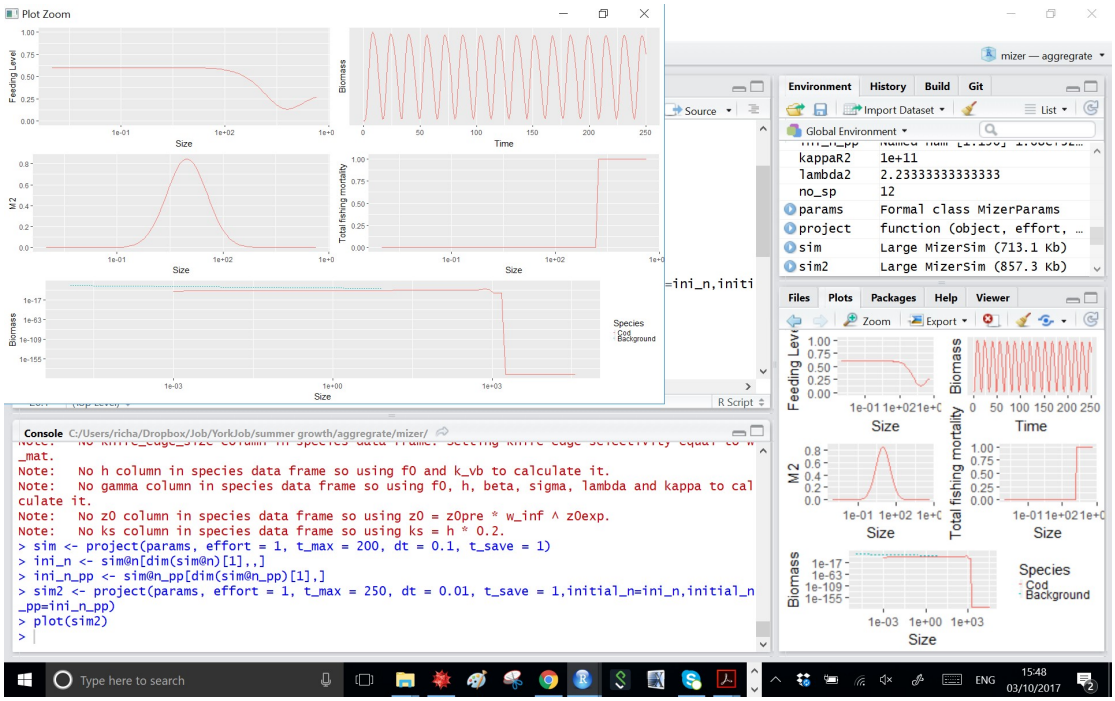
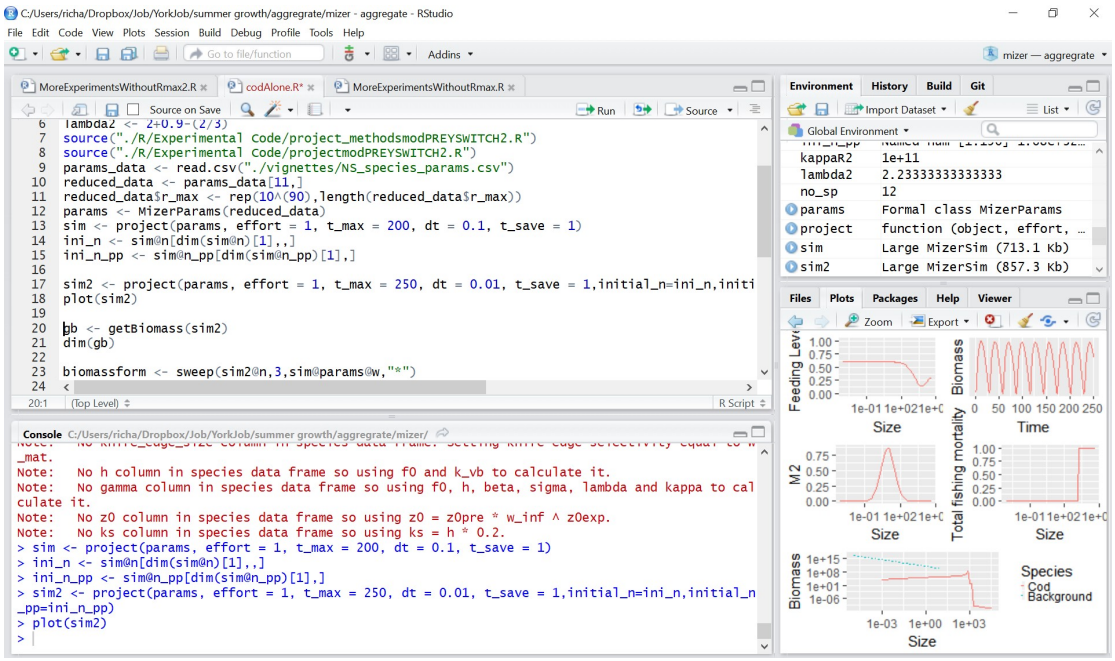
cod alone, Rmax=inf, chi=0

