Meta-analysis investigating P and N*P addition impacts on plant functional traits

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Script that explores the effect of P addition on leaf and whole-plant functional traits using P fertilization and N*P fertilization experiments. The meta-analysis includes data from the MESI database as of January 07, 2025 and additional experiments compiled by Evan Perkowski.

Script summarizes the number of observations per trait and then conducts a meta-analysis to summarize plant responses to P addition, then conducts a second meta-analysis that summarizes responses when P is added in concert with N.

NOTE: NEED TO CHECK THAT ADDED SAMPLE SIZE OF ADDED EXPERIMENTS IS APPROPRIATE FOR MESI (SHOULD BE LISTED AS 'PLOT' REPS, NOT INDIVIDUAL REP NUMBER)

```
# Libraries
library(dplyr)
library(tidyr)
library(stringr)
library(ggplot2)
library(readr)
library(metafor)
library(MAd)
library(patchwork)

# MESI data
df_mesi <- read_csv("../data/mesi_main.csv")

# Manual data compilation
df_manual <- read_csv("../data/CNP_compiled_data.csv") %>%
  mutate(sampling_year = as.character(sampling_year),
         treatment = ifelse(treatment == FALSE, "f", treatment),
         sampling_date = as.character(sampling_date))

# Merge MESI database with manual data compilation
df_total <- df_mesi %>%
  full_join(df_manual)
```

Explore data availability in combined dataset for N-fertilization experiments

```
explore_nfert_exps <- df_total %>%

  # field experiments only
```

```
  filter(experiment_type == "field") %>%

  # fertilisation experiments only
  filter(treatment == "f") %>%

  # P-fertilisation only (without N or K addition)
  filter(npk == "_100")

head(explore_nfert_exps)
```

```
## # A tibble: 6 x 60
##   db      id    duplicate_id citation    response site  study exp     lat    lon
##   <chr>   <chr> <chr>        <chr>       <chr>    <chr> <chr> <chr> <dbl>  <dbl>
## 1 hebei   h962  h962         stape_et_a~ agb      -11.~ -11.~ -11.~ -12.0  -38.1
## 2 hebei   h963  h963         stape_et_a~ agb      -11.~ -11.~ -11.~ -12.0  -38.1
## 3 hebei   h964  h964         stape_et_a~ agb      -11.~ -11.~ -11.~ -12.0  -38.1
## 4 hebei   h965  h965         stape_et_a~ agb      -11.~ -11.~ -11.~ -12.0  -38.1
## 5 alberta a72   a72          collins_et~ agb      34.2~ 34.2~ 34.2~  34.2 -106.
## 6 alberta a71   a71          collins_et~ agb      34.2~ 34.2~ 34.2~  34.2 -106.
## # i 50 more variables: elevation <dbl>, mat <dbl>, map <dbl>,
## #   ecosystem_type <chr>, vegetation_type <chr>, experiment_type <chr>,
## #   community_type <chr>, dominant_species <chr>, growth_form <chr>, age <dbl>,
## #   disturbance_type <chr>, treatment <chr>, npk <chr>, w_t1 <chr>, c_c <dbl>,
## #   c_t <dbl>, d_t <dbl>, d_t2 <dbl>, n_c <dbl>, n_t <dbl>, p_c <dbl>,
## #   p_t <dbl>, k_c <dbl>, k_t <dbl>, i_c <dbl>, i_t <dbl>, i_t2 <dbl>,
## #   s_c <dbl>, s_t <dbl>, w_t2 <dbl>, w_t3 <dbl>, start_year <dbl>, ...
```

```
## How many experiments?
length(unique(explore_nfert_exps$exp))
```

```
## [1] 417
```

```
## What traits are available?
unique(explore_nfert_exps$response)
```

```
##  [1] "agb"
##  [2] "fine_root_biomass"
##  [3] "total_biomass"
##  [4] "bgb"
##  [5] "r_soil"
##  [6] "npp"
##  [7] "agb_group"
##  [8] "anpp_group"
##  [9] "soil_total_c_org_layer"
## [10] "soil_total_c_min_layer"
## [11] "soil_total_c"
## [12] "mbc"
## [13] "anpp"
## [14] "mbn"
## [15] "litter_decomposition"
## [16] "bgb_n"
## [17] "leaf_c"
## [18] "leaf_cn"
## [19] "leaf_n_mass"
## [20] "soil_nh4_min_layer"
```

```
##  [21] "soil_no3_min_layer"
##  [22] "bgb_n_stock"
##  [23] "soil_total_n_min_layer"
##  [24] "soil_n2o_flux"
##  [25] "agb_n_stock"
##  [26] "som_n"
##  [27] "soil_nh4"
##  [28] "soil_no3"
##  [29] "root_production"
##  [30] "root_shoot_ratio"
##  [31] "mb"
##  [32] "anet"
##  [33] "agb_n"
##  [34] "asat"
##  [35] "leaf_n_area"
##  [36] "soil_potential_net_n_mineralization"
##  [37] "soil_nh4-n"
##  [38] "soil_no3-n"
##  [39] "soil_total_n"
##  [40] "soil_total_cn"
##  [41] "soil_n_immobilization"
##  [42] "mbcn"
##  [43] "lwp"
##  [44] "soil_total_p"
##  [45] "r_soilh"
##  [46] "fine_root_turnover"
##  [47] "leaf_biomass_eco"
##  [48] "stem_biomass"
##  [49] "litter_n"
##  [50] "litter_p"
##  [51] "litter_k"
##  [52] "fine_root_production"
##  [53] "r_eco"
##  [54] "soc"
##  [55] "soil_p"
##  [56] "leaf_p_mass"
##  [57] "leaf_k_mass"
##  [58] "leaf_np"
##  [59] "bgb_coarse"
##  [60] "r_root"
##  [61] "som"
##  [62] "vcmax"
##  [63] "anpp_leaf"
##  [64] "fine_root_respiration"
##  [65] "jmax"
##  [66] "lai"
##  [67] "leaf_litterfall"
##  [68] "gpp"
##  [69] "nep"
##  [70] "swc"
##  [71] "nee"
##  [72] "amax"
##  [73] "litter_biomass"
##  [74] "bgb_group"
```

```
##  [75] "total_biomass_group"
##  [76] "litterfall"
##  [77] "leaf_nue"
##  [78] "soil_total_c_profile"
##  [79] "r_leaf"
##  [80] "lai_max"
##  [81] "wue_leaf"
##  [82] "gs"
##  [83] "wood_n"
##  [84] "soil_net_n_mineralization"
##  [85] "wue"
##  [86] "wue_eco"
##  [87] "grain_n"
##  [88] "root_n"
##  [89] "root_n_uptake"
##  [90] "grain_c"
##  [91] "bgb_c"
##  [92] "stem_n"
##  [93] "soil_total_cn_org_layer"
##  [94] "soil_total_cn_min_layer"
##  [95] "anpp_grain"
##  [96] "bnpp"
##  [97] "soil_in"
##  [98] "leaf_cp"
##  [99] "leaf_litter_p"
## [100] "leaf_litter_np"
## [101] "agb_p_stock"
## [102] "agb_ndvi"
## [103] "agb_height"
## [104] "agb_p"
## [105] "agb_cn"
## [106] "bgb_cn"
## [107] "leaf_biomass_plant"
## [108] "root_length"
## [109] "soil_gross_nitrification"
## [110] "soil_net_nitrification"
## [111] "soil_denitrification"
## [112] "anpp_woody"
## [113] "leaf_biomass_leaf"
## [114] "coarse_root_n"
## [115] "fine_root_n"
## [116] "leaf_litter_n"
## [117] "bai"
## [118] "leaf_area_leaf"
## [119] "soil_phkcl"
## [120] "soil_pbray"
## [121] "agb_np"
## [122] "soil_n_leaching"
## [123] "soil_net_ammonification"
## [124] "agb_c"
## [125] "root_p_uptake"
## [126] "rmf"
## [127] "rootshoot"
## [128] "lma"
```

```
## [129] "leaf_p_area"
## [130] "spad"
## [131] "tpu"
## [132] "rd"
## [133] "leaf_pue"
## [134] "leaf_structure_p"
## [135] "leaf_metabolic_p"
## [136] "leaf_nucleic_p"
## [137] "leaf_residual_p"
## [138] "leaf_thickness"
## [139] "sla"
## [140] "ldmc"
## [141] "leaf_pi"
## [142] "leaf_sugar_p"
## [143] "E"
## [144] "leaf_wue"
```

Select variables

```
use_response_n <- c("total_biomass",
                    "agb",
                    "bgb",
                    "leaf_n_mass",
                    "leaf_n_area",
                    "leaf_p_mass",
                    "leaf_p_area",
                    "leaf_np",
                    "gs",
                    "lma",
                    "sla",
                    "spad",
                    "amax",
                    "vcmax",
                    "jmax",
                    "leaf_nue",
                    "leaf_pue",
                    "rd",
                    "tpu",
                    "asat",
                    "cica",
                    "ci",
                    "leaf_strucure_p",
                    "leaf_metabolic_p",
                    "leaf_nucleic_p",
                    "leaf_residual_p",
                    "leaf_pi",
                    "leaf_sugar_p"
)

nfert_responses <- explore_nfert_exps %>%
  filter(response %in% use_response_n) %>%
  mutate(myvar = response) %>%
  mutate(myvar = ifelse(myvar %in% c("cica", "ci"),
```

```
                        "cica", myvar)) %>%
  mutate(myvar = ifelse(myvar %in%  c("leaf_", "amax"),
                        "anet", myvar))

use_vars_n <- unique(nfert_responses$myvar)
```

