Practical Setup

https://github.com/microbiome/miaSim

https://github.com/danielriosgarza/microbialTimeSeries

Per-capita based model

- Unified neutral theory of biodiversity

Metacommunity: represented as a fixed multinomial distribution

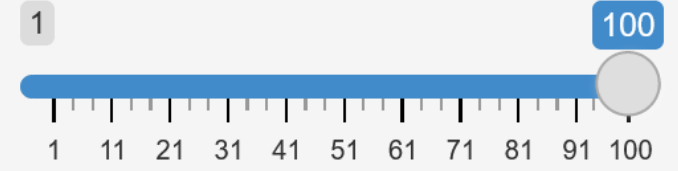Local community: represented as continuously changing multinomial distribution

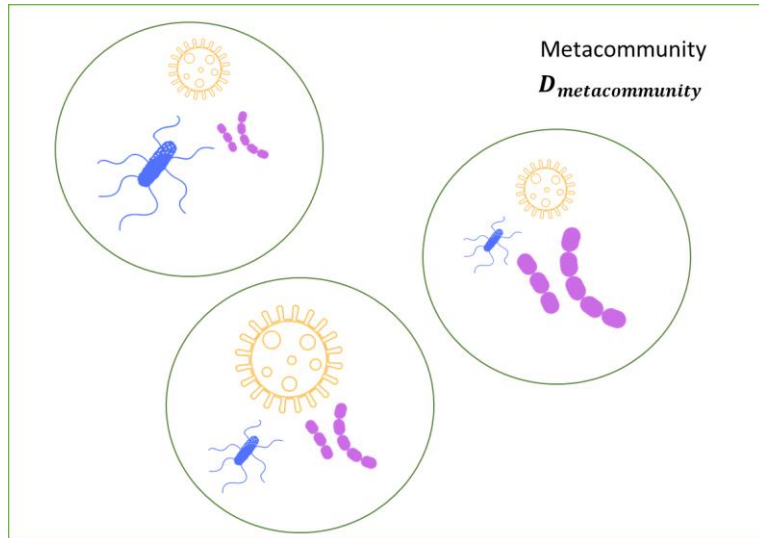Time-steps are discrete

Metacommunity

Metacommunity species abundance

Meta community

0.05
0.04
0.03
0.02
0.01

Number of species in metacommunity

1   100

1   11 21 31 41 51 61 71 81 91 100

Metacommunity eveness

1   1,000

1   101 201 301 401 501 601 701 801 9011,000

Metacommunity

$D_{metacommunity}$

Constant multinomial distribution

Local community

Initial composition
local community

Local
community
40
30
20
10
0

Represented as "dynamic" multinomial distribution that Follows a "Moran-like process"
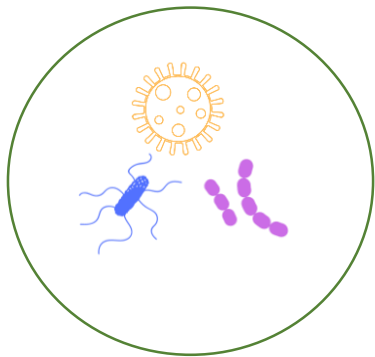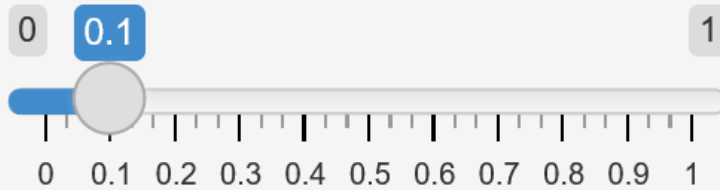
1) Pick an individual (or k individuals) from D_{local}
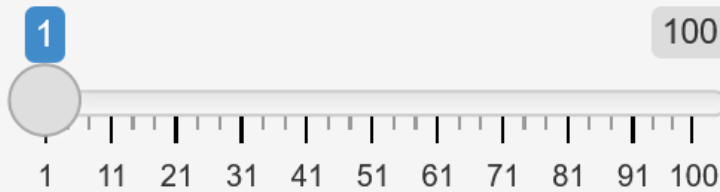
2) Replace it by an individual from a local species or a migrant from the metacommunity

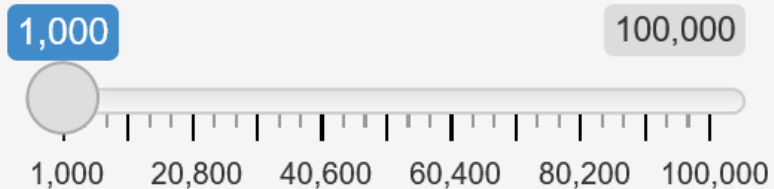$$(1 - \lambda) \quad \text{or} \quad \lambda$$

