TUrf production modelling

2022-06-28

Packages

Loading data compiled and reworked by Tebbett and Bellwood 2021 Mar Env Res.

Depth data were added manually by looking at each individual study

```
data <- read_csv('turf_prod_val.csv') |>
  filter(!is.na(depth))
```

```
## Rows: 214 Columns: 4
## -- Column specification --------------------------------------------------------
## Delimiter: ","
## chr (3): mean_prod (g C m-2 day-1), obs, Ref
## dbl (1): depth
##
## 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.
```

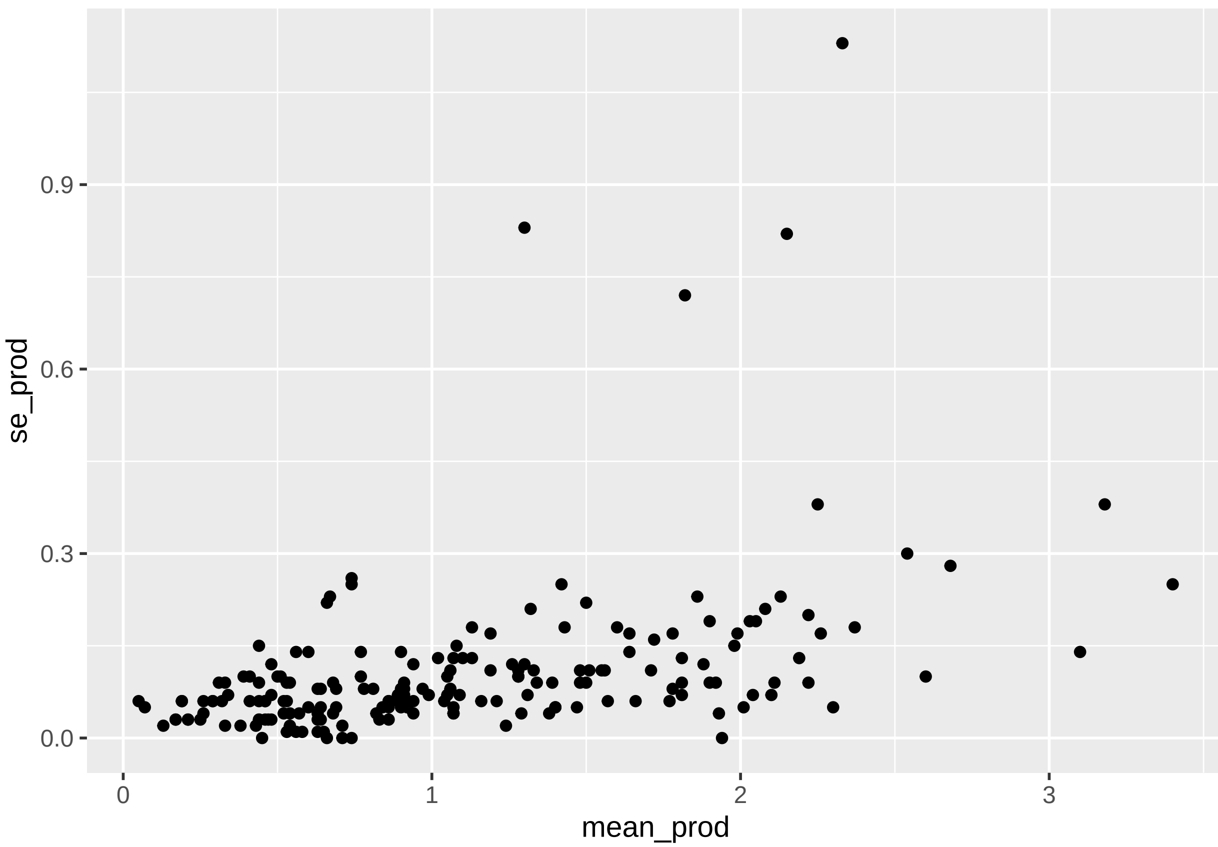
```
unit <- names(data)[1]
names(data)[1] <- 'prod'

x <- str_split(data$prod, '\xb1')
data$mean_prod <- as.numeric(substr(unlist(lapply(x, function(x)x[1])),1,4))
data$se_prod <- as.numeric(substr(unlist(lapply(x, function(x)x[2])),2,5))
```

```
## Warning: NAs introduced by coercion
```

```
data <- data %>% filter(mean_prod != 0)
```

