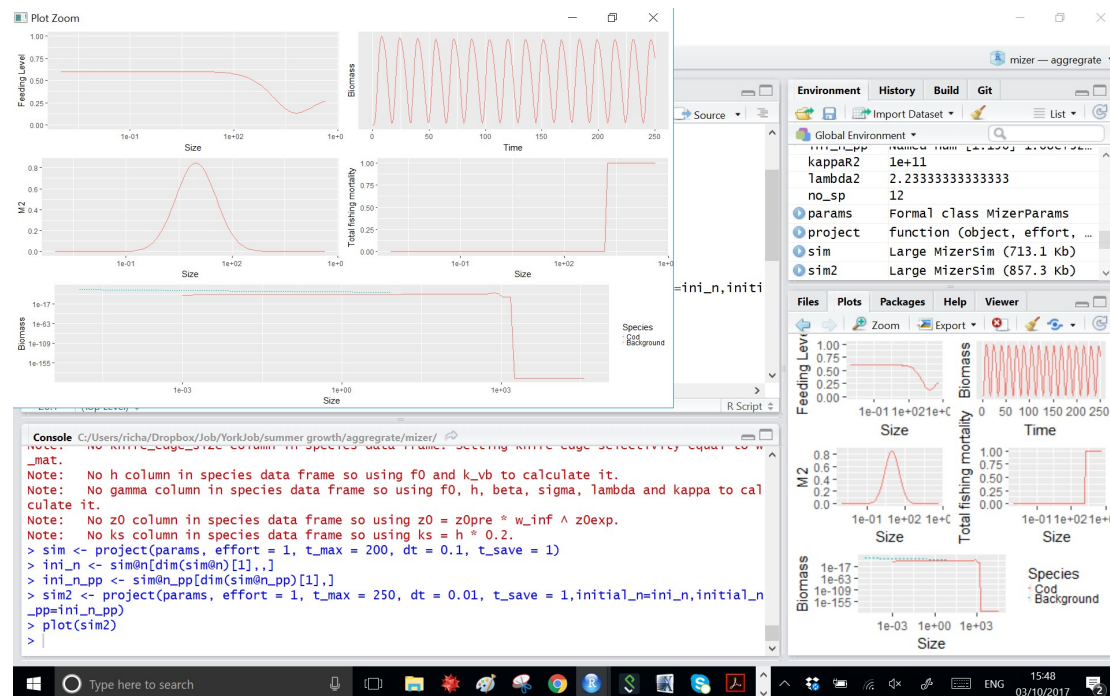
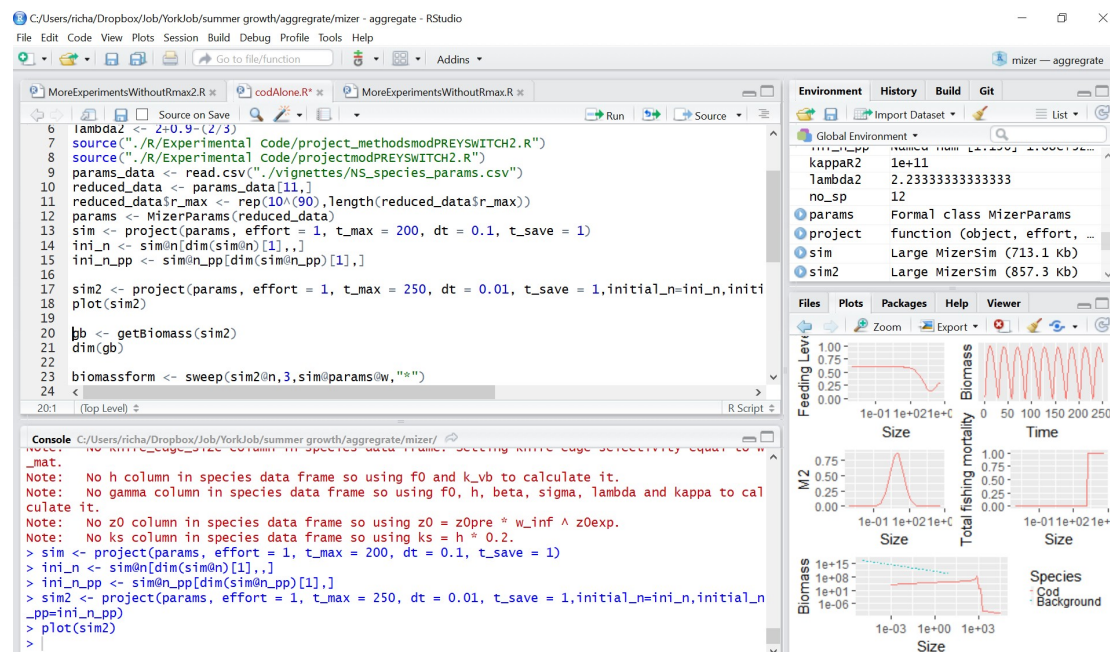


