

Comparing C^r Values with Network Perturbation Results - Focal Species: Monarchs

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Contents

1 Monarch Notes and Generalized C^r	1
2 Baseline Simulation	2
3 Perturbation Experiment - Perturbing Node Survival Rates	3
4 Monarch Plots - June 2018 - to Match Pintail Outputs	4
4.1 Population weighted average C^r	5
4.2 Population Distribution W^r	6
4.3 Proportional Dependence D_s	7
4.4 Criticality - NEW K^r	8

1 Monarch Notes and Generalized C^r

We model a population of Monarchs building our model based on the formulation in *A general modeling framework for describing spatially structured population dynamics* by Sample et. al.

We track the population at four nodes: node 1 (Winter - nonbreeding), node 2 (South - breeding), node 3 (Central - breeding), node 4 (North - breeding). The population is modeled through seven times steps for each season:

- In the fall, monarch butterflies migrate from the northern US and southern Canada to the non-breeding area in Mexico. The non-breeding season lasts six months, then the monarchs migrate to the southern US where the butterflies lay their eggs and die. The eggs turn into caterpillars, then into butterflies where the cycle continues as they migrate North until September.

We use a generalized network model formulation where we define one time step as

$$\vec{N}_{t+1} = \mathbf{A}_t \vec{N}_t \quad (1)$$

Where \vec{N}_t contains the population at each of the n nodes and c classes at time t . The matrix \mathbf{A}_t contains all of the demographic node update and migration data for time t . (Christine and Joanna have a draft of a paper with this construction).

Within the monarch code we calculate the C^r values for both the origin and the intermediate nodes during each season. We use a generalized one equation definition of C^r in matrix form. *This generalized version is from Joanna and Christine and has not yet been published, currently in draft form. It allows for complete generality in the number of nodes, classes, and seasons.*

$$\vec{C}_t = \left(\prod_{\tau=t}^{t+s-1} \mathbf{A}_\tau^T \right) \vec{1}_{nc} \quad (2)$$

where s is the total number of seasons in one anual cycle, for the monarchs $s = 7$ and \vec{C}_t is a column vector that contains the C^r values at each node for each class for focal season, or time, t .

We note that because the code is run to equilibrium, the overall growth rate of the network is equal to one. We can calculate the growth rate using:

$$\lambda_t = \frac{\vec{N}_t^T}{N_t^{tot}} \vec{C}_t \quad (3)$$

where N_t^{tot} is the sum of the equilibrium population values across all nodes and all classes in the network and is represented by the following summation

$$N_t^{tot} = \sum_{r=1}^n \sum_{x=1}^c N_{r,t}^x \quad (4)$$

2 Baseline Simulation

The baseline simulation gives us identical results to *A general modeling framework for describing spatially structured population dynamics* by Sample et. al. We find that the long term carrying capacity for each node during the nonbreeding season, including all classes, is

```
season 1 : k= 104369867 0 0 0
season 2 : k= 0 50678505 0 0
season 3 : k= 0 45341487 20370029 0
season 4 : k= 0 0 53525729 33199558
season 5 : k= 0 0 45933321 88548303
season 6 : k= 0 0 72219163 70020140
season 7 : k= 0 62180832 66308229 0
```

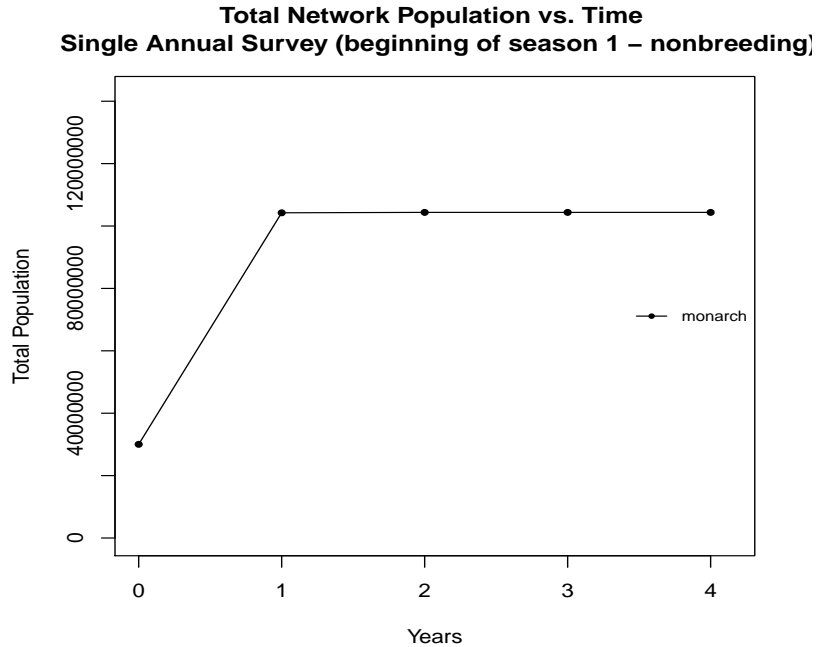


Figure 1: Baseline results: population over time at nonbreeding node.

