#Calculate correlation
cor_result <- cor(
  plant_with_light$daily_growth,
  plant_with_light$weekly_avg_SlrW,
use = "complete.obs"
)

print(cor_result)
```

```
## [1] 0.1299395
```

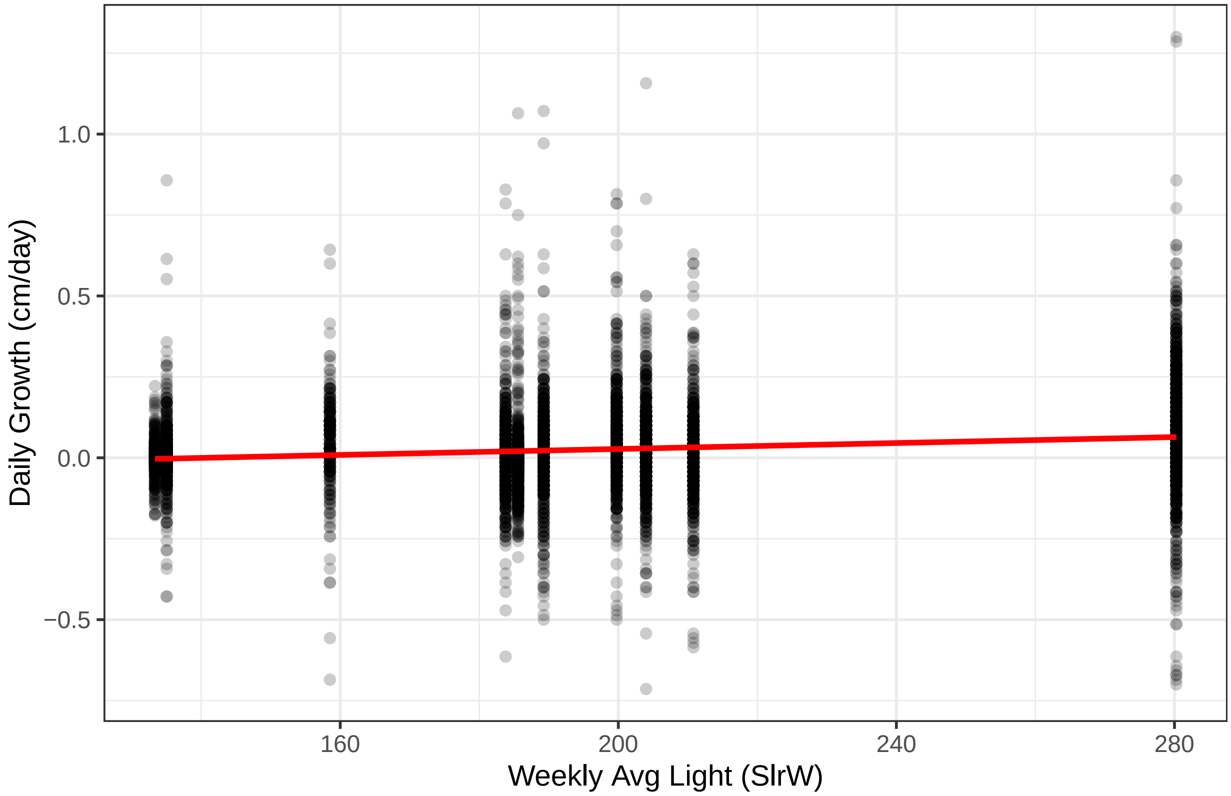
```
#Plot correlation
ggplot(plant_with_light, aes(x = weekly_avg_SlrW, y = daily_growth)) +
  geom_point(alpha = 0.2) +
  geom_smooth(method = "lm", color = "red") +
  labs(title = "Figure B: Correlation between Light and Growth", x = "Weekly Avg Light (SlrW)", y = "Da
  theme_bw()
```

```
## `geom_smooth()` using formula = 'y ~ x'