Now, for the data points we do not have standard error values,

determine them from the relationship between mean and se:



Predicting variability using the mean for 14 points and also adjusting McClure 2019, ## which is a ci and not se, and also adding a small non zero value to all zero se

```
mod_se <- lm(se_prod ~ mean_prod, data=data)
## Model sucks, but better than to consider zero

data[is.na(data$se_prod),'se_prod'] <- round(predict(mod_se, newdata=data[is.na(data$se_prod),]),2)
data[data$Ref == 'McClure 2019', 'se_prod'] <- data[data$Ref == 'McClure 2019', 'se_prod'] / 1.96
nzmin <- function(x) min(x[x>0])
data[data$se_prod == 0,'se_prod'] <- nzmin(data$se_prod)
```

And finally modelling algal turf productivity using a meta-analysis

Bayesian model with depth as the only predictor

Loading and tidying data to predict for

```
## Constrained max depth of site to 15m

pred_depth <- read.csv('moorea_depth.csv') %>%
```

```
  mutate(site=tolower(site)) %>%
  group_by(site) %>%
  mutate(depth=if_else(depth < -15,-15, depth)*-1) %>%
  slice_max(depth)

pred_data <- read.csv('moorea_benthos.csv') %>%
  mutate(site=gsub('\\s','_',tolower(site)))
```

Filtering and manipulating the time series for the categories of interest.

For Moorea, at the moment, these could be algal turfs, halimeda and macroalgae

```
ts_data <- left_join(pred_data,pred_depth, by='site') %>%
  filter(Habitat=='Outer slope' & Season=='Mar') %>%
  mutate(subs_group=case_when(
      Substrate == 'Dead coral' ~ 'algal_turf',
      Substrate == 'Stegastes Turf' ~ 'algal_turf',
      Substrate == 'Rubble' ~ 'algal_turf',
      Substrate == 'Pavement' ~ 'algal_turf',
      Substrate == 'Macroalgae' ~ 'macroalgae',
      Substrate == 'Turbinaria' ~ 'macroalgae',
      Substrate == 'Halimeda' ~ 'halimeda',
      TRUE ~ Substrate,
  )) %>%
  filter(subs_group %in% c('algal_turf','macroalgae')) %>%
  group_by(Year, site, Transect, lat, long, depth, subs_group) %>%
  summarise(prop=sum(proportion), .groups='drop_last') %>%
  pivot_wider(names_from=subs_group,values_from=prop,values_fill=0)
```

Now, how about trying to predict benthic reef productivity

by merging area specific turf productivity predicted

using the data compiled by Tebbett and Bellwood and turf cover?

