

Supplementary Figures

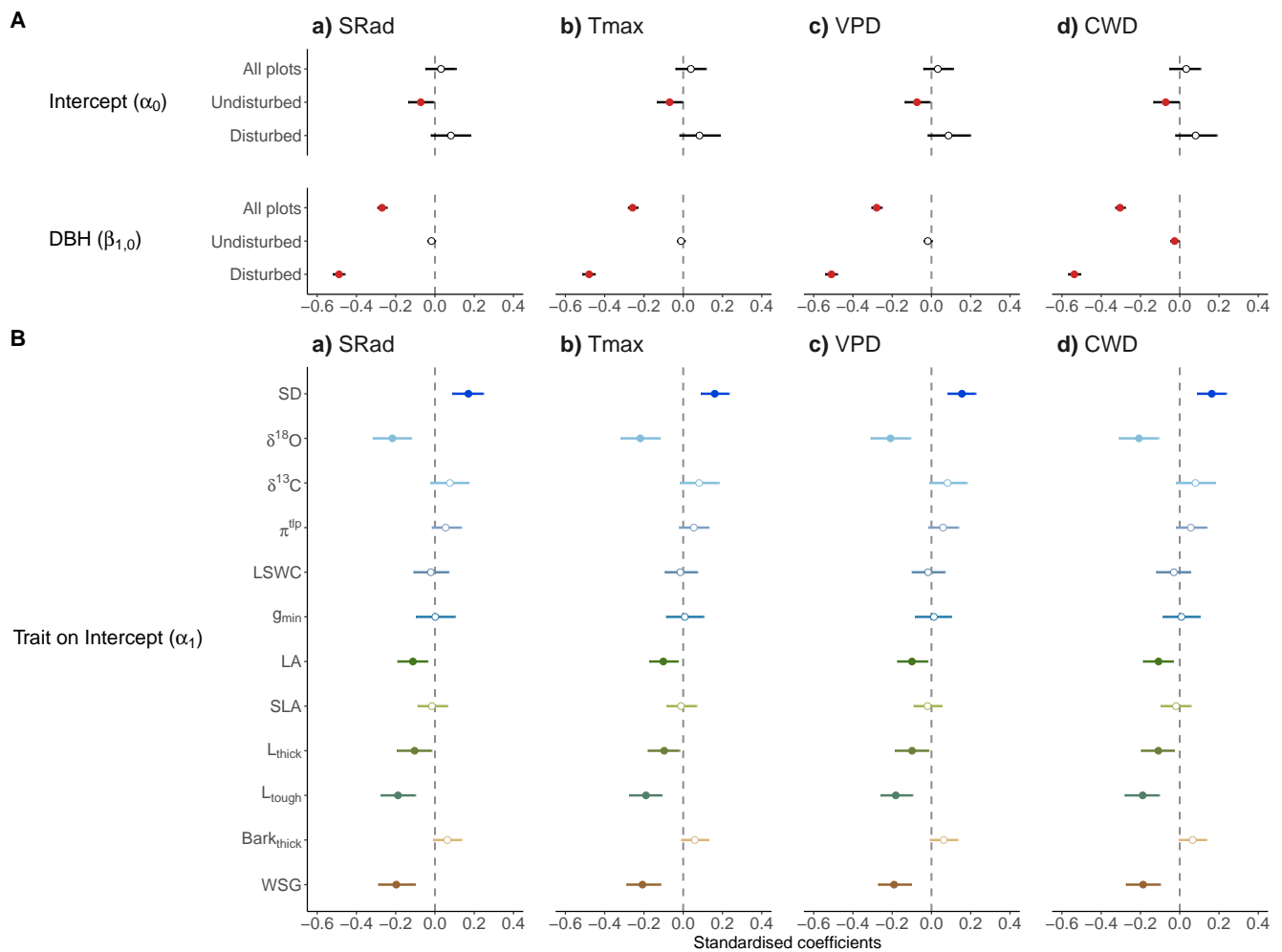


Figure S1. Standardised coefficients from a) SRad, b) Tmax, c) VPD and d) CWD models of A) M1: Community level intrinsic AGR (α_0) and community level AGR response to tree size (DBH, $\beta_{3,0}$ on tree growth for all 15 plots combined, the 6 undisturbed plots and the 9 disturbed plots respectively and B) M2: trait effects on intrinsic AGR α_1 (see: eqn 5) for each of the eleven trait models: stomata density (SD), leaf oxygen ($\delta^{18}\text{O}$) and carbon $\delta^{13}\text{C}$ isotope composition, water potential at turgor loss point (π_{tlp}), leaf saturated water content (LSWC), minimum conductance (g_{min}), leaf area (LA), specific leaf area (SLA), leaf thickness (L_{thick}), leaf toughness (L_{tough}), bark thickness (BarkThick) and wood specific gravity (WSG). Circles show posterior medians of standardised coefficients, and lines indicate 90% highest posterior density intervals [HPDI]. Filled circles indicate negative (red) and positive (blue) effects (i.e. slope coefficient 90%-HPDI not encompassing zero) and empty circles indicate no effects. Positive parameter estimates values indicate faster growth with increasing values of the model covariate, while negative parameter estimates values indicate slower growth with increasing model covariate. For details on parameter estimates see: Table S2 and Table S5.

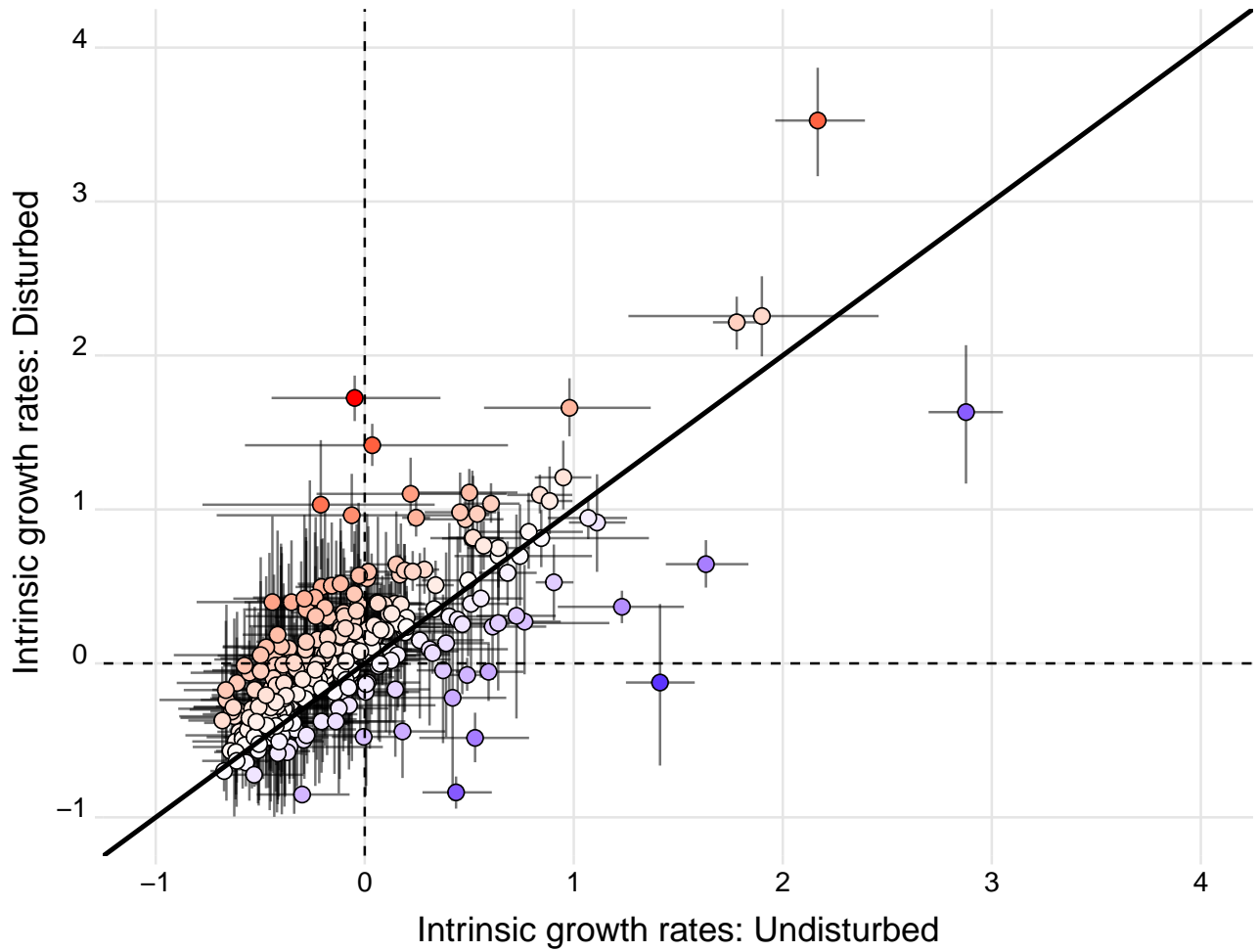


Figure S2. M1: Standardised coefficients of species-level intrinsic growth rate (i.e. species median posterior of species-specific intercept, α_s) in undisturbed (x-axis) and disturbed (y-axis) plots using the outputs from the CWD models. Vertical and horizontal lines represent coefficients 90%-highest posterior density intervals (HPDI). Species on the 1:1 line show the same intrinsic growth rates on both plot types. Species above the 1:1 (in red shade) have faster growth on disturbed than undisturbed plots, while species below the 1:1 line (in blue shade) have slower growth on disturbed than undisturbed plots.

