

Predicting pollinator-mediated gene flow in a fragmented landscape

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Background

- Gene flow, the exchange of genes among populations, helps maintain genetic diversity and prevent inbreeding in small, isolated populations.
- Most models of gene flow assume that (1) *gene flow is random with respect to genotype* and (2) that *gene flow can be predicted by distance* (Ellstrand 2014).
- Pollinator foraging is often sensitive to variation in floral traits and abundance. Thus, standard gene flow models may inaccurately predict gene flow of animal-pollinated plants.
- The ability to predict pollinator-mediated gene flow would advance conservation strategies in fragmented landscapes.

How does individual variation in spatial isolation and timing of flowering influence potential for gene flow in fragmented landscapes?

Results

Methods

Data Collection



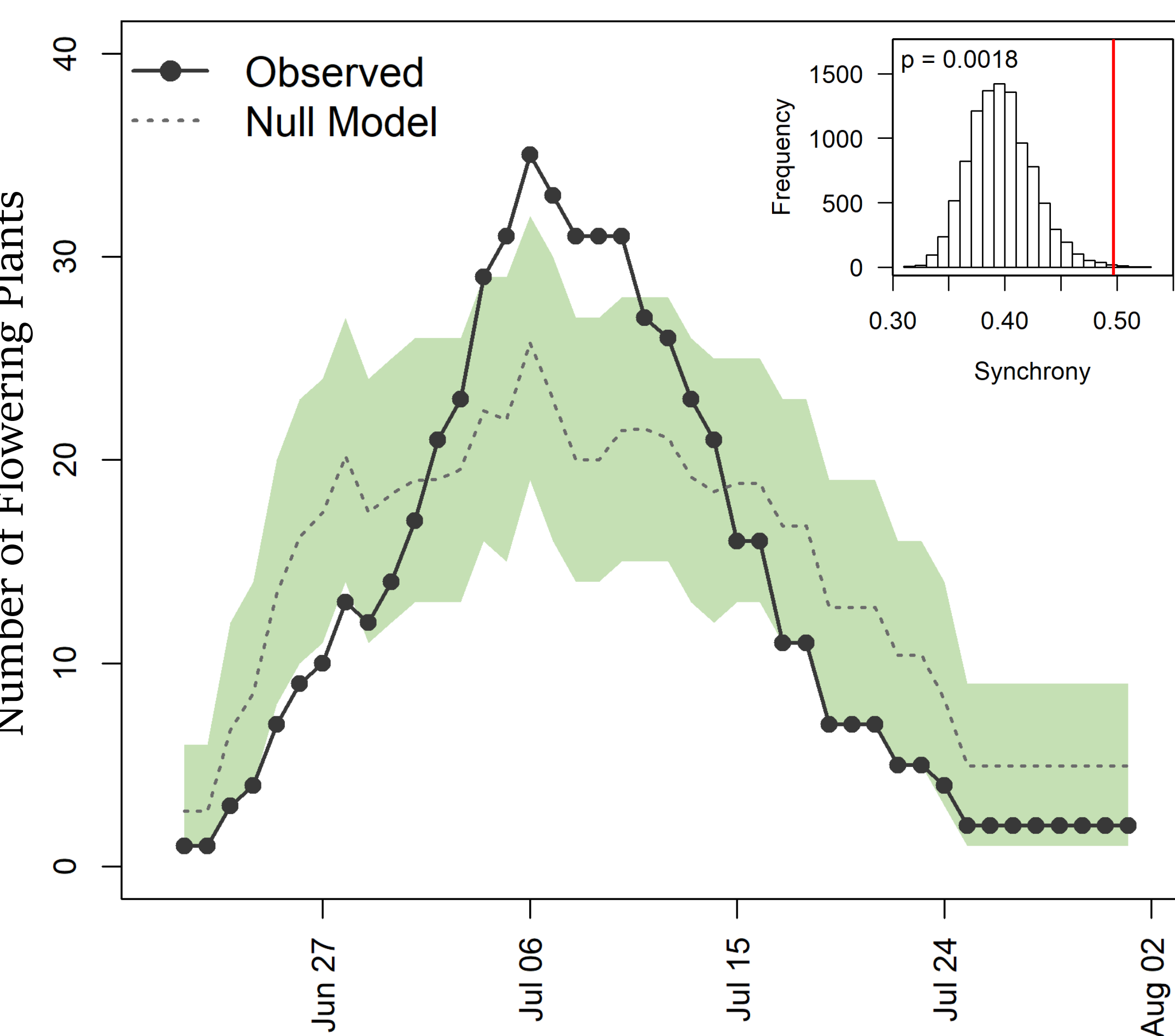
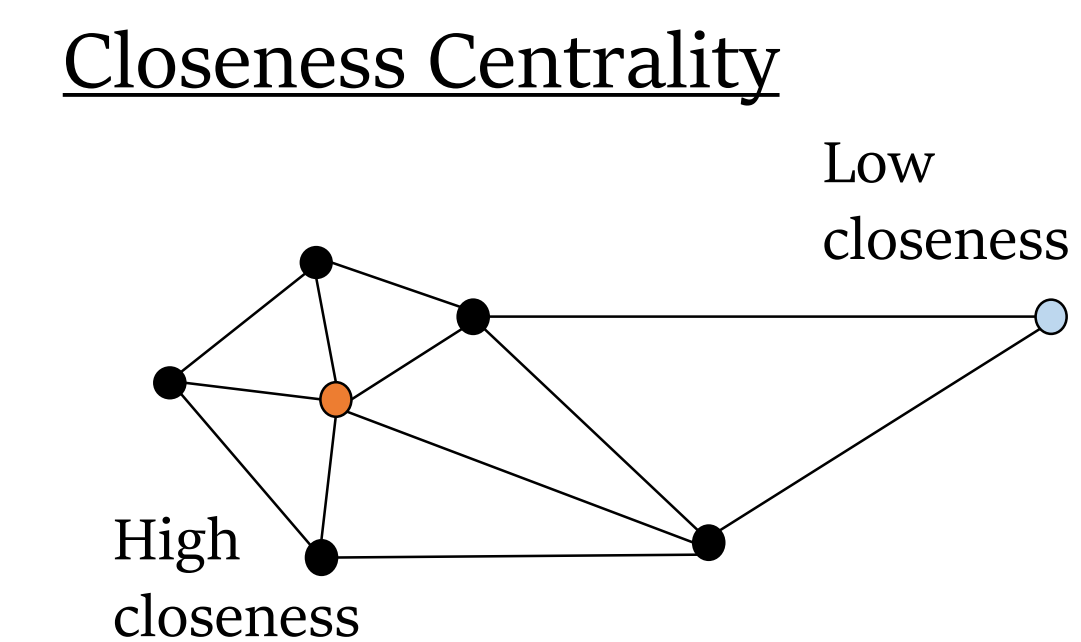
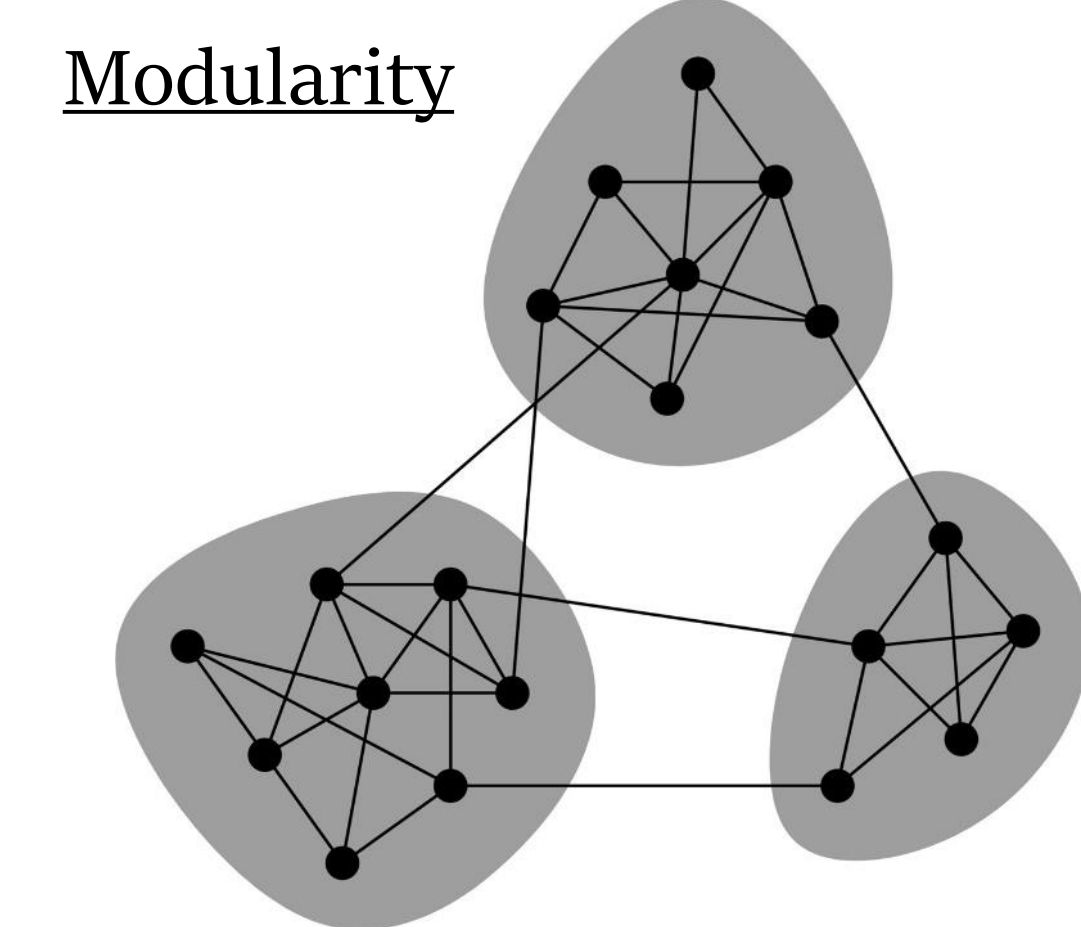
Map all flowering *Echinacea angustifolia* in 516 ha study area