cod alone, $R_{max} = \infty$, $\chi = 0$

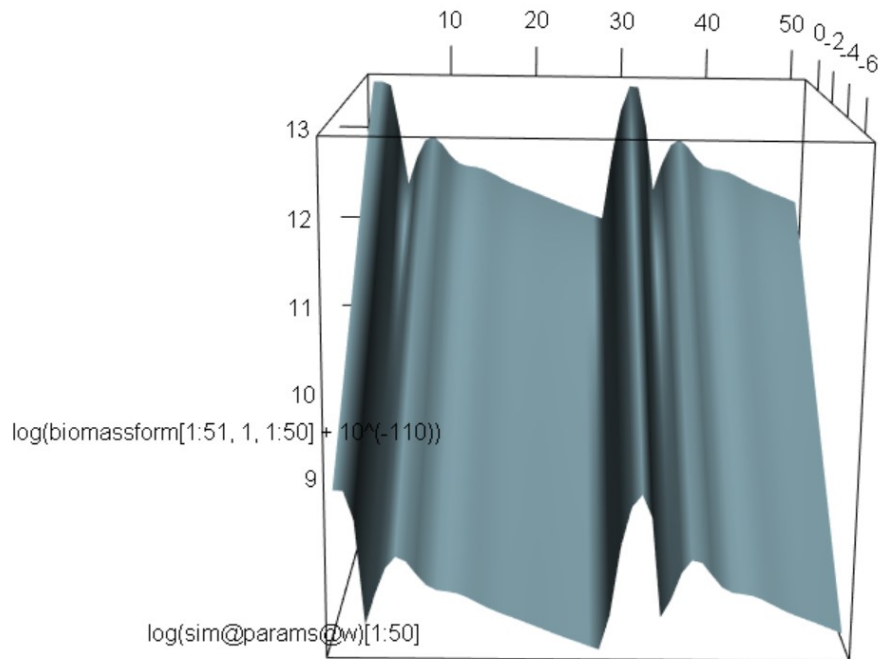
With no prey switching the period is short and the biomass spectrum is flat (so oscillations are a consequence of a lack of R_{max} , not the new prey switching mechanism)



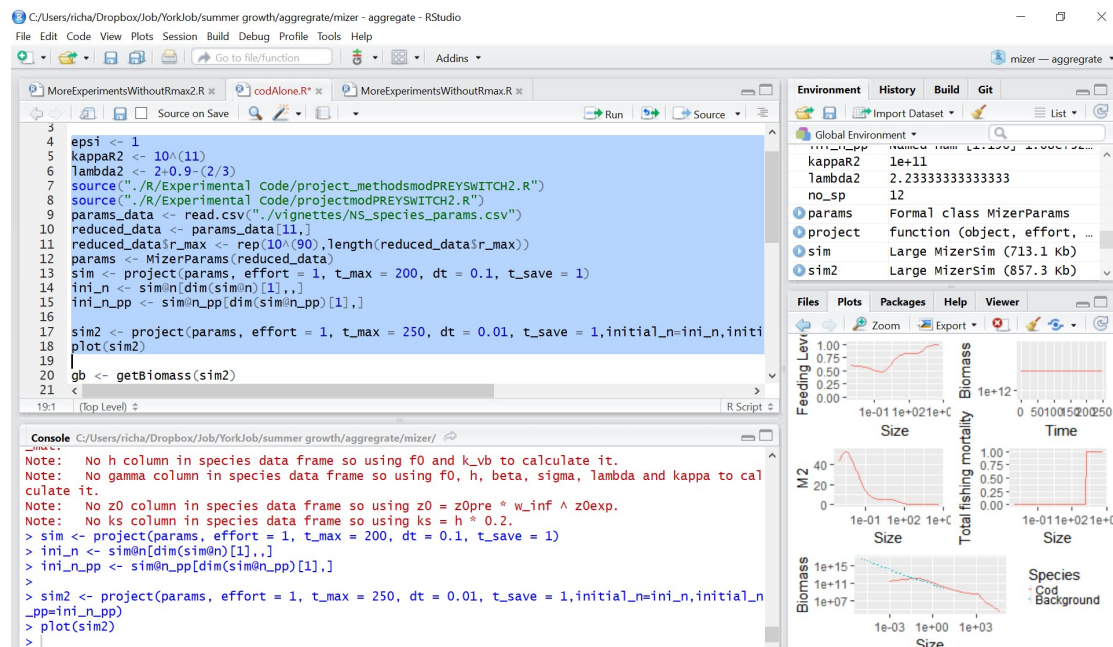
cod alone, now with $\chi = 0.1$, the period is larger (30 yrs) and the biomass curve slopes the wrong way



