compare growth estimates

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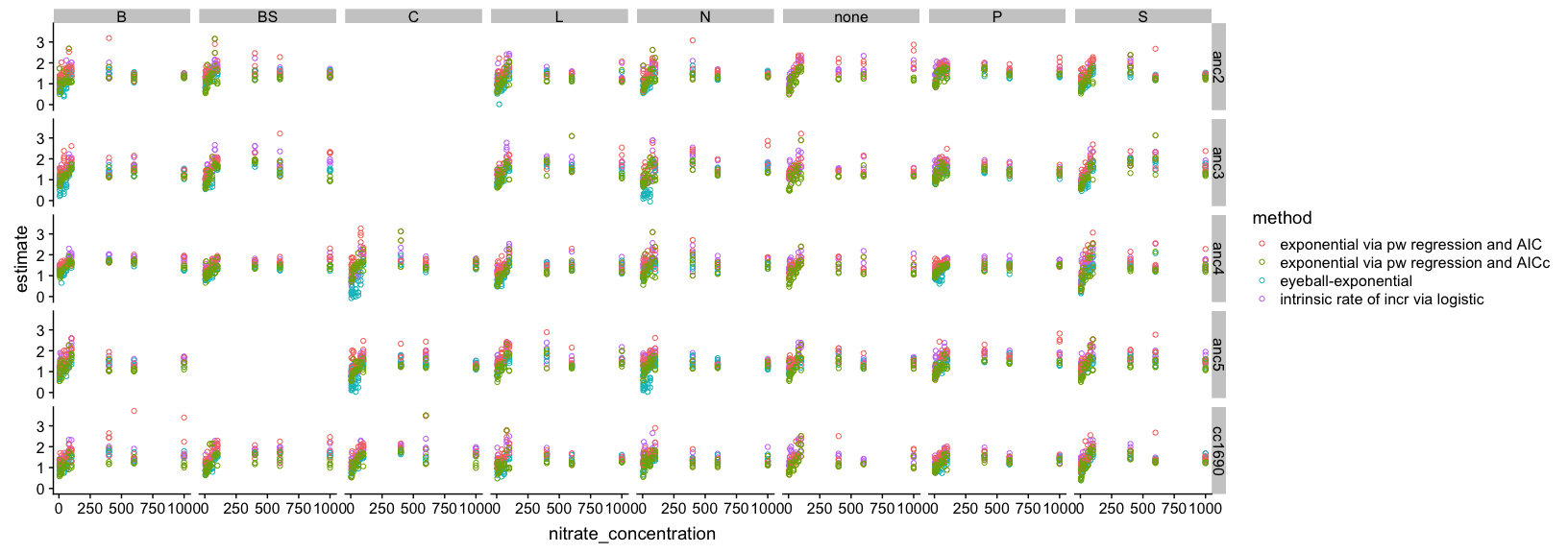
Wed Feb 20 10:45:43 2019

knitr::opts\_chunk$set(echo = TRUE)  
knitr::opts\_chunk$set(message = FALSE)  
knitr::opts\_chunk$set(warning = FALSE)  
knitr::opts\_chunk$set(cache = TRUE)

library(tidyverse)  
library(cowplot)  
library(broom)  
library(readxl)  
library(janitor)  
library(plotrix)  
library(here)  
  
  
  
treatments <- read\_excel(here("data-general", "ChlamEE\_Treatments\_JB.xlsx")) %>%   
 clean\_names() %>%   
 mutate(treatment = ifelse(is.na(treatment), "none", treatment)) %>%   
 filter(population != "cc1629")   
  