Analysis

Calculate "ROM" - the log transformed ratio of means (Hedges et al., 1999; Lajeunesse, 2011) for each observation pair (ambient and elevated).

```
nfert_responses2 <- nfert_responses %>%

  ## keep only essential variables and drop rows containing missing values for
  ## essential variables
  select(id, duplicate_id, exp, myvar, treatment, sampling_year,
         x_t, x_c, sd_t, sd_c, rep_t, rep_c) %>%

  ## Get logarithm of response ratio and its variance
  metafor::escalc(
    measure = "ROM",
    m1i = x_t, sd1i = sd_t, n1i = rep_t,
    m2i = x_c, sd2i = sd_c, n2i = rep_c,
    data = .,
    append = TRUE,
    var.names = c("logr", "logr_var")
  ) %>%

  ## to keep the output readable from the console output
  as_tibble() %>%

  ## get standard error
  mutate( logr_se = sqrt(logr_var) / sqrt(rep_t) )

head(nfert_responses2)
```

```
## # A tibble: 6 x 15
##   id    duplicate_id exp      myvar treatment sampling_year    x_t    x_c   sd_t
##   <chr> <chr>        <chr>    <chr> <chr>     <chr>          <dbl>  <dbl>  <dbl>
## 1 h962  h962         -11.97_~ agb   f         <NA>          3.89e3 3.38e3 4.62e2
## 2 h963  h963         -11.97_~ agb   f         <NA>          7.86e3 7.26e3 7.04e2
## 3 h964  h964         -11.97_~ agb   f         <NA>          1.00e4 9.48e3 7.46e2
## 4 h965  h965         -11.97_~ agb   f         <NA>          1.10e4 1.06e4 1.48e3
## 5 a72   a72          34.2_10~ agb   f         2             7.72e1 4.89e1 6.07e0
## 6 a71   a71          34.2_10~ agb   f         3             5.6 e1 3.75e1 4.36e0
## # i 6 more variables: sd_c <dbl>, rep_t <dbl>, rep_c <dbl>, logr <dbl>,
## #   logr_var <dbl>, logr_se <dbl>
```

```
# Aggregate all measurements (multiple years, sampling dates and plots) by experiment (and response var
nfert_responses3 <- nfert_responses2 %>%

  # suggested addition by Kevin, email 02.10.2023 10:03
  dplyr::distinct(duplicate_id, x_t, x_c, .keep_all = TRUE) |>
```

```
  filter(!is.na(logr_var) & !is.na(logr)) %>%

  # re-create ID (common ID per experiment and response variable)
  select(-id) %>%
  mutate( id = paste(exp, myvar, sep = "_XXX_")) %>%

  MAd::agg(
    id = id,
    es = logr,
    var = logr_var,
    cor = 1.0,
    method = "BHHR",
    data = .
  ) %>%

  ## to keep the output readable from the console output
  as_tibble() %>%

  # separate ID again for ease of data use
  mutate( id = str_split(id, "_XXX_") ) %>%
  mutate( exp = purrr::map_chr(id, 1),
          myvar = purrr::map_chr(id, 2) ) %>%

  ## rename again
  select(exp, myvar, logr = es, logr_var = var) %>%

  ## add number of observations (sum of plots and repeated samplings)
  left_join(
    nfert_responses2 %>%
      group_by(exp, myvar, treatment) %>%
      summarise(n_c = sum(rep_c), n_t = sum(rep_t)),
    by = c("exp", "myvar")
  ) %>%

  ## get standard error. Verify if number available observations are identical
  ## for ambient and elevated. Use N from control here (n_c).
  mutate( logr_se = sqrt(logr_var) / sqrt(n_c) ,

          # merge SLA and LMA measurements by taking inverse of logr (keep SE)
          logr = ifelse(myvar == "sla", -logr, logr),
          myvar = ifelse(myvar == "sla", "lma", myvar))
```

```
## `summarise()` has grouped output by 'exp', 'myvar'. You can override using the
## `.groups` argument.
```

```
head(nfert_responses3)
```

```
## # A tibble: 6 x 8
##   exp                  myvar       logr logr_var treatment   n_c   n_t logr_se
##   <chr>                <chr>      <dbl>    <dbl> <chr>     <dbl> <dbl>   <dbl>
## 1 -11.97_-38.12_f      agb       0.0789 0.00489  f            16    16 0.0175
## 2 34.2_106.43_f        agb       0.429  0.00271  f            10    10 0.0165
## 3 37.25_-121.75_forb_fn agb      0      0.00292  f             3     3 0.0312
## 4 37.25_-121.75_grass_fn agb    -0.121  0.00305  f             3     3 0.0319
```

```
## 5 38.53_-76.33_f         agb       1.01   0.00544  f            35    35 0.0125
## 6 38.53_-76.33_f         total_b~  0.465  0.000154 f            15    15 0.00320
```

Meta-analysis

Aggregate log-ratios across multiple experiments, taking into account their respective variance and using the experiment identity as a grouping factor for random intercepts.

```
source("../helper_fxns/analyse_meta.R")

out_n  <- purrr::map(as.list(use_vars_n),
                     ~analyse_meta(nfert_responses3 %>%
                                     rename(var = myvar), nam_target = .))
names(out_n) <- use_vars_n
df_box_n <- purrr::map_dfr(out_n, "df_box") |>
  left_join(
    nfert_responses3 |>
      group_by(myvar) |>
      summarise(logr_min = min(logr), logr_max = max(logr)) |>
      rename(var = myvar),
    by = "var"
  )
saveRDS(df_box_n, file = paste0(here::here(), "df_box_nfert.rds"))
```

Final data size

Number of data points (plot-level measurements) per variable:

```
nfert_responses3 %>%
  group_by(myvar) %>%
  summarise(n_plots = sum(n_c, na.rm = TRUE), n_exp = n()) %>%
  rename("Variable"="myvar", "N observations"="n_plots", "N experiments"="n_exp") %>%
  knitr::kable()
```

Variable	N observations	N experiments
agb	3764	154
anet	12	1
asat	284	11
bgb	1262	104
gs	12	1
jmax	162	6
leaf_metabolic_p	25	1
leaf_n_area	442	33
leaf_n_mass	808	50
leaf_np	511	40
leaf_nucleic_p	35	2
leaf_nue	52	4
leaf_p_area	316	28
leaf_p_mass	620	51
leaf_pi	10	1
leaf_pue	25	1
leaf_residual_p	35	2
leaf_sugar_p	10	1
lma	382	29

Variable	N observations	N experiments
rd	85	2
spad	107	3
total_biomass	870	28
tpu	33	2
vcmax	158	6

Some quick plots:

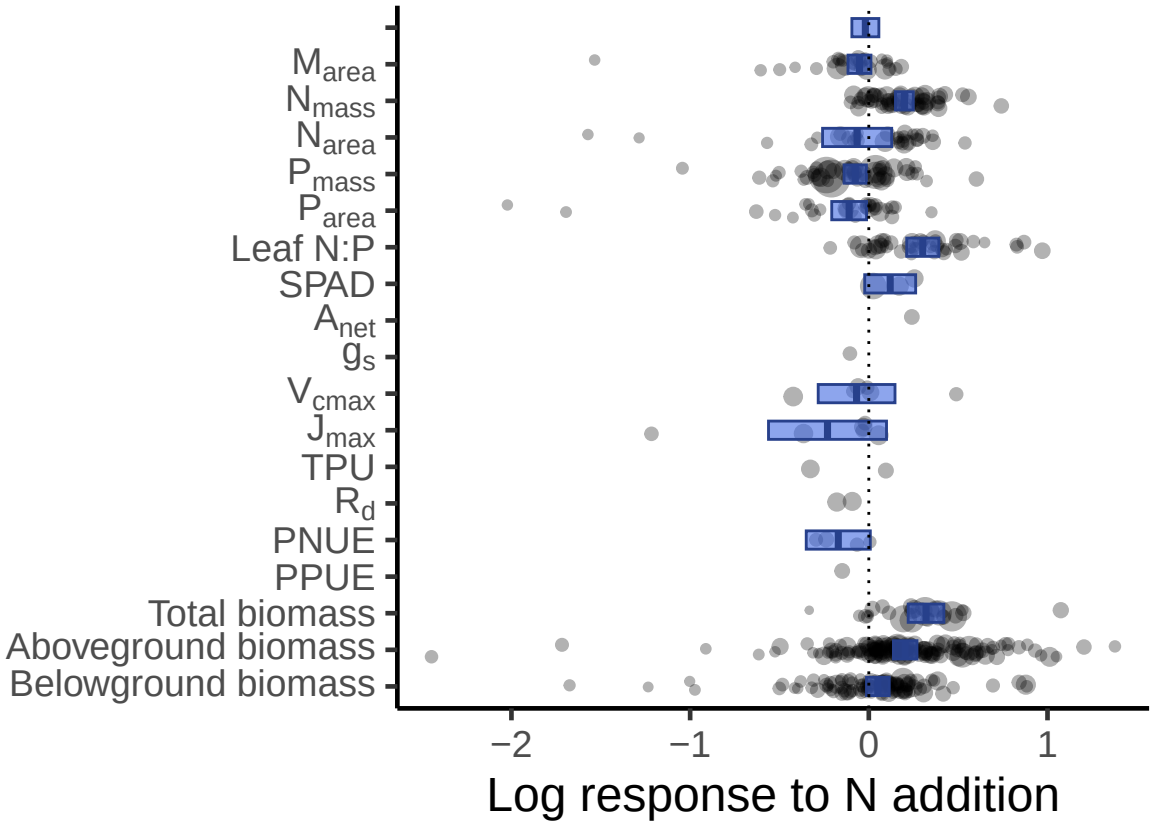
```
nfert_responses3 <- nfert_responses3 %>%
  mutate(myvar = factor(myvar, levels = c("bgb", "agb", "total_biomass", "leaf_pue",
                                          "leaf_nue", "rd", "tpu", "jmax", "vcmax",
                                          "cica", "gs", "anet", "spad", "leaf_np",
                                          "leaf_p_area", "leaf_p_mass", "leaf_n_area",
                                           "leaf_n_mass", "lma")))

meta_plot_n <- ggplot(data = subset(nfert_responses3, myvar != "cica"),
                      aes(x = myvar, y = logr)) +
  geom_jitter(color = rgb(0,0,0,0.3),
              aes( size = 1/logr_se ),
              position = position_jitter(w = 0.2, h = 0),
              show.legend = FALSE) +
  geom_crossbar( data = df_box_n %>% drop_na(var),
                 aes(x = var, y = middle, ymin = ymin, ymax = ymax),
                 fill = "royalblue",
                 color = "royalblue4",
                 alpha = 0.6,
                 width = 0.5 ) +
  geom_hline( yintercept = 0.0, linewidth = 0.5, linetype = "dotted" ) +
  scale_x_discrete(labels = c("Belowground biomass",
                              "Aboveground biomass",
                              "Total biomass",
                              "PPUE",
                              "PNUE",
                              expression("R"["d"]),
                              "TPU",
                              expression("J"["max"]),
                              expression("V"["cmax"]),
                              expression("g"["s"]),
                              expression("A"["net"]),
                              "SPAD",
                              "Leaf N:P",
                              expression("P"["area"]),
                              expression("P"["mass"]),
                              expression("N"["area"]),
                              expression("N"["mass"]),
                              expression("M"["area"]))) +

  #scale_x_discrete("", labels = mylabl) +
  labs(x = "",
       y = "Log response to N addition") +
  coord_flip() +
```

```
  theme_classic(base_size = 18)
meta_plot_n
```

```
## Warning: Removed 2 rows containing missing values (`geom_point()`).
```