3 Perturbation Experiment - Perturbing Node Survival Rates

To investigate the utility of the metrics as an indicator of the change in carrying capacity K we consider the following perturbations to the survival rate at each node:

$$PERT = .9, .8, .7, .6, .5, 1.0$$

Some notes about the simulations:

- All simulations are run to equilibrium with an error tolerance of within 1 animal, meaning the network growth rate $\lambda = 1$.
- We only carry out negative perturbations because positive perturbations will cause survival rates to exceed 1.

4 Monarch Plots - June 2018 - to Match Pintail Outputs

We will consider metrics for the x-axis of our graph:

- Baseline C^r vs K perturbations - this is the population weighted C^r value averaged across classes and seasons Figure 2
- Baseline W^r vs K perturbations - the population proportions averaged across seasons Figure 3
- Baseline D_s vs K perturbations - the proportional dependence as defined in Bagstad et al, generalizing to account for larval: Figure 4
- NEW - Baseline Criticality KR_i vs K perturbations - defined as the network growth rate in the absence of node i using a population weighted average across seasons: Figure 5. Note that because we are at equilibrium the baseline network growth rate is $\lambda = 1$.

4.1 Population weighted average C^r

In order to be consistent across case studies we decide to calculate C^r using a population weighted average. The general matrix form of C^r results in a C^r values for each node, class, and season. To combine these into a single full year network wide C^r value we first do a population weighted average by class within each node and then do a population weighted average across seasons. This results in a single C^r values for each node.

The Monarch model has seven seasons (Winter and April-September) and one class.

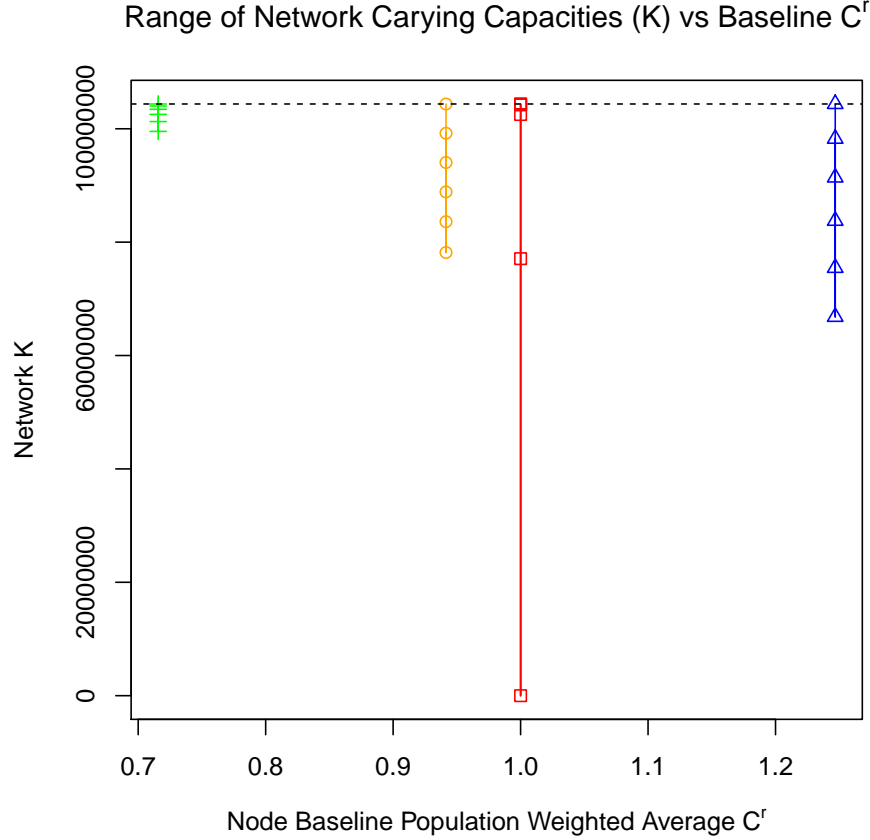


Figure 2: Perturbation results: Range of K values after perturbations to each node, X-axis represents **baseline population weighted C^r values** for each node

Winter	□	Winter
South	○	Breeding
Central	△	Breeding
North	◦	Breeding

4.2 Population Distribution W^r

W^r is calculated as the percent of the total population residing at a node. This calculation results in W^r values for each node during each seasons. To get a consistent value for the network, we average (not weighted) across the seasons. The final numbers should sum to one.