Track flowering phenology to obtain start and end date of flowering

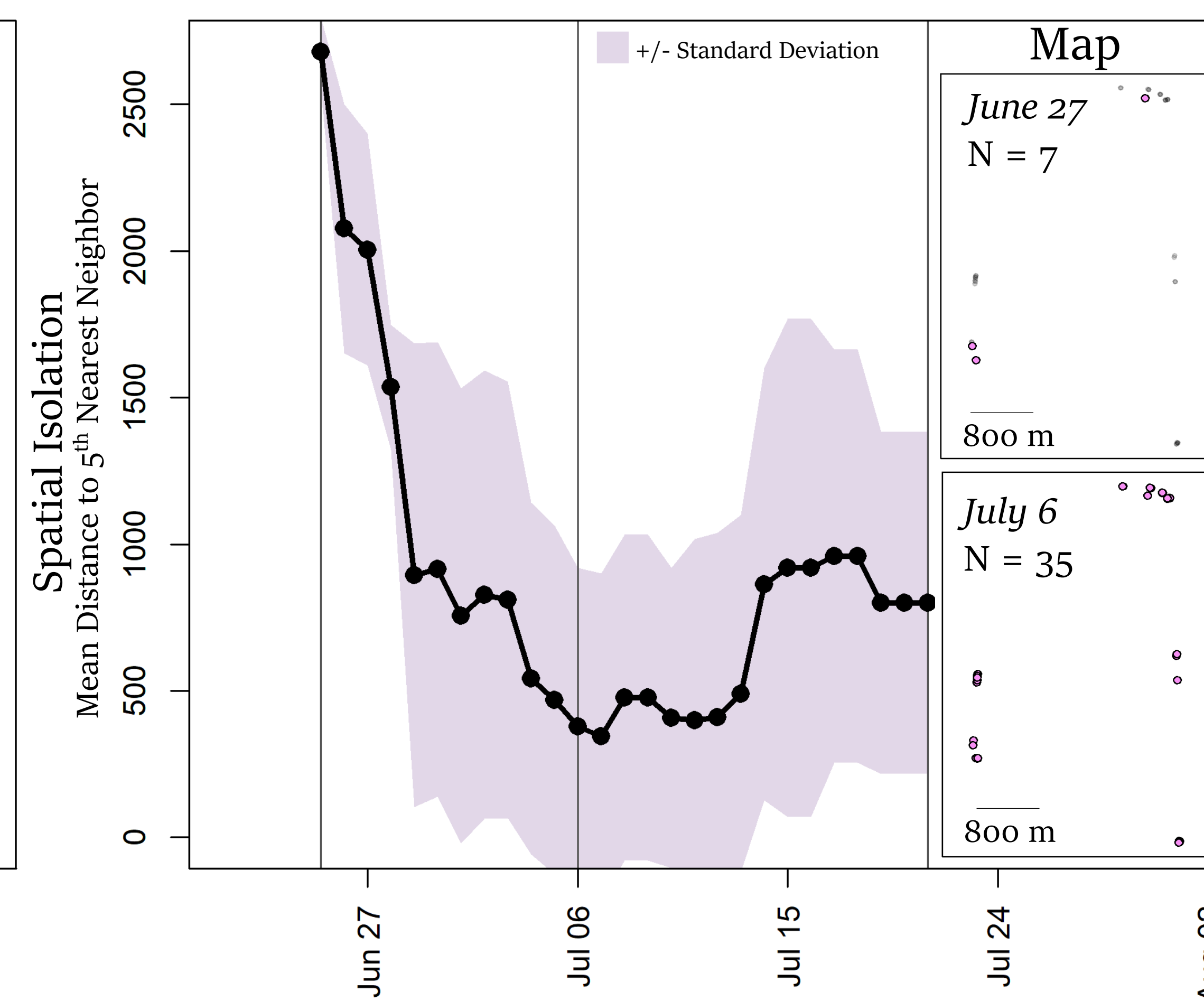
Network Analysis

- I calculated population *flowering synchrony* using Augspurger's index (Augspurger, 1983) and compared observed synchrony to mid-domain effect null models (Waananen et al., 2018).
- I assessed daily *spatial isolation* as distance to 5th nearest flowering conspecific throughout flowering season (Wagenius, 2006).
- Then, I built *weighted network models* of pollen movement based on an exponential-decay function of distance between individuals and calculated individual *closeness centrality* and network *modularity*.



