The eigenmove package

Efficient modelling of patch structure and connectivity via low-rank approximation of random walk models

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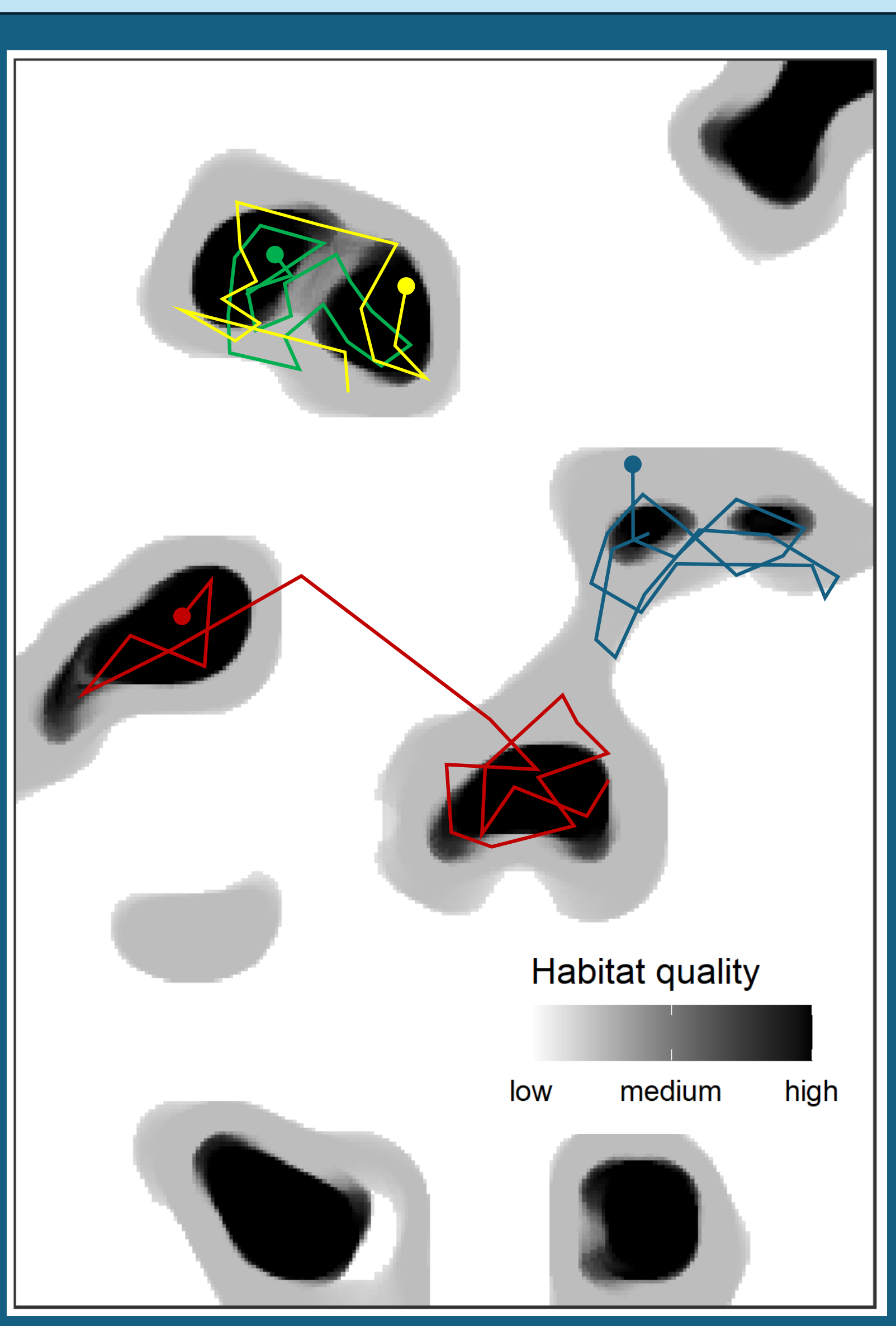
The problem:

- Metapopulation models assume individuals interact within *well-mixed patches with rare movement through matrix between patches* **but we have never determined how to define what a patch is**
- Rates of interaction between individuals will depend not only on *landscape structure*, but also on individual decisions about how to *move through* that landscape



