

Synchrony notes

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Some mathematical details

From Loreau and de Mazancourt (2008, American Naturalist: [link](#)), here is the “expected synchrony of per capita population growth rate” under neutral community dynamics:

$$\phi_r = \frac{\sigma_c^2 + \sigma_e^2 + \sigma_d^2/(S\tilde{N})}{[(1/S)(\sum_i \sqrt{\sigma_c^2 + \sigma_e^2 + \sigma_d^2/\tilde{N}})]^2} \quad (1)$$

Here are parameter definitions:

Parameter	Definition
ϕ_r	expected synchrony in per capita growth rates
σ_c^2	community response variance (see definition below)
σ_e^2	environmental variance (equal among species)
σ_d^2	demographic variance (equal among species)
S	species richness in community
\tilde{N}	harmonic temporal mean of population or community size

Community response variance is defined as:

$$\sigma_c^2 = (r_m^2/K^2)\sigma_{N_T}^2 \quad (2)$$

All these expressions are derived from Lotka-Volterra model with environmental and demographic stochasticity:

$$r_i(t) = \ln N_i(t+1) - \ln N_i(t) \quad (3)$$

$$= r_m[1 - \frac{N_T(t)}{K}] + \sigma_e U_e(t) + \frac{\sigma_d U_{di}(t)}{\sqrt{N_i(t)}} \quad (4)$$

The model above is a neutral case where species are equivalent. So there are no competition coefficients needed. Likewise, density-dependence takes place at the community level as if it is a single population (thus, $N_T(t)/K$). Supposedly, if we can estimate σ_c , σ_e , and σ_d we can get a null approximation of species synchrony.

Recreate ML and CdM’s results

I’m going to try and reproduce their figure 1 to make sure I understand the model well. Here is model in code:

```

neutral_model <- function(N, NT, r, K, sigE, Ue, n_spp){
  r_out <- numeric(n_spp)
  N_out <- numeric(n_spp)
  for(i in 1:n_spp){
    lambda <- exp(r[i] * (1-(NT/K)) + sigE*Ue)
    N_out[i] <- sum(rpois(N[i], lambda))
  }
  return(N_out)
}

```

#Independent random variables for stochasticity

```

t_limit <- 130
Ue <- rnorm(t_limit,0,1)
Ud <- rnorm(t_limit,0,1)

```

#Other parameters

```

r <- c(1,1) #neutral
K <- c(20000,20000) #neutral
sigE <- c(0.01, 0.01) #neutral

```

OK, try simulating the model to get figure 1.

```

r_save <- matrix(nrow=t_limit, ncol=length(r))
N_save <- matrix(nrow=t_limit, ncol=length(r))
N_save[1,] <- K
for(t in 2:t_limit){
  mod_out <- neutral_model(N=N_save[t-1,], NT=sum(N_save[t-1,]), r=r, K=K,
                           sigE=sigE, Ue=Ue[t-1], n_spp=length(r))
  N_save[t,] <- mod_out
}
N_save <- as.data.frame(N_save)
N_save$year <- c(1:t_limit)
N_lag <- N_save
N_lag$lagyear <- N_lag$year+1
colnames(N_lag)[1:2] <- c("lagN1", "lagN2")
N_merge <- merge(N_save, N_lag[,c(1,2,4)], by.x = "year", by.y = "lagyear")
N_merge$pgr1 <- with(N_merge, log(V1/lagN1))
N_merge$pgr2 <- with(N_merge, log(V2/lagN2))