## Warning: Removed 1069 rows containing non-finite outside the scale range
## (`stat_smooth()`).

## Warning: Removed 1069 rows containing missing values or values outside the scale range
## (`geom_point()`).
```

Figure B: Correlation between Light and Growth



Process data

```
#Standardization
plant_with_light$weekly_avg_SlrW2 <- scale(plant_with_light$weekly_avg_SlrW, center = TRUE, scale = TRU
mean_light <- mean(plant_with_light$weekly_avg_SlrW, na.rm = TRUE)
sd_light   <- sd(plant_with_light$weekly_avg_SlrW, na.rm = TRUE)

#Change Data type
plant_with_light <- plant_with_light %>%
  mutate(
    parent_pop = factor(parent_pop),
    PID        = factor(PID),
    block      = factor(block)
  )
```

use mixed-effect model to fit relationship between plant growth and light radiation with population as random effect #Q: Does weekly solar radiation positively affect daily growth rate across all populations? #Test: Fit a mixed-effect model with population as a random slope.

```
growth_light.lmer <- lmer(
  daily_growth ~ weekly_avg_SlrW2 +
    (1 + weekly_avg_SlrW2 | parent_pop),
  data = plant_with_light, REML = TRUE
)
summary(growth_light.lmer)
```

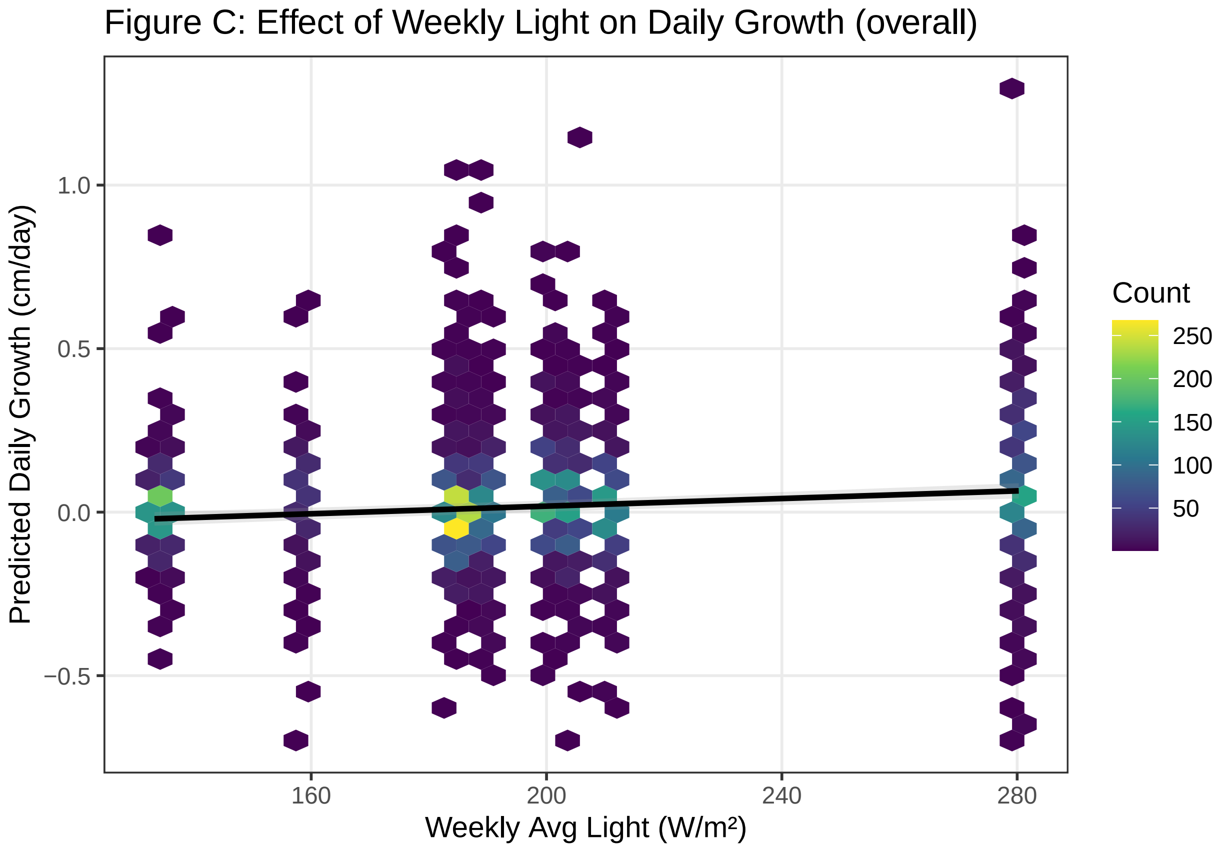
```
## Linear mixed model fit by REML ['lmerMod']
## Formula: daily_growth ~ weekly_avg_SlrW2 + (1 + weekly_avg_SlrW2 | parent_pop)
##    Data: plant_with_light
##
## REML criterion at convergence: -6464.1
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -6.2096 -0.4715  0.0094  0.4415  8.3380
##
## Random effects:
##  Groups     Name             Variance  Std.Dev. Corr
##  parent_pop (Intercept)      0.0015837 0.0398
##             weekly_avg_SlrW2 0.0002495 0.0158   0.03
##  Residual                    0.0191023 0.1382
## Number of obs: 5870, groups:  parent_pop, 22
##
## Fixed effects:
##                  Estimate Std. Error t value
## (Intercept)      0.017235   0.008784   1.962
## weekly_avg_SlrW2 0.024127   0.003973   6.073
##
## Correlation of Fixed Effects:
##             (Intr)
## wkly_vg_SW2 0.020
```

overall effect of solar radiation on plant daily growth #Figure C: Relationship between weekly average solar radiation and predicted daily growth rate (cm/day), aggregated across all populations. Each hexagon represents the density of observations. The black line shows the fitted regression slope .