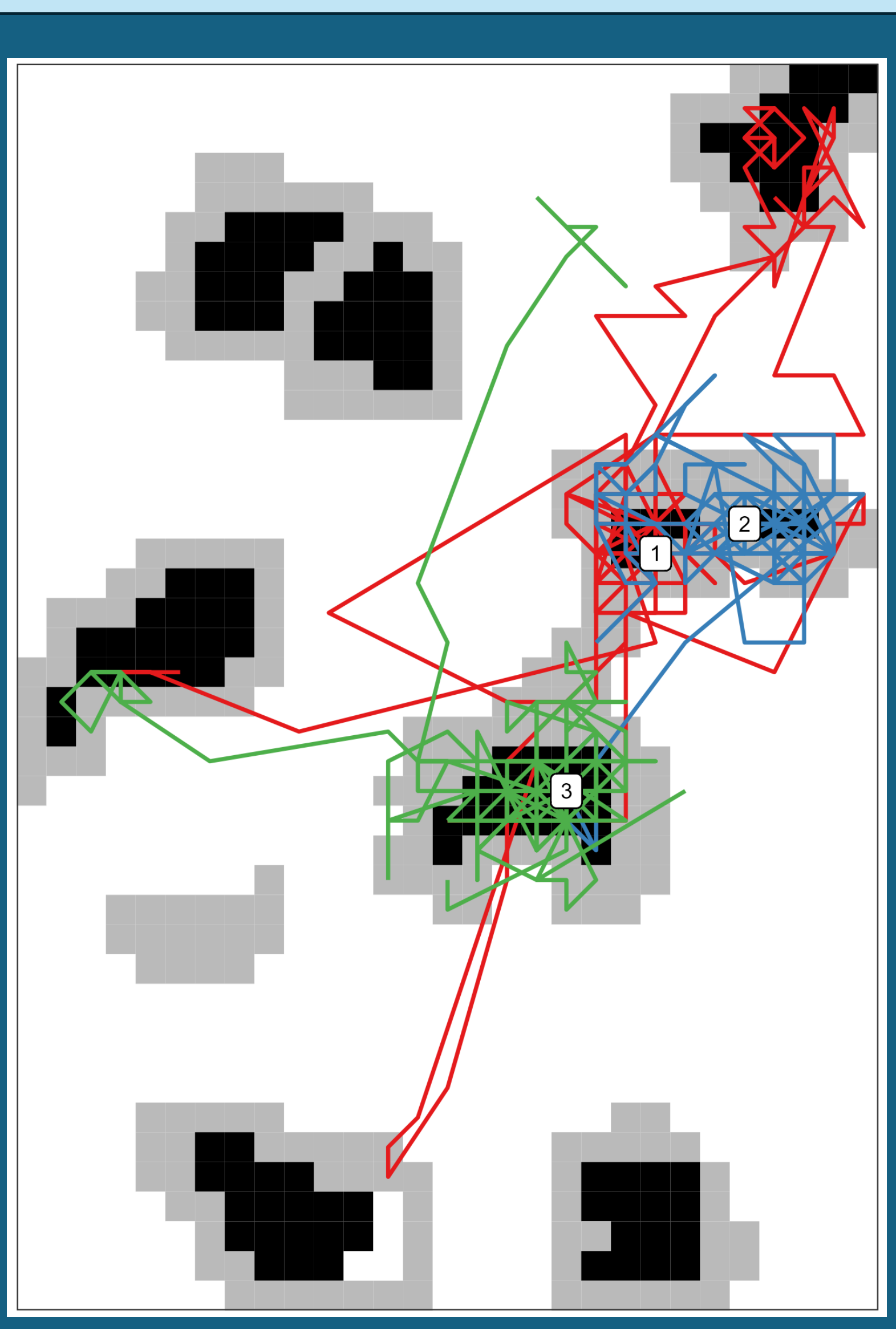
Example landscape: Animals breed within black regions, and forage within grey regions. White is matrix where animals will move through but cannot survive. Lines show movement trajectories of individuals starting from circles

Can we derive landscape structure directly from movement models?