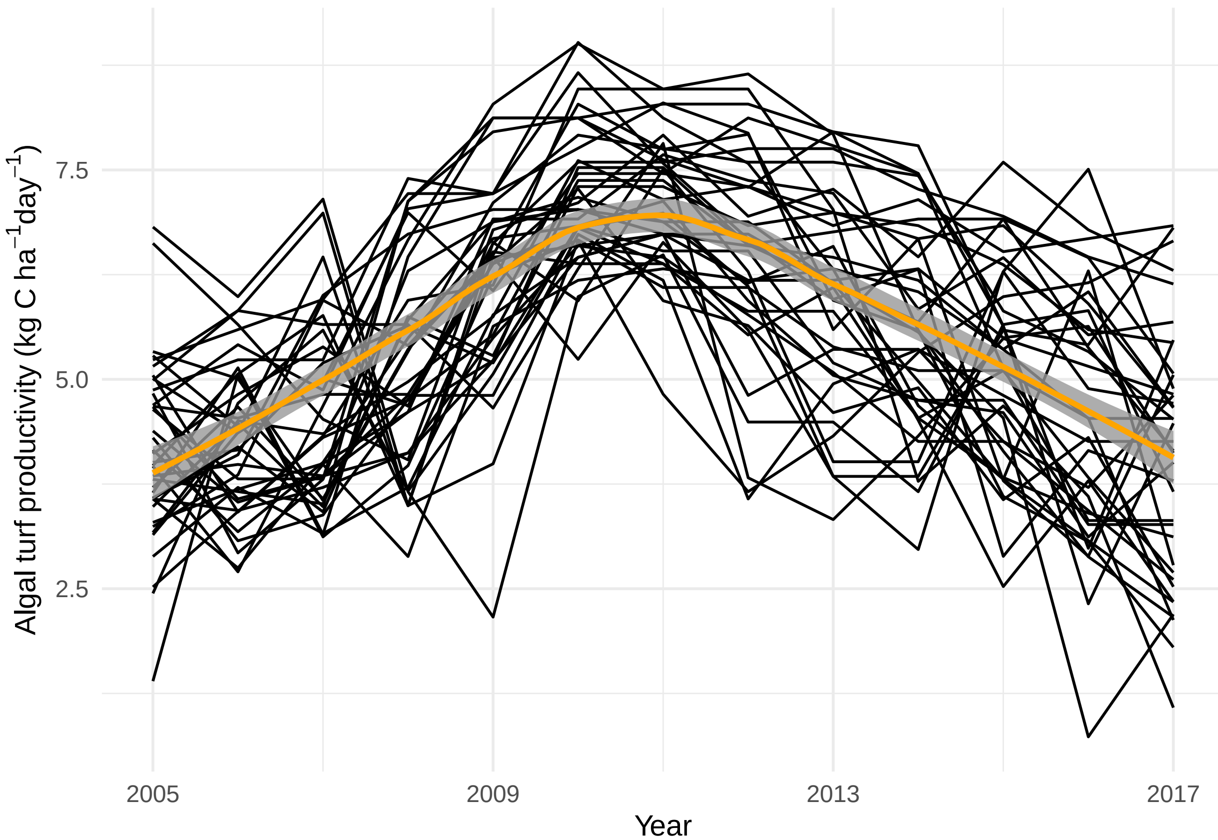
```
pred_val <- posterior_epred(brmod,
      newdata=ts_data %>% mutate(se_prod=0.1), ndraws=1000)

tot_turf_prod <- ((ts_data$algal_turf * t(pred_val)) * 10000)/1000
## in kg C ha day-1


# aggregating

fts_data <- cbind(ts_data,
      turf_prod_kghaday_med=apply(tot_turf_prod,1,median),
      turf_prod_kghaday_lhd=apply(tot_turf_prod,1,function(x) median_hdci(x)$ymin),
      turf_prod_kghaday_uhd=apply(tot_turf_prod,1,function(x) median_hdci(x)$ymax))
```

```
## in kg C ha-1 day-1
```

Now plotting

First the time series of turf productivity over time in Moorea

```
ggplot(data=fts_data) +
  geom_line(aes(x=Year,y=turf_prod_kghaday_med,group=interaction(Transect,site))) +
  geom_smooth(aes(x=Year,y=turf_prod_kghaday_med),
              method = 'loess', formula = y ~ x,
              colour='orange', alpha=0.8) +
  scale_x_continuous(breaks=c(2005,2009,2013,2017)) +
  ylab(expression(Algal~turf~productivity~'('*kg~C~ha^-1*day^-1*')')) +
  theme_minimal()
```