```
#Unscaling
pred_all <- ggpredict(growth_light.lmer, terms = "weekly_avg_SlrW2") %>%
  as.data.frame() %>%
  mutate(light_orig = x * sd_light + mean_light)

#Plot
p_overall <- ggplot() +
  geom_hex(data = plant_with_light,
           aes(x = weekly_avg_SlrW, y = daily_growth), bins = 35) +
  scale_fill_viridis_c(name = "Count") +
  geom_ribbon(data = pred_all,
              aes(x = light_orig, ymin = conf.low, ymax = conf.high),
              alpha = .22, fill = "grey60") +
  geom_line(data = pred_all,
            aes(x = light_orig, y = predicted), linewidth = 1) +
  labs(title = "Figure C: Effect of Weekly Light on Daily Growth (overall)",
       x = "Weekly Avg Light (W/m²)",
       y = "Predicted Daily Growth (cm/day)") +
  theme_bw() +
  theme(panel.grid.minor = element_blank())
p_overall
```

```
## Warning: Removed 1069 rows containing non-finite outside the scale range
## (`stat_binhex()`).
```



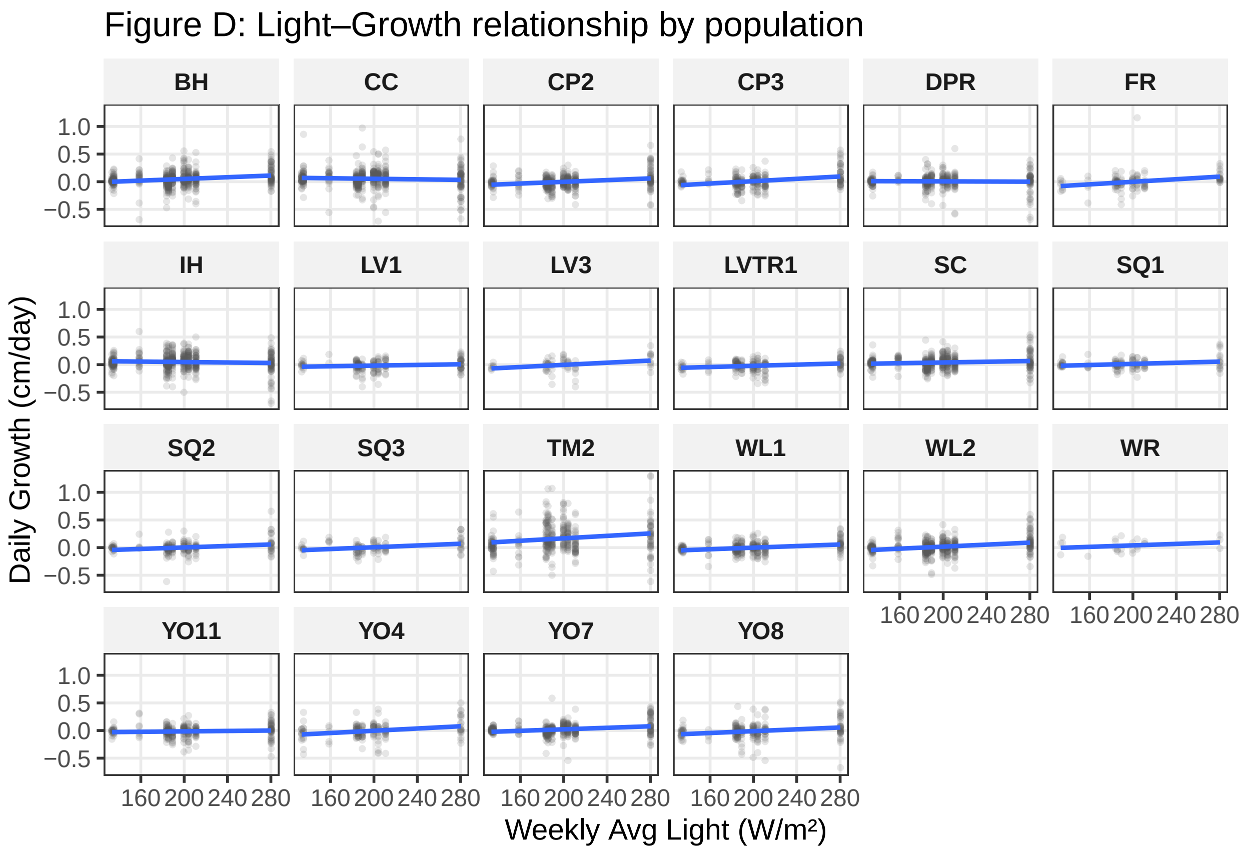
Effect of solar radiation on plant daily growth by population #Q: Do different populations vary in their growth response to weekly solar radiation? #Test: For visualization, scatter plots with fitted regression lines were drawn separately for each population. #Figure D: Light–growth relationship by population. #Scatter plots show daily growth rate (cm/day) against weekly average solar radiation (W/m^2) for 22 populations. Each panel corresponds to one population, with the blue line indicating the fitted linear trend.

```
p_facet <- ggplot(plant_with_light,
                  aes(weekly_avg_SlrW, daily_growth)) +
  facet_wrap(~ parent_pop, ncol = 6) +
  geom_point(alpha = .15, size = .6, color = "grey35") +
  geom_smooth(method = "lm", se = FALSE, linewidth = .8) +
  labs(title = "Figure D: Light-Growth relationship by population",
       x = "Weekly Avg Light (W/m²)",
       y = "Daily Growth (cm/day)") +
  theme_bw() +
  theme(strip.background = element_rect(fill = "grey95", color = NA),
        strip.text = element_text(face = "bold"),
        panel.grid.minor = element_blank())
p_facet
```