Explore data availability in combined dataset for P-fertilization experiments

```
explore_pfert_exps <- df_total %>%

  # field experiments only
  # filter(experiment_type == "field") %>%

  # fertilisation experiments only
  filter(treatment == "f") %>%

  # P-fertilisation only (without N or K addition)
  filter(npk == "_010")

head(explore_pfert_exps)
```

```
## # A tibble: 6 x 60
##   db      id    duplicate_id citation    response site  study exp      lat   lon
##   <chr>   <chr> <chr>        <chr>       <chr>    <chr> <chr> <chr>  <dbl> <dbl>
## 1 sichuan s885  s885         lawrence_2~ total_b~ 0.12~ 0.12~ 0.12~   0.12 110.
## 2 sichuan s888  s888         lawrence_2~ total_b~ 0.12~ 0.12~ 0.12~   0.12 110.
```

```
## 3 sichuan s879  s879         lawrence_2~ total_b~ 0.12~ 0.12~ 0.12~   0.12 110.
## 4 sichuan s882  s882         lawrence_2~ total_b~ 0.12~ 0.12~ 0.12~   0.12 110.
## 5 sichuan s385  s385         augustine_~ anpp     0.28~ 0.28~ 0.28~   0.28  37.9
## 6 sichuan s172  s172         ohalloran_~ agb      -15.~ -15.~ -15.~ -15.4   23.2
## # i 50 more variables: elevation <dbl>, mat <dbl>, map <dbl>,
## #   ecosystem_type <chr>, vegetation_type <chr>, experiment_type <chr>,
## #   community_type <chr>, dominant_species <chr>, growth_form <chr>, age <dbl>,
## #   disturbance_type <chr>, treatment <chr>, npk <chr>, w_t1 <chr>, c_c <dbl>,
## #   c_t <dbl>, d_t <dbl>, d_t2 <dbl>, n_c <dbl>, n_t <dbl>, p_c <dbl>,
## #   p_t <dbl>, k_c <dbl>, k_t <dbl>, i_c <dbl>, i_t <dbl>, i_t2 <dbl>,
## #   s_c <dbl>, s_t <dbl>, w_t2 <dbl>, w_t3 <dbl>, start_year <dbl>, ...
```

```
## How many experiments?
length(unique(explore_pfert_exps$exp))
```

```
## [1] 255
```

```
## What traits are available?
unique(explore_pfert_exps$response)
```

```
##  [1] "total_biomass_group"    "anpp"                   "agb"
##  [4] "total_biomass"          "mbc"                    "soil_total_c"
##  [7] "bgb"                    "leaf_c"                 "agb_group"
## [10] "anpp_group"             "agb_n"                  "agb_p"
## [13] "soil_total_n"           "agb_p_stock"            "gpp"
## [16] "fine_root_biomass"      "leaf_n_mass"            "leaf_p_mass"
## [19] "lai"                    "mbn"                    "r_soil"
## [22] "gs"                     "lwp"                    "fine_root_production"
## [25] "soil_no3-n_supply_rate" "soil_nh4-n_supply_rate" "soil_p_supply_rate"
## [28] "leaf_biomass_eco"       "root_shoot_ratio"       "bpe"
## [31] "total_biomass_p_stock"  "total_biomass_n_stock"  "total_biomass_np"
## [34] "agb_pod_n"              "wood_n"                 "agb_pod_p"
## [37] "wood_p"                 "agb_grain_n"            "agb_grain_p"
## [40] "anpp_grain"             "soil_p"                 "agb_ndvi"
## [43] "agb_height"             "bgb_n"                  "bgb_p"
## [46] "root_n_uptake"          "nee"                    "soil_np"
## [49] "leaf_np"                "litter_decomposition"   "r_root"
## [52] "nep"                    "lma"                    "leaf_n_area"
## [55] "leaf_p_area"            "rgr"                    "amax"
## [58] "vcmax"                  "jmax"                   "leaf_nue"
## [61] "leaf_pue"               "leaf_pi"                "leaf_ester_p"
## [64] "leaf_nucleic_p"         "leaf_lipid_p"           "leaf_residual_p"
## [67] "asat"                   "tpu"                    "rd"
## [70] "cica"                   "rmf"                    "rootshoot"
## [73] "sla"                    "stom_lim"               "gsw"
## [76] "spad"                   "anet"                   "leaf_structure_p"
## [79] "leaf_metabolic_p"       "leaf_thickness"         "ldmc"
## [82] "fine_root_p_mass"       "coarse_root_p_mass"     "stem_p_mass"
## [85] "total_p_uptake_eff"     "E"                      "iwue"
## [88] "leaf_sugar_p"           "leaf_wue"
```

Select variables

```
use_response_p <- c("total_biomass",
                    "agb",
```

```
                    "bgb",
                    "rmf",
                    "rootshoot",
                    "leaf_n_mass",
                    "leaf_n_area",
                    "leaf_p_mass",
                    "leaf_p_area",
                    "leaf_np",
                    "gs",
                    "lma",
                    "sla",
                    "spad",
                    "amax",
                    "vcmax",
                    "jmax",
                    "leaf_nue",
                    "leaf_pue",
                    "rd",
                    "tpu",
                    "asat",
                    "cica",
                    "ci",
                    "leaf_strucure_p",
                    "leaf_metabolic_p",
                    "leaf_nucleic_p",
                    "leaf_residual_p",
                    "leaf_pi",
                    "leaf_sugar_p"
)

pfert_responses <- explore_pfert_exps %>%
  filter(response %in% use_response_p) %>%
  mutate(myvar = response) %>%
  mutate(myvar = ifelse(myvar %in% c("cica", "ci"),
                        "cica", myvar)) %>%
  mutate(myvar = ifelse(myvar %in%  c("asat", "amax"),
                        "anet", myvar))

use_vars_p <- unique(pfert_responses$myvar)
```

Analysis

Calculate `"ROM"` - the log transformed ratio of means (Hedges et al., 1999; Lajeunesse, 2011) for each observation pair (ambient and elevated).

```
pfert_responses2 <- pfert_responses %>%

  ## keep only essential variables and drop rows containing missing values for
  ## essential variables
  select(id, duplicate_id, exp, myvar, treatment, sampling_year,
         x_t, x_c, sd_t, sd_c, rep_t, rep_c) %>%

  ## Get logarithm of response ratio and its variance
  metafor::escalc(
```

```
    measure = "ROM",
    m1i = x_t, sd1i = sd_t, n1i = rep_t,
    m2i = x_c, sd2i = sd_c, n2i = rep_c,
    data = .,
    append = TRUE,
    var.names = c("logr", "logr_var")
  ) %>%

  ## to keep the output readable from the console output
  as_tibble() %>%

  ## get standard error
  mutate( logr_se = sqrt(logr_var) / sqrt(rep_t) )

head(pfert_responses2)
```

```
## # A tibble: 6 x 15
##   id    duplicate_id exp       myvar treatment sampling_year    x_t    x_c  sd_t
##   <chr> <chr>        <chr>     <chr> <chr>     <chr>          <dbl>  <dbl> <dbl>
## 1 s172  s172         -15.44_2~ agb   f         2               6.29   9.43  5.76
## 2 s3497 s3497        17.25_-8~ agb   f         3             488.   106.   43.7
## 3 s3500 s3500        17.25_-8~ agb   f         3             418.   200.   83.7
## 4 s3503 s3503        17.25_-8~ agb   f         3             247.    80.1  43.7
## 5 s1524 s1524        -18.66_2~ tota~ f         2              76.4   46.7  18.8
## 6 s168  s168         -18.66_2~ agb   f         1              80.0   51.1  19.6
## # i 6 more variables: sd_c <dbl>, rep_t <dbl>, rep_c <dbl>, logr <dbl>,
## #   logr_var <dbl>, logr_se <dbl>
```

```
# Aggregate all measurements (multiple years, sampling dates and plots) by experiment (and response var
pfert_responses3 <- pfert_responses2 %>%

  # suggested addition by Kevin, email 02.10.2023 10:03
  dplyr::distinct(duplicate_id, x_t, x_c, .keep_all = TRUE) |>

  filter(!is.na(logr_var) & !is.na(logr)) %>%

  # re-create ID (common ID per experiment and response variable)
  select(-id) %>%
  mutate( id = paste(exp, myvar, sep = "_XXX_")) %>%

  MAd::agg(
    id = id,
    es = logr,
    var = logr_var,
    cor = 1.0,
    method = "BHHR",
    data = .
  ) %>%

  ## to keep the output readable from the console output
  as_tibble() %>%

  # separate ID again for ease of data use
  mutate( id = str_split(id, "_XXX_") ) %>%
```

```
  mutate( exp = purrr::map_chr(id, 1),
          myvar = purrr::map_chr(id, 2) ) %>%

  ## rename again
  select(exp, myvar, logr = es, logr_var = var) %>%

  ## add number of observations (sum of plots and repeated samplings)
  left_join(
    pfert_responses2 %>%
      group_by(exp, myvar, treatment) %>%
      summarise(n_c = sum(rep_c), n_t = sum(rep_t)),
    by = c("exp", "myvar")
  ) %>%

  ## get standard error. Verify if number available observations are identical
  ## for ambient and elevated. Use N from control here (n_c).
  mutate( logr_se = sqrt(logr_var) / sqrt(n_c) ,

          # merge SLA and LMA measurements by taking inverse of logr (keep SE)
          logr = ifelse(myvar == "sla", -logr, logr),
          myvar = ifelse(myvar == "sla", "lma", myvar))
```

```
## `summarise()` has grouped output by 'exp', 'myvar'. You can override using the
## `.groups` argument.
```

```
head(pfert_responses3)
```

```
## # A tibble: 6 x 8
##   exp             myvar           logr logr_var treatment   n_c   n_t logr_se
##   <chr>           <chr>          <dbl>    <dbl> <chr>     <dbl> <dbl>   <dbl>
## 1 -15.44_23.25_f  agb           -0.405 0.287    f             4     4  0.268
## 2 17.25_-88.77_f  agb            1.13  0.0572   f             9     9  0.0797
## 3 -18.66_25.5_f   total_biomass  0.491 0.0285   f             3     3  0.0974
## 4 -18.66_25.5_f   agb            0.158 0.418    f             8     8  0.229
## 5 19.6_-155.33_fp bgb            0.142 0.0124   f             3     3  0.0644
## 6 -2.98_-47.52_f  agb            0.269 0.000881 f             4     4  0.0148
```

Meta-analysis

Aggregate log-ratios across multiple experiments, taking into account their respective variance and using the experiment identity as a grouping factor for random intercepts.

```
source("../helper_fxns/analyse_meta.R")

out_p  <- purrr::map(as.list(use_vars_p),
                     ~analyse_meta(pfert_responses3 %>%
                                     rename(var = myvar), nam_target = .))
names(out_p) <- use_vars_p
df_box_p <- purrr::map_dfr(out_p, "df_box") |>
  left_join(
    pfert_responses3 |>
      group_by(myvar) |>
      summarise(logr_min = min(logr), logr_max = max(logr)) |>
      rename(var = myvar),
```

```
    by = "var"
  )
saveRDS(df_box_p, file = paste0(here::here(), "df_box_pfert.rds"))
```

Final data size

Number of data points (plot-level measurements) per variable:

```
pfert_responses3 %>%
  group_by(myvar) %>%
  summarise(n_plots = sum(n_c, na.rm = TRUE), n_exp = n()) %>%
  rename("Variable"="myvar", "N observations"="n_plots", "N experiments"="n_exp") %>%
  knitr::kable()
```

Variable	N observations	N experiments
agb	918	126
anet	608	12
bgb	250	56
cica	116	3
gs	69	5
jmax	473	8
leaf_metabolic_p	25	1
leaf_n_area	727	33
leaf_n_mass	885	44
leaf_np	807	44
leaf_nucleic_p	87	3
leaf_nue	382	5
leaf_p_area	701	33
leaf_p_mass	821	47
leaf_pi	62	2
leaf_pue	381	5
leaf_residual_p	87	3
leaf_sugar_p	5	1
lma	761	33
rd	309	4
rmf	91	29
rootshoot	91	29
spad	107	3
total_biomass	101	14
tpu	160	5
vcmax	473	8

Number of data points (plot-level measurements) per experiment:

```
pfert_responses3 %>%
  group_by(exp) %>%
  summarise(n_plots = sum(n_c), n_exp = n()) %>%
  rename_("Experiment"="exp", "N observations"="n_plots", "N experiments"="n_exp") %>%
  knitr::kable()
```