```

#Calculate correlations

```

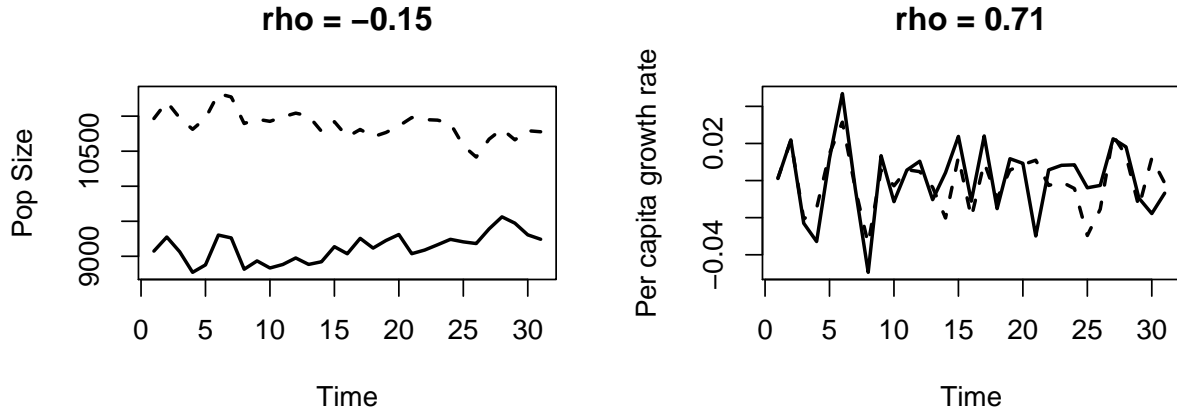
rho_n <- cor(N_merge[c(99:129),"V1"], N_merge[c(99:129),"V2"])
rho_r <- cor(N_merge[c(99:129),"pgr1"], N_merge[c(99:129),"pgr2"])

```

```

par(mfrow=c(1,2))
matplot(as.matrix(N_merge[c(99:129),c("V1", "V2")]), type="l",
        col="black", lwd=2, xlab="Time", ylab="Pop Size",
        main=paste("rho =", round(rho_n,2)))
matplot(as.matrix(N_merge[c(99:129),c("pgr1", "pgr2")]), type="l",
        col="black", lwd=2, xlab="Time", ylab="Per capita growth rate",
        main=paste("rho =", round(rho_r,2)))

```



Parameters to estimate

OK, if the idea is to estimate the expected synchrony of per capita growth rates under the neutral assumption, then we need to estimate the following parameters (table include parameters and my idea for estimating them). The key here is to estimate these parameters statistically and using the IPM assuming species equivalence, so instead of modeling by species, we treat the whole community as a single population.

Parameter	Estimation method
K	the time-invariant equilibrium area cover (no year reandom effects)
r_m	intrinsic growth rate of the “combined species” (grow it alone at low density)
σ_{N_T}	temporal standard deviation of total community cover directly from data
σ_c	estimated from K , R_m , and σ_{N_T} ($(r_m^2/K^2)\sigma_{N_T}^2$)
σ_e	standard deviation of “combined species” yearly growth rate time series
σ_d	average individual-level effect standard deviation from hierarchical vital rate models

Parameter estimation with one species

Just to see what we can expect, I am going to try the above approach with *Artemesia triparta* only fromt the Idaho site. These are the steps:

1. Fit vital rate models with year and individual effects
2. Average vital rate individual effect variance (σ_D)
3. Simulate IPM without year effects for equilibrium cover (K)
4. Simulate IPM with year effects (random order) at low density many times to estimate r_m (average over time series)
5. Simulate IPM with year effects at low density (in order) to get the yearly growth rate time series (σ_e)
6. Put it all together for neutral expecteation of synchrony.

Vital rate regressions

First we fit the vital rate regressions using INLA. Note that INLA gives us the precision (τ) for the individual-level effect, which we can convert to standard deviation as: $\sigma_D^G = \sqrt{\tau^{-1}}$.

```
formula2 <- logarea.t1 ~ logarea.t0+crowd+
  f(yearID, model="iid", prior="normal",param=c(0,0.001))+
  f(GroupID, model="iid", prior="normal",param=c(0,0.001))+
  f(plantID, model="iid", prior="normal",param=c(0,0.001))+
  f(year, logarea.t0, model="iid", prior="normal",param=c(0,0.001))

outINLA <- inla(formula2, data=D,
  family=c("gaussian"), verbose=TRUE,
  control.predictor = list(link = 1),
  control.compute=list(dic=T,mlik=T),
  control.inla = list(h = 1e-6))
```

So, the demographic variance (as we have defined it, individual-level variation) for growth is: $\sigma_d^G = 0.3273$ (that is $1/\sqrt{(\tau^{-1})}$, where τ is the precision of the individual plant effect in the model). We can do this for the other vital rates too, and we get the following results:

Vital Rate	σ_d	σ_d^2
Growth	0.3273	0.1071
Survival	0.9643	0.9299
AVERAGE	0.6458	0.5185