

Supplementary Material

Bayesian inference to partition determinants of community dynamics

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1. Description

This file includes the BUGS code for fitting the reduced model and the full model to the data. The reduced model does not explicitly include resource limitation as opposed to the full model. In the reduced model, the density-independent growth rate of the i th phytoplankton functional type from one week to the next is denoted as r_i . The full model incorporates resource limitation by describing the realized density-independent growth rate of the i th phytoplankton functional type from week $w - 1$ to w as $r_{i,w} = \mu_i f_i(w)$, where $\mu_i > 0$ is the maximum net growth rate of the i th functional type from one week to the next at average environmental conditions (temperature and salinity) and optimal resource combination, and

$$f_i(w) = \min \left[\frac{PAR_w}{PAR_w + KE_i}, \frac{Nit_w}{Nit_w + KN_i}, \frac{Sil_w}{Sil_w + KS_i} \right]$$

where $KE_i > 0$, $KN_i > 0$ and $KS_i > 0$ denote respectively the irradiance, nitrogen and silicate half-saturation constants representing the level of each resource at which $r_{i,w} = \mu_i/2$, provided that none of the other resources is limiting.

2. BUGS Code for the reduced and the full (extended model)

Nobs and Npop denote respectively the length of the time series (number of weeks) and the number of populations (functional groups) under consideration. Note that in BUGS, the normal distribution is parameterized with the mean and the precision (inverse variance).

2.1. *Reduced model*

```
model{
##### DYNAMICAL MODEL #####
for(t in 2:Nobs){
# Incorporating "residual" environmental stochasticity
w[t,1:Npop]~dmnorm(m[t,1:Npop], Tau[,])
for(i in 1: Npop){
# Adding biotic interactions and environmental forcing through environmental
variables
m[t,i]<- y[t-1,i]+r[i]*(1+ inprod(alpha[i,], y[t-1,])/k[i]) +
beta[i,1]*temperature[t] + beta[i,2]*salinity[t]
# Incorporating demographic stochasticity
y[t,i]~dnorm(w[t,i], Dem.prec[t,i])
ypred[t,i]~dnorm(w[t,i], Dem.prec[t,i])
eps[t,i]<-(y[t,i]-ypred[t,i])
Dem.var[t,i]<-1/Dem.prec[t,i]
# Scaling of demographic variance with the (population size) FG biomass
Dem.prec[t,i]<-tau.d[i]*exp(y[t,i])
}## end i
}## end t
## r[i] is the intrinsic growth rate for FG i
## alpha[i,j] effect of Functional Group (FG) j on the growth rate of FG i
## alpha[i,i] intraspecific effect #####
## Specifying Priors #####
for(s in 1:Npop){
for(v in 1:Nvar){
beta[s,v]~dnorm(0,tau.b[s,v])
tau.b[s,v]<-v.b[s,v]
v.b[s,v]~dexp(lambda.b)
}
}
}
```

```

alpha[Npop, Npop]<- -1
for(i in 1:Npop-1){
  alpha[i,i]<- -1
  for(j in i+1:Npop){
    alpha[i,j]~dnorm(0, tau.a[i,j])
    alpha[j,i]~dnorm(0, tau.a[j,i])
    tau.a[i,j]<-1/ v.a[i,j]
    tau.a[j,i]<-1/ v.a[j,i]
    v.a[i,j]~dexp(lambda.a)
    v.a[j,i]~dexp(lambda.a)
  }
}
Tau[1:Npop,1:Npop] ~ dwish(R[ , ], Npop)
# Environmental covariance matrix
sigma[1:Npop,1:Npop]<-inverse(Tau[,])
# Cross-species environmental correlations
for(i in 1:Npop){
  for(j in 1:Npop){
    rho[i,j]<-sigma[i,j]/sqrt(sigma[i,i]*sigma[j,j])
    alpha.square[i,j]<-pow(alpha[i,j],2)
  }
}
for(i in 1:Npop){
  r[i]~dgamma(6,4)
  k[i]~dgamma(6,4)
  h[i]<-r[i]/k[i]
  tau.d[i]~dgamma(1,1)
  demVar[i]<-1/tau.d[i]
  ## Variance due to Env. forcing and intra/inter-spec. interactions
  stress1[i]<-(beta[i,1]*beta[i,1])
  stress2[i]<-(beta[i,2]*beta[i,2])
  intra[i]<-pow((r[i]/k[i]),2)*svar[i]
  ## svar[i] is the variance of y[,i]
  totinteract[i]<-pow((r[i]/k[i]),2)*inprod(alpha.square[i,],svar[])
  inter[i]<-totinteract[i]-intra[i]
  ## Total variance for population i (excluding demographic stochasticity)
  totvar[i]<- totinteract[i]+ stress1[i]+ stress2[i] + sigma[i,i]
  ## contributions of environmental and biotic factors

