

salmon_nutrient_pollution

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This markdown uses models and species specific parameters from the paper *Hindcasts and Future Projections of Global Inland and Coastal Nitrogen and Phosphorus Loads Due to Finfish Aquaculture* (2013 Bouwman et al)

Set up

```
library(tidyverse)
library(sf)
library(raster)
library(readr)
library(data.table)

path<-"/home/shares/food-systems/Food_footprint/_raw_data/"
path2 <- "/home/shares/food-systems/Food_footprint/Data/"

parameters <- fread(paste0(path, "Bouwman_aquaculture_nutrient/trout_parameters.csv"))

production <- fread(paste0(path2, "Regional_aquaculture_production/FAO_Adjusted_regional_production.csv"))
dplyr::select(IS03, Region_name, Salmon_tonnes_adj)
```

Add in all the parameters we will need

```
## read in all the parameter values we will need for the calculations
Frac_WG <- as.numeric(parameters$Value[parameters$Parameter == "Frac_WG"])
Frac_Comp <- as.numeric(parameters$Value[parameters$Parameter == "Frac_Comp"])
FCR_Comp <- as.numeric(parameters$Value[parameters$Parameter == "FCR_Comp"])
Frac_Comp_N <- as.numeric(parameters$Value[parameters$Parameter == "Frac_Comp_N"])
Frac_Comp_P <- as.numeric(parameters$Value[parameters$Parameter == "Frac_Comp_P"])
Frac_Fish_N <- as.numeric(parameters$Value[parameters$Parameter == "Frac_Fish_N"])
Frac_Fish_P <- as.numeric(parameters$Value[parameters$Parameter == "Frac_Fish_P"])
ADC_Comp_N <- as.numeric(parameters$Value[parameters$Parameter == "ADC_Comp_N"])
ADC_Comp_P <- as.numeric(parameters$Value[parameters$Parameter == "ADC_Comp_P"])
```

```
## add all the parameter values to the production by each region and country
produc_param <- production %>%
  rename(Fish_Prod = Salmon_tonnes_adj) %>%
  mutate(Frac_WG = Frac_WG,
         Frac_Comp = Frac_Comp,
         FCR_Comp = FCR_Comp,
         Frac_Comp_N = Frac_Comp_N,
         Frac_Comp_P = Frac_Comp_P,
         Frac_Fish_N = Frac_Fish_N,
         Frac_Fish_P = Frac_Fish_P,
         ADC_Comp_N = ADC_Comp_N,
         ADC_Comp_P = ADC_Comp_P)
```

in the end will need to apply the same numbers for each value to all the countries so that they can merge

1. Calculating the amount of nutrients (N and P) entering the system from compound feed

$$In_Comp_N = Fish_Prod * Frac_WG * Frac_Comp * FCR_Comp * Frac_Comp_N$$

The same equation is used for calculating nitrogen and phosphorous, using the nitrogen/phosphorous specific variables when needed

Fish_Prod = production in tonnes

Frac_WG = production that is actual weight gain

Frac_Comp = fraction of fish feed that is compound feed

FCR_Comp = amount of feed used to produce 1 kg of fish

Frac_Comp_N = fraction of nitrogen present in the feed

Frac_Comp_P = fraction of phosphorous present in the feed

In_Comp_N = the amount of N entering the system

In_Comp_P = the amount of P entering the system

N_In = total amount of nitrogen entering the system (this is the same as In_Comp_N here because salmon are only fed compound feeds)

P_In = total amount of phosphorous entering the system (this is the same as In_Comp_P here because salmon are only fed compound feeds)

```
nutrients_entering <- produc_param %>%
  mutate(In_Comp_N = Fish_Prod*Frac_WG*Frac_Comp*FCR_Comp*Frac_Comp_N,
         In_Comp_P = Fish_Prod*Frac_WG*Frac_Comp*FCR_Comp*Frac_Comp_P,
         N_In = In_Comp_N, ## since salmon are only feed compound feeds this value is the same
         P_In = In_Comp_P) %>%
  dplyr::select(IS03, Region_name, In_Comp_N, In_Comp_P, N_In, P_In)

all_parameters_1 <- produc_param %>%
  mutate(In_Comp_N = Fish_Prod*Frac_WG*Frac_Comp*FCR_Comp*Frac_Comp_N,
         In_Comp_P = Fish_Prod*Frac_WG*Frac_Comp*FCR_Comp*Frac_Comp_P,
         N_In = In_Comp_N, ## since salmon are only feed compound feeds this value is the same
         P_In = In_Comp_P)
```

2. Calculating the amount of nutrients (N and P) entering the system from non-compound feed

We are not doing this here because we know that salmon are only fed compound feed. However, for future analysis with species that are also fed non-compound feed we will need to do this. The equations are the same as with compound except $Frac_Comp$ is replaced by $(1-Frac_Comp)$ and the parameter values for non-compound feeds replaces the compound feed ones.