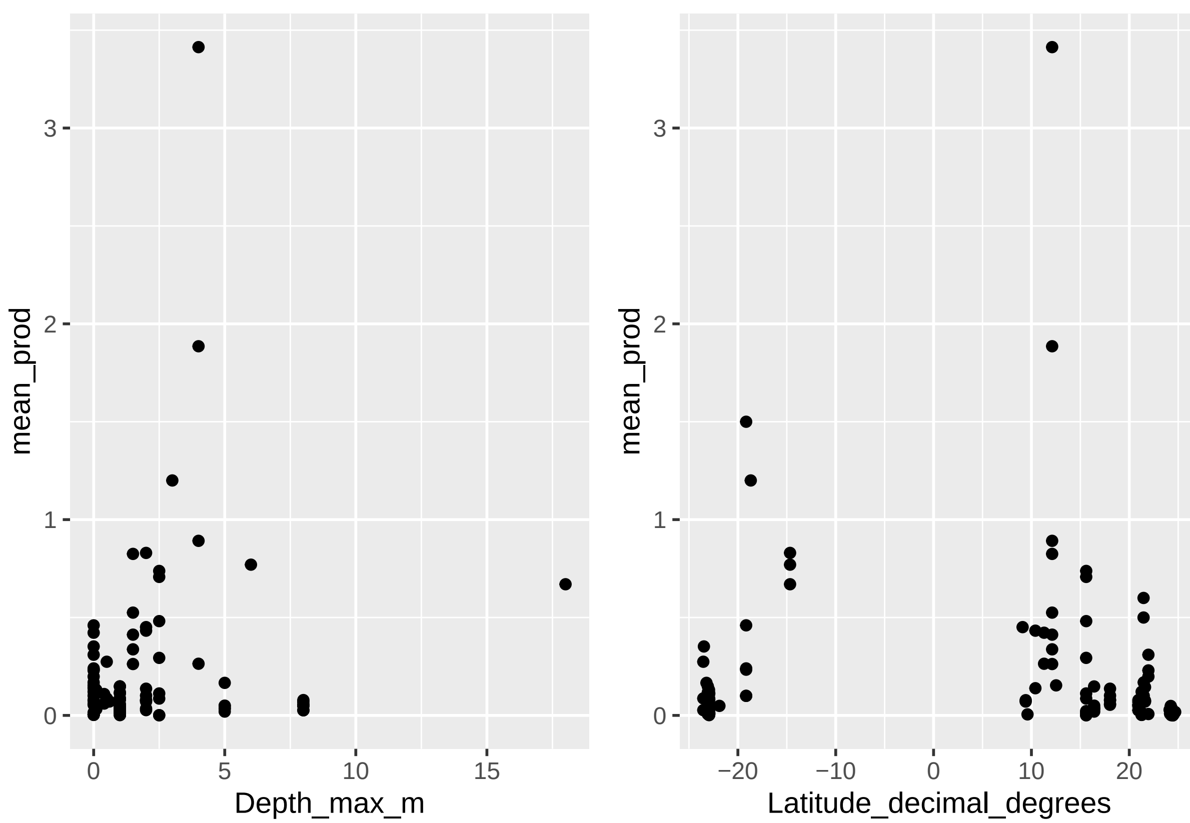
And using Duarte's et al 2022's data to explore a model for macroalgae

It could be possible to do the same for Halimeda, but there are less values

Maybe return to this possibility later?