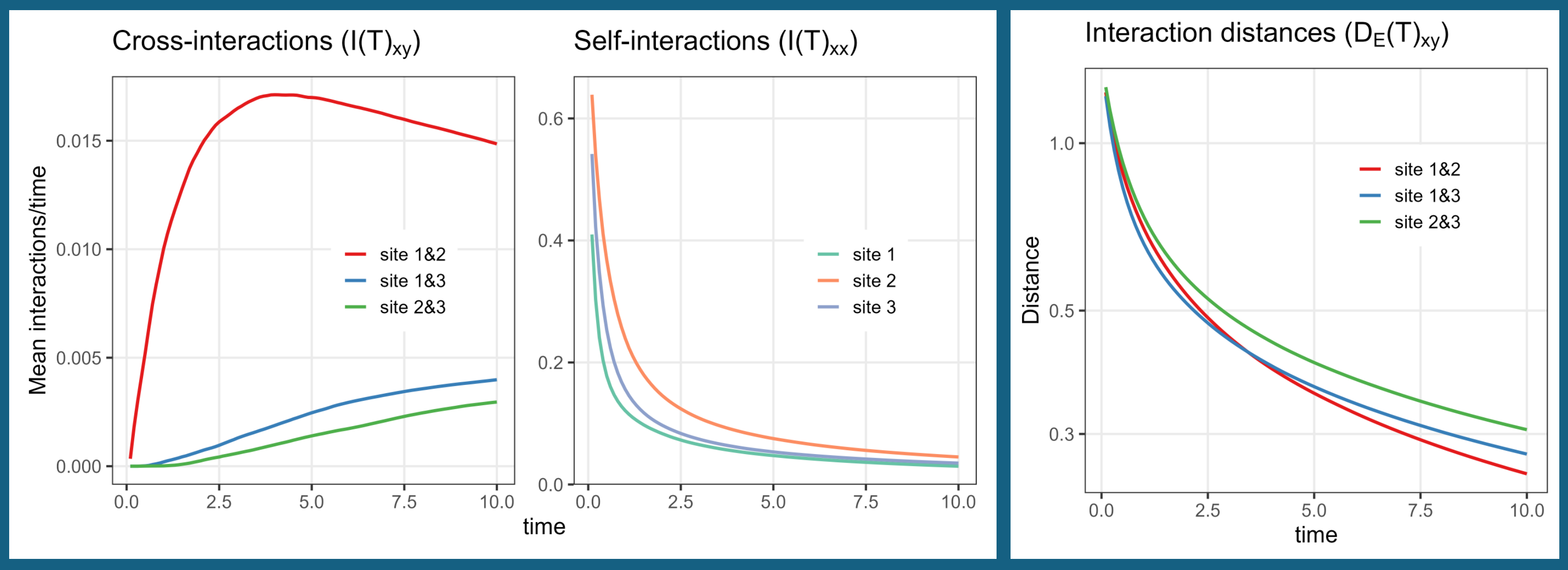
Encounter-based distances

- If we follow movement of individuals born in different locations x, y across their lifespans, we can count the average number of times they encounter each other (end up in the same site z) in their lifespan T as $\mathrm{I(T)}_{xy}$
- Using this, we can define an **encounter *distance function*** between sites:

$$\boldsymbol{D_E(x,y) = I_{xy} + I_{yy} - 2I_{xy}}$$



Simulated random-walk movement paths for individuals starting from sites 1, 2, and 3 at time 0



Interaction rates and distances calculated via simulations between random walkers that start from different starting sites (1-3) on the landscape

But directly simulating encounters is computationally costly. Is there a more efficient way to calculate these distances?