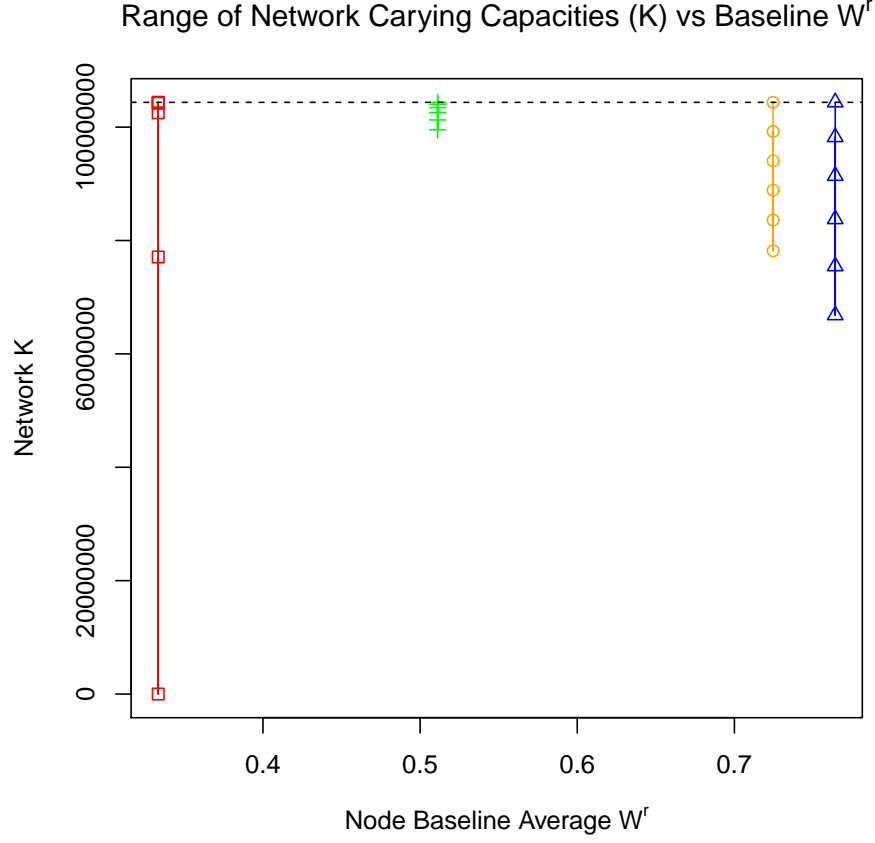


Figure 3: Perturbation results: Range of K values after perturbations to each node, X-axis represents baseline average W^r value for each node

Winter	□	Winter
South	○	Breeding
Central	△	Breeding
North	◦	Breeding

4.3 Proportional Dependence D_s

D_s is calculated following Bagstad et al. We first find the population weighted C^r values for each of the seasons and then average across the annual cycle.