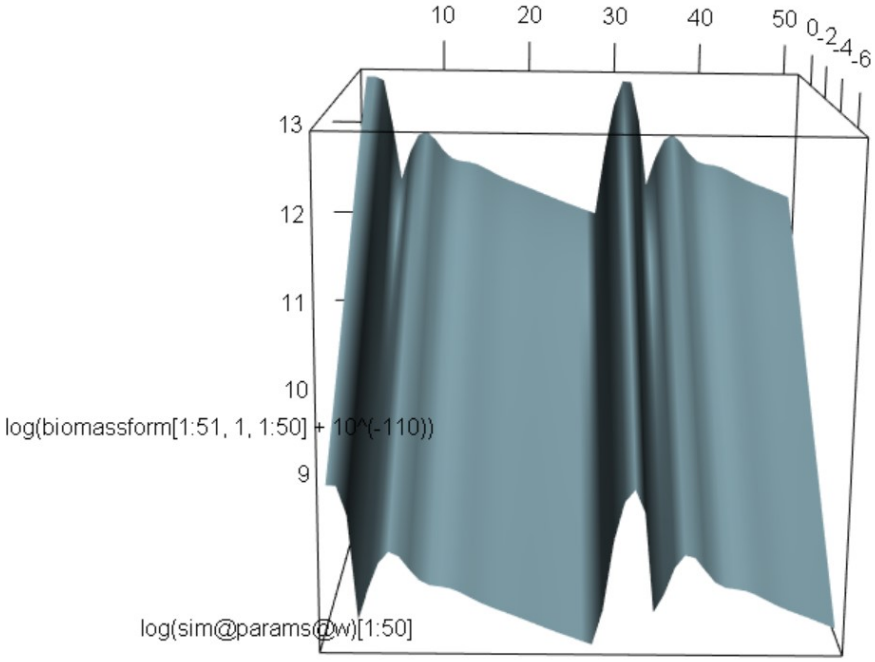
With no prey switching the period is short and the biomass spectrum is flat (so oscillations are a consequence of a lack of Rmax, not the new prey switching mechanism)



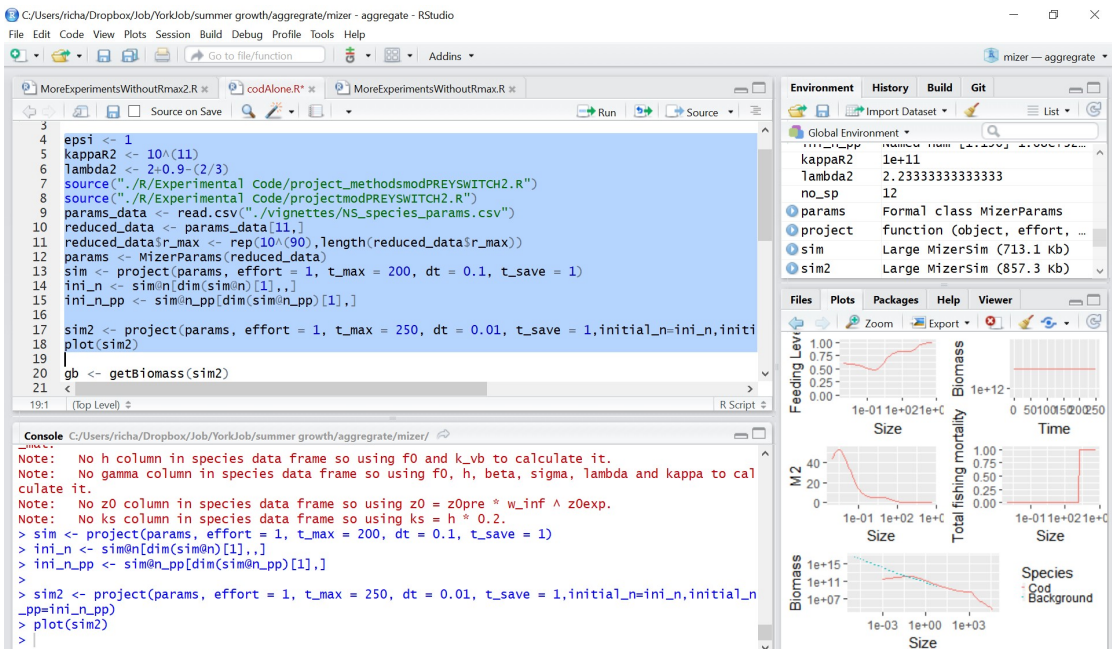
cod alone, now with chi = 0.1, the period is larger (30 yrs) and the biomass curve slopes the wrong way