The theory behind eigenmove

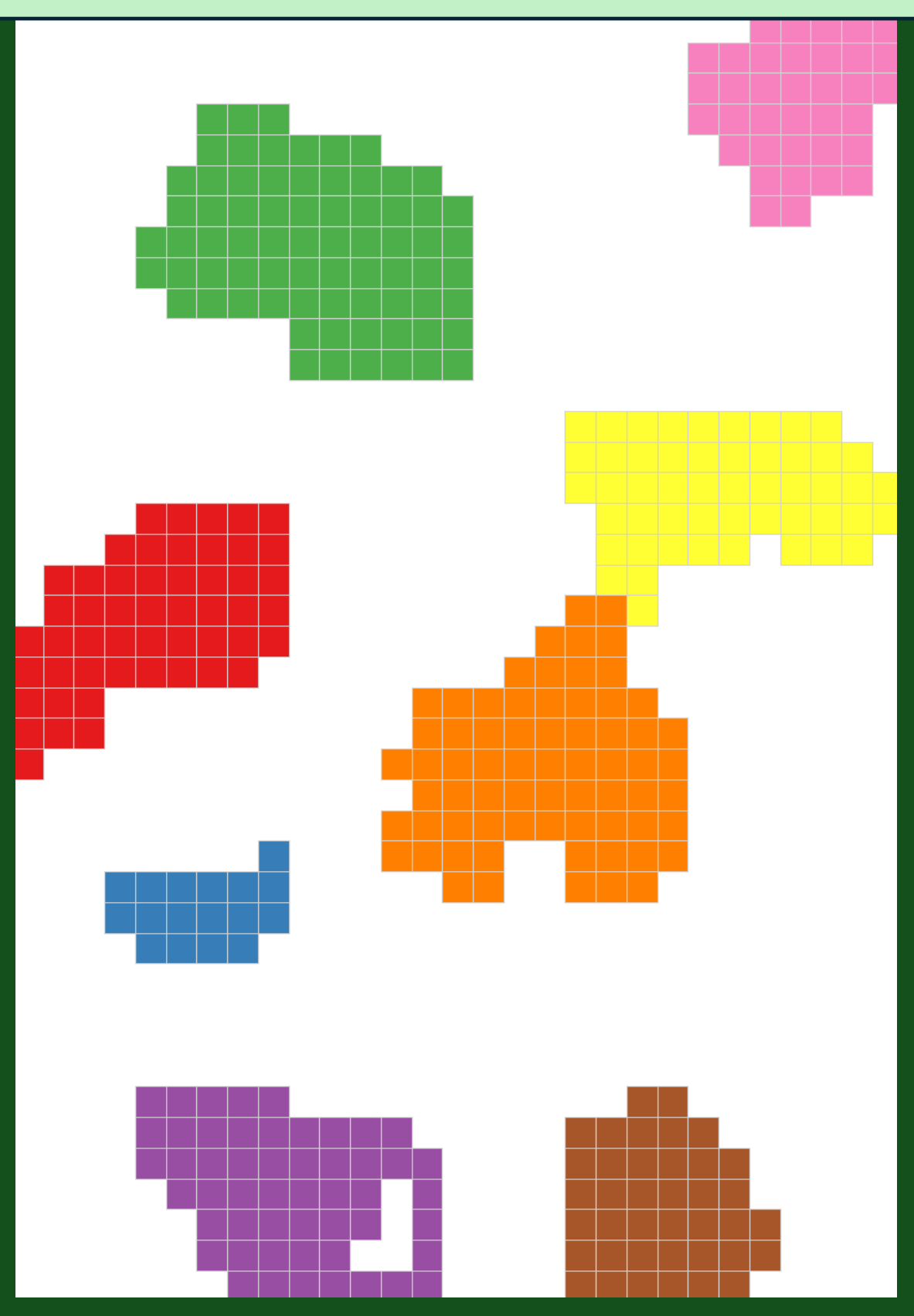
1. Assume movement follows a Continuous-time Markov Chain (CTMC[1]): individuals starting from site x wait for some time w_x then jump to a new site y with probability p_{xy}. w_x and p_{xy} depend on site-level characteristics (Hanks et al. 2015). Gives a Generator matrix Q
2. Matrix of interaction rates $I(T)$ can be calculated as:
$$I(T) = \frac{1}{T}\int_0^T \exp(\tau Q)' \exp(\tau Q)\, d\tau$$
3. Eigendecompose $Q = \Phi\Lambda\Psi$, retain k leading eigenvalues / vectors: $\tilde{Q} = \Phi_\mathrm{k}\Lambda_\mathrm{k}\Psi_\mathrm{k}$
4. Use the low-rank representation to efficiently calculate approximate interactions / distances[2]:
$$\tilde{I}(T) = \frac{1}{T}\Psi_k' \int_0^T \exp(\tau\Lambda_k)\, \Phi_k{}'\phi_K \exp(\tau\Lambda_k)\, d\tau\Psi_k$$

What can eigenmove do?

