### Paige E. Howell, Erin Muths, Blake R. Hossack, Brent H. Sigafus, and Richard B. Chandler. Increasing connectivity between metapopulation ecology and landscape ecology. *Ecology*

### Data S1

### R code for the custom Metropolis-within-Gibbs sampler and data used to quantify the influence of landscape features on landscape resistance and colonization dynamics in a spatially-explicit metapopulation model.

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### File list (files found within DataS1.zip)

lich-resist-hydroCol-2017-S1.R

lich-resist-hydroCol-mcmc-S1.R

coords.dryad.csv

water.dryad.csv

y.wide.dryad.csv

wind.wide.dryad.csv

temp.wide.dryad.csv

dem

**File descriptions**

The file lich-resist-hydroCol-2017-S1.R contains R code for running the custom mcmc sampler lich-resist-hydroCol-mcmc-S1.R with data collected for the Chiricahua leopard frog in the Altar Valley, Arizona, USA.

The file lich-resist-hydroCol-mcmc-S1.R contains the custom Metropolis-within-Gibbs sampler used to fit a spatially-explicit metapopulation occupancy model to presence-absence data collected at a subset of sites. The R code allows users to estimate the influence of up to two landscape features, represented as raster files, on landscape resistance and colonization rate. The code contains an explanation of each of the parameters estimated in the model and the data that can be input by the user.

The file y.wide.dryad.csv contains the presence-absence data.

The file wind.wide.dryad.csv contains wind speed data collected during each sampling occasion.

The file temp.wide.dryad.csv contains ambient temperature collected during each sampling occasion.

The file coords.dryad.csv contains coordinates for each site.

The file water.dryad.csv contains the hydroperiod for each site.

The file dem contains the digital elevation model used in our analysis. The resolution (pixel size) of the raster is 900x900m.

**Note:** All of the files in DataS1 must be within your working directory for the analysis to work. The data are provided as csv files and a raster format for the elevation covariate. In the R code provided, we show an example of running the sampler out of parallel. To improve processing time, we recommend running the sampler in parallel on multiple cores (1 chain per core), in order to run multiple chains at the same time to assess convergence.