* **Experiment 0 (non-selective ­­­global dispersal)**
  + gives similar results to Jonsson and Watson 2016 (???)
  + No temperature preference (1 global phenotype)
  + 341 'invaders' at 341 global sites
    - passive tracer - use deterministic advection
    - stochastic demography
  + check global dispersal times
* **Experiment 1 (spin up)**
  + 77 Temperature optima, 60646 locations
  + 77x60646 matrix
  + Seeded with biomass in each location equal among all 77 phenotypes
    - need to also seed with single common ancestor (e.g. warm and cold)
    - ...to test robustness
  + Mutation and circulation - on/off
  + Seasonality - on\off (temperature and carrying capacity)
  + Run for 100 years
  + Reaches equilibrium quickly (probably < decade)
    - Phenotypes selected in optimal environment
    - Broader range maintained by dispersal
* **Experiment 2 (global dispersal of 'ancestral species')**
  + 77 phenotypes separated into distinct 'species' (no mutational flux)
  + Each column now has 77 columns, so matrix is 772x60646
  + Seeded with distributions from experiment 1
  + Each 'species' now in optimal habitat
  + Can disperse globally, but competes neutrally with other 'species'  
    **but** each must adapt to new environments.
* **Experiment 3**
  + Repeat Exp.2 but without temperature selection or mutation
  + i.e. just dispersal from initial distribution
    - turn off mutational flux but leave temperature selection
      * reveals diversity attributable solely to dispersal
    - turn off mutational flux and temperature selection
      * reveals strictly neutral scenario (i.e. rapid dispersal)

**Repeat all experiments for *prochlorococcus* and diatoms**

**Mutation, no dispersal (diversity maintained by mutation)**

**Dispersal, no mutation (diversity maintained by dispersal)**

**No dispersal, no mutation (competitive exclusion)**

**What happens under differing degrees of selection?**