The oscillation seems quite simple

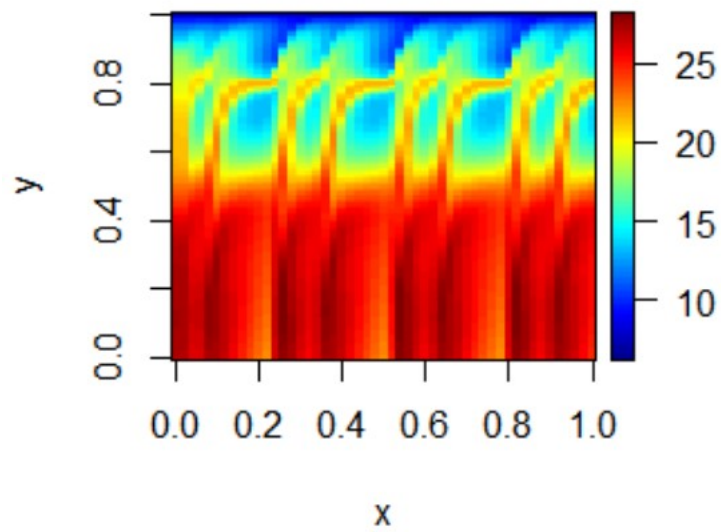
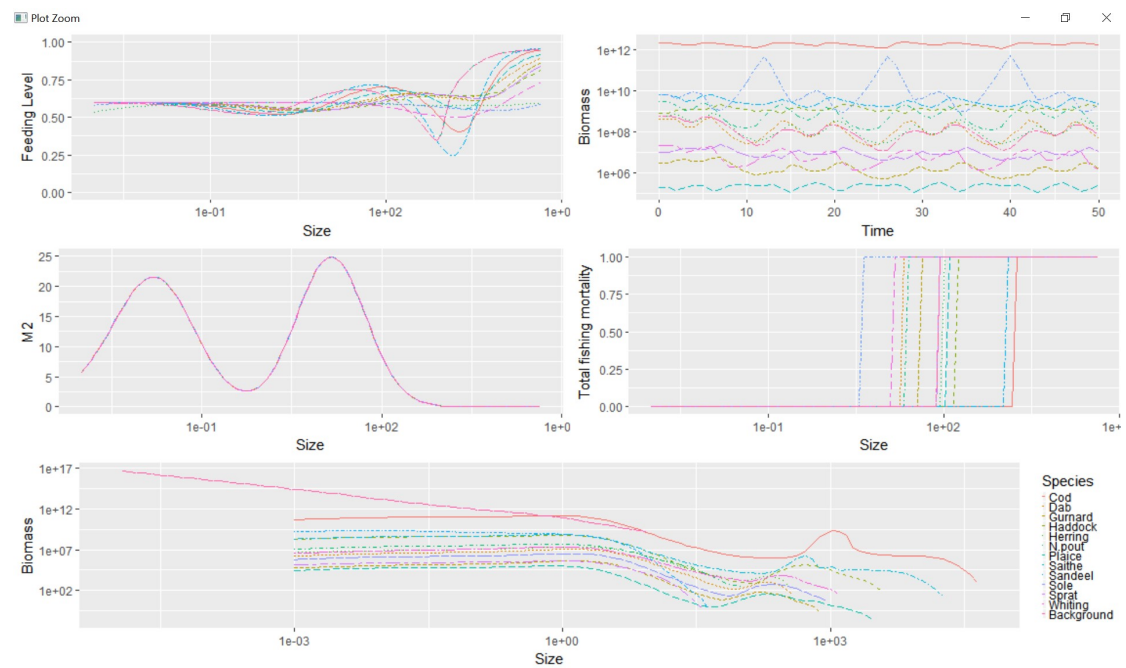