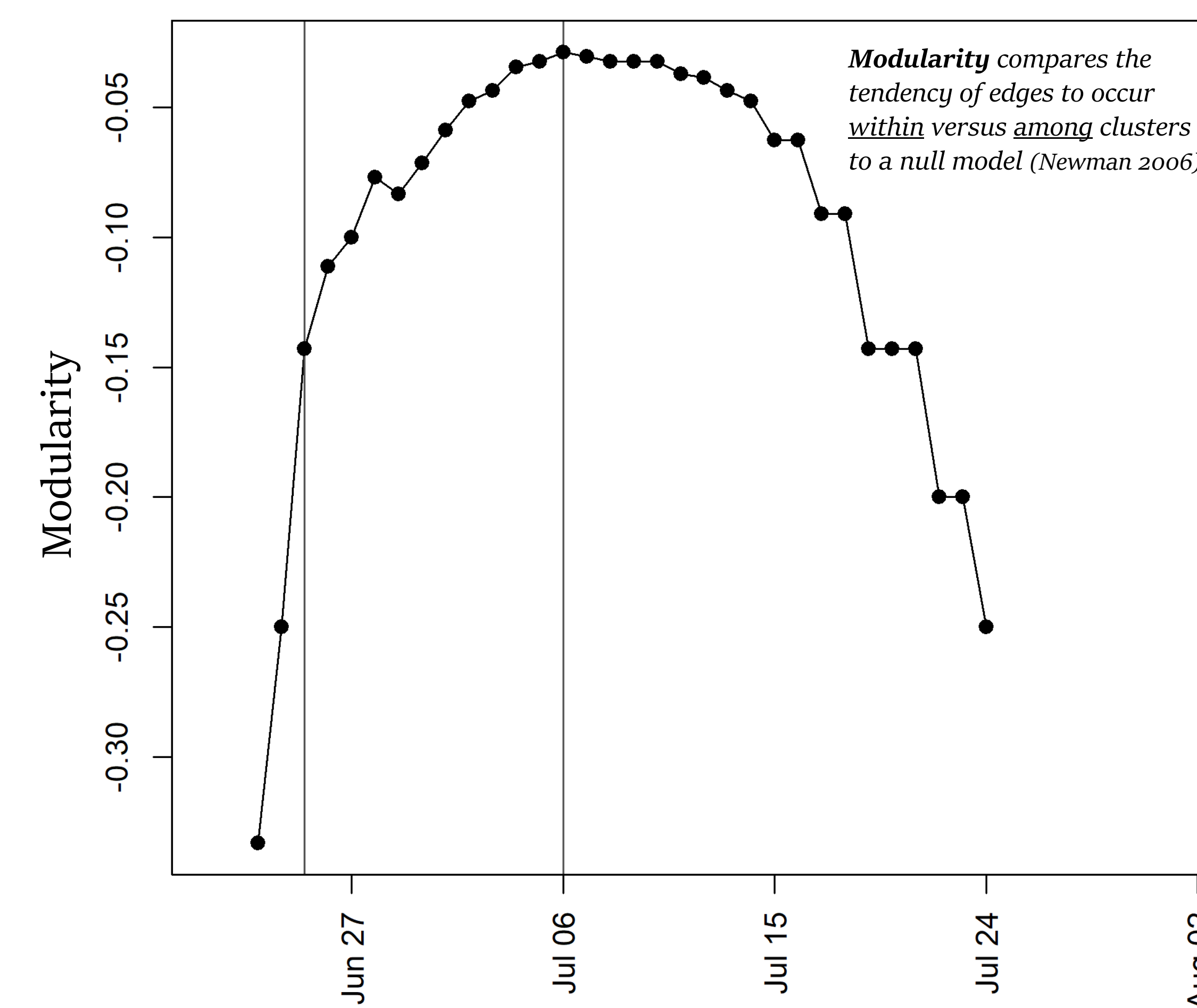
Flowering was more synchronous than expected given random timing within seasonal constraints.

Asynchronous flowering could increase an individual's effective isolation.