Experiment	N observations	N experiments
-15.44_23.25_f	4	1
-18.66_25.5_f	11	2

Experiment	N observations	N experiments
-2.98_-47.52_f	4	1
-21.65_21.81_f	3	1
-22.283_117.666_f	6	1
-22.41_21.71_f	4	1
-22.78_31.25_f	16	2
-23.75_31.43_f	16	2
-24.17_21.89_f	7	2
-24.4_31.75_f	16	2
-25.12_31.23_f	16	2
-25.29_31.91_f	16	2
-3.5_36_f	6	1
-3.95_-79.03_f	12	2
-33.35_150.3_f	9	3
-35.73_-58.05_f	12	1
17.25_-88.77_f	9	1
19.6_-155.33_fp	3	1
22.13_-159.63_f	11	1
26.52_109.78_fp	3	1
31.37_90.02_f	24	1
31.3_-81.28_f	4	1
31.55_-81.78_f	4	1
32.54_-116.7_fp	12	1
33.7_120.3_f	15	1
34.92_102.88_f2p	5	1
34.92_102.88_f3p	5	1
34.92_102.88_fp	5	1
37.25_-121.75_forb_fp	3	1
37.25_-121.75_grass_fp	3	1
37.48_101.2_fp	18	3
37.55_-122.3_f	3	1
37.6_101.32_fp	20	3
37.87_-122.52_f	18	2
39.25_-121.28_fp	20	1
39.75_-74.75_fp	4	1
41.35_36.25_fp	4	1
41.35_36.25_fp2	4	1
41.62_-71.32_fp	8	2
42.28_-85.58_f	6	2
42.58_122.21_fp	12	2
44.8_116.03_fp	6	2
47.57_7.6_f	6	1
51.85_5.62_fp	3	1
52.07_5.58_fp	3	1
52.37_5.1_fp	6	1
52.5_5.7_fp	6	1
53.83_-8.83_fp	10	1
54.63_8.83_fp	5	1
64.83_-147.72_fp	3	1
69.43_-133.02_fp	10	1
69.43_-133.02_fp2	10	1
9.6_-79.5_f	3	1
alpflix_fp	60	1

Experiment	N observations	N experiments
bennekom_drained_fp	5	1
bennekom_undrained_fp	5	1
bloomfield2014_fp	1462	14
bordeaux_fp	40	3
bown2007_fnp	80	8
buitengoor_1992_fp	5	1
buitengoor_1993_fp	5	1
carswell2005_fnp	80	4
cleland2019_bldr.us_fnp	8	4
cleland2019_bnch.us_fnp	12	4
cleland2019_bogong.au_fnp	12	4
cleland2019_burrawan.au_fnp	12	4
cleland2019_cbgb.us_fnp	24	4
cleland2019_cdcr.us_fnp	12	4
cleland2019_cdpt.us_fnp	12	4
cleland2019_cowi.ca_fnp	12	4
cleland2019_elliot.us_fnp	12	4
cleland2019_frue.ch_fnp	12	4
cleland2019_gilb.za_fnp	12	4
cleland2019_hall.us_fnp	12	4
cleland2019_hart.us_fnp	12	4
cleland2019_konz.us_fnp	12	4
cleland2019_lancaster.uk_fnp	8	4
cleland2019_look.us_fnp	12	4
cleland2019_mtca.au_fnp	12	4
cleland2019_sage.us_fnp	12	4
cleland2019_saline.us_fnp	12	4
cleland2019_sgs.us_fnp	12	4
cleland2019_shps.us_fnp	12	4
cleland2019_sier.us_fnp	12	4
cleland2019_smith.us_fnp	12	4
cleland2019_spin.us_fnp	12	4
cleland2019_summ.za_fnp	12	4
cleland2019_trel.us_fnp	12	4
cleland2019_ukul.za_fnp	24	4
cleland2019_unc.us_fnp	12	4
cleland2019_valm.ch_fnp	12	4
crous2017_fnp	2351	12
daqinggou_fp	12	2
drentsche_aa_drained_fp	5	1
drentsche_aa_wet_fp	5	1
ewenke_f_p	6	1
fan2024_fp	773	14
firn2019_bldr.us_fnp	21	6
firn2019_bnch.us_fnp	51	6
firn2019_bogong.au_fnp	72	6
firn2019_burrawan.au_fnp	73	6
firn2019_cbgb.us_fnp	54	6
firn2019_comp.pt_fnp	78	6
firn2019_cowi.ca_fnp	45	6
firn2019_elliot.us_fnp	54	6
firn2019_frue.ch_fnp	46	6

Experiment	N observations	N experiments
firn2019_gilb.za_fnp	48	6
firn2019_hopl.us_fnp	51	6
firn2019_kiny.au_fnp	45	6
firn2019_konz.us_fnp	29	6
firn2019_lancaster.uk_fnp	51	6
firn2019_look.us_fnp	54	6
firn2019_mcla.us_fnp	51	6
firn2019_mtca.au_fnp	53	6
firn2019_sage.us_fnp	31	6
firn2019_sgs.us_fnp	39	6
firn2019_shps.us_fnp	24	6
firn2019_sier.us_fnp	48	6
firn2019_smith.us_fnp	54	6
firn2019_summ.za_fnp	72	6
firn2019_unc.us_fnp	54	6
firn2019_valm.ch_fnp	120	6
flottbek_fp	30	1
gusewell_s1_fp	4	1
gusewell_s2_fp	4	1
gusewell_t1_fp	4	1
gusewell_t2_fp	4	1
gusewell_v1_fp	4	1
gusewell_v2_fp	4	1
gusewell_v3_fp	4	1
gusewell_w1_p	4	1
gusewell_w2_p	4	1
gusewell_w3_p	4	1
gusewell_w4_p	4	1
herschgreen2024_cbgb.us_fnp	88	4
herschgreen2024_cdcr.us_fnp	70	4
herschgreen2024_churn.us_fnp	50	4
herschgreen2024_kbs.us_fnp	50	4
herschgreen2024_konz.us_fnp	69	4
herschgreen2024_spin.us_fnp	77	4
hol_kortenhoef_fp	5	1
imgers_ng_2006np_fp	6	1
indoneisa_f	54	3
kansasf_fp	12	1
kansask_fp	12	1
katelijne_2016_fp	5	1
katelijne_2017_f2	10	1
katelijne_2017_f3	10	1
kisa_grahamiana_f	20	1
luneburg_field_2006_fp	10	1
luneburg_field_2008_fp	10	1
luneburg_gh_drought_molinia_fp	NA	2
luneburg_gh_fert_molinia_fp	10	1
michigan_underc_bog_fp	19	1
michigan_underc_intermfen_fp	17	1
michigan_underc_richfen_fp	20	1
mo2019_fnp	275	11
mo2021_fnp	10	2

Experiment	N observations	N experiments
molenpolder_fp	5	1
nashfield_pooled_fp	8	2
niwot_ridge2_dm_fp	5	1
niwot_ridge2_wm_fp	5	1
sanjiang_mire_pfert_fp	9	1
sanjiang_mire_pfert_fp2	9	1
sanjiang_mire_pfert_fp3	9	1
sanpedro_fp	6	3
schiermonnikoog_old_fp	12	1
schiermonnikoog_old_fp2	12	1
schiermonnikoog_young_fp	12	1
schiermonnikoog_young_fp2	12	1
shaaxi_330_fp	3	1
shaaxi_6_fp	3	1
tambopata_fp	6	3
teberda_fp	8	1
tono_fp	6	3
toolik_nonacidic_fp	6	2
verryckt2022_nouragues_fnp	472	11
verryckt2022_paracou_fnp	420	11
wang2019_fnp	25	5
warren2002_fp	30	2
warren2011_fp	120	8
wayqecha_fp	6	3
westbroek_polder_fp	5	1
yu2022_fnp	120	5
yucatan_marsh_highsalinity_fp	30	1
yucatan_marsh_lowsalinity_fp	30	1
yucatan_marsh_mediumsalinity_fp	30	1
zavisic2018_Bad_Bruckenau_fp	26	4
zavisic2018_Unterluus_fp	26	4
zwarte_beek_drained_fp	5	1
zwarte_beek_wet_fp	5	1

Some quick plots:

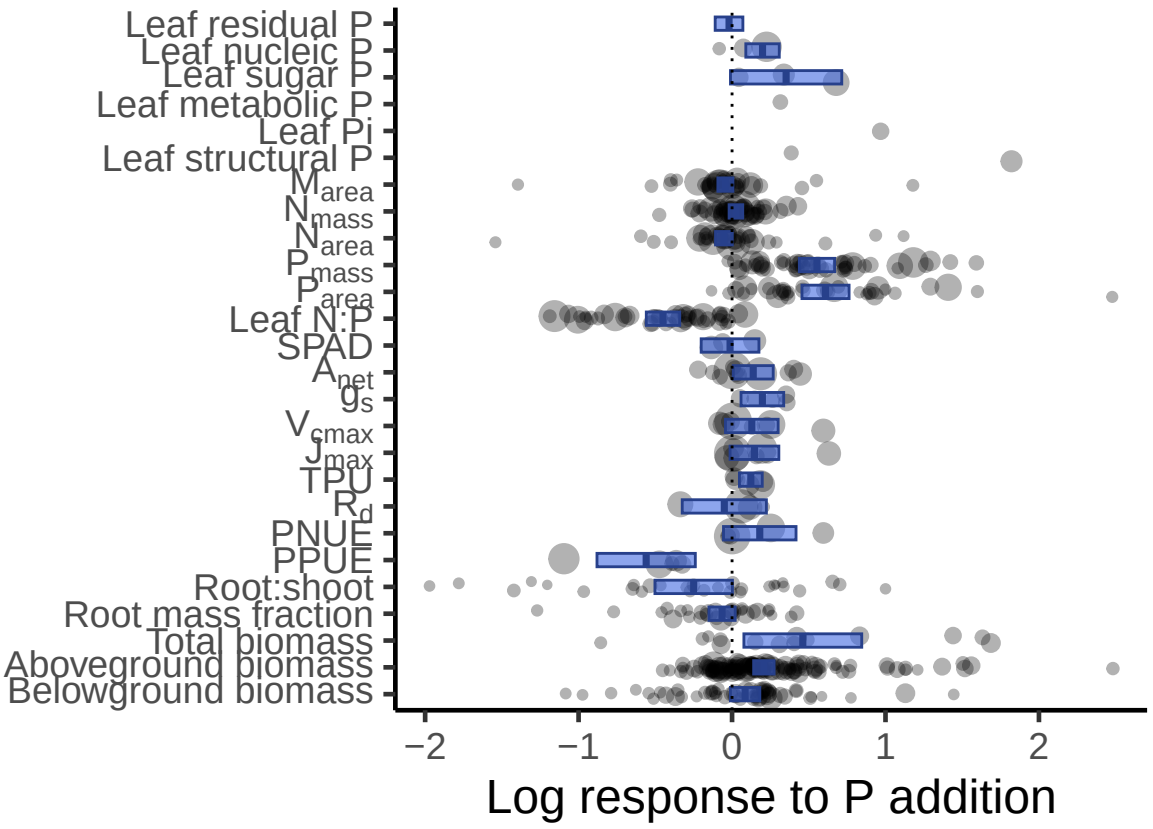
```
pfert_responses3 <- pfert_responses3 %>%
  mutate(myvar = factor(myvar, levels = c("bgb", "agb", "total_biomass", "rmf", "rootshoot",
                                          "leaf_pue", "leaf_nue", "rd", "tpu", "jmax", "vcmax",
                                          "cica", "gs", "anet", "spad", "leaf_np",
                                          "leaf_p_area", "leaf_p_mass", "leaf_n_area",
                                           "leaf_n_mass", "lma", "leaf_strucure_p", "leaf_pi",
                                          "leaf_metabolic_p", "leaf_sugar_p", "leaf_nucleic_p",
                                          "leaf_residual_p")))

meta_plot_p <- ggplot(data = subset(pfert_responses3, myvar != "cica"),
                      aes(x = myvar, y = logr)) +
  geom_jitter(color = rgb(0,0,0,0.3),
              aes( size = 1/logr_se ),
              position = position_jitter(w = 0.2, h = 0),
              show.legend = FALSE) +
```

```
  geom_crossbar( data = df_box_p %>% drop_na(var),
                 aes(x = var, y = middle, ymin = ymin, ymax = ymax),
                 fill = "royalblue",
                 color = "royalblue4",
                 alpha = 0.6,
                 width = 0.5 ) +
  geom_hline( yintercept = 0.0, linewidth = 0.5, linetype = "dotted" ) +
  scale_x_discrete(labels = c("Belowground biomass",
                              "Aboveground biomass",
                              "Total biomass",
                              "Root mass fraction",
                              "Root:shoot",
                              "PPUE",
                              "PNUE",
                              expression("R"["d"]),
                              "TPU",
                              expression("J"["max"]),
                              expression("V"["cmax"]),
                              expression("g"["s"]),
                              expression("A"["net"]),
                              "SPAD",
                              "Leaf N:P",
                              expression("P"["area"]),
                              expression("P"["mass"]),
                              expression("N"["area"]),
                              expression("N"["mass"]),
                              expression("M"["area"]),
                              "Leaf structural P",
                              "Leaf Pi",
                              "Leaf metabolic P",
                              "Leaf sugar P",
                              "Leaf nucleic P",
                              "Leaf residual P")) +

  #scale_x_discrete("", labels = mylabl) +
  labs(x = "",
       y = "Log response to P addition") +
  coord_flip() +
  theme_classic(base_size = 18)
meta_plot_p
```

```
## Warning: Removed 2 rows containing missing values (`geom_point()`).
```