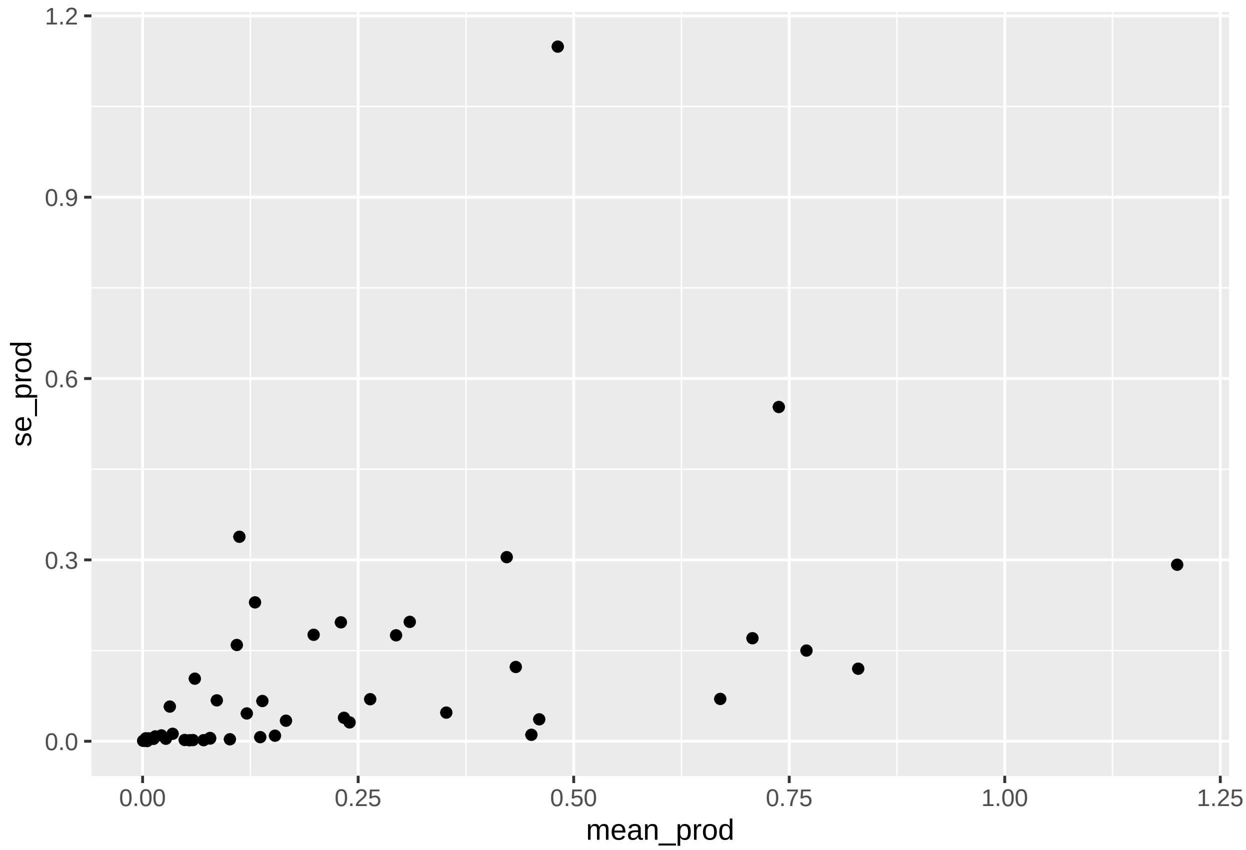
```
dmachal <- read.csv('macroalgae_npp_dataset.csv') %>%
  filter(Habitat_category_Duarte_etal_2021 %in% c('Coral Reef Algae','Subtidal brown algae') & abs(Lati
  mutate(mean_prod = ((Avg_NPP_kg_C_m2_y) * 1000) / 365,
         se_prod   = ((stdev_NPP_kg_C_m2_y) * 1000) / 365)
# in g C m-2 day-1


## Having a look at the data from a few perspectives

p1 <- ggplot(dmachal) +
  geom_point(aes(x=Depth_max_m, y=mean_prod))

p2 <-ggplot(dmachal) +
  geom_point(aes(x=Latitude_decimal_degrees, y=mean_prod))

p1 + p2
```

```
## Warning: Removed 19 rows containing missing values (geom_point).
```



```
## Get outta here, nothing useful to predict so just including variability in a meta-analysis
```

Can we predict standard error values from a relationship between mean and se as we did for algal turfs?




```
mod_se2 <- lm(se_prod ~ mean_prod, data=dmachal)
## Again, Model sucks, but better than to consider zero

dmachal[is.na(dmachal$se_prod),'se_prod'] <- round(predict(mod_se2, newdata=dmachal[is.na(dmachal$se_pro
```