  
# compare growth rate estimates -------------------------------------------

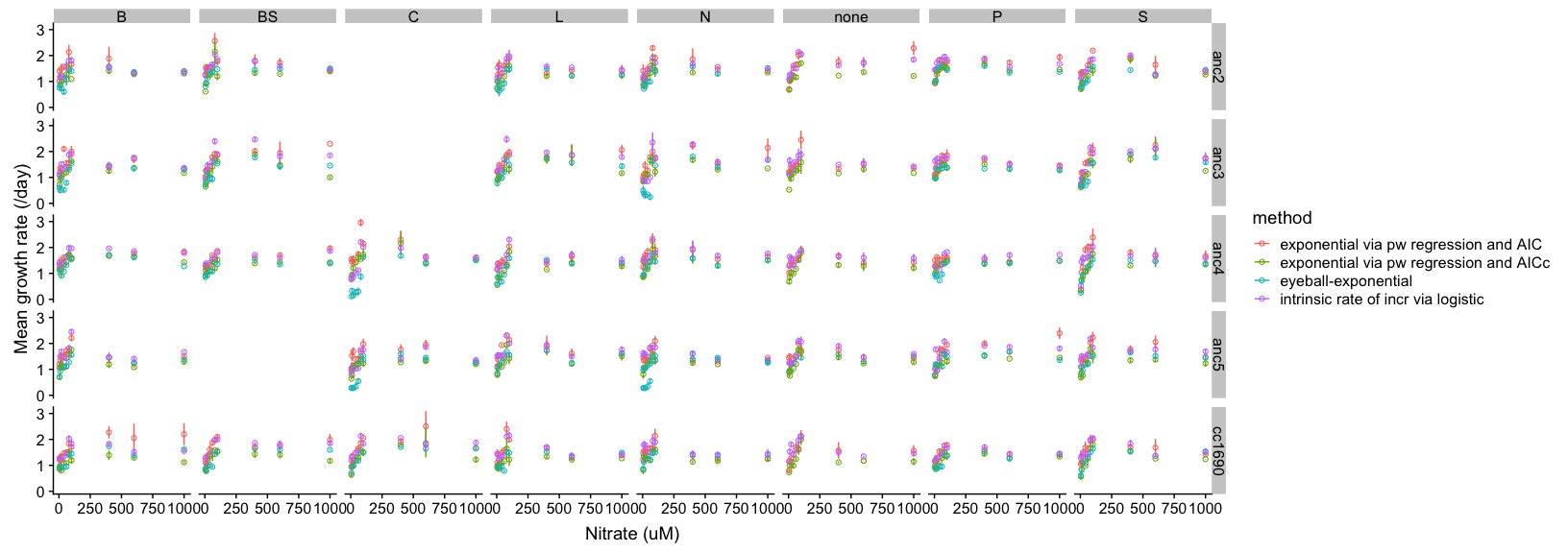
logistic <- read\_csv(here("data-processed", "nitrate\_exp\_growth\_logistic.csv")) %>%   
 select(population, ancestor\_id, treatment, nitrate\_concentration, estimate) %>%   
 mutate(method = "logistic") %>%   
 distinct(population, ancestor\_id, treatment, nitrate\_concentration, estimate) %>%   
 filter(!is.na(ancestor\_id)) %>%   
 mutate(population = as.character(population)) %>%   
 mutate(method = "intrinsic rate of incr via logistic")  
eyeball <- read\_csv(here("data-processed", "nitrate\_exp\_growth\_eyeball.csv")) %>%   
 select(population, ancestor\_id, treatment, nitrate\_concentration.x, estimate) %>%  
 rename(nitrate\_concentration = nitrate\_concentration.x) %>%   
 distinct(population, ancestor\_id, treatment, nitrate\_concentration, estimate) %>%   
 filter(!is.na(population))%>%   
 mutate(population = as.character(population)) %>%   
 mutate(method = "eyeball-exponential")  
AIC\_exp <- read\_csv(here("data-processed", "nitrate\_exp\_growth\_w\_growthtools\_AIC.csv")) %>%   
 rename(estimate = mu) %>%   
 mutate(method = "exponential via pw regression and AIC") %>%   
 mutate(population = as.character(population))  
AIC\_exp <- left\_join(AIC\_exp, treatments)  
  
AICc\_exp <- read\_csv(here("data-processed", "nitrate\_exp\_growth\_w\_growthtools.csv")) %>%   
 rename(estimate = mu) %>%   
 mutate(method = "exponential via pw regression and AICc") %>%   
 mutate(population = as.character(population))  
AICc\_exp <- left\_join(AICc\_exp, treatments)  
  
all\_growth\_estimates <- bind\_rows(logistic, eyeball, AIC\_exp, AICc\_exp)

all\_growth\_estimates %>%  
 group\_by(population, nitrate\_concentration) %>%   
 ggplot(aes(x = nitrate\_concentration, y = estimate, color = method)) + geom\_point(shape = 1) +  
 facet\_grid(ancestor\_id ~ treatment)



ggsave(here("figures", "comparison\_nitrate\_monod.png"), width = 15, height = 6)

all\_growth\_estimates %>%   
 group\_by(population, nitrate\_concentration, ancestor\_id, treatment, method) %>%   
 summarise\_each(funs(mean, std.error), estimate) %>%   
 ggplot(aes(x = nitrate\_concentration, y = mean, color = method)) + geom\_point(shape=1) +  
 geom\_errorbar(aes(ymin = mean - std.error, ymax = mean + std.error), width = 0.1) +  
 facet\_grid(ancestor\_id ~ treatment) + ylab("Mean growth rate (/day)") + xlab("Nitrate (uM)")



ggsave(here("figures", "comparison\_nitrate\_monod\_means.png"), width = 17, height = 6)