Ecography

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Supplementary material

Supplementary appendices

Appendix 1. Additional methodological details

Details of construction of alternative scenario layers

No set-aside strips

Raster layer at 500m resolution where the value of each cell represents the area of semi-natural grassland (SNG) (according to the 2015 Land Cover Map; Rowland et al. 2017) within that cell.

AES set-aside strips

Raster layer at 500m resolution where the value of each cell represents the area of SNG plus area of set-aside strip within that cell. Set-aside strip areas/locations were sourced from the Environmental Stewardship Scheme (ESS) Options (points) dataset by Natural England (accessed November 2016, https://data.gov.uk/dataset/6c0f19e7-9a2d-4c50-b548-3b7d4b9c18bb/environmental-stewardship-scheme-options-points). Only set-aside strips in place as of July 2015 were included in analyses and this date was chosen because 2015 represented the peak of ESS agreements.

Randomized set-aside strips

As for 'AES set-aside strips', except for the spatial location of set-aside strip patches. Set-aside strips as present in the ESS dataset were redistributed by randomly assigning set-aside strips to grid cells across England.

Aggregated set-aside strips

As for 'AES set-aside strips', except that for each individual farm/holding (as identified by 'AGREF' agreement codes in the ESS dataset) all set-aside strip patches were aggregated such that the total set-aside strip area on each farm was assigned to a single patch at the centroid of the farm.

Doubled set-aside strips

As for 'AES set-aside strips', except the area of set-aside strip within each grid cell is doubled. Equivalent to, for example, doubling the width (or carrying capacity) of each set-aside strip.

Construction of metapopulation models

Metapopulation capacity

Specifically, the metapopulation capacity is defined as the leading eigenvalue of the landscape matrix, M, consisting of elements

$$m_{\mathrm{ij}} = \begin{cases} f(d_{\mathrm{ij}})A_i & i \neq j \\ 0 & i = j \end{cases}$$

where A_i is the area of patch i and $f(d_{\mathrm{ij}})$ is a function describing the effect of inter-patch distance (d_{ij}) on dispersal. Dispersal is defined here as a negative exponential function,

$$f(d_{\mathrm{ij}}) = \frac{\alpha^2}{2\pi} A_i A_j exp(-\alpha d_{\mathrm{ij}})$$

where α is the parameter setting the slope of the curve and therefore the dispersal ability of the species and the mean dispersal distance is $2/\alpha$.

Incidence Function Model

The effect of inter-patch distance (d_{ij}) on dispersal, $f(d_{\mathrm{ij}})$, was defined by a negative exponential function as follows:

$$f(d_{\mathrm{ij}}) = \frac{\alpha^2}{2\pi} A_i A_j e^{-\alpha d_{\mathrm{ij}}}$$

where A_i and A_j are the areas of patch i and j respectively and α is the parameter setting the slope of the curve and therefore the dispersal ability of the species (the mean dispersal distance is $2/\alpha$).

Selection of species parameters

Dispersal

Mean dispersal distances calculated from negative exponential dispersal kernels fitted to mark-release-recapture (MMR) data from European butterflies can be as high as 1.3 km within individual studies (less than one generation) (1). As MMR data underestimate dispersal (2, 3) and because colonization distances at the leading edge of the expanding range of UK butterflies have been shown to be as high as 12 km over $\sim$ 10 years (from 1995-1999 to 2005-2009; 4), we set our 'high' mean dispersal to 2 km. We set our lower mean dispersal value at 0.5 km; this value approximately corresponds to mean dispersal values calculated for more sedentary European butterflies (1) and below this value metapopulations generally failed to expand their ranges at all in our IFM simulations.

Population density

Published literature estimates population densities of European butterfly species as low as <5 individuals ha^{-1} (5) and as high as >4,000 individuals ha^{-1} (6); in our models we define 'low' density at 10 individuals ha^{-1} and 'high' density at 1,000 individuals ha^{-1} to capture this variation.