Estimate patch structure

Distances can be used to cluster locations into patches that account for movement behaviour (via Q) and lifespan (T)

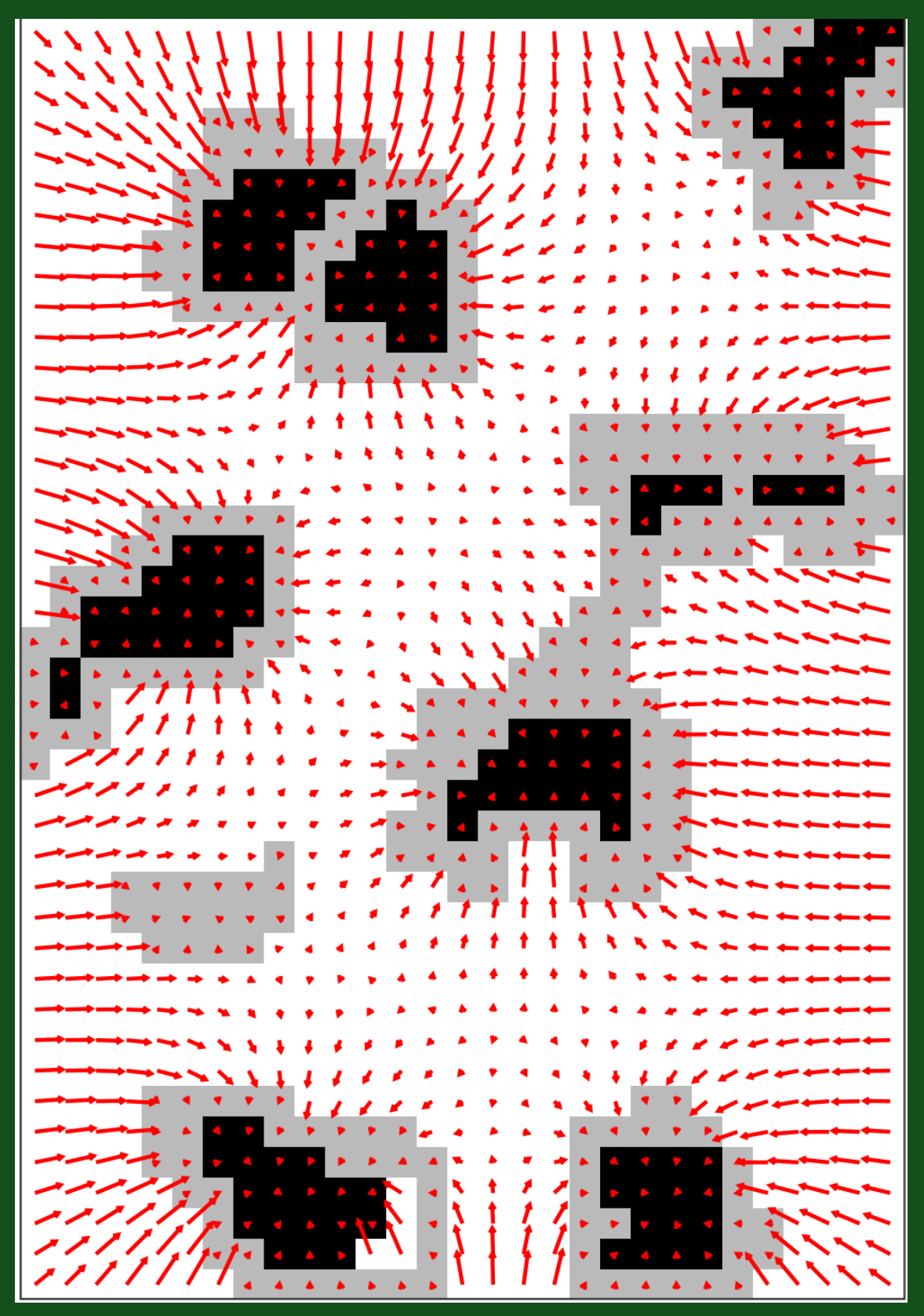
$\widetilde{D}_E$ from site 2 to other sties at time scale = 4, k = 100