And finally modelling macroalgae productivity using a meta-analysis Bayesian model with depth as the only predictor

```
pri2 <- get_prior(mean_prod | se(se_prod, sigma=TRUE) ~ 1,
          data = dmachal,
          family=skew_normal())

brmod2 <- brm(mean_prod | se(se_prod, sigma=TRUE) ~ 1,
             data = dmachal,
```

```
            family=skew_normal(),
            prior = pri2,
            chains = 4, iter = 5000, thin = 3)
```

```
## Compiling Stan program...

## Trying to compile a simple C file

## Running /Library/Frameworks/R.framework/Resources/bin/R CMD SHLIB foo.c
## clang -arch arm64 -I"/Library/Frameworks/R.framework/Resources/include" -DNDEBUG   -I"/Library/Frame
## In file included from <built-in>:1:
## In file included from /Library/Frameworks/R.framework/Versions/4.2-arm64/Resources/library/StanHeade
## In file included from /Library/Frameworks/R.framework/Versions/4.2-arm64/Resources/library/RcppEigen
## In file included from /Library/Frameworks/R.framework/Versions/4.2-arm64/Resources/library/RcppEigen
## /Library/Frameworks/R.framework/Versions/4.2-arm64/Resources/library/RcppEigen/include/Eigen/src/Core
## namespace Eigen {
## ^
## /Library/Frameworks/R.framework/Versions/4.2-arm64/Resources/library/RcppEigen/include/Eigen/src/Core
## namespace Eigen {
##                ^
##                ;
## In file included from <built-in>:1:
## In file included from /Library/Frameworks/R.framework/Versions/4.2-arm64/Resources/library/StanHeade
## In file included from /Library/Frameworks/R.framework/Versions/4.2-arm64/Resources/library/RcppEigen
## /Library/Frameworks/R.framework/Versions/4.2-arm64/Resources/library/RcppEigen/include/Eigen/Core:96
## #include <complex>
##          ^~~~~~~~~
## 3 errors generated.
## make: *** [foo.o] Error 1

## Start sampling

##
## SAMPLING FOR MODEL '65e53fdc92b4dc47b3a716bb70bf19ac' NOW (CHAIN 1).
## Chain 1:
## Chain 1: Gradient evaluation took 4.1e-05 seconds
## Chain 1: 1000 transitions using 10 leapfrog steps per transition would take 0.41 seconds.
## Chain 1: Adjust your expectations accordingly!
## Chain 1:
## Chain 1:
## Chain 1: Iteration:    1 / 5000 [  0%]  (Warmup)
## Chain 1: Iteration:  500 / 5000 [ 10%]  (Warmup)
## Chain 1: Iteration: 1000 / 5000 [ 20%]  (Warmup)
## Chain 1: Iteration: 1500 / 5000 [ 30%]  (Warmup)
## Chain 1: Iteration: 2000 / 5000 [ 40%]  (Warmup)
## Chain 1: Iteration: 2500 / 5000 [ 50%]  (Warmup)
## Chain 1: Iteration: 2501 / 5000 [ 50%]  (Sampling)
## Chain 1: Iteration: 3000 / 5000 [ 60%]  (Sampling)
## Chain 1: Iteration: 3500 / 5000 [ 70%]  (Sampling)
## Chain 1: Iteration: 4000 / 5000 [ 80%]  (Sampling)
## Chain 1: Iteration: 4500 / 5000 [ 90%]  (Sampling)
## Chain 1: Iteration: 5000 / 5000 [100%]  (Sampling)
```

```