Tasks:

1) Simulate the Hubbell model in RStudio

2) Generate "moments" for multiple instances of the model

3) Correlate alpha diversity with metacommunity evenness

4) Generate a UMAP with an evenness gradient

5) Generate a UMAP with evenness = 1 and evenness = 20

Adding rates

Treat events as "reactions" in the Gillespie algorithm

- When will the next event occur?

$$nA \xrightarrow{R} nB \qquad \tau = \frac{1}{nA * R} * \log(\frac{1}{r_1})$$
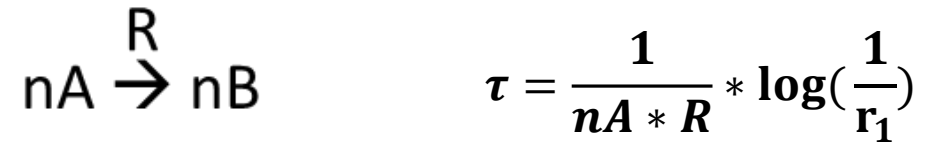
- When will the next K events occur?

$$Gamma(shape = k, scale = \frac{1}{nA * R})$$

K-leap method for accelerating stochastic simulation of coupled chemical reactions

Xiaodong Cai[a] *and* Zhouyi Xu

Use growth rates?

○ yes

◉ no

Distribution of growth rates (beta distribution **) if used**

alpha

| 0.5 | 10 |

0 1 2 3 4 5 6 7 8 9 10
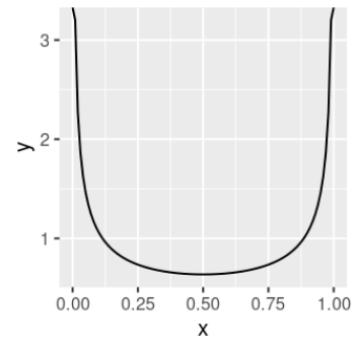
beta

| 0.5 | 10 |

0 1 2 3 4 5 6 7 8 9 10
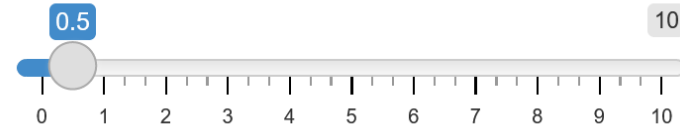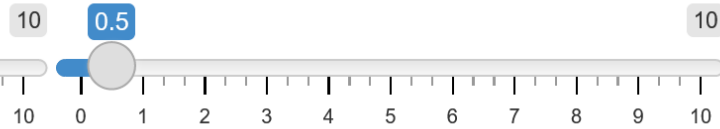
Growth rates are:

```
 [1] "0.40" "0.37" "0.00" "0.06" "0.98" "0.79" "0.99" "0.93" "0.62" "0.67"
[11] "0.90" "0.60" "0.06" "0.22" "0.04" "0.98" "0.98" "0.70" "0.15" "1.00"
[21] "0.66" "0.64" "0.58" "0.45"
```
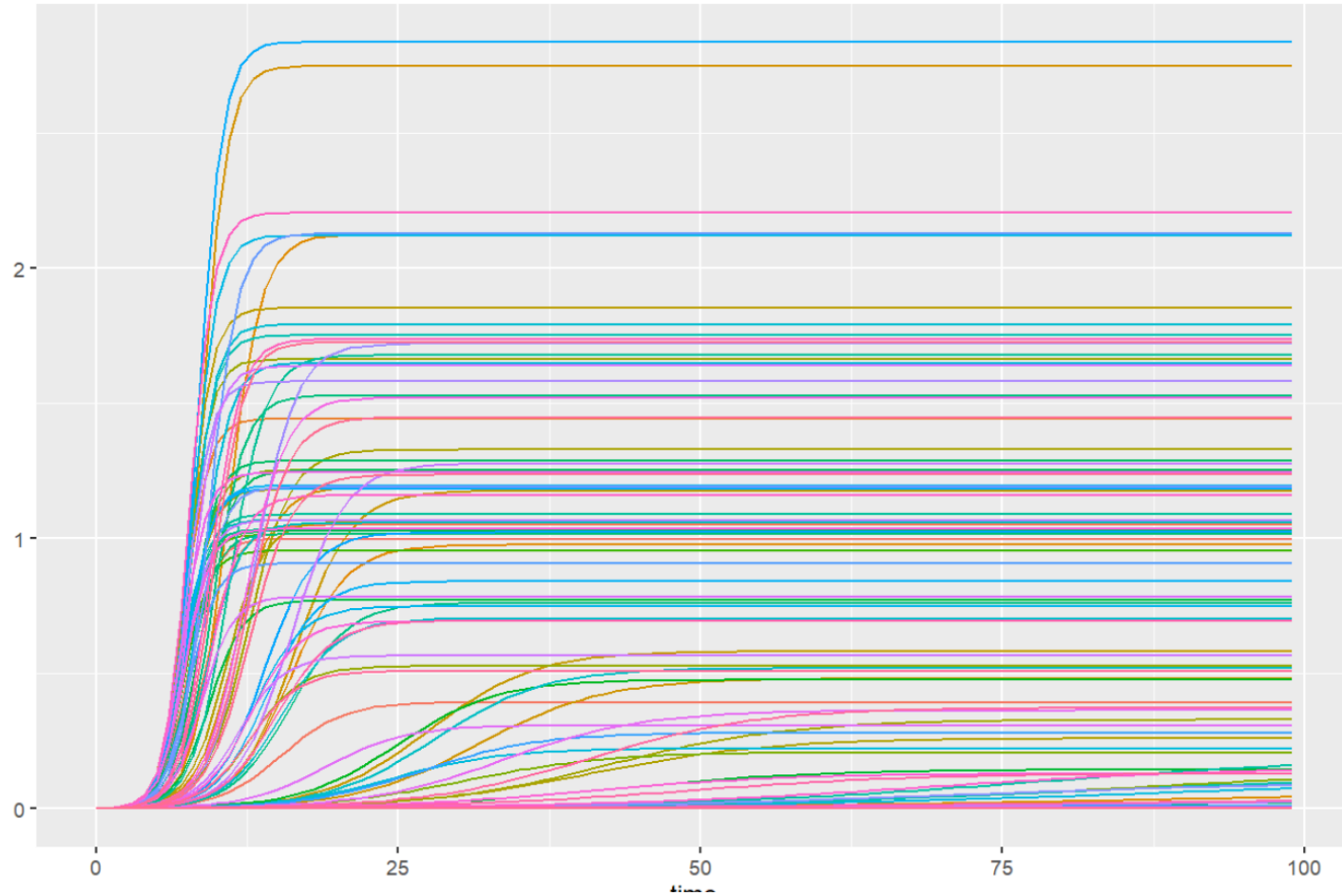
The expected distribution is:

Tasks:

6) Generate a simulation of a per-capita based model with growth rates

7) Compare neutral and non-neutral simulations with the Kullback-Leibler divergence

8) Check if communities generated with a per-capita model cluster based on their neutral and non-neutral origin
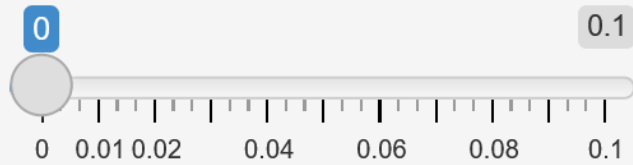
Population-based models

Logistic model

Species do not interact

Abundance only depends on two parameters: growth rate and Carrying capacities

Death rates

Initial populations are set to constant and equal to 0.001

constant death rates

0   0.1

0   0.01 0.02   0.04   0.06   0.08   0.1

Metacommunity	Growth rates	Stochasticity	Simulation

Eveness

1   504.1   1,000

1   100.9 200.8 300.7 400.6 500.5 600.4 700.3 800.2 900.1 1,000

Migration rate   **sd of migration**

0   1   0.01   1

0   0.1   0.2   0.3   0.4   0.5   0.6   0.7   0.8   0.9   1   0   0.1   0.2   0.3   0.4   0.5   0.6   0.7   0.8   0.9   1

Metacommunity
species abundance

Meta
community

- 0.23
- 0.22
- 0.21
- 0.20
- 0.19

Tasks:

1) Find a parameter setting in the APP and reproduce with a script in RStudio; For now, keep "stochastic=FALSE"

2) Compare moments of a "stabilized" migration/death rate community with the Hubbell model, using the same metacommunity (use norm =TRUE)

3) Check if the Hubbell and SLM separate in a UMAP space

4) What happens to the community if it gets "invaded" by an extremely fast growing species?

Noise and perturbation

Use stochasticity?

