# Turf and macroalgae productivity on coral reefs: a modelling exercise in Moorea

Renato

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#### **Packages**

```
library(tidyverse)
library(brms)
library(tidybayes)
library(patchwork)
```

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('data/turf_prod_val.csv') |>
    filter(!is.na(depth))

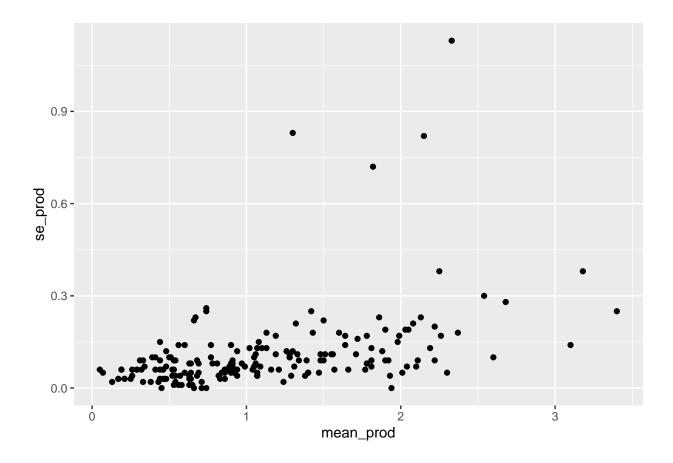
unit <- names(data)[1]
names(data)[1] <- 'prod'

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))</pre>
```

```
## 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:

```
ggplot(data %>% filter(!is.na(se_prod))) +
  geom_point(aes(x=mean_prod,y=se_prod))
```



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)</pre>
```

And finally modelling algal turf productivity using a meta-analysis

Bayesian model with depth as the only predictor

```
brmod <- brm(mean_prod | se(se_prod, sigma=TRUE) ~ 1 + log(depth),</pre>
             data = data,
             family=skew_normal(),
             prior = pri,
             chains = 4, iter = 5000, thin = 3)
## Compiling Stan program...
## Start sampling
##
## SAMPLING FOR MODEL '10f63a45fd17e5d9181b383b6c1bd659' NOW (CHAIN 1).
## Chain 1:
## Chain 1: Gradient evaluation took 6e-05 seconds
## Chain 1: 1000 transitions using 10 leapfrog steps per transition would take 0.6 seconds.
## Chain 1: Adjust your expectations accordingly!
## Chain 1:
## Chain 1:
## Chain 1: Iteration:
                          1 / 5000 [ 0%]
                                            (Warmup)
## Chain 1: Iteration: 500 / 5000 [ 10%]
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## Chain 1: Iteration: 2000 / 5000 [ 40%]
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## Chain 1: Iteration: 2500 / 5000 [ 50%]
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## Chain 1: Iteration: 2501 / 5000 [ 50%]
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## Chain 1: Iteration: 3000 / 5000 [ 60%]
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## Chain 1: Iteration: 4500 / 5000 [ 90%]
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## Chain 1: Iteration: 5000 / 5000 [100%]
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## Chain 1:
## Chain 1:
             Elapsed Time: 0.632871 seconds (Warm-up)
## Chain 1:
                           0.806597 seconds (Sampling)
## Chain 1:
                           1.43947 seconds (Total)
## Chain 1:
##
## SAMPLING FOR MODEL '10f63a45fd17e5d9181b383b6c1bd659' NOW (CHAIN 2).
## Chain 2:
## Chain 2: Gradient evaluation took 3.3e-05 seconds
## Chain 2: 1000 transitions using 10 leapfrog steps per transition would take 0.33 seconds.
## Chain 2: Adjust your expectations accordingly!
## Chain 2:
## Chain 2:
## Chain 2: Iteration:
                          1 / 5000 [ 0%]
                                            (Warmup)
## Chain 2: Iteration: 500 / 5000 [ 10%]
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                                            (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: 0.664687 seconds (Warm-up)
## Chain 2:
                           0.621663 seconds (Sampling)
## Chain 2:
                           1.28635 seconds (Total)
## Chain 2:
##
## SAMPLING FOR MODEL '10f63a45fd17e5d9181b383b6c1bd659' NOW (CHAIN 3).
## Chain 3:
## Chain 3: Gradient evaluation took 3.2e-05 seconds
## Chain 3: 1000 transitions using 10 leapfrog steps per transition would take 0.32 seconds.
## Chain 3: Adjust your expectations accordingly!
## Chain 3:
## Chain 3:
## Chain 3: Iteration:
                          1 / 5000 [ 0%]
                                            (Warmup)
## Chain 3: Iteration: 500 / 5000 [ 10%]
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## Chain 3: Iteration: 1000 / 5000 [ 20%]
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## Chain 3: Iteration: 2501 / 5000 [ 50%]
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## Chain 3: Iteration: 3500 / 5000 [ 70%]
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## Chain 3: Iteration: 4000 / 5000 [ 80%]
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## Chain 3: Iteration: 4500 / 5000 [ 90%]
                                            (Sampling)
## Chain 3: Iteration: 5000 / 5000 [100%]
                                            (Sampling)
## Chain 3:
## Chain 3:
            Elapsed Time: 0.660888 seconds (Warm-up)
## Chain 3:
                           0.762042 seconds (Sampling)
## Chain 3:
                           1.42293 seconds (Total)
## Chain 3:
##
## SAMPLING FOR MODEL '10f63a45fd17e5d9181b383b6c1bd659' NOW (CHAIN 4).
## Chain 4:
## Chain 4: Gradient evaluation took 3.5e-05 seconds
## Chain 4: 1000 transitions using 10 leapfrog steps per transition would take 0.35 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)
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## 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%]
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## Chain 4: Iteration: 3500 / 5000 [ 70%]
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## 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: 0.660058 seconds (Warm-up)
```