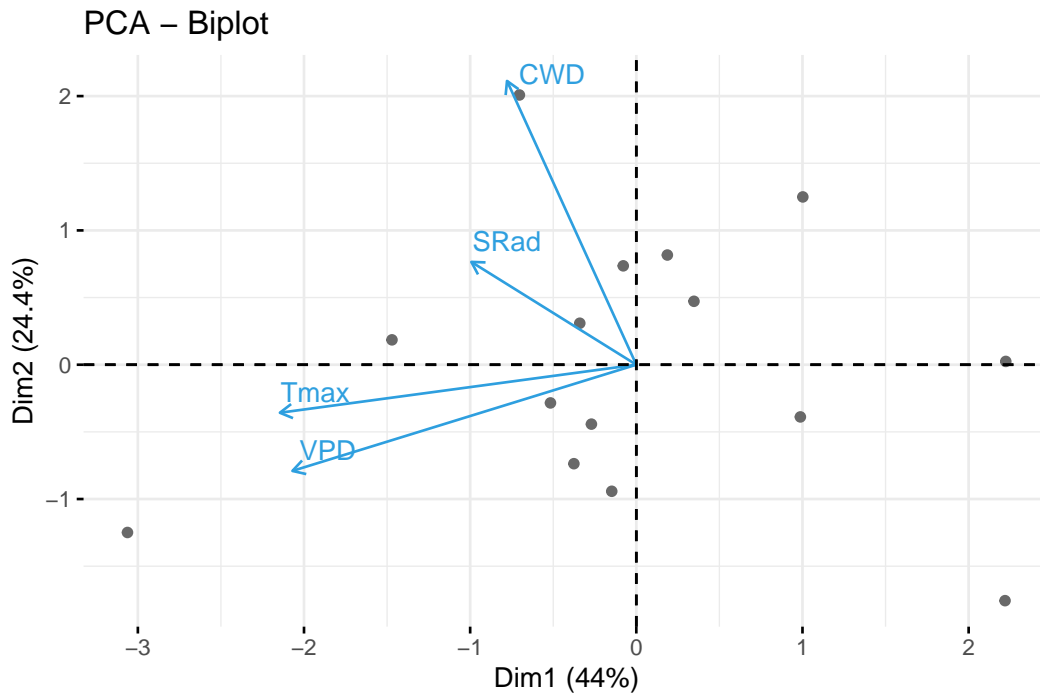


Figure **S3**. Bi-plot of principal component analysis (PCA) performed on climate anomalies (arrows) in solar radiation (SRad), maximum temperature (Tmax), vapour pressure deficit (VPD) and climatic water deficit (CWD). Dots represent individual census intervals. The first axis explains 44% of the variance and is driven by anomalies in Tmax and VPD. The second axis explains 24.4% of the variance and is driven by anomalies in CWD.

Supplementary Methods

Supplementary Methods S1: Corrections of tree inventory data

To ensure the quality of the inventory data set and the completeness of the neighbourhood several corrections have been made. We estimated tree circumference from the individual's growth trajectory for census years in which trees were not observed or falsely classified as dead, thus reappearing as alive at a later census. We further corrected abnormal annual increases (> 5 cm) and absolute decreases (< 2 cm) in DBH by aligning the concerned DBH measurement to the overall growth trajectory of the individual (Page et al. 2021). Abnormal decreases in DBH were likely due to changes in point of measurements. While trees with abnormal growth were excluded from the focal individuals they were kept as neighbours with their corrected diameter. We further discarded individuals with DBH estimations due to buttresses, human induced damage (e.g. through logging treatments) as well as missing or uncertain botanical determination from the focal tree data set.