Appendix 2. MPC code

```
 #####function for unscaled metapopulation capacity
# x & y: coordinates of patches (km)
# area: areas of habitat patches (km2)
# alpha: parameter which sets slope of negative
#        exponential dispersal kernel

mpc<-function(x,y,area,alpha=0.2){

  d<- as.matrix(dist(cbind(x,y)))
  M<- alpha^2/2/pi*exp(-alpha*d)*outer(area^2,area,'*')
  diag(M)<-0
  eg<-eigen(M, symmetric=F, only.values = FALSE)
  l_M=eg$values[1]
  return(l_M=eg$values[1])
}
```

Appendix 3. IFM code

```
##########################################################################
# ifm()                                                                  #
#                                                                        #
# Adapted from Hodgson et al. (2011)                                     #
#                                                                        #
# IFM function. Seeds occupancy in single cell at base of invasion axis, #
# which it gives 100% habitat cover, and simulation continues until cell #
# at opposite edge of landscape (also given 100% cover) is occupied, or  #
# else number of generations > 'simtime', the population goes globally   #
# extinct, or global occupancy >95%.                                     #
#                                                                        #
##########################################################################
# Arguments:                                                             #
#                                                                        #
# x - vector of x-coordinates of habitat patches (in km)                 #
# y - vector of y-coordinates of habitat patches (in km)                 #
# n - vector of carrying capacity of habitat patches (calculated as      #
#   patch area * density)                                                #
# alpha - slope of negative exponential dispersal kernel                 #
# density - population density (in individuals per km2)                  #
# simtime - number of generations at which to cut off simulations        #
# rot - angle of invasion (0 = South to North)                           #
# cellsize - cell size of gridded data (used for creating habitat start  #
#   and end cells), measured in km                                       #
```

```r
# landscapesize - radius of landscape in km                              #
##########################################################################


ifm <- function(x,y,n,alpha,density,
                rot, simtime=200, cellsize=0.5, landscapesize=10){

  x <- x-min(x)-landscapesize # make all coordinates relative, where the
                              # centre of the landscape is (0,0)
  y <- y-min(y)-landscapesize
  le <- length(x)
  D <-( -sin(rot)*x + cos(rot)*y ) # distance along invasion axis
                                   # (start at low end)
  far <- max(D)
  W <-  x*cos(rot) + y*sin(rot) # width-ways distance from centre of axis
  dw <- data.frame(D, W)

  start_edge_cand <- dw[which(dw$D == min(D)),] # cells at starting edge
                                                # of landscape

  # Where there are multiple cells at starting edge, pick the one that is
  # nearest the centre of axis of invasion. Where the axis goes between 2
  # cells, pick the one adjacent & offset anti-clockwise from the axis.

  if (nrow(start_edge_cand > 1)){
```

```
  start_edge_cand$Wplus <- start_edge_cand$W - 0.1
  start <- as.numeric(
            rownames(start_edge_cand)[
              which(
                abs(
                  start_edge_cand$Wplus) == min(
                    abs(start_edge_cand$Wplus)))])
} else {
  start <- as.numeric(rownames(start_edge_cand))
}

# start = cell number of starting cell (of all cells incl. zeros)

# x- and y-coordinates of starting cell
start_x <- x[start]
start_y <- y[start]

# Where there are multiple cells at ending edge, pick the one that
# is nearest the centre of axis of invasion. Where the axis goes
# between 2 cells, pick the one adjacent & offset anti-clockwise from
# the axis.

endedge <- D[rank(D) == max(rank( D ))]
end_edge_cand <- dw[which(dw$D == max(D)),]
if (nrow(end_edge_cand > 1)){
```

```
    end_edge_cand$Wplus <- end_edge_cand$W + 0.1
    end <- as.numeric(
              rownames(
                end_edge_cand)[
                  which(
                    abs(
                      end_edge_cand$Wplus) == min(
                        abs(end_edge_cand$Wplus)))])
  } else {
    end <- as.numeric(rownames(end_edge_cand))
  }

  # end = cell number of ending cell (of all cells incl. zeros)

  # x- and y-coordinates of ending cell

  end_x <- x[end]
  end_y <- y[end]

  # Set up starting occupancy (all cells)
  occ0 <- rep(FALSE, times=le)
  occ0[start] <- TRUE

  # Give starting and ending cells 100% habitat cover
  n[start] <- cellsize^2 * density
```

```r
n[end] <- cellsize^2 * density

# Get rownumbers of non-habitat containing cells
zeros <- which(n==0)

# Get rid of x, y, n elements with no habitat & redefine objects
x <- x[-zeros]
y <- y[-zeros]
n <- n[-zeros]
occ0 <- occ0[-zeros]
D <-( -sin(rot)*x + cos(rot)*y )
le <- length(x)

# Dataframe of non-zero cell coordinates
xy <- data.frame(x,y)

# Non-zero index of ending cell
end_new <- which(xy$x==end_x & xy$y==end_y)



# Baseline probability of extinction
pex<- pmin(1,1/n)