```
## Chain 4: 0.718078 seconds (Sampling)
## Chain 4: 1.37814 seconds (Total)
## Chain 4:
saveRDS(brmod,'mods/turf_prod_brms.RDS')
```

#### Loading and tidying data to predict for

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

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

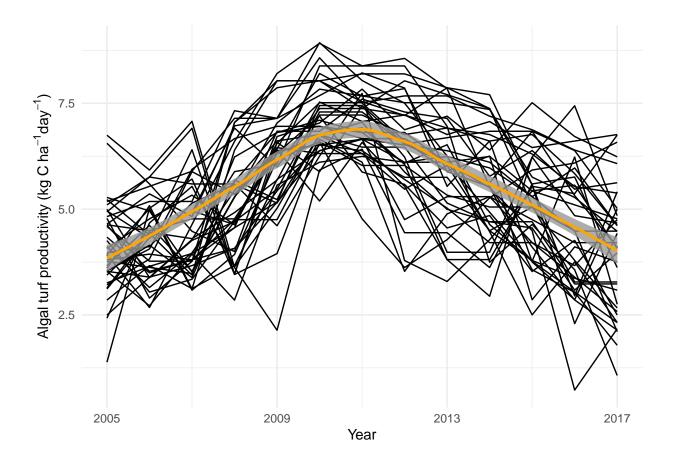
Filtering and manipulating the time series for the categories of interest.

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

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?

#### Now plotting

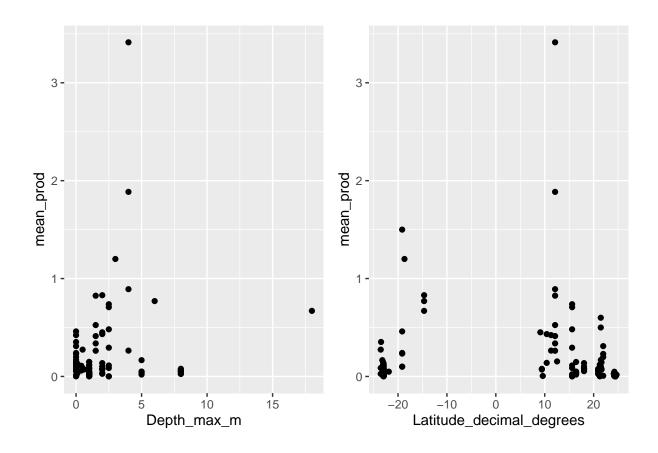
First the time series of turf productivity over time in Moorea



#### 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

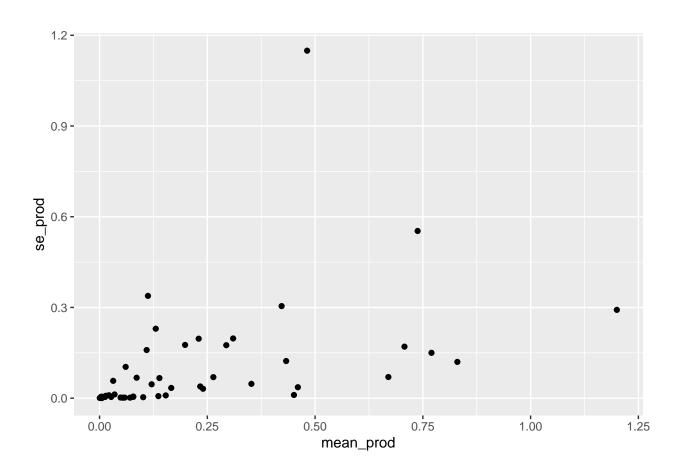
Maybe return to this possibility later?



## 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?