Explore data availability in combined dataset for N*P-fertilization experiments

```
explore_npfert_exps <- df_total %>%

  # fertilisation experiments only
  filter(treatment == "f") %>%

  # P-fertilization in concert with N-fertilization (without K addition)
  filter(npk == "_110")

head(explore_npfert_exps)
```

```
## # A tibble: 6 x 60
##   db      id    duplicate_id citation    response site  study exp      lat   lon
##   <chr>   <chr> <chr>        <chr>       <chr>    <chr> <chr> <chr>  <dbl> <dbl>
## 1 sichuan s886  s886         lawrence_2~ total_b~ 0.12~ 0.12~ 0.12~   0.12 110.
## 2 sichuan s889  s889         lawrence_2~ total_b~ 0.12~ 0.12~ 0.12~   0.12 110.
## 3 sichuan s880  s880         lawrence_2~ total_b~ 0.12~ 0.12~ 0.12~   0.12 110.
## 4 sichuan s883  s883         lawrence_2~ total_b~ 0.12~ 0.12~ 0.12~   0.12 110.
## 5 sichuan s386  s386         augustine_~ anpp     0.28~ 0.28~ 0.28~   0.28  37.9
## 6 sichuan s171  s171         ohalloran_~ agb      -15.~ -15.~ -15.~ -15.4   23.2
## # i 50 more variables: elevation <dbl>, mat <dbl>, map <dbl>,
## #   ecosystem_type <chr>, vegetation_type <chr>, experiment_type <chr>,
## #   community_type <chr>, dominant_species <chr>, growth_form <chr>, age <dbl>,
## #   disturbance_type <chr>, treatment <chr>, npk <chr>, w_t1 <chr>, c_c <dbl>,
```

```
## #   c_t <dbl>, d_t <dbl>, d_t2 <dbl>, n_c <dbl>, n_t <dbl>, p_c <dbl>,
## #   p_t <dbl>, k_c <dbl>, k_t <dbl>, i_c <dbl>, i_t <dbl>, i_t2 <dbl>,
## #   s_c <dbl>, s_t <dbl>, w_t2 <dbl>, w_t3 <dbl>, start_year <dbl>, ...
```

```
## How many experiments?
length(unique(explore_npfert_exps$exp))
```

```
## [1] 286
```

```
## What traits are available?
unique(explore_npfert_exps$response)
```

```
##  [1] "total_biomass_group"      "anpp"
##  [3] "agb"                      "total_biomass"
##  [5] "agb_c"                    "bgb_c"
##  [7] "soil_total_c"             "mbc"
##  [9] "bgb"                      "leaf_c"
## [11] "leaf_biomass_eco"         "agb_group"
## [13] "stem_biomass"             "agb_n"
## [15] "agb_p"                    "soil_total_n"
## [17] "agb_p_stock"              "gpp"
## [19] "fine_root_biomass"        "soil_no3"
## [21] "r_soil"                   "total_biomass_production"
## [23] "soil_total_cn"            "root_production"
## [25] "soc"                      "lwp"
## [27] "gs"                       "soil_no3_leaching"
## [29] "soil_nh4"                 "soil_drp"
## [31] "soil_p"                   "fine_root_production"
## [33] "soil_no3-n_supply_rate"   "soil_nh4-n_supply_rate"
## [35] "soil_p_supply_rate"       "root_shoot_ratio"
## [37] "bpe"                      "total_biomass_np"
## [39] "agb_cn"                   "agb_cp"
## [41] "agb_ndvi"                 "agb_height"
## [43] "bgb_n"                    "bgb_p"
## [45] "root_n_uptake"            "nee"
## [47] "swc"                      "soil_phkcl"
## [49] "soil_pbray"               "som_cn"
## [51] "soil_np"                  "leaf_n_mass"
## [53] "leaf_p_mass"              "leaf_np"
## [55] "litter_decomposition"     "r_root"
## [57] "nep"                      "agb_k_stock"
## [59] "rmf"                      "rootshoot"
## [61] "lma"                      "leaf_n_area"
## [63] "leaf_p_area"              "sla"
## [65] "stom_lim"                 "vcmax"
## [67] "jmax"                     "tpu"
## [69] "leaf_nue"                 "leaf_pue"
## [71] "asat"                     "rd"
## [73] "gsw"                      "spad"
## [75] "anet"                     "leaf_structure_p"
## [77] "leaf_metabolic_p"         "leaf_nucleic_p"
## [79] "leaf_residual_p"          "leaf_thickness"
## [81] "ldmc"                     "leaf_pi"
## [83] "leaf_sugar_p"             "E"
## [85] "leaf_wue"
```

Select variables

```
use_response_np <- c("total_biomass",
                     "agb",
                     "bgb",
                     "leaf_n_mass",
                     "leaf_n_area",
                     "leaf_p_mass",
                     "leaf_p_area",
                     "leaf_np",
                     "gs",
                     "lma",
                     "sla",
                     "spad",
                     "amax",
                     "vcmax",
                     "jmax",
                     "leaf_nue",
                     "leaf_pue",
                     "rd",
                     "tpu",
                     "asat",
                     "cica",
                     "ci"
)

npfert_responses <- explore_npfert_exps %>%
  filter(response %in% use_response_np) %>%
  mutate(myvar = response) %>%
  mutate(myvar = ifelse(myvar %in% c("cica", "ci"),
                        "cica", myvar)) %>%
  mutate(myvar = ifelse(myvar %in%  c("asat", "amax"),
                        "anet", myvar))

use_vars_np <- unique(npfert_responses$myvar)
```

Analysis

Calculate "ROM" - the log transformed ratio of means (Hedges et al., 1999; Lajeunesse, 2011) for each observation pair (ambient and elevated).

```
npfert_responses2 <- npfert_responses %>%

  ## keep only essential variables and drop rows containing missing values for
  ## essential variables
  select(id, duplicate_id, exp, myvar, treatment, sampling_year,
         x_t, x_c, sd_t, sd_c, rep_t, rep_c) %>%

  ## Get logarithm of response ratio and its variance
  metafor::escalc(
    measure = "ROM",
    m1i = x_t, sd1i = sd_t, n1i = rep_t,
    m2i = x_c, sd2i = sd_c, n2i = rep_c,
    data = .,
```

```
    append = TRUE,
    var.names = c("logr", "logr_var")
  ) %>%

  ## to keep the output readable from the console output
  as_tibble() %>%

  ## get standard error
  mutate( logr_se = sqrt(logr_var) / sqrt(rep_t) )

head(npfert_responses2)
```

```
## # A tibble: 6 x 15
##   id    duplicate_id exp       myvar treatment sampling_year    x_t    x_c  sd_t
##   <chr> <chr>        <chr>     <chr> <chr>     <chr>          <dbl>  <dbl> <dbl>
## 1 s171  s171         -15.44_2~ agb   f         2               8.38   9.43  5.76
## 2 s3499 s3499        17.25_-8~ agb   f         3             506.   106.   40.0
## 3 s3502 s3502        17.25_-8~ agb   f         3             364.   200.   76.4
## 4 s3505 s3505        17.25_-8~ agb   f         3             262.    80.1  76.4
## 5 s1525 s1525        -18.66_2~ tota~ f         2              59.5   46.7  27.1
## 6 s169  s169         -18.66_2~ agb   f         1             163.    51.1  64.3
## # i 6 more variables: sd_c <dbl>, rep_t <dbl>, rep_c <dbl>, logr <dbl>,
## #   logr_var <dbl>, logr_se <dbl>
```

```
# Aggregate all measurements (multiple years, sampling dates and plots) by experiment (and response var
npfert_responses3 <- npfert_responses2 %>%

  # suggested addition by Kevin, email 02.10.2023 10:03
  dplyr::distinct(duplicate_id, x_t, x_c, .keep_all = TRUE) |>

  filter(!is.na(logr_var) & !is.na(logr)) %>%

  # re-create ID (common ID per experiment and response variable)
  select(-id) %>%
  mutate( id = paste(exp, myvar, sep = "_XXX_")) %>%

  MAd::agg(
    id = id,
    es = logr,
    var = logr_var,
    cor = 1.0,
    method = "BHHR",
    data = .
  ) %>%

  ## to keep the output readable from the console output
  as_tibble() %>%

  # separate ID again for ease of data use
  mutate( id = str_split(id, "_XXX_") ) %>%
  mutate( exp = purrr::map_chr(id, 1),
          myvar = purrr::map_chr(id, 2) ) %>%

  ## rename again
```

```
  select(exp, myvar, logr = es, logr_var = var) %>%

  ## add number of observations (sum of plots and repeated samplings)
  left_join(
    npfert_responses2 %>%
      group_by(exp, myvar, treatment) %>%
      summarise(n_c = sum(rep_c), n_t = sum(rep_t)),
    by = c("exp", "myvar")
  ) %>%

  ## get standard error. Verify if number available observations are identical
  ## for ambient and elevated. Use N from control here (n_c).
  mutate( logr_se = sqrt(logr_var) / sqrt(n_c) ,

          # merge SLA and LMA measurements by taking inverse of logr (keep SE)
          logr = ifelse(myvar == "sla", -logr, logr),
          myvar = ifelse(myvar == "sla", "lma", myvar))
```

```
## `summarise()` has grouped output by 'exp', 'myvar'. You can override using the
## `.groups` argument.
```

```
head(npfert_responses3)
```

```
## # A tibble: 6 x 8
##   exp              myvar          logr logr_var treatment   n_c   n_t logr_se
##   <chr>            <chr>         <dbl>    <dbl> <chr>     <dbl> <dbl>   <dbl>
## 1 -15.44_23.25_f   agb          -0.118 0.195    f             4     4  0.221
## 2 17.25_-88.77_f   agb           1.11  0.0634   f             9     9  0.0839
## 3 -18.66_25.5_f    total_biomass 0.242 0.0776   f             3     3  0.161
## 4 -18.66_25.5_f    agb           1.01  0.287    f             8     8  0.190
## 5 19.6_-155.33_fnp bgb           0.636 0.0174   f             3     3  0.0762
## 6 -2.98_-47.52_f   agb           0.245 0.000560 f             4     4  0.0118
```