```

```
conn<-rep(0,le)#the connectivity
for(j in 1:le){
  if( occ0[j] ){
    conn[-j] <- conn[-j]+(n[-j]/density)*alpha^2/2/pi*
      n[j]*exp(-alpha*
                 sqrt( (x[-j] - x[j])^2 + (y[-j] - y[j])^2 )
      )#close kernel
  }#close if
}#close j loop

###########output for t=0#############
tis<- data.frame(t=0,no=sum(n*occ0)/sum(n),co=mean(occ0),
                 do=far-max(D[occ0])
)

######here is the actual simulation#######
for(i in 1:simtime){
  pcol<- 1-exp(-conn)
  pext<- pex*(1-pcol)#extinction prob with rescue effect
  occ1<- (occ0*(1-pext) + (!occ0)*(pcol)) > runif(le)#the new occupancy
  tis<- rbind(tis,c(t=i,no=sum(n*occ1)/sum(n),co=mean(occ1),
                    do= if(mean(occ1)>0){far-max( D[occ1])}else{
                      far-min( D )}
  ))#the results
  ###########test for ending###########
```

```
    if( sum(occ1)==0 ){break}
    if( (mean(occ1)>=0.95)){break}
    if( occ1[end_new]==TRUE ) {break} # end id not same here - NAs removed
    ###########update connectivity#######
    for(j in 1:le){
      if( occ0[j] & !occ1[j]){
        conn[-j] <- conn[-j] - (n[-j]/density)*
          alpha^2/2/pi*n[j]*exp(-alpha*
                                  sqrt( (x[-j] - x[j])^2 + (y[-j] - y[j])^2 )
          )#close kernel
      }#close if
      if( !occ0[j] & occ1[j]){
        conn[-j] <- conn[-j] + (n[-j]/density)*
          alpha^2/2/pi*n[j]*exp(-alpha*
                                  sqrt( (x[-j] - x[j])^2 + (y[-j] - y[j])^2 )
          )#close kernel
      }#close if
    }#close j loop
    ##############
    occ0<- occ1
  }#end time series
  return(list(tis=tis,time=i,rot=rot))#return this
}#end the function
```

Supplementary references

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Hanski, I. and Thomas, C. D. 1994. Metapopulation dynamics and conservation: A spatially explicit model applied to butterflies. - Biol. Conserv. 68: 167–180.

Krauss, J. et al. 2003. How does landscape context contribute to effects of habitat fragmentation on diversity and population density of butterflies? - J. Biogeogr. 30: 889–900.

Mair, L. et al. 2014. Abundance changes and habitat availability drive species' responses to climate change. - Nat. Clim. Chang. 4: 127–131.

Rowland, C.S.; Morton, R.D.; Carrasco, L.; McShane, G.; O'Neil, A.W.; Wood, C.M. (2017). Land Cover Map 2015 (25m raster, GB). NERC Environmental Information Data Centre. https://doi.org/10.5285/bb15e200-9349-403c-bda9-b430093807c7

Schneider, C. 2003. The influence of spatial scale on quantifying insect dispersal: An analysis of butterfly data. - Ecol. Entomol. 28: 252–256.

Stevens, V. M. et al. 2010. A meta-analysis of dispersal in butterflies. - Biol. Rev. Camb. Philos. Soc. 85: 625–642.