When $\chi=1$ the oscillation vanishes

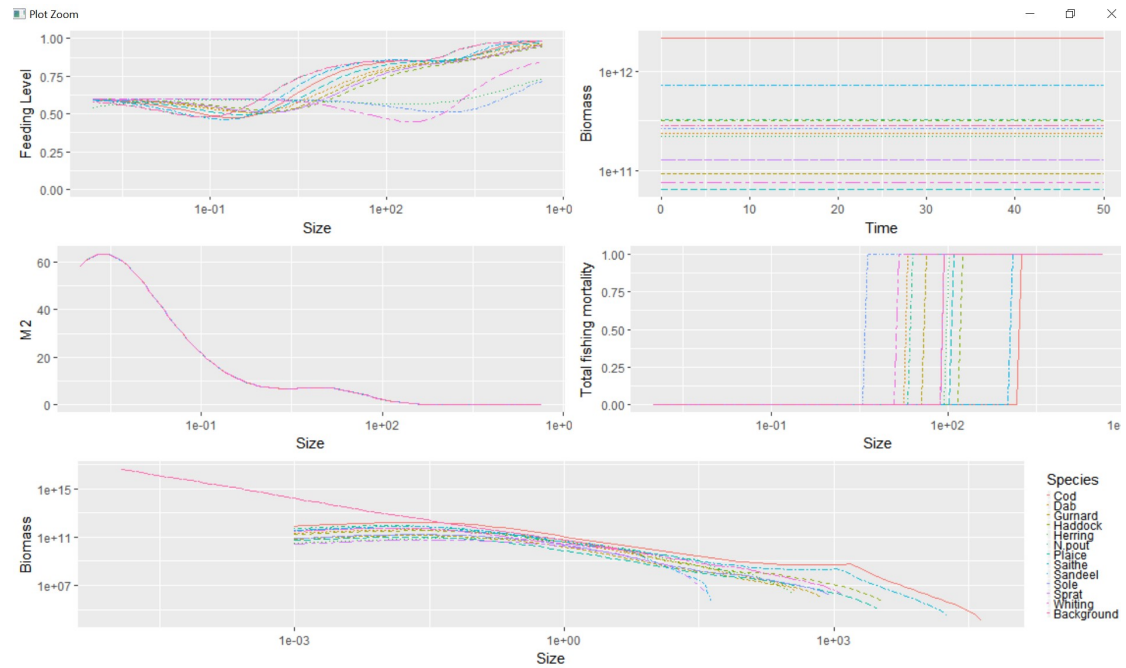


#####

12 species, with $\chi=0.1$ (oscillations occur)



12 species with $\chi=0.5$ (oscillations are gone)



Code used

```
#####
```

```
library(mizer)
```

```
library(plyr)
```

```
epsi <- .1
```

```
kappaR2 <- 10^(11)
```

```
lambda2 <- 2+0.9-(2/3)
```

```
source("./R/Experimental Code/project_methodsmodPREY SWITCH2.R")
```

```
source("./R/Experimental Code/projectmodPREY SWITCH2.R")
```

```
params_data <- read.csv("./vignettes/NS_species_params.csv")
```

```
reduced_data <- params_data[11,]
```

```
reduced_data$r_max <- rep(10^(90),length(reduced_data$r_max))
```

```
params <- MizerParams(reduced_data)
```

```
sim <- project(params, effort = 1, t_max = 200, dt = 0.1, t_save = 1)
```

```
ini_n <- sim@n[dim(sim@n)[1],]
```