Meta-analysis

Aggregate log-ratios across multiple experiments, taking into account their respective variance and using the experiment identity as a grouping factor for random intercepts.

```
out_np  <- purrr::map(as.list(use_vars_np),
                  ~analyse_meta(npfert_responses3 %>%
                                  rename(var = myvar), nam_target = .))
names(out_np) <- use_vars_np
df_box_np <- purrr::map_dfr(out_np, "df_box") |>
  left_join(
    npfert_responses3 |>
      group_by(myvar) |>
      summarise(logr_min = min(logr), logr_max = max(logr)) |>
      rename(var = myvar),
    by = "var"
  )
saveRDS(df_box_np, file = paste0(here::here(), "df_box_npfert.rds"))
```

Final data size

Number of data points (plot-level measurements) per variable:

```
npfert_responses3 %>%
  group_by(myvar) %>%
  summarise(n_plots = sum(n_c, na.rm = TRUE), n_exp = n()) %>%
  rename("Variable"="myvar", "N observations"="n_plots", "N experiments"="n_exp") %>%
  knitr::kable()
```

Variable	N observations	N experiments
agb	1439	140
anet	323	7
bgb	385	68
gs	35	2
jmax	304	5
leaf_n_area	552	30
leaf_n_mass	710	41
leaf_np	633	41
leaf_nue	230	3
leaf_p_area	527	30
leaf_p_mass	642	42
leaf_pue	230	3
lma	599	31
rd	275	3
spad	107	3
total_biomass	90	14
tpu	43	3
vcmax	304	5

Number of data points (plot-level measurements) per experiment:

```
npfert_responses3 %>%
  group_by(exp) %>%
  summarise(n_plots = sum(n_c), n_exp = n()) %>%
  rename_("Experiment"="exp", "N observations"="n_plots", "N experiments"="n_exp") %>%
  knitr::kable()
```

Experiment	N observations	N experiments
-15.44_23.25_f	4	1
-18.66_25.5_f	11	2
-2.98_-47.52_f	4	1
-21.65_21.81_f	3	1
-22.283_117.666_f	6	1
-22.41_21.71_f	4	1
-22.78_31.25_f	16	2
-23.75_31.43_f	16	2
-24.17_21.89_f	7	2
-24.4_31.75_f	16	2
-25.12_31.23_f	16	2
-25.29_31.91_f	16	2
-3.5_36_f	6	1
-3.95_-79.03_f	12	2
17.25_-88.77_f	9	1

Experiment	N observations	N experiments
19.6_-155.33_fnp	3	1
22.13_-159.63_f	11	1
26.52_109.78_fn2p	3	1
31.37_90.02_f	48	1
31.3_-81.28_f	4	1
31.42_-88.45_f	8	2
31.55_-81.78_f	4	1
32.54_-116.7_fnp	12	1
33.7_120.3_f	15	1
34.92_102.88_f2np	5	1
34.92_102.88_f3np	5	1
34.92_102.88_fnp	5	1
35.97_101.88_f	40	2
37.25_-121.75_forb_fnp	3	1
37.25_-121.75_grass_fnp	3	1
37.48_101.2_fnp	18	3
37.55_-122.3_f	3	1
37.6_101.32_fnp	20	3
37.87_-122.52_f	14	2
39.25_-121.28_fnp	20	1
41.35_36.25_fn2p	4	1
41.35_36.25_fn2p2	4	1
41.35_36.25_fn3p	4	1
41.35_36.25_fn3p2	4	1
41.35_36.25_fnp	4	1
41.35_36.25_fnp2	4	1
41.62_-71.32_fnp	8	2
42.58_122.21_fnp	12	2
44.8_116.03_fnp	24	2
51.85_5.62_fnp	3	1
52.07_5.58_fnp	3	1
52.37_5.1_fnp	6	1
52.5_5.7_fnp	6	1
53.83_-8.83_fnp	10	1
54.63_8.83_fnp	5	1
64.83_-147.72_fnp	3	1
68.2_-149.6_f	16	2
68.38_-104.54_f	4	1
69.43_-133.02_fn2p2	10	1
69.43_-133.02_fnp	10	1
9.6_-79.5_f	3	1
alpflix_fnp	60	1
bennekom_drained_fnp	5	1
bennekom_undrained_fnp	5	1
bown2007_fnp	80	8
buitengoor_1992_fnp	5	1
carswell2005_fnp	80	4
cleland2019_bldr.us_fnp	4	2
cleland2019_bnch.us_fnp	6	2
cleland2019_bogong.au_fnp	6	2
cleland2019_burrawan.au_fnp	6	2
cleland2019_cbgb.us_fnp	12	2

Experiment	N observations	N experiments
cleland2019_cdcr.us_fnp	6	2
cleland2019_cdpt.us_fnp	6	2
cleland2019_cowi.ca_fnp	6	2
cleland2019_elliot.us_fnp	6	2
cleland2019_frue.ch_fnp	6	2
cleland2019_gilb.za_fnp	6	2
cleland2019_hall.us_fnp	6	2
cleland2019_hart.us_fnp	6	2
cleland2019_konz.us_fnp	6	2
cleland2019_lancaster.uk_fnp	4	2
cleland2019_look.us_fnp	6	2
cleland2019_mtca.au_fnp	6	2
cleland2019_sage.us_fnp	6	2
cleland2019_saline.us_fnp	6	2
cleland2019_sgs.us_fnp	6	2
cleland2019_shps.us_fnp	6	2
cleland2019_sier.us_fnp	6	2
cleland2019_smith.us_fnp	6	2
cleland2019_spin.us_fnp	6	2
cleland2019_summ.za_fnp	6	2
cleland2019_trel.us_fnp	6	2
cleland2019_ukul.za_fnp	12	2
cleland2019_unc.us_fnp	6	2
cleland2019_valm.ch_fnp	6	2
crous2017_fnp	2351	12
cuiliugou_f	80	1
cuiliugou_f2	72	1
cuiliugou_f3	72	1
damxung_f	30	1
damxung_f2	30	1
daqinggou_fnp	12	2
drentsche_aa_drained_fnp	5	1
drentsche_aa_wet_fnp	5	1
duolun15_fn2p	4	1
duolun15_fnp	4	1
duolun1_f	4	1
escambia_county_f	8	2
ewenke_f_np	6	1
firn2019_bldr.us_fnp	21	6
firn2019_bnch.us_fnp	51	6
firn2019_bogong.au_fnp	72	6
firn2019_burrawan.au_fnp	73	6
firn2019_cbgb.us_fnp	54	6
firn2019_comp.pt_fnp	78	6
firn2019_cowi.ca_fnp	45	6
firn2019_elliot.us_fnp	54	6
firn2019_frue.ch_fnp	46	6
firn2019_gilb.za_fnp	48	6
firn2019_hopl.us_fnp	51	6
firn2019_kiny.au_fnp	45	6
firn2019_konz.us_fnp	29	6
firn2019_lancaster.uk_fnp	51	6

Experiment	N observations	N experiments
firn2019_look.us_fnp	54	6
firn2019_mcla.us_fnp	51	6
firn2019_mtca.au_fnp	53	6
firn2019_sage.us_fnp	31	6
firn2019_sgs.us_fnp	39	6
firn2019_shps.us_fnp	24	6
firn2019_sier.us_fnp	48	6
firn2019_smith.us_fnp	54	6
firn2019_summ.za_fnp	72	6
firn2019_unc.us_fnp	54	6
firn2019_valm.ch_fnp	120	6
flottbek_fnfp	25	1
gusewell_s1_fnp	4	1
gusewell_s2_fnp	4	1
gusewell_t1_fnp	4	1
gusewell_t2_fnp	4	1
gusewell_v1_fnp	4	1
gusewell_v2_fnp	4	1
gusewell_v3_fnp	4	1
gusewell_w1_fnp	4	1
gusewell_w2_fnp	4	1
gusewell_w3_fnp	4	1
gusewell_w4_fnp	4	1
haibei_fn1p	33	1
haibei_fn1pp	33	1
haibei_fn2p	33	1
haibei_fn2pp	33	1
haibei_fn3p	33	1
haibei_fn3pp	33	1
herschgreen2024_cbgb.us_fnp	88	4
herschgreen2024_cdcr.us_fnp	70	4
herschgreen2024_churn.us_fnp	50	4
herschgreen2024_kbs.us_fnp	50	4
herschgreen2024_konz.us_fnp	69	4
herschgreen2024_spin.us_fnp	77	4
imgers_ng_2006np_fn2	6	1
imgers_ng_2006np_fn3	6	1
imgers_ng_2006np_fn4	6	1
imgers_ng_2006np_fn5	6	1
imgers_ng_2006np_fn6	6	1
imgers_ng_2006np_fp2	6	1
imgers_ng_2006np_fp3	6	1
imgers_ng_2006np_fp4	6	1
imgers_ng_2006np_fp5	6	1
imgers_ng_2006np_fp6	6	1
jingtai_f	32	1
jingtai_f2	32	1
jingtai_f3	32	1
kansasf_fnp	12	1
kansask_fnp	12	1
katelijne_2016_fnp	5	1
katelijne_2017_f	5	1

Experiment	N observations	N experiments
luneburg_field_2006_fnp	10	1
luneburg_field_2008_fnp	10	1
luneburg_gh_drought_molinia_fnp	NA	2
luneburg_gh_fert_molinia_fnp	10	1
michigan_underc_bog_fnp	19	1
michigan_underc_intermfen_fnp	17	1
michigan_underc_richfen_fnp	20	1
mo2019_fnp	200	8
mo2021_fnp	10	2
nashfield_pooled_fnp	8	2
niwot_ridge2_dm_fnp	10	1
niwot_ridge2_wm_fnp	10	1
sanpedro_fnp	6	3
schiermonnikoog_old_fn2p	12	1
schiermonnikoog_old_fn2p2	12	1
schiermonnikoog_old_fnp	12	1
schiermonnikoog_old_fnp2	12	1
schiermonnikoog_young_fn2p	12	1
schiermonnikoog_young_fn2p2	12	1
schiermonnikoog_young_fnp	12	1
schiermonnikoog_young_fnp2	12	1
shaaxi_330_fnp	3	1
shaaxi_6_fnp	3	1
tambopata_fnp	6	3
teberda_fnp	8	1
tono_fnp	6	3
toolik_acidic_1981_f	4	1
toolik_acidic_f	4	1
toolik_nonacidic_fnp	18	3
toolik_shrub_f	6	3
verryckt2022_nouragues_fnp	472	11
verryckt2022_paracou_fnp	420	11
wang2019_fnp	10	1
wayqecha_fnp	6	3
yu2022_fnp	120	5
yucatan_marsh_highsalinity_fnp	30	1
yucatan_marsh_lowsalinity_fnp	30	1
yucatan_marsh_mediumsalinity_fnp	30	1
zwarte_beek_drained_fnp	5	1
zwarte_beek_wet_fnp	5	1

Some quick plots:

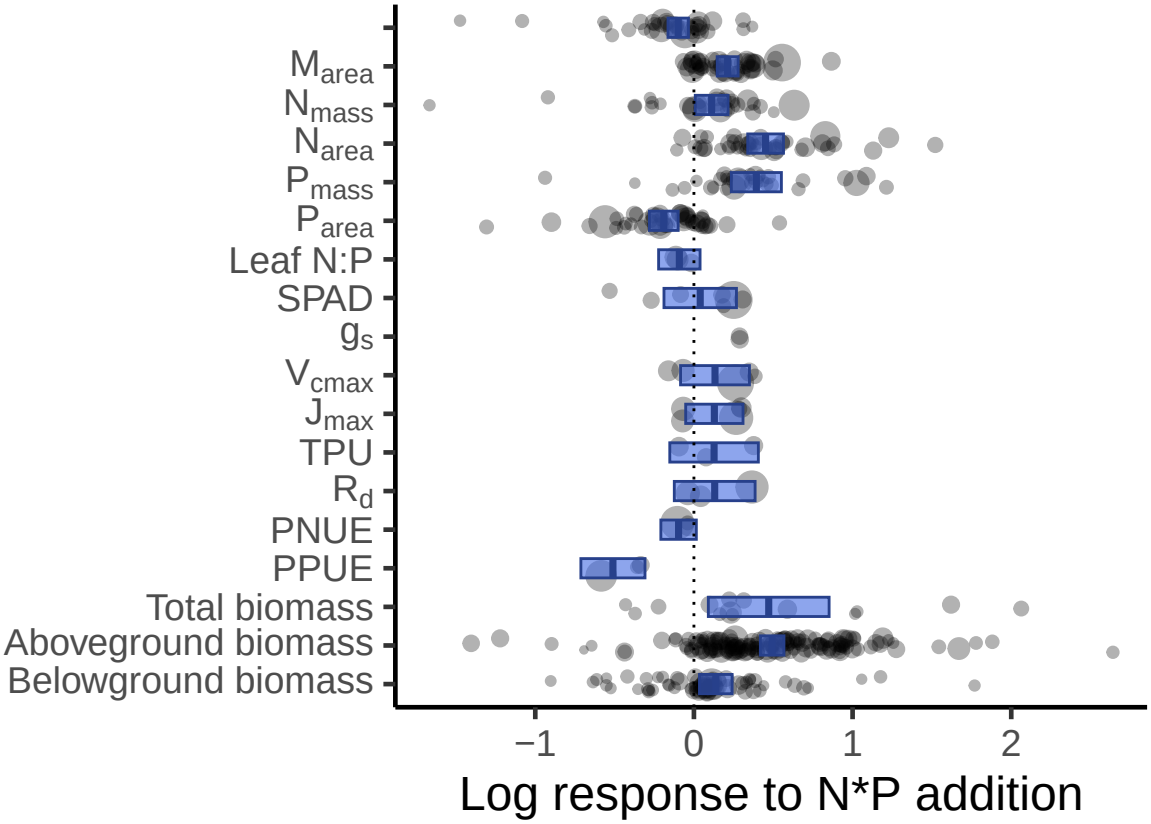
```
npfert_responses3 <- npfert_responses3 %>%
  mutate(myvar = factor(myvar, levels = c("bgb", "agb", "total_biomass", "leaf_pue",
                                          "leaf_nue", "rd", "tpu", "jmax", "vcmax",
                                          "cica", "gs", "anet", "spad", "leaf_np",
                                          "leaf_p_area", "leaf_p_mass", "leaf_n_area",
                                           "leaf_n_mass", "lma")))

meta_plot_np <- ggplot(data = subset(npfert_responses3, myvar != "cica"),
```

```
                    aes(x = myvar, y = logr)) +
  geom_jitter(color = rgb(0,0,0,0.3),
              aes( size = 1/logr_se ),
              position = position_jitter(w = 0.2, h = 0),
              show.legend = FALSE) +
  geom_crossbar( data = df_box_np %>% drop_na(var),
                 aes(x = var, y = middle, ymin = ymin, ymax = ymax),
                 fill = "royalblue",
                 color = "royalblue4",
                 alpha = 0.6,
                 width = 0.5 ) +
  geom_hline( yintercept = 0.0, linewidth = 0.5, linetype = "dotted" ) +
  scale_x_discrete(labels = c("Belowground biomass",
                              "Aboveground biomass",
                              "Total biomass",
                              "PPUE",
                              "PNUE",
                              expression("R"["d"]),
                              "TPU",
                              expression("J"["max"]),
                              expression("V"["cmax"]),
                              expression("g"["s"]),
                              "SPAD",
                              "Leaf N:P",
                              expression("P"["area"]),
                              expression("P"["mass"]),
                              expression("N"["area"]),
                              expression("N"["mass"]),
                              expression("M"["area"]))) +

  #scale_x_discrete("", labels = mylabl) +
  labs(x = "",
       y = "Log response to N*P addition") +
  coord_flip() +
  theme_classic(base_size = 18)
meta_plot_np
```

```
## Warning: Removed 2 rows containing missing values (`geom_point()`).
```




```
# Add exp type to all data frames to merge together
df_box_np$manip_type <- "np"
df_box_p$manip_type <- "p"
df_box_n$manip_type <- "n"

npfert_responses3$manip_type <- "np"
pfert_responses3$manip_type <- "p"
nfert_responses3$manip_type <- "n"

# Merge P and NP meta results
df_box_all <- df_box_n %>%
  full_join(df_box_p) %>%
  full_join(df_box_np) %>%
  mutate(manip_type = factor(manip_type, levels = c("np", "p", "n")))
```

```
## Joining with `by = join_by(var, middle, ymin, ymax, middle_scaled, ymin_scaled,
## ymax_scaled, logr_min, logr_max, manip_type)`
## Joining with `by = join_by(var, middle, ymin, ymax, middle_scaled, ymin_scaled,
## ymax_scaled, logr_min, logr_max, manip_type)`
```

```
fert_exp_responses_all <- nfert_responses3 %>%
  full_join(pfert_responses3) %>%
  full_join(npfert_responses3) %>%
  mutate(manip_type = factor(manip_type, levels = c("np", "p", "n")))
```

```
## Joining with `by = join_by(exp, myvar, logr, logr_var, treatment, n_c, n_t,
## logr_se, manip_type)`
## Joining with `by = join_by(exp, myvar, logr, logr_var, treatment, n_c, n_t,
```

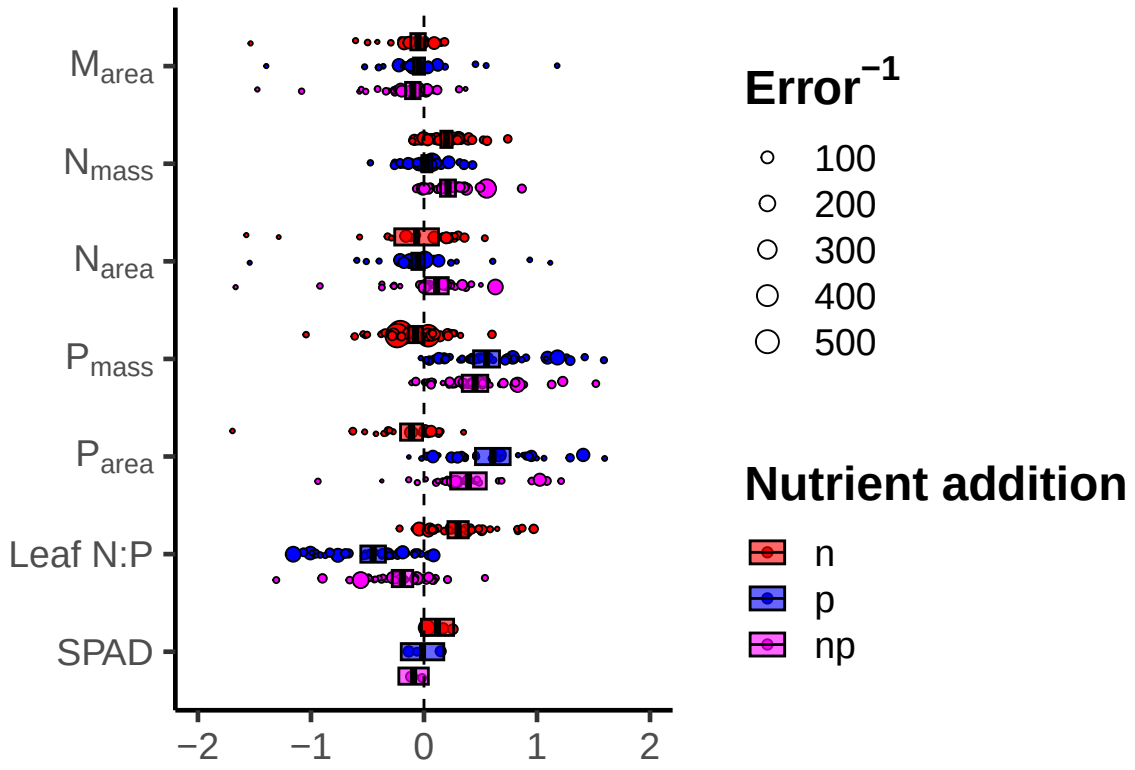
```
## logr_se, manip_type)`
```

```
head(fert_exp_responses_all)
```

```
## # A tibble: 6 x 9
##   exp            myvar    logr logr_var treatment   n_c   n_t logr_se manip_type
##   <chr>          <fct>   <dbl>    <dbl> <chr>     <dbl> <dbl>   <dbl> <fct>
## 1 -11.97_-38.12~ agb    0.0789 0.00489  f            16    16 0.0175  n
## 2 34.2_106.43_f  agb    0.429  0.00271  f            10    10 0.0165  n
## 3 37.25_-121.75~ agb    0      0.00292  f             3     3 0.0312  n
## 4 37.25_-121.75~ agb   -0.121  0.00305  f             3     3 0.0319  n
## 5 38.53_-76.33_f agb    1.01   0.00544  f            35    35 0.0125  n
## 6 38.53_-76.33_f tota~  0.465  0.000154 f            15    15 0.00320 n
```

```
# Plot nutrients. Separating by trait type to avoid plot overwhelm
meta_plot_all_leaf_nutrients <- ggplot(
  data = subset(fert_exp_responses_all,
                myvar %in% c("lma", "leaf_n_mass", "leaf_n_area", "leaf_p_mass",
                             "leaf_p_area", "leaf_np", "spad")),
  aes(x = myvar, y = logr, fill = manip_type)) +
  geom_jitter(position = position_jitterdodge(jitter.width = 0.1,
                                              dodge.width = 0.75),
              shape = 21, aes(size = 1/logr_se)) +
  geom_crossbar(data = df_box_all %>% drop_na(var) %>%
                  filter(var %in% c("lma", "leaf_n_mass", "leaf_n_area",
                                    "leaf_p_mass", "leaf_p_area", "leaf_np",
                                    "spad")),
                aes(x = var, y = middle, ymin = ymin, ymax = ymax),
                alpha = 0.6, width = 0.5,
                position = position_dodge(width = 0.75)) +
  geom_hline(yintercept = 0, linewidth = 0.5, linetype = "dashed") +
  scale_x_discrete(labels = c("SPAD",
                              "Leaf N:P",
                              expression("P"["area"]),
                              expression("P"["mass"]),
                              expression("N"["area"]),
                              expression("N"["mass"]),
                              expression("M"["area"]))) +
  scale_y_continuous(limits = c(-2, 2), breaks = seq(-2, 2, 1)) +
  scale_fill_manual(limits = c("n", "p", "np"),
                    values = c("red", "blue", "magenta")) +
  scale_size(range = c(0.25, 4)) +
  labs(x = "",
       y = "Log response to N, P, or N+P addition",
       fill = "Nutrient addition",
       size = expression(bold("Error"^"-1"))) +
  coord_flip() +
  theme_classic(base_size = 18) +
  theme(legend.position = "right",
        legend.title = element_text(face = "bold"),
        axis.title.x = element_text(face = "bold"))
meta_plot_all_leaf_nutrients
```