```

```

cenv[i]<-(stress1[i]+ stress2[i] + sigma[i,i])/ totvar[i]
cbio[i]<-totinteract[i] / totvar[i]
cintra[i]<-intra[i]/totvar[i]
cinter[i]<-inter[i]/totvar[i]
}
lambda.b~dgamma(10,1)
lambda.a~dgamma(10,1)
}## end model

```

#####

2.2. Full model

```

model{
for(t in 2:Nobs){
w[t,1:Npop]~dmnorm(m[t,1: Npop], Tau[,])
for(i in 1: Npop){
# Including biotic interactions and environmental forcing
m[t,i]<- y[t-1,i]+g[t,i]
g[t,i]<-r[t,i]*(1+ inprod(alpha[i,], y[t-1,])/k[i]) +
beta[i,1]*temperature[t] + beta[i,2]*salinity[t]
r[t,i]<-mu[i]*min(nitrogen[t]/(KN[i]+nitrogen[t]), min(PAR[t]/(KE[i]+PAR[t]),
silicate[t]/(KS[i]+silicate[t])) ) )
h[t,i]<-r[t,i]/k[i]
# Incorporating demographic stochasticity
y[t,i]~dnorm(w[t,i], Dem.prec[t,i])
Dem.var[t,i]<-1/Dem.prec[t,i]
# Inverse scaling of demographic variance with the (population size) FG
biomass
Dem.prec[t,i]<-tau.d[i]*exp(y[t,i])
}## end i
}## end t
## r[i] is the intrinsic growth rate for FG i at time t ####
# alpha[i,j] effect of FG j on the growth rate of FG i
## alpha[i,i] intraspecific effect #####
##### Specifying Priors #####
for(s in 1:Npop){
for(v in 1:Nvar){
beta[s,v]~dnorm(0,tau.b[s,v])
}
}
}

```

```

        tau.b[s,v]<-v.b[s,v]
        v.b[s,v]~dexp(lambda.b)
    }
}
alpha[Npop, Npop]<- -1
for(i in 1:Npop-1){
  alpha[i,i]<- -1
  for(j in i+1:Npop){
    alpha[i,j]~dnorm(0, tau.a[i,j])
    alpha[j,i]~dnorm(0, tau.a[j,i])
    tau.a[i,j]<-1/v.a[i,j]
    tau.a[j,i]<-1/v.a[j,i]
    v.a[i,j]~dexp(lambda.a)
    v.a[j,i]~dexp(lambda.a)
  }
}
Tau[1:Npop,1:Npop] ~ dwish(R[ , ], Npop)
# Environmental covariance matrix
sigma[1:Npop,1:Npop]<-inverse(Tau[,])
# Cross-species environmental correlations
for(i in 1:Npop){
  for(j in 1:Npop){
    rho[i,j]<-sigma[i,j]/sqrt(sigma[i,i]*sigma[j,j])
  }
}
for(i in 1:Npop){
  mu[i]~dgamma(6,4)
  k[i]~dgamma(6,4)
  # h[i]<-r[i]/k[i]
  tau.d[i]~dgamma(1,1)
  demVar[i]<-1/tau.d[i]
  KN[i]~dnorm(0,100)I(0,)
  KS[i]~dnorm(0,tauS[i])I(0,)
  KE[i]~dnorm(15,0.01)I(0,)
  tauS[i]<-1/varS[i]
  varS[i]<-gam[i]*1 +(1-gam[i])*0.001
  #varS[i]~dexp(1)
  gam[i]~dbern(0.25)
}

```

```
    r[1,i]<-mu[i]*min(nitrogen[1]/(KN[i]+nitrogen[1]),
min(PAR[1]/(KE[i]+PAR[1]), silicate[1]/(KS[i]+silicate[1])) ) )
}
lambda.b~dgamma(10,1)
lambda.a~dgamma(10,1)
}## end model
#####
```