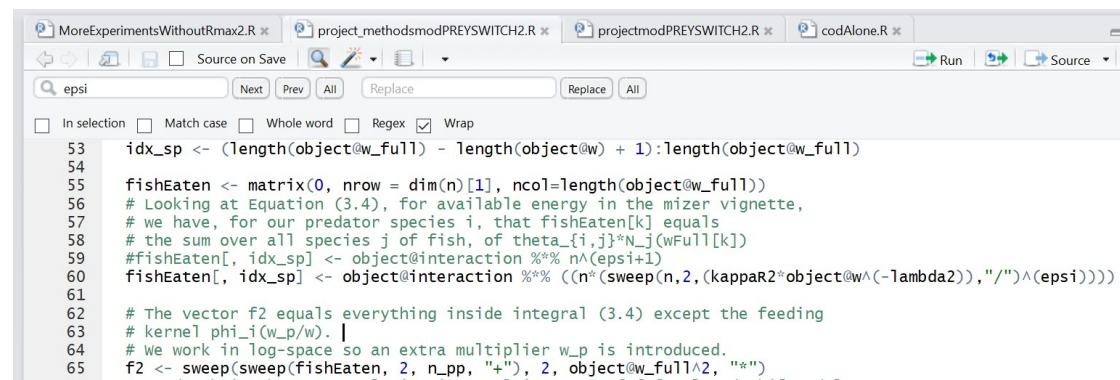
```
ini_n_pp <- sim@n_pp[dim(sim@n_pp)[1],]
```

```
sim2 <- project(params, effort = 1, t_max = 250, dt = 0.01, t_save =  
1, initial_n = ini_n, initial_n_pp = ini_n_pp)
```

```
plot(sim2)
```

#####

#####Changes to project_methods #####



```
53 idx_sp <- (length(object@w_full) - length(object@w) + 1):length(object@w_full)
54
55 fishEaten <- matrix(0, nrow = dim(n)[1], ncol=length(object@w_full))
56 # Looking at Equation (3.4), for available energy in the mizer vignette,
57 # we have, for our predator species i, that fishEaten[k] equals
58 # the sum over all species j of fish, of theta_{i,j}*N_j(wFull[k])
59 fishEaten[, idx_sp] <- object@interaction %>% n^(epsi+1)
60 fishEaten[, idx_sp] <- object@interaction %>% ((n*(sweep(n,2,(kappaR2*object@w^(-lambda2)),"/")^(epsi))))
61
62 # The vector f2 equals everything inside integral (3.4) except the feeding
63 # kernel phi_i(w_p/w).
64 # We work in log-space so an extra multiplier w_p is introduced.
65 f2 <- sweep(sweep(fishEaten, 2, n_pp, "+"), 2, object@w_full^2, "*")
```

#####Changes to project #####

```
229 # Iterate species one time step forward:
230 # See Ken's PDF
231 # A_{ij} = - g_i(w_{j-1}) / dw_j dt
232 A[,idx] <- sweep(-e_growth[,idx-1,drop=FALSE]*dt, 2, sim@params@dw[idx], "/")
233 # B_{ij} = 1 + g_i(w_j) / dw_j dt + \mu_i(w_j) dt
234 #B[,idx] <- 1 + sweep(e_growth[,idx,drop=FALSE]*dt,2,sim@params@dw[idx],"/") + z[,idx,drop=FALSE]*(n[,idx,drop=FALSE]^epsi)*dt
235 B[,idx] <- 1 + sweep(e_growth[,idx,drop=FALSE]*dt,2,sim@params@dw[idx],"/") + z[,idx,drop=FALSE]*(sweep(n[,idx,drop=FALSE],2,(kappa
236 # S_{ij} <- N_i(w_j)
237
238
239 S[,idx] <- n[,idx,drop=FALSE]
240 # Boundary condition upstream end (recruitment)
241 #B[w_min_idx_array_ref] <- 1+e_growth[w_min_idx_array_ref]*dt/sim@params@dw[sim@params@species_params$w_min_idx]+z[w_min_idx_array
242 B[w_min_idx_array_ref] <- 1+e_growth[w_min_idx_array_ref]*dt/sim@params@dw[sim@params@species_params$w_min_idx]+z[w_min_idx_array_
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Code is at

<https://github.com/gustavdelius/mizer/blob/aggregate/R/Experimental%20Code/MoreExperimentsWithoutRmax2.R>