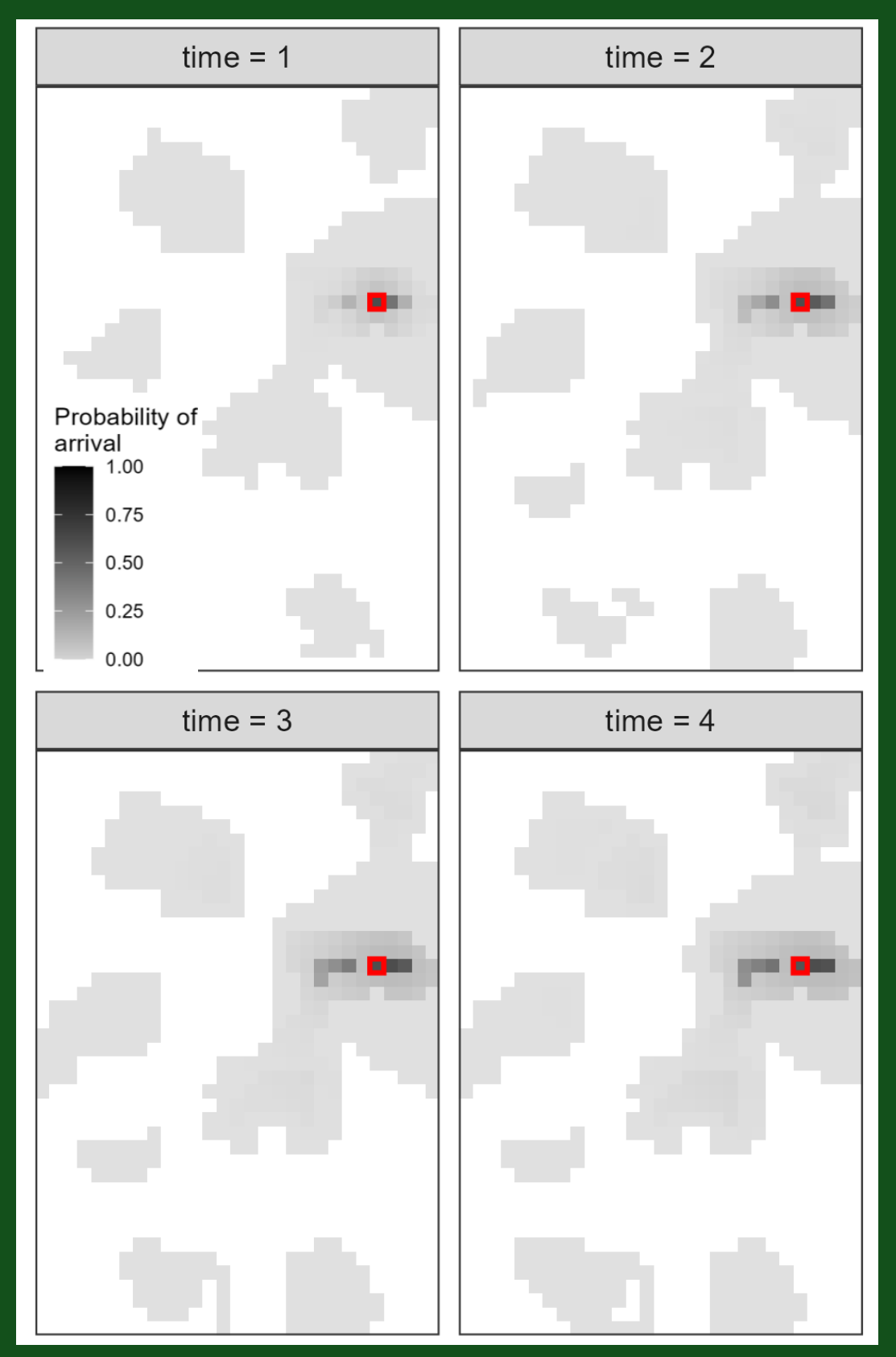
Estimated patch structure based on $\widetilde{D}_E$(T=4)

Calculate connectivity

Approximate movement matrix $\Phi_\mathrm{k}\exp(\tau\Lambda_\mathrm{k})\Psi_\mathrm{k}$ can be used to calculate instantaneous flow fields and time-dependent dispersal probabilities between different sites / patches



Average direction of travel (flow) from each starting site



Time-dependent movement probabilities from site 2

Follow us for more on our work:

eigenmove R package (in development):
github.com/pedersen-fisheries-lab/eigenmove
Pedersen lab website:
www.pedersenfisherieslab.com/

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1. Hanks, E., Hooten, M.B., Alldredge, M.W. 2015: Continuous-time discrete-space models for animal movement. Ann. Appl. Stat. 9: 145-165
2. Noé, F., Clementi, C. 2015: Kinetic distance and kinetic maps from molecular dynamics simulation. J. of Chem. Theory & Comp. 11:5002-5011