Appendix 4

Supplementary Figures

Figure A1. Summary of habitat quantity and composition within landscapes

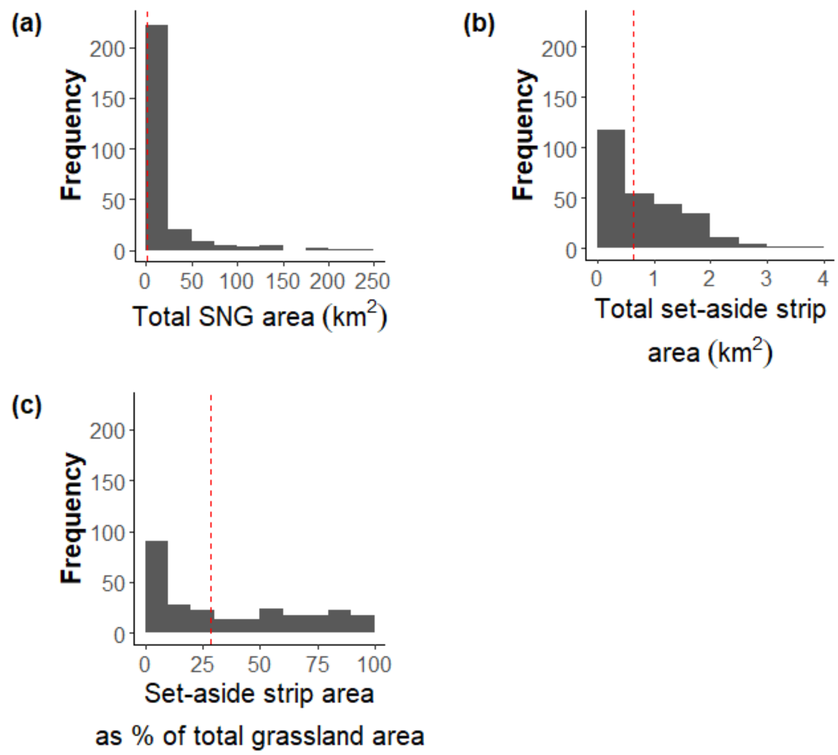

Figure A1: The frequency of landscapes (n=267) according to (a)total quantity of semi-natural grassland (SNG), (b) set-aside strip, and (c) the % of total habitat amount made up of set-aside strips.

Figure A2. Additional MPC scenarios

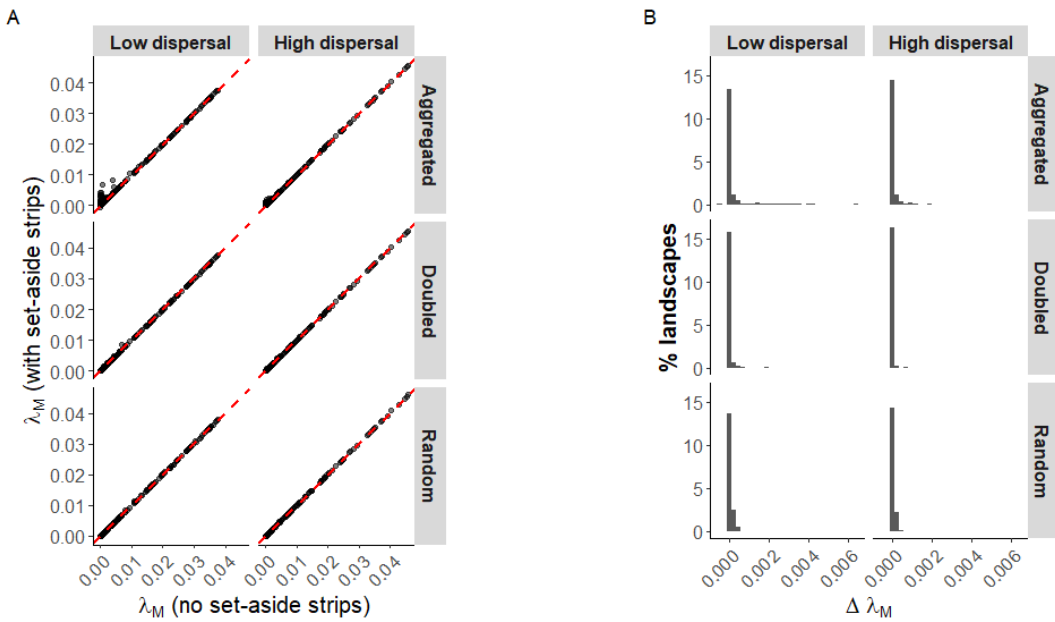

Figure A2: The impact of alternative set-aside strip spatial scenarios on metapopulation persistence. (A) Comparison of the metapopulation capacity λ_M of landscapes (n=267) under scenarios in the absence and presence of set-aside strips. Red dashed line indicates 1:1 line of no change inλ_M between scenarios. Blue dotted lines indicate hypothetical persistence thresholds. (B) Distribution of the effect of set-aside strips on metapopulation capacity under each scenario ($\Delta\lambda_M = \lambda_M$ [scenario with set-aside strips present] - λ_M [scenario with set-aside strips absent]).