```
## ‘geom_smooth()‘ using formula = ’y ~ x’
```

```
## Warning: Removed 1069 rows containing non-finite outside the scale range
## (‘stat_smooth()‘).
```

```
## Warning: Removed 1069 rows containing missing values or values outside the scale range
## (‘geom_point()‘).
```



Find slope of plant growth and solar radiation for each population #Q: Which populations show significantly positive or negligible slopes in the light–growth relationship? #Method: Extract slopes and 95% confidence intervals for each population from the mixed-effects model #Figure E. Population-specific slopes with 95% confidence intervals. #Forest plot showing estimated slopes of daily growth rate against weekly average solar radiation for 22 populations. Points represent population-specific slopes (cm/day per W/m²) and horizontal lines show 95% CIs. Several populations (e.g., TM2, CP3, FR, WL2, YO4) exhibit significantly positive slopes with CIs entirely above zero, indicating stronger growth response to light. Others (e.g., CC, IH, DPR) have slopes not significantly different from zero, suggesting little or no detectable response to light.

```
#slope and standard deviation of fixed effects
b_fix  <- fixef(growth_light.lmer)["weekly_avg_SlrW2"]
V_fix  <- vcov(growth_light.lmer)["weekly_avg_SlrW2","weekly_avg_SlrW2"]
```

```
#slope and standard deviation of random effects
re <- ranef(growth_light.lmer, condVar = TRUE)
re_pop <- re$parent_pop
postVar <- attr(re$parent_pop, "postVar")
sl_col <- which(colnames(re_pop) == "weekly_avg_SlrW2")

#create the tibble of slopes for each population
pop_slope <- tibble(
  parent_pop   = rownames(re_pop),
  rand_slope   = re_pop[ , "weekly_avg_SlrW2"],
  rand_var     = sapply(seq_len(dim(postVar)[3]), function(i) postVar[sl_col, sl_col, i])
) %>%
  mutate(
    slope_SD   = b_fix + rand_slope,
    se_SD      = sqrt(V_fix + rand_var),
    lower_SD   = slope_SD - 1.96*se_SD,
    upper_SD   = slope_SD + 1.96*se_SD
  )

sd_light <- sd(plant_with_light$weekly_avg_SlrW, na.rm = TRUE)

pop_slope <- pop_slope %>%
  mutate(
    slope_per_Wm2 = slope_SD / sd_light,
    lower_per_Wm2 = lower_SD / sd_light,
    upper_per_Wm2 = upper_SD / sd_light
  )%>%
  select(parent_pop, slope_per_Wm2, lower_per_Wm2, upper_per_Wm2)
pop_slope
```

```
## # A tibble: 22 x 4
##    parent_pop slope_per_Wm2 lower_per_Wm2 upper_per_Wm2
##    <chr>              <dbl>         <dbl>         <dbl>
##  1 BH             0.000742      0.000409       0.00108
##  2 CC            -0.000128     -0.000461       0.000205
##  3 CP2            0.000744      0.000376       0.00111
##  4 CP3            0.000949      0.000542       0.00136
##  5 DPR            0.0000489    -0.000316       0.000413
##  6 FR             0.000918      0.000402       0.00143
##  7 IH            -0.000105     -0.000433       0.000223
##  8 LV1            0.000373     -0.0000792      0.000825
##  9 LV3            0.000755      0.000174       0.00134
## 10 LVTR1          0.000540      0.0000734      0.00101
## # i 12 more rows
```

```
write.csv(pop_slope, "population_slopes.csv", row.names = FALSE)

