obsTimData2011.csv

**id**: unique plant patch ID code.

**host**: host-plant species. A = *Adenostoma*, C = *Ceanothus*

**x:** longitudinal location on map in metres

**y**: latitudinal location in map in metres

**height:** max height of patch in cm

**length**: max length of patch in cm

**width**: max width of patch in cm

**ln.size:** natural log of length x width\*\*

**occupied:** 1 = occupied by at least one *Timema*, 0 = no *Timema*

**total**: number of *Timema* in patch

**ln.total**: natural log of total number of *Timema*

**no\_grn**: number of green (unstriped) *Timema*

**no\_str**: number of striped *Timema*

**no\_dark**: number of dark (melanic) *Timema*

**no\_mal**: number of maladapted *Timema*. For host =A, no\_grn. For host = C, no\_str

**no\_cam**: number of camouflaged *Timema*. For host = A, no\_str. For host = C, no\_grn

**mal**: proportion of maladapted *Timema*. For host = A, no\_grn/(no\_grn + no\_str),

for host = C, no\_str/(no\_grn+no\_str)

**con**: connectivity (), where N is population size, *a* is reciprocal of avg. dispersal distance, and d is distance to patch. Sum across all patches *j*. *a* = 1/2

**conA**: connectivity to *Adenostoma* patches

**conC**: connectivity to *Ceanothus* patches

**pcon\_mal**: proportion of total connectivity due to populations on alternate host. For host = A, conC/con. For host = C, conA/con.

**qimm**: expected morph frequency among immigrants

**qimmA**: expected morph frequency among immigrants from *Adenostoma*

**qimmC**: expected morph frequency among immigrants from *Ceanothus*

**qimm\_mal**: expected frequency of the maladapted morph among immigrants

**qimmA\_mal**: expected frequency of the maladapted morph among immigrants from *Adenostoma*

**qimmC\_mal**: expected frequency of the maladapted morph among immigrants from *Ceanothus*