The oscillation seems quite simple

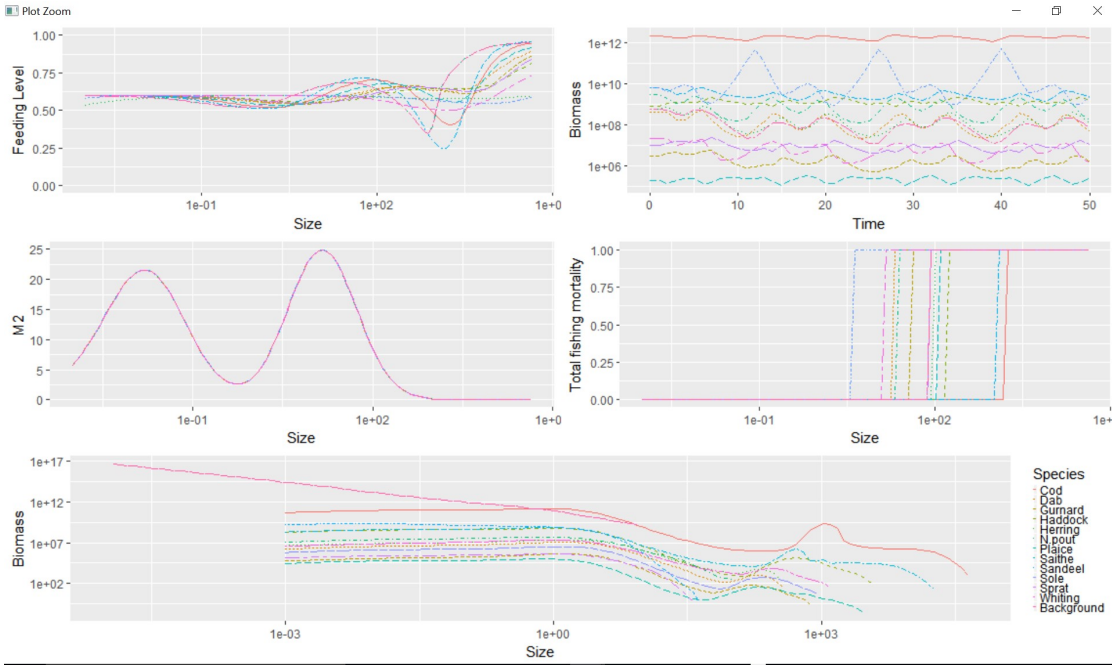


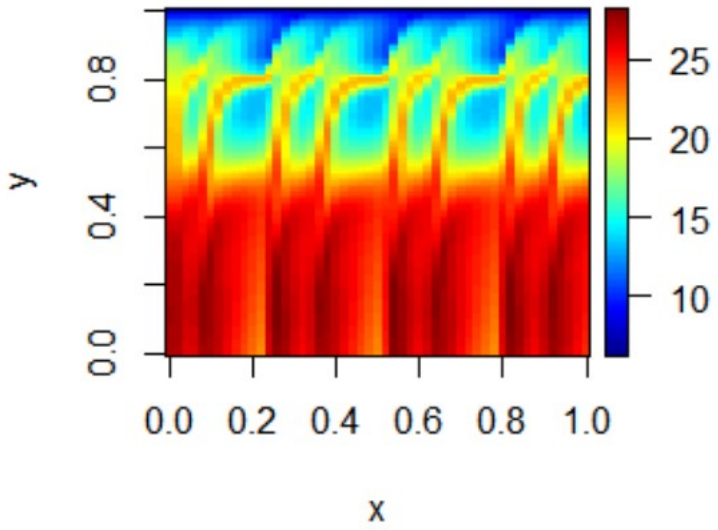
When chi=1 the oscillation vanishes



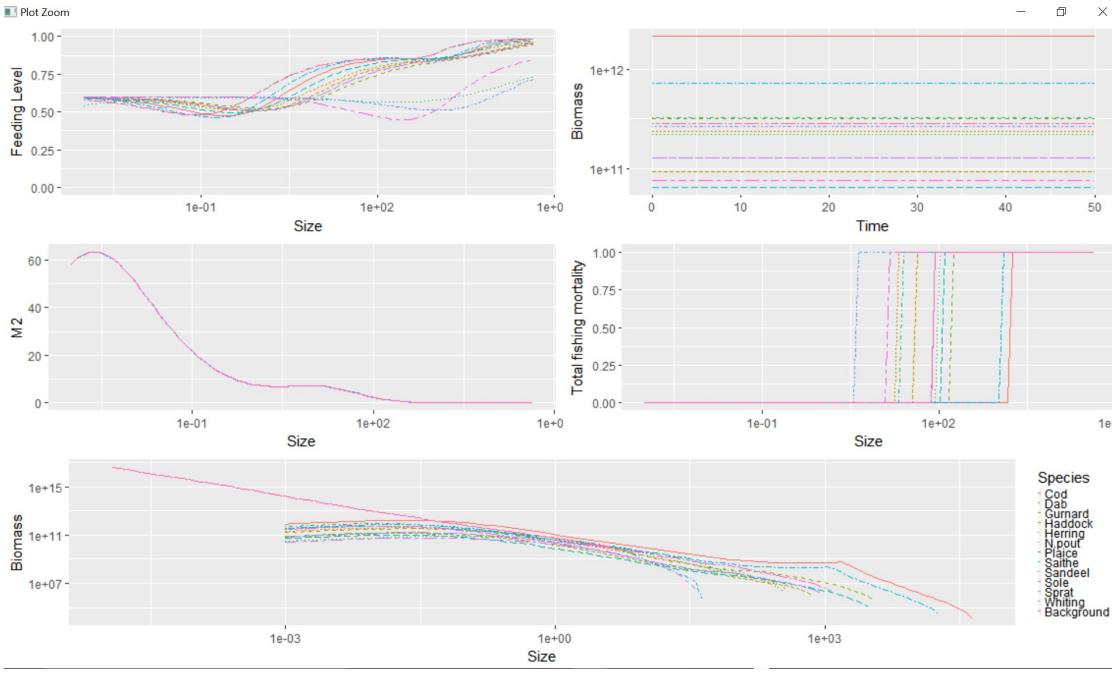
##########

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_methodsmodPREYSWITCH2.R")

source("./R/Experimental Code/projectmodPREYSWITCH2.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],,]

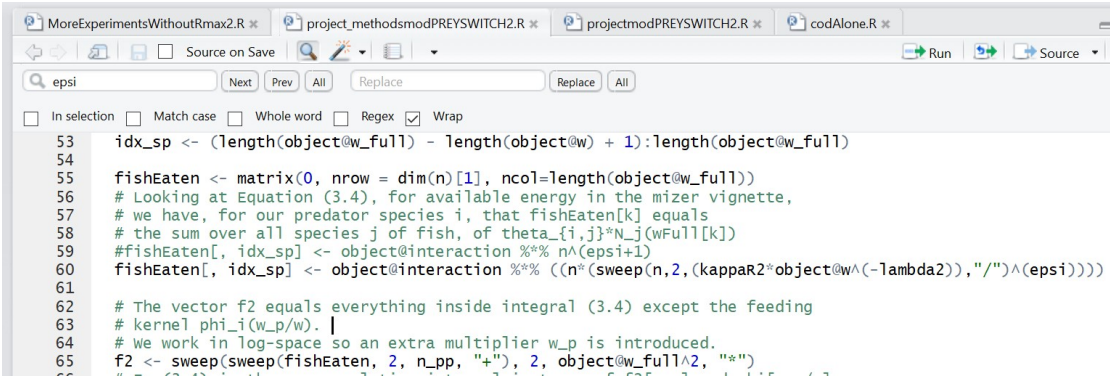
ini_n_pp <- sim@n_pp[dim(sim@n_pp)[1],]

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 #################



###########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,(kapp
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_
```

```
234  arams@dw[idx],"/") + z[,idx,drop=FALSE]*(n[,idx,drop=FALSE]^epsi)*dt
235  rams@dw[idx],"/") + z[,idx,drop=FALSE]*(sweep(n[,idx,drop=FALSE],2,(kappaR2*sim@params@w[idx]^(-lambda2)),"/")^(epsi))*dt
236
237
238
239
240
241  *dt/sim@params@dw[sim@params@species_params$w_min_idx]+z[w_min_idx_array_ref]*(n[w_min_idx_array_ref]^epsi)*dt
242  dt/sim@params@dw[sim@params@species_params$w_min_idx]+z[w_min_idx_array_ref]*((n[,1]/(kappaR2*sim@params@w[1]^(-lambda2)))^(epsi))*dt
```

Code is at

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