#plot
ggplot(pop_slope, aes(x = reorder(parent_pop, slope_per_Wm2), y = slope_per_Wm2)) +
  geom_hline(yintercept = 0, linetype = 2) +
  geom_pointrange(aes(ymin = lower_per_Wm2, ymax = upper_per_Wm2), linewidth = .6) +
  coord_flip() +
  labs(title = "Figure E: Population-specific slopes with 95% CI",
       x = "Population", y = "Slope (cm/day per W/m²)") +
  theme_bw()
```

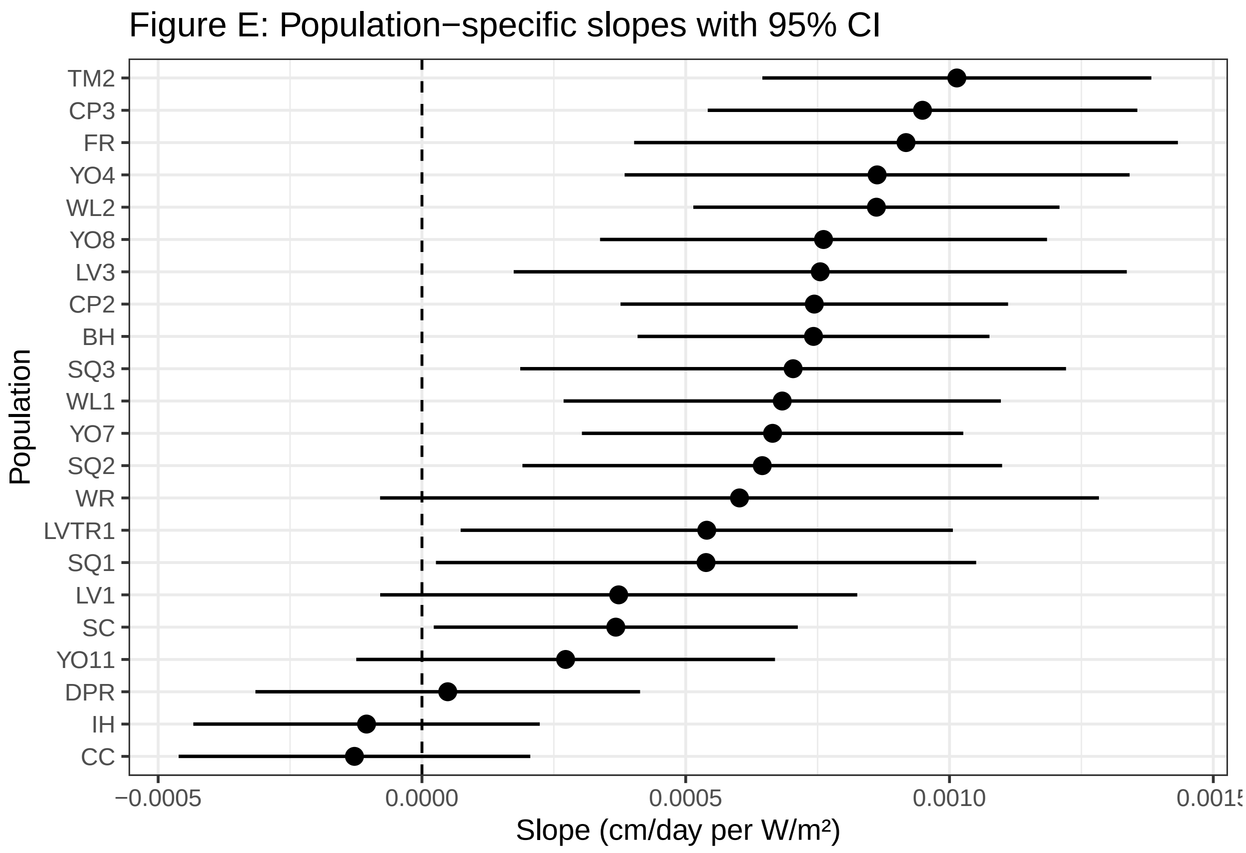


Figure E: Population−specific slopes with 95% CI
Population
TM2
CP3
FR
YO4
WL2
YO8
LV3
CP2
BH
SQ3
WL1
YO7
SQ2
WR
LVTR1
SQ1
LV1
SC
YO11
DPR
IH
CC
Slope (cm/day per W/m²)