Supplementary Methods S2: R code for M1- and M2-models

Required packages

```
library(tidyverse)
library(rstan)
library(cmdstanr)
library(brms)
library(Rcpp)
library(parallel)
library(StanHeaders)
library(dplyr)
```

M1 models

Data preparation for M1 models

Here the data preparation code at the example of all plots combined (i.e. not subsetting for undisturbed or disturbed forest plots). Note that processing of inventory data and growth calculations took place before hand.

```
growth <- read.csv("~/MyPath/My_growth_data_file.csv")
```

We excluded palms from focal tree data.

```
growth <- growth %>%
  filter(Family != "Arecaceae")
```

We only kept species with more than 100 growth observations.

```
My_species <- growth %>%
  group_by(spName) %>%
  summarize(N_years = n_distinct(CensusYear_t),
            N_observation = n()) %>%
  arrange(N_observation) %>%
  filter(N_observation >= 100)
growth <- growth %>%
  filter(spName %in% My_species$spName)
```

Required columns and information for M1 models.

PlotType contains the information whether the plot belongs to undisturbed or disturbed plots. idTree is a unique identifier for tree individuals at Paracou.

```
growth <- growth %>%
  select(AGR_dbh_year, DBH, NCI, SRad, Tmax, VPD,
         CWD, spName, PlotType, Plot, idTree) %>%
  mutate(AGR_dbh_year = as.numeric(AGR_dbh_year),
         DBH = as.numeric(DBH),
         NCI = as.numeric(NCI),
         SRad = as.numeric(SRad),
         Tmax = as.numeric(Tmax),
         VPD = as.numeric(VPD),
         CWD = as.numeric(CWD),
         spName = as.character(spName),
         PlotType = as.character(PlotType),
         Plot = as.character(Plot),
         idTree = as.character(idTree))
```

Transformations of response variable and model covariates.

```
# calculate minimum growth (AGR)
min_agr <- min(growth$AGR_dbh_year, na.rm = T)

# Log response variable (AGR) + minimum AGR + 1/10 of minimum AGR avoid 0s
growth_mod <- growth %>%
  mutate(AGRlog = log(AGR_dbh_year + abs(min_agr +
                                         min_agr/10)))

# Log transform model covariates (DBH, NCI)
growth_mod <- growth_mod %>%
  mutate(NCIlog = log(NCI),
         DBHlog = log(DBH))

# Scale and center DBH within species
growth_mod <- growth_mod %>%
  group_by(spName) %>%
  mutate(DBHlogsc = scale(DBHlog, center = TRUE)) %>%
  ungroup()

# Scale and center growth (AGR) and NCI across all species
growth_mod <- growth_mod %>%
  mutate(AGRlogsc = scale(AGRlog, center = TRUE),
         NCIlogsc = scale(NCIlog, center = TRUE))
```

Running models

Here an example of the model set up for the CWD model for all plots combined

Specify your priors:

```
# priors for # grand intercept
prior_brms <- c(prior(normal(0, 0.5), class = "Intercept"),
               # grand slopes
               prior(normal(0, 0.5), class = "b"),
               # overall sigma
               prior(exponential(1), class = "sigma"),
               # varying intercepts and slopes
               prior(exponential(1), class = "sd"),
               # variance-covariance matrix
               prior(lkj(2), class = "cor")
               )
```

Definition of the model and model specifications.

```
# Set the number of available cores
NrCores <- 16

# Specify the model formula
fit_allplots_CWD <-
brm(formula = AGRlogsc ~
     DBHlogsc + CWD + NCIlogsc + CWD:NCIlogsc +
     # add varying intercept and slopes for species
     (1 + DBHlogsc + CWD + NCIlogsc + CWD:NCIlogsc | spName) +
     # add varying intercepts for plots and tree individuals
     (1 | Plot) + (1 | idTree),
     data = datamod,
     family = gaussian(),
     prior = prior_brms,
     warmup = 2000, # warm up iterations
     iter = 4000, # total iterations
     chains = 4, # number of chains
     cores = NrCores, # the defined number of cores
     backend = "cmdstanr", # call cmd stan to do interchain parallelisation
     threads = threading(4), # the number of cores per chain
     refresh = 10, # will print you the progress every 10 iterations
     seed = 35,
     control = list(adapt_delta = 0.98, max_treedepth = 15)
     )
```

```

# print overall model summary
fit_allplots_CWD

# save model fit
save(fit_allplots_CWD,
     file=paste0("fit_allplots_CWD", "_FIT.RData"))

# save data on which model was fitted
save(datamod,
     file=paste0("fit_allplots_CWD", "_DATA.RData"))

```

M2 models

Data preparation for M1 models

Here the data preparation code at the example of the CWD - π_{tlp} model. M2 models were run on all plots combined. Note that processing of inventory data and growth calculations took place before hand.

```
growth <- read.csv("~/MyPath/My_growth_data_file.csv")
```