3. Calculating the amount of nutrients retained in fish biomass

$$N_Fish = Fish_Prod * Frac_WG * Frac_Fish_N$$

$Frac_Fish_N$ = nitrogen content of fish biomass

$Frac_Fish_P$ = phosphorous content of fish biomass

N_Fish = amount of N in the weight gained during each year (tonnes)

P_Fish = amount of P in the weight gained during each year (tonnes)

```
nutrients_retained_biomass <- all_parameters_1 %>%
  mutate(N_Fish = Fish_Prod*Frac_WG*Frac_Fish_N,
         P_Fish = Fish_Prod*Frac_WG*Frac_Fish_P) %>%
  dplyr::select(IS03, Region_name, N_Fish, P_Fish)

all_parameters_3 <- all_parameters_1 %>%
  mutate(N_Fish = Fish_Prod*Frac_WG*Frac_Fish_N,
         P_Fish = Fish_Prod*Frac_WG*Frac_Fish_P)
```

4. Calculating solid particulate nutrient release

**there is also a component here for the non-compound feed that would need to be included for species that do have this in their diet

$$PN = (1 - ADC_Comp_N) * In_Comp_N$$

ADC_Comp_N = apparent digestibility of compound feed for nitrogen

ADC_Comp_P = apparent digestibility of compound feed for phosphorous

In_Comp_N = the amount of N entering the system

In_Comp_P = the amount of P entering the system

PN = particulate nitrogen in tonnes

PP = particulate phosphorous in tonnes

```
particulate_nutrients_released <- all_parameters_3 %>%
  mutate(PN = (1- ADC_Comp_N)*In_Comp_N,
         PP = (1- ADC_Comp_P)*In_Comp_P)

all_parameters_4 <- all_parameters_3 %>%
  mutate(PN = (1- ADC_Comp_N)*In_Comp_N,
         PP = (1- ADC_Comp_P)*In_Comp_P)
```

5. Calculating dissolved nutrient release

$$DN = N_In - N_Fish - PN$$

N_In = total amount of nitrogen entering the system (this is the same as In_Comp_N here because salmon are only fed compound feeds)

P_In = total amount of phosphorous entering the system (this is the same as In_Comp_P here because salmon are only fed compound feeds)

N_Fish = amount of N in the weight gained during each year (tonnes)

P_Fish = amount of P in the weight gained during each year (tonnes)

PN = particulate nitrogen in tonnes

PP = particulate phosphorous in tonnes

DN = dissolved nitrogen

DP - dissolved phosphorus

```
dissolved_nutrients_released <- all_parameters_4 %>%
  mutate(DN = N_In - N_Fish - PN,
         DP = P_In - P_Fish - PP)

all_parameters_5 <- all_parameters_4 %>%
  mutate(DN = N_In - N_Fish - PN,
         DP = P_In - P_Fish - PP)
```

6. Calculating the actual nutrient release to the water column

$$DN_out = DN * (1 - Frac_N_removal * Frac_Integer_Aqua)$$

The parameters are as follows:

Frac_N_removal = fraction of N released that is retained in the integrated system or removed by waste water treatment

Frac_P_removal = fraction of P released that is retained in the integrated system or removed by waste water treatment

Frac_integer_Aqua = fraction of production in integrated aquaculture systems with effluent treatment

Since salmon aquaculture is not an indoor system but an open in the environment one, this part of the model is zero for salmon. So the DN and DP calculated in the previous step is the total nutrient released into the environment

DN_out = total nitrogen released into system

DP_out = total phosphorous released into system

```
total_nutrients_released <- all_parameters_5 %>%
  mutate(DN_out = DN,
         DP_out = DP)

all_parameters <- all_parameters_5 %>%
  mutate(DN_out = DN,
         DP_out = DP)
```

Compare the Norway values to the results Caitie posted in the issue to see if it's the same

I don't have P out

The values calculated in the models are in kg/tonnes, so we need to do some math in order to get the total tonnes of nutrients released

```
norway <- all_parameters %>%
  filter(IS03 == "NOR") %>%
  dplyr::select(IS03, Fish_Prod, PP, PN, DP_out, DN_out, P_In, N_In) %>%
  mutate(PP_tot = (Fish_Prod*PP)/1000,
         PN_tot = (Fish_Prod*PN)/1000,
         DN_out_tot = (Fish_Prod*DN_out)/1000,
         DP_out_tot = (Fish_Prod*DP_out)/1000,
         P_In_tot = (Fish_Prod*P_In)/1000,
         N_In_tot = (Fish_Prod*N_In)/1000) %>%
  group_by(IS03) %>%
  summarize(PP = sum(PP_tot),
           PN = sum(PN_tot),
           DP_Out = sum(DP_out_tot),
           DN_Out = sum(DN_out_tot),
           P_In = sum(P_In_tot),
           N_In = sum(N_In_tot)) %>%
  ungroup() %>%
  dplyr::select(IS03, PP, PN, DP_Out, DN_Out, P_In, N_In) %>%
  gather(parameter, value, 2:7)
```

Values are different than what Caitie posted in Github

Lex model outputs: totals PP = 16126.78 PN = 25086.11 DP_Out = -5674.239 (apparently there is an error in it) DN_Out = 124982.6 P_in = 40316.96 N_in = 250861.1

P_out = 10452.55 N_out = 150068.7

do i need to add particulate and dissolved together to get the P and N out?