```
ggplot(dmachal %>% filter(!is.na(se_prod))) +
geom_point(aes(x=mean_prod,y=se_prod))
```



```
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_prod)))</pre>
```

### And finally modelling macroalgae productivity using a meta-analysis

#### Bayesian model with depth as the only predictor

```
## Compiling Stan program...
## Start sampling
##
## SAMPLING FOR MODEL '65e53fdc92b4dc47b3a716bb70bf19ac' NOW (CHAIN 1).
## Chain 1:
## Chain 1: Gradient evaluation took 3.8e-05 seconds
## Chain 1: 1000 transitions using 10 leapfrog steps per transition would take 0.38 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%]
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## Chain 1: Iteration: 2500 / 5000 [ 50%]
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## Chain 1: Iteration: 2501 / 5000 [ 50%]
                                            (Sampling)
## Chain 1: Iteration: 3000 / 5000 [ 60%]
                                            (Sampling)
## Chain 1: Iteration: 3500 / 5000 [ 70%]
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## 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: 0.721783 seconds (Warm-up)
## Chain 1:
                           0.571532 seconds (Sampling)
## Chain 1:
                           1.29331 seconds (Total)
## Chain 1:
##
## SAMPLING FOR MODEL '65e53fdc92b4dc47b3a716bb70bf19ac' NOW (CHAIN 2).
## Chain 2:
## Chain 2: Gradient evaluation took 1.7e-05 seconds
## Chain 2: 1000 transitions using 10 leapfrog steps per transition would take 0.17 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%]
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## Chain 2: Iteration: 1500 / 5000 [ 30%]
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## Chain 2: Iteration: 2500 / 5000 [ 50%]
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## Chain 2: Iteration: 2501 / 5000 [ 50%]
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## Chain 2: Iteration: 3500 / 5000 [ 70%]
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## Chain 2: Iteration: 4500 / 5000 [ 90%]
                                            (Sampling)
## Chain 2: Iteration: 5000 / 5000 [100%]
                                            (Sampling)
## Chain 2:
## Chain 2:
            Elapsed Time: 0.786121 seconds (Warm-up)
## Chain 2:
                           0.591157 seconds (Sampling)
## Chain 2:
                           1.37728 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%]
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## Chain 3: Iteration: 1000 / 5000 [ 20%]
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## Chain 3: Iteration: 1500 / 5000 [ 30%]
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## Chain 3: Iteration: 2000 / 5000 [ 40%]
                                            (Warmup)
## Chain 3: Iteration: 2500 / 5000 [ 50%]
                                            (Warmup)
## Chain 3: Iteration: 2501 / 5000 [ 50%]
                                            (Sampling)
```

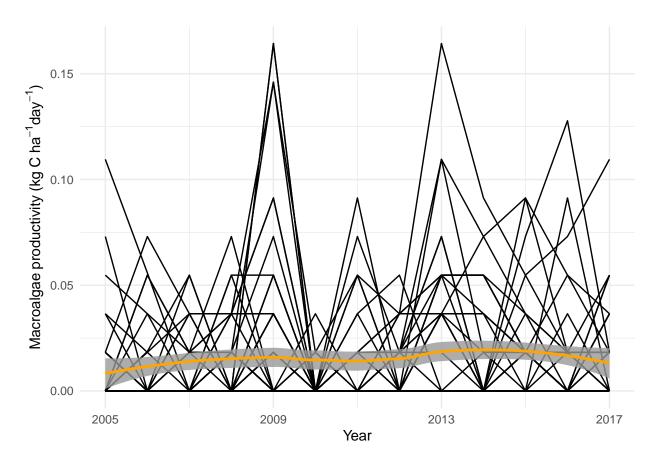
```
## Chain 3: Iteration: 3000 / 5000 [ 60%]
                                            (Sampling)
## Chain 3: Iteration: 3500 / 5000 [ 70%]
                                            (Sampling)
## Chain 3: Iteration: 4000 / 5000 [ 80%]
                                            (Sampling)
## Chain 3: Iteration: 4500 / 5000 [ 90%]
                                            (Sampling)
## Chain 3: Iteration: 5000 / 5000 [100%]
                                            (Sampling)
## Chain 3:
## Chain 3: Elapsed Time: 0.905476 seconds (Warm-up)
## Chain 3:
                           0.623952 seconds (Sampling)
                           1.52943 seconds (Total)
## Chain 3:
## Chain 3:
##
## SAMPLING FOR MODEL '65e53fdc92b4dc47b3a716bb70bf19ac' NOW (CHAIN 4).
## Chain 4:
## Chain 4: Gradient evaluation took 2e-05 seconds
## Chain 4: 1000 transitions using 10 leapfrog steps per transition would take 0.2 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%]
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## Chain 4: Iteration: 2500 / 5000 [ 50%]
                                            (Warmup)
## Chain 4: Iteration: 2501 / 5000 [ 50%]
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## Chain 4: Iteration: 4500 / 5000 [ 90%]
                                            (Sampling)
## Chain 4: Iteration: 5000 / 5000 [100%]
                                            (Sampling)
## Chain 4:
## Chain 4: Elapsed Time: 0.802426 seconds (Warm-up)
## Chain 4:
                           0.571068 seconds (Sampling)
## Chain 4:
                           1.37349 seconds (Total)
## Chain 4:
```

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?

```
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



# Saving the final estimates fro Moorea

saveRDS(fts\_data,'preds/Moorea\_TurfMacroalgaeProd\_preds.RDS')