## Chain 1:
## Chain 1:  Elapsed Time: 0.799554 seconds (Warm-up)
## Chain 1:                0.557864 seconds (Sampling)
## Chain 1:                1.35742 seconds (Total)
## Chain 1:
##
## SAMPLING FOR MODEL '65e53fdc92b4dc47b3a716bb70bf19ac' NOW (CHAIN 2).
## Chain 2:
## Chain 2: Gradient evaluation took 1.9e-05 seconds
## Chain 2: 1000 transitions using 10 leapfrog steps per transition would take 0.19 seconds.
## Chain 2: Adjust your expectations accordingly!
## Chain 2:
## Chain 2:
## Chain 2: Iteration:    1 / 5000 [  0%]  (Warmup)
## Chain 2: Iteration:  500 / 5000 [ 10%]  (Warmup)
## Chain 2: Iteration: 1000 / 5000 [ 20%]  (Warmup)
## Chain 2: Iteration: 1500 / 5000 [ 30%]  (Warmup)
## Chain 2: Iteration: 2000 / 5000 [ 40%]  (Warmup)
## Chain 2: Iteration: 2500 / 5000 [ 50%]  (Warmup)
## Chain 2: Iteration: 2501 / 5000 [ 50%]  (Sampling)
## Chain 2: Iteration: 3000 / 5000 [ 60%]  (Sampling)
## Chain 2: Iteration: 3500 / 5000 [ 70%]  (Sampling)
## Chain 2: Iteration: 4000 / 5000 [ 80%]  (Sampling)
## Chain 2: Iteration: 4500 / 5000 [ 90%]  (Sampling)
## Chain 2: Iteration: 5000 / 5000 [100%]  (Sampling)
## Chain 2:
## Chain 2:  Elapsed Time: 0.750525 seconds (Warm-up)
## Chain 2:                0.54311 seconds (Sampling)
## Chain 2:                1.29364 seconds (Total)
## Chain 2:
##
## SAMPLING FOR MODEL '65e53fdc92b4dc47b3a716bb70bf19ac' NOW (CHAIN 3).
## Chain 3:
## Chain 3: Gradient evaluation took 1.8e-05 seconds
## Chain 3: 1000 transitions using 10 leapfrog steps per transition would take 0.18 seconds.
## Chain 3: Adjust your expectations accordingly!
## Chain 3:
## Chain 3:
## Chain 3: Iteration:    1 / 5000 [  0%]  (Warmup)
## Chain 3: Iteration:  500 / 5000 [ 10%]  (Warmup)
## Chain 3: Iteration: 1000 / 5000 [ 20%]  (Warmup)
## Chain 3: Iteration: 1500 / 5000 [ 30%]  (Warmup)
## Chain 3: Iteration: 2000 / 5000 [ 40%]  (Warmup)
## Chain 3: Iteration: 2500 / 5000 [ 50%]  (Warmup)
## Chain 3: Iteration: 2501 / 5000 [ 50%]  (Sampling)
## Chain 3: Iteration: 3000 / 5000 [ 60%]  (Sampling)
## Chain 3: Iteration: 3500 / 5000 [ 70%]  (Sampling)
## Chain 3: Iteration: 4000 / 5000 [ 80%]  (Sampling)
## Chain 3: Iteration: 4500 / 5000 [ 90%]  (Sampling)
## Chain 3: Iteration: 5000 / 5000 [100%]  (Sampling)
## Chain 3:
## Chain 3:  Elapsed Time: 0.760787 seconds (Warm-up)
## Chain 3:                0.557037 seconds (Sampling)
## Chain 3:                1.31782 seconds (Total)
```

```
## Chain 3:
##
## SAMPLING FOR MODEL '65e53fdc92b4dc47b3a716bb70bf19ac' NOW (CHAIN 4).
## Chain 4:
## Chain 4: Gradient evaluation took 1.9e-05 seconds
## Chain 4: 1000 transitions using 10 leapfrog steps per transition would take 0.19 seconds.
## Chain 4: Adjust your expectations accordingly!
## Chain 4:
## Chain 4:
## Chain 4: Iteration:    1 / 5000 [  0%]  (Warmup)
## Chain 4: Iteration:  500 / 5000 [ 10%]  (Warmup)
## Chain 4: Iteration: 1000 / 5000 [ 20%]  (Warmup)
## Chain 4: Iteration: 1500 / 5000 [ 30%]  (Warmup)
## Chain 4: Iteration: 2000 / 5000 [ 40%]  (Warmup)
## Chain 4: Iteration: 2500 / 5000 [ 50%]  (Warmup)
## Chain 4: Iteration: 2501 / 5000 [ 50%]  (Sampling)
## Chain 4: Iteration: 3000 / 5000 [ 60%]  (Sampling)
## Chain 4: Iteration: 3500 / 5000 [ 70%]  (Sampling)
## Chain 4: Iteration: 4000 / 5000 [ 80%]  (Sampling)
## Chain 4: Iteration: 4500 / 5000 [ 90%]  (Sampling)
## Chain 4: Iteration: 5000 / 5000 [100%]  (Sampling)
## Chain 4:
## Chain 4:  Elapsed Time: 0.767665 seconds (Warm-up)
## Chain 4:                0.561687 seconds (Sampling)
## Chain 4:                1.32935 seconds (Total)
## Chain 4:
```

```
saveRDS(brmod2,'macro_prod_brms.RDS')
```