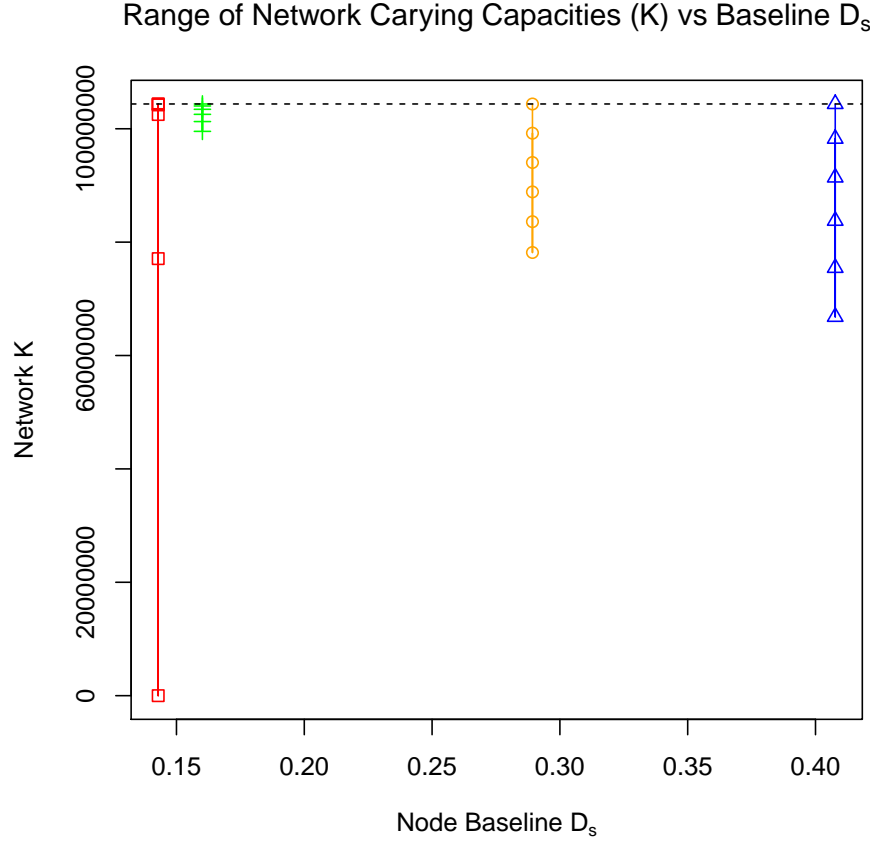


Figure 4: Perturbation results: Range of K values after perturbations to each node, X-axis represents baseline D_s value for each node

Winter	□	Winter
South	○	Breeding
Central	△	Breeding
North	◦	Breeding

4.4 Criticality - NEW K^r

Criticality K^r is a new metric conceived of by Christine and her colleagues. The basic idea is that from C^r we can calculate the network growth rate λ . In the case of a population in equilibrium, like our simulations, $\lambda = 1$. Then one could also calculate a theoretical C^r value as if one of the nodes was removed. From this theoretical C^r value we could calculate a new network growth rate γ . We define criticality as

$$K^r = \lambda - \gamma$$

In other words K^r represents the amount of the network growth rate that flows through the focal node r . In our equilibrium case if $K^r = 1$ then all of the network growth rate must flow through r and removal of r reduces the new growth rate γ to zero. Alternatively, if $K^r = 0$ then none of the original network growth rate flows through r and removal of r does not change the growth rate, $\lambda = \gamma = 1$.

The K^r calculation results in criticality values for each node during each season. To get a single yearly value we use a population weighted average.

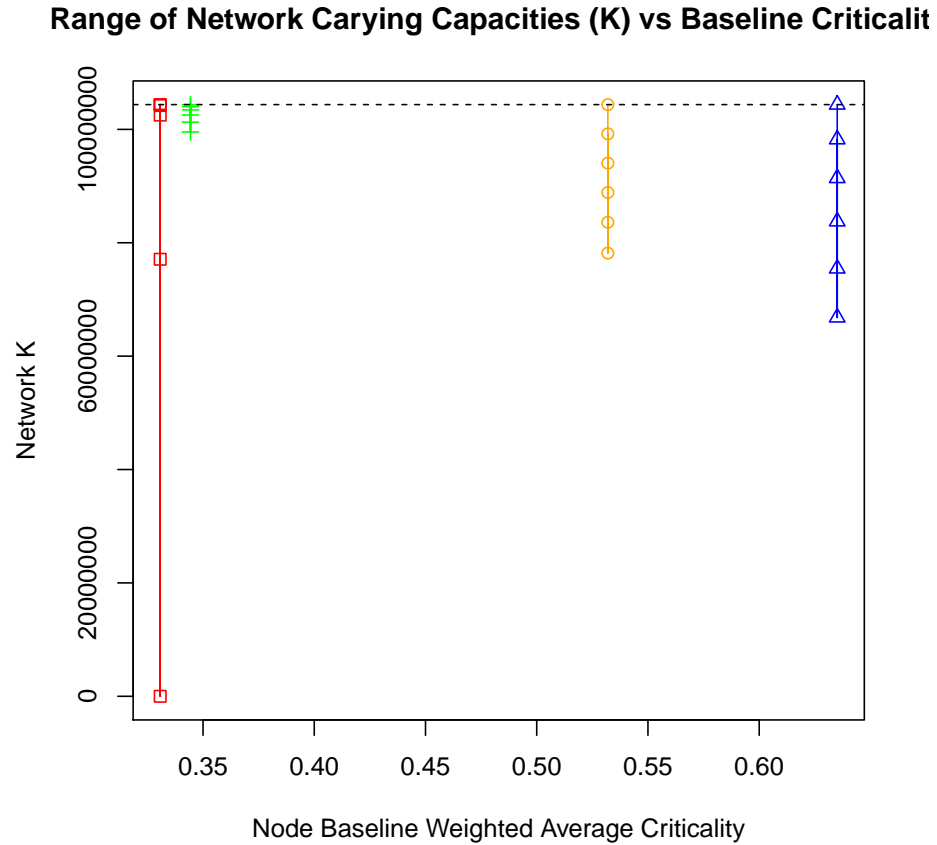


Figure 5: Perturbation results: Range of K values after perturbations to each node, X-axis represents baseline Criticality value for each node

Winter	□	Winter
South	○	Breeding
Central	△	Breeding
North	◦	Breeding