Figure A3. MPC under increasing set-aside area

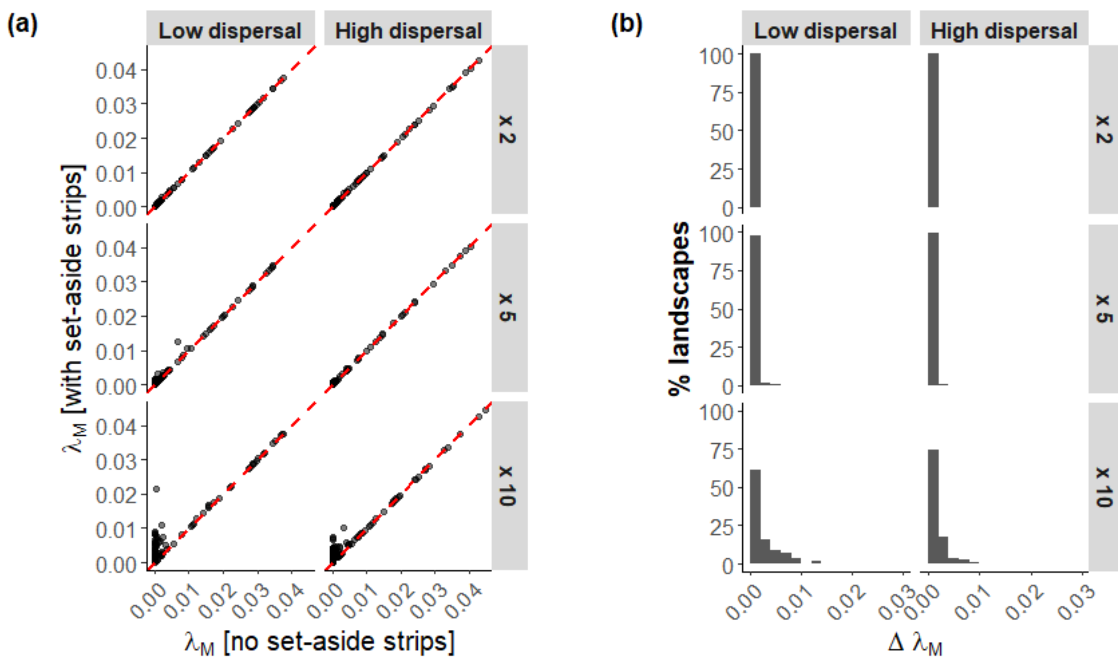

Figure A3. Metaopulation capacity (λ_M) values of landscapes under increasing quantities of set-aside strips, equivalent to multiplying the areas of existing strips in their current locations by 2, 5 and 10. (a) Metapopulation capacity of landscapes with and without set-aside strips. Red dashed line indicates 1:1. (b) The frequency distribution of $\Delta\lambda_{M,}$ calculated as the difference between λ_M with and without set-aside strips

Figure A4. Number of species types for which set-aside strips benefit range expansion in each landscape

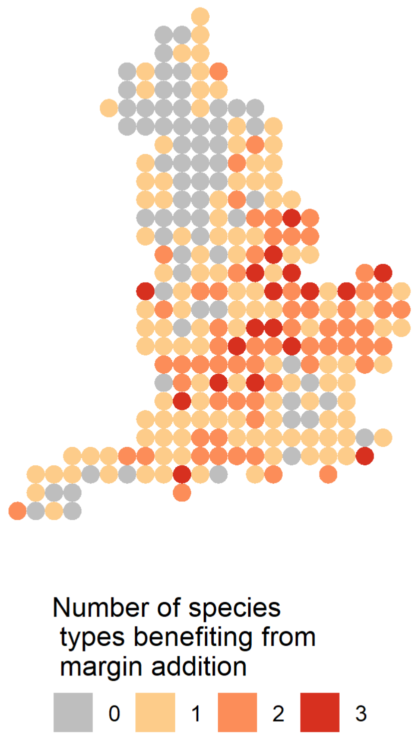

Figure A4: The number of species types (out of four) benefiting in range expansion from set-aside strips across all landscapes (n=267). Benefit is defined as >5% improvement in expansion success. At least one species benefited in 74% of landscapes (198/267).

Figure A5. Maps indicating the 'best scenario' for range expansion in each landscape