Now, how about trying to predict benthicmacroalgae productivity

by merging area specific turf productivity predicted

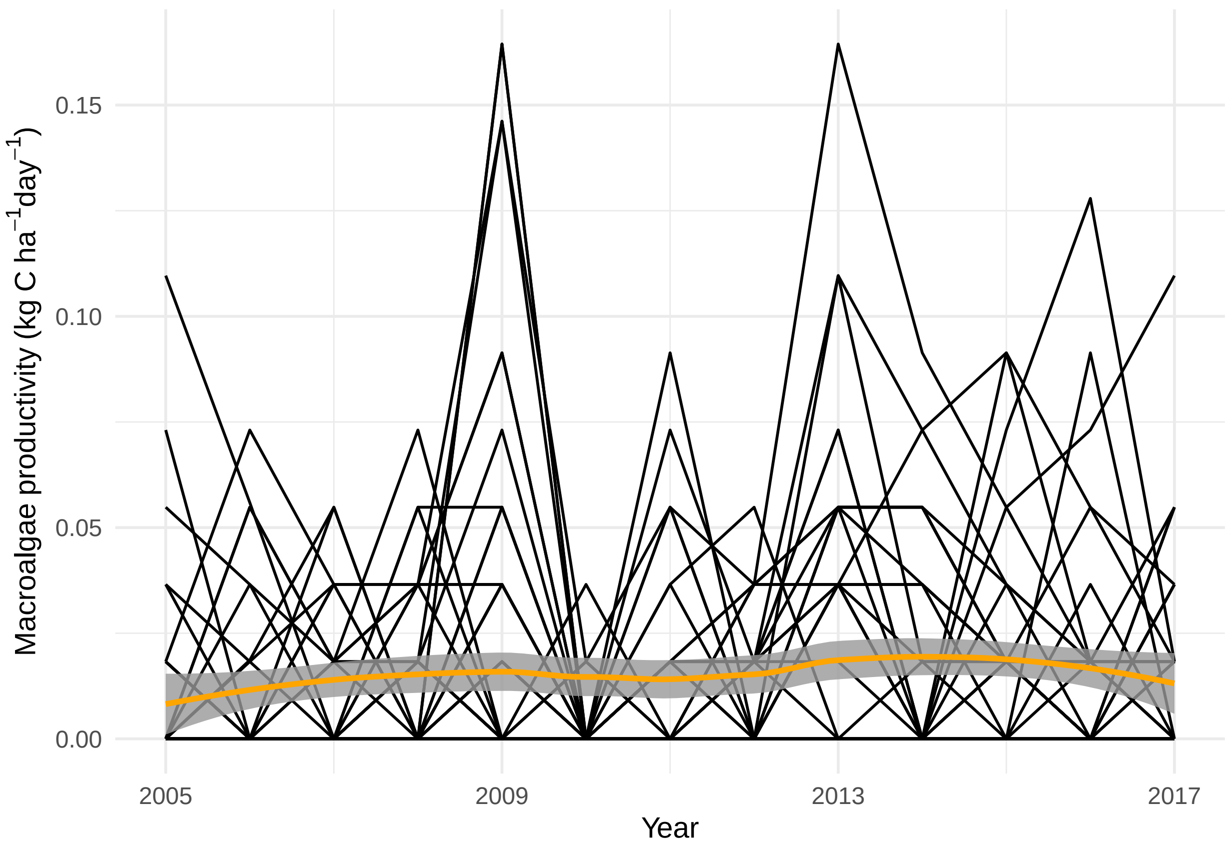
using the data compiled by Duarte et al 2022 and macroalgae cover?

```
pred_val2 <- posterior_epred(brmod2,
      newdata=ts_data %>% mutate(se_prod=0.1), ndraws=1000)

tot_macr_prod <- ((ts_data$macroalgae * t(pred_val2)) * 10000)/1000
## in kg C ha day-1


# aggregating

fts_data <- cbind(fts_data,
      macr_prod_kghaday_med=apply(tot_macr_prod,1,median),
      macr_prod_kghaday_lhd=apply(tot_macr_prod,1,function(x) median_hdci(x)$ymin),
      macr_prod_kghaday_uhd=apply(tot_macr_prod,1,function(x) median_hdci(x)$ymax))

## in g C ha-1 day-1
```

Now plotting

First the time series of macroalgae productivity over time in Moorea

```
ggplot(data=fts_data) +
  geom_line(aes(x=Year,y=macr_prod_kghaday_med,group=interaction(Transect,site))) +
  geom_smooth(aes(x=Year,y=macr_prod_kghaday_med),
              method = 'loess', formula = y ~ x,
              colour='orange', alpha=0.8) +
  scale_x_continuous(breaks=c(2005,2009,2013,2017)) +
  ylab(expression(Macroalgae~productivity~'('*kg~C~ha^-1*day^-1*')')) +
  theme_minimal()
```



Saving the final estimates fro Moorea

```
write.csv(fts_data,'Moorea_turf_macr_prod.csv', row.names=FALSE)
```