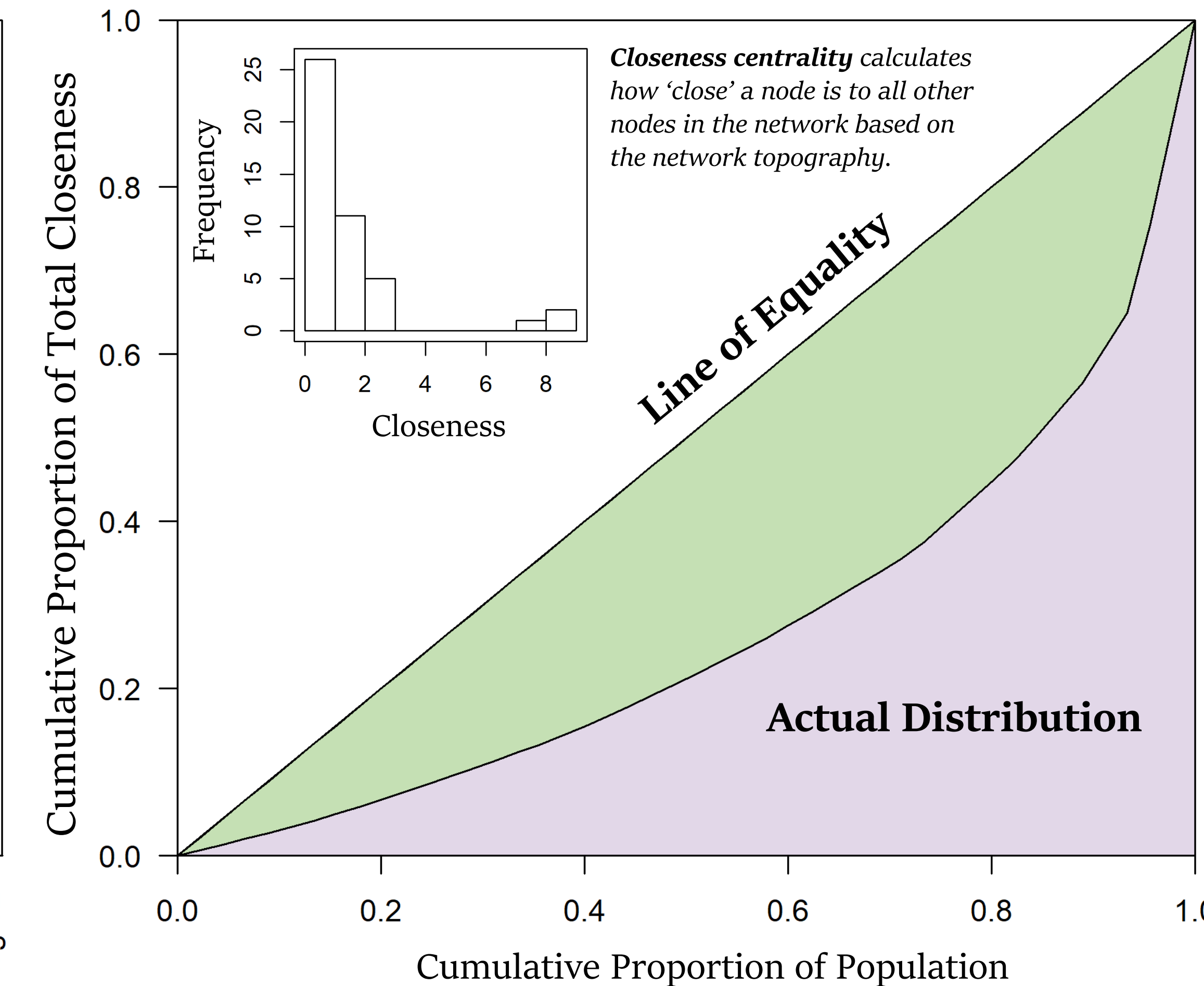
Spatial isolation varies temporally, so mean isolation may be insufficient to predict movement.

If pollinators favor movements between nearest neighbors, movement distance might be greatest when plants are isolated.



Distance-based networks predict connectivity will be lowest at the beginning and end of flowering.

However, at no point is the network predicted to be strongly modular. Non-distance-based foraging may lead to deviations from these predictions.



Mating opportunities and contribution to gene flow may vary among individuals.

When factors other than distance increase isolation of individuals, inequality in network position could be even more extreme.

Work in Progress



Tracking pollen movement

Evaluate predictions by observing pollen movement within and among populations using microsatellite paternity analysis.



Tracking pollinator movement

Assess paternity of pollen loads of *Echinacea* floral visitors to estimate pollinator movement among populations using microsatellites.



Measuring fitness outcomes

Assess population genetics of *Echinacea* populations and use common garden experiment to test population outcomes of gene flow.

Acknowledgments

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