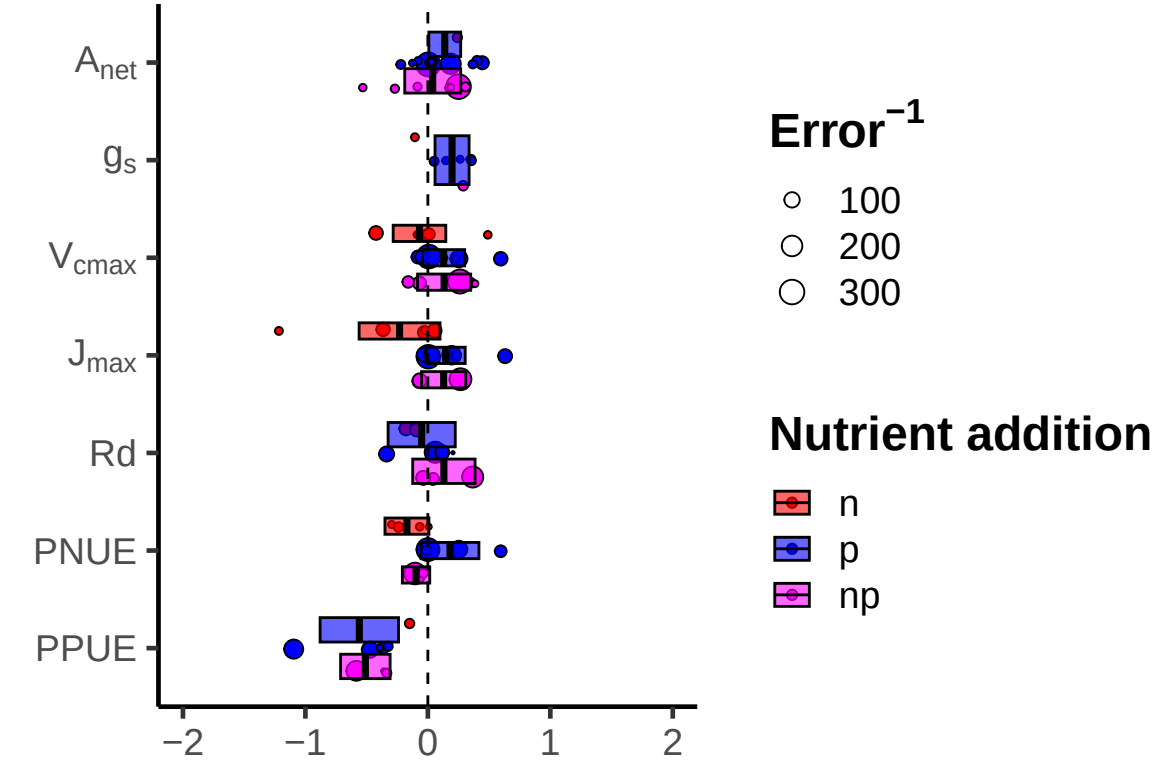
```
## Warning: Removed 4 rows containing missing values (`geom_point()`).
```



Log response to N, P, or N+P addition

```
# Plot photosynthetic traits. Separating by trait type to avoid plot overwhelm
meta_plot_all_photo <- ggplot(
  data = subset(fert_exp_responses_all,
                myvar %in% c("anet", "gs", "vcmax", "jmax",
                             "rd", "leaf_nue", "leaf_pue")),
  aes(x = myvar, y = logr, fill = manip_type)) +
  geom_jitter(position = position_jitterdodge(jitter.width = 0.1,
                                              dodge.width = 0.75),
              shape = 21, aes(size = 1/logr_se)) +
  geom_crossbar(data = df_box_all %>% drop_na(var) %>%
                  filter(var %in% c("anet", "gs", "vcmax", "jmax",
                                    "rd", "leaf_nue", "leaf_pue")),
                aes(x = var, y = middle, ymin = ymin, ymax = ymax),
                alpha = 0.6, width = 0.5,
                position = position_dodge(width = 0.75)) +
  geom_hline(yintercept = 0, linewidth = 0.5, linetype = "dashed") +
  scale_x_discrete(labels = c("PPUE",
                              "PNUE",
                              expression("Rd"),
                              expression("J"["max"]),
                              expression("V"["cmax"]),
                              expression("g"["s"]),
                              expression("A"["net"]))) +
  scale_y_continuous(limits = c(-2, 2), breaks = seq(-2, 2, 1)) +
  scale_fill_manual(limits = c("n", "p", "np"),
                    values = c("red", "blue", "magenta")) +
  scale_size(range = c(0.25, 4)) +
```

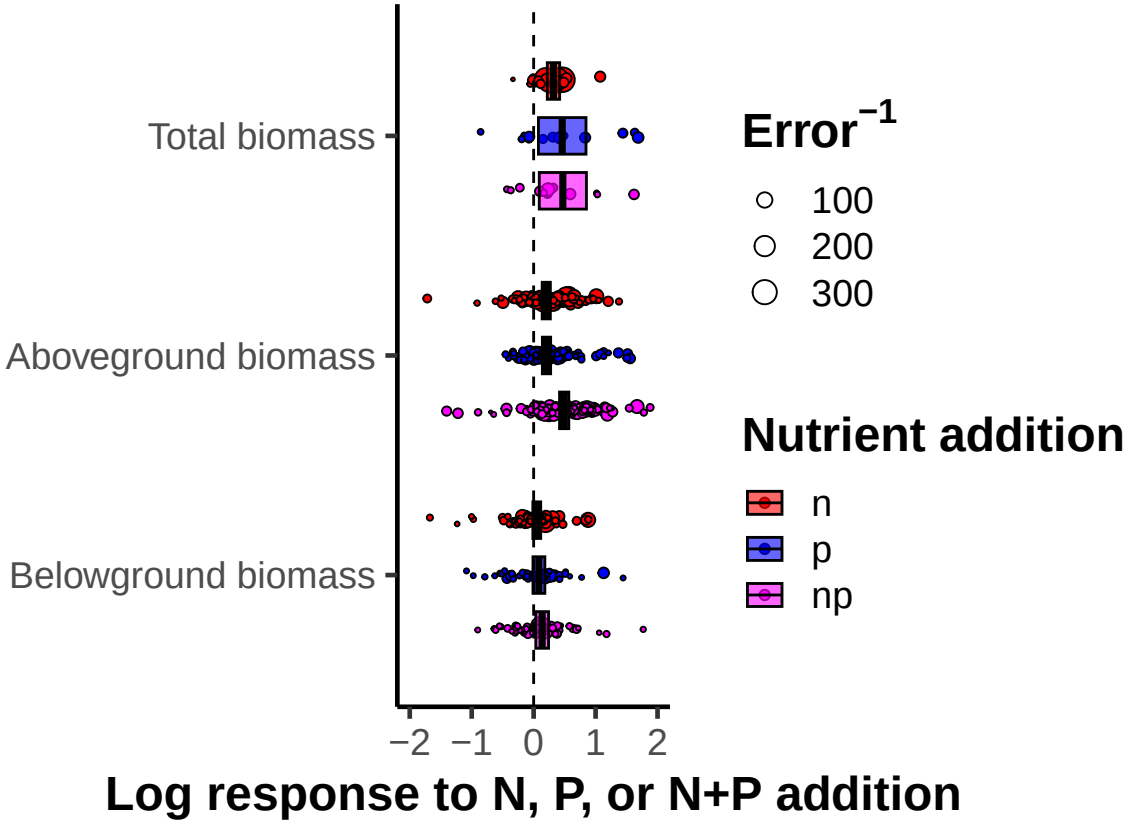
```
  labs(x = "",
       y = "Log response to N, P, or N+P addition",
       fill = "Nutrient addition",
       size = expression(bold("Error"^"-1"))) +
  coord_flip() +
  theme_classic(base_size = 18) +
  theme(legend.position = "right",
        legend.title = element_text(face = "bold"),
        axis.title.x = element_text(face = "bold"))
meta_plot_all_photo
```




```
# Plot biomass traits. Separating by trait type to avoid plot overwhelm
meta_plot_all_biomass <- ggplot(
  data = subset(fert_exp_responses_all,
                myvar %in% c("bgb", "agb", "total_biomass")),
  aes(x = myvar, y = logr, fill = manip_type)) +
  geom_jitter(position = position_jitterdodge(jitter.width = 0.1,
                                              dodge.width = 0.75),
              shape = 21, aes(size = 1/logr_se)) +
  geom_crossbar(data = df_box_all %>% drop_na(var) %>%
                  filter(var %in% c("bgb", "agb", "total_biomass")),
                aes(x = var, y = middle, ymin = ymin, ymax = ymax),
                alpha = 0.6, width = 0.5,
                position = position_dodge(width = 0.75)) +
  geom_hline(yintercept = 0, linewidth = 0.5, linetype = "dashed") +
  scale_x_discrete(labels = c("Belowground biomass",
                              "Aboveground biomass",
```

```
                              "Total biomass")) +
  scale_y_continuous(limits = c(-2, 2), breaks = seq(-2, 2, 1)) +
  scale_fill_manual(limits = c("n", "p", "np"),
                    values = c("red", "blue", "magenta")) +
  scale_size(range = c(0.25, 4)) +
  labs(x = "",
       y = "Log response to N, P, or N+P addition",
       fill = "Nutrient addition",
       size = expression(bold("Error"^"-1"))) +
  coord_flip() +
  theme_classic(base_size = 18) +
  theme(legend.position = "right",
        legend.title = element_text(face = "bold"),
        axis.title.x = element_text(face = "bold"))
meta_plot_all_biomass
```

```
## Warning: Removed 8 rows containing missing values (`geom_point()`).
```



Write plots

```
# N meta-analysis
# png("../plots/meta_results_n.png", width = 9, height = 6,
#     units = "in", res = 600)
# meta_plot_n
# dev.off()
#
# # P meta-analysis
```

```
png("../plots/meta_results_p.png", width = 9, height = 6,
    units = "in", res = 600)
meta_plot_p
```

```
## Warning: Removed 2 rows containing missing values (`geom_point()`).
```

```
dev.off()
```

```
## pdf
##   2
```

```
#
# # NP meta-analysis
# png("../plots/meta_results_np.png", width = 9, height = 6,
#     units = "in", res = 600)
# meta_plot_np
# dev.off()
#
# # Combine N, P, NP meta-analysis into single figure. First, leaf nutrients
# png("../plots/CNPmeta_plot_nutrients_combined.png", width = 9, height = 6,
#     units = "in", res = 600)
# meta_plot_all_leaf_nutrients
# dev.off()
#
# # Second, photosynthetic traits
# png("../plots/CNPmeta_plot_photo_combined.png", width = 9, height = 6,
#     units = "in", res = 600)
# meta_plot_all_photo
# dev.off()
#
# # Third, biomass
# png("../plots/CNPmeta_plot_biomass_combined.png", width = 9, height = 6,
#     units = "in", res = 600)
# meta_plot_all_biomass
# dev.off()
#
# # Finally, lets arange all of the combined plots into a 3-panel figure
# png("../plots/CNPmeta_plot_all_combined.png", height = 16, width = 9,
#     units = "in", res = 600)
# ggarrange(meta_plot_all_leaf_nutrients, meta_plot_all_photo,
#           meta_plot_all_biomass, nrow = 3, ncol = 1, common.legend = TRUE,
#           legend = "right", labels = c("(a)", "(b)", "(c)", align = "hv"))
# dev.off()
```