We only kept species with information for a given trait (here π_{tlp} , TLP).

```
growth <- growth %>%
  filter(!is.na(TLP)) #trait
```

Required columns and information for M1 models. PlotType contains the information whether the plot belongs to undisturbed or disturbed plots. idTree is a unique identifier for tree individuals at Paracou.

```

growth <- growth %>%
  select(AGR_dbh_year, DBH, NCI, SRad, Tmax, VPD, CWD, TLP,
         spName, PlotType, Plot, idTree) %>%
  mutate(AGR_dbh_year = as.numeric(AGR_dbh_year),
         DBH = as.numeric(DBH),
         NCI = as.numeric(NCI),
         SRad = as.numeric(SRad),
         Tmax = as.numeric(Tmax),
         VPD = as.numeric(VPD),
         CWD = as.numeric(CWD),
         TLP = as.numeric(TLP), #trait
         spName = as.character(spName),
         PlotType = as.character(PlotType),
         Plot = as.character(Plot),
         idTree = as.character(idTree)
  )

```


Transformations of response variable and model covariates including the trait. In the case of π_{tlp} (here TLP) no log transformation was applied.

```
# calculate minimum growth (minimum AGR)
min_agr <- min(growth$AGR_dbh_year, na.rm = T)

# Log response variable (AGR) + minimum AGR + 1/10 of minimum AGR avoid 0s
growth_mod <- growth %>%
  mutate(AGRlog = log(AGR_dbh_year + abs(min_agr +
    min_agr/10)))

# Log transform model covariates (DBH, NCI)
growth_mod <- growth_mod %>%
  mutate(NCIlog = log(NCI), DBHlog = log(DBH))

# Scale and center DBH within species
growth_mod <- growth_mod %>%
  group_by(spName) %>%
  mutate(DBHlogsc = scale(DBHlog, center = TRUE)) %>%
  ungroup()

# Scale and center growth (AGR), NCI and the trait (here TLP) across all species
growth_mod <- growth_mod %>%
  mutate(AGRlogsc = scale(AGRlog, center = TRUE),
    NCIlogsc = scale(NCIlog, center = TRUE), TLPsc = scale(TLP,
    center = TRUE))
```

Running models

Here an example of the model set up for the CWD - π_{tlp} (here TLP) model.

Specify your priors:

```
# priors for # grand intercept
prior_brms <- c(prior(normal(0, 0.5), class = "Intercept"),
  # grand slopes
  prior(normal(0, 0.5), class = "b"),
  # overall sigma
  prior(exponential(1), class = "sigma"),
  # varying intercepts and slopes
  prior(exponential(1), class = "sd"),
  # variance-covariance matrix
  prior(lkj(2), class = "cor")
)
```

Definition of the model and model specifications.

```
# Set the number of available cores
NrCores <- 16

fit_allplots_CWD_TLP <-
brm(formula = AGRlogsc ~ DBHlogsc + CWD + NCILogsc + CWD:NCILogsc +
      # add trait effect on intercept and slopes which will be
      modeled in lower species-level regression
      TLP + CWD:TLP + NCILogsc:TLP + CWD:NCILogsc:TLP +
      # add varying intercept and slopes for species
      (1 + DBHlogsc + CWD + NCILogsc + CWD:NCILogsc | spName) +
      # add varying intercepts for plots and tree individuals
      (1 | Plot) + (1 | idTree),
  data = datamod,
  family = gaussian(),
  prior = prior_brms,
  warmup = 2000, # warm up iterations
  iter = 4000, # total iterations
  chains = 4, # number of chains
  cores = NrCores, # the defined number of cores
  backend = "cmdstanr", # call cmd stan to do interchain parallelisation
  threads = threading(4), # the number of cores per chain
  refresh = 10, # will print you the progress every 10 iterations
  seed = 35,
  control = list(adapt_delta = 0.98, max_treedepth = 15)
)

# print overall model summary
fit_allplots_CWD_TLP

# save model fit
save(fit_allplots_CWD_TLP,
      file=paste0("fit_allplots_CWD_TLP", "_FIT.RData")) # save MODEL FIT

# save data on which model was fitted
save(datamod,
      file=paste0("fit_allplots_CWD_TLP", "_DATA.RData"))
```

References

Page, N., Derroire, G., Hérault, B., Marcon, E., Guedj, E., Jaouen, G., and Piponiot, C. ForestData: Post-inventory processing of forest plot data, 2021.