⦿ yes

◯ no

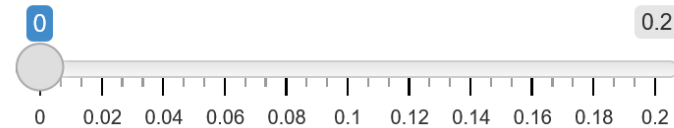**sd of random drift**

| 0 | 0.2 |

0   0.02 0.04 0.06 0.08 0.1 0.12 0.14 0.16 0.18 0.2

frequency of strong episodic drift

| 0.01 | 0.5 |

0 0.05 0.1 0.15 0.2 0.25 0.3 0.35 0.4 0.45 0.5

sd of strong episodic drift

| 0.01 | 0.5 |

0 0.05 0.1 0.15 0.2 0.25 0.3 0.35 0.4 0.45 0.5
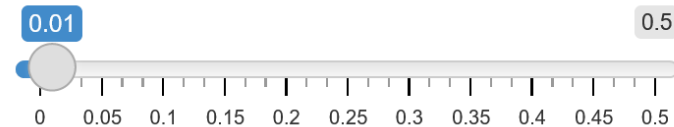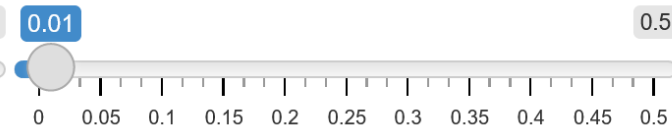
number of perturbation events

| 0 | 10 | | 100 |

0 10 20 30 40 50 60 70 80 90 100
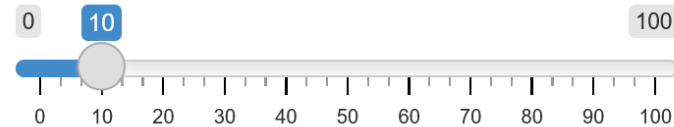
duration of perturbation events (t)

| 0.1 | 10 |

0 1 2 3 4 5 6 7 8 9 10

sd of perturbation

| 0.01 | 0.5 |

0 0.05 0.1 0.15 0.2 0.25 0.3 0.35 0.4 0.45 0.5
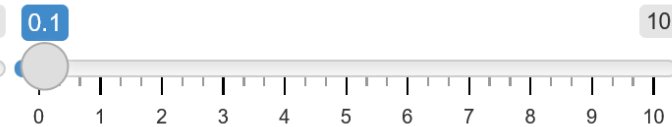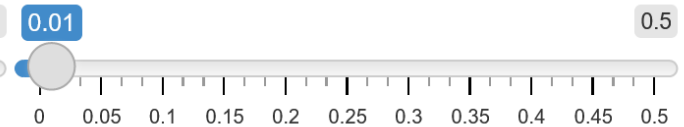
Times of perturbations are: 9.1, 18, 27, 36, 46, 55, 64, 73, 82, 91

Tasks:

- Compare alpha diversity and rank abundances in a "stochastic" vs. a "deterministic" model

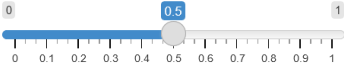- Measure their distance to a Hubbell model (open)

- Any other ideas? (open)
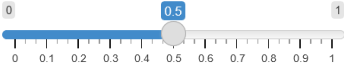
GLV

Interaction matrix
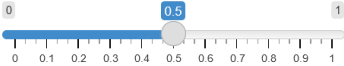
sd of interaction matrix

| 0 | 1 | 10 |

0 1 2 3 4 5 6 7 8 9 10

scaling of interaction matrix

| 0 | 0.5 | 1 |

0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 1

Connectance of interaction matrix

| 0 | 0.5 | 1 |

0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 1

mutualism (1,1)

| 0 | 0.5 |

0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 1

commensalism (1,0)

| 1 | 0 | 0.5 |

0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 1

parasitism (1,-1)

| 1 | 0 | 0.5 |

0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 1

amensalism (0,-1)

| 1 | 0 | 0.5 |

0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 1

competition (-1,-1)

| 1 | 0 | 0.5 | 1 |
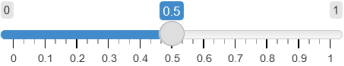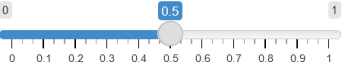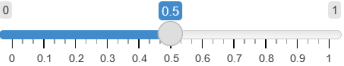
0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 1
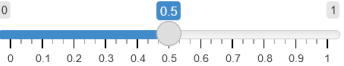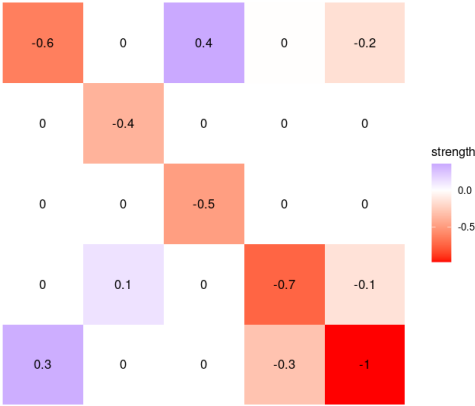
Use symmetric interactions?

○ yes
◉ no

Interaction frequencies are:

```
[1] "0.20" "0.20" "0.20" "0.20" "0.20"
```

Interaction
matrix

Tasks:

- Explore the conditions for a community to "explode" in the GLV interactions

- Can random drift "mask" the interactions? (open)

- Add some structure to the matrix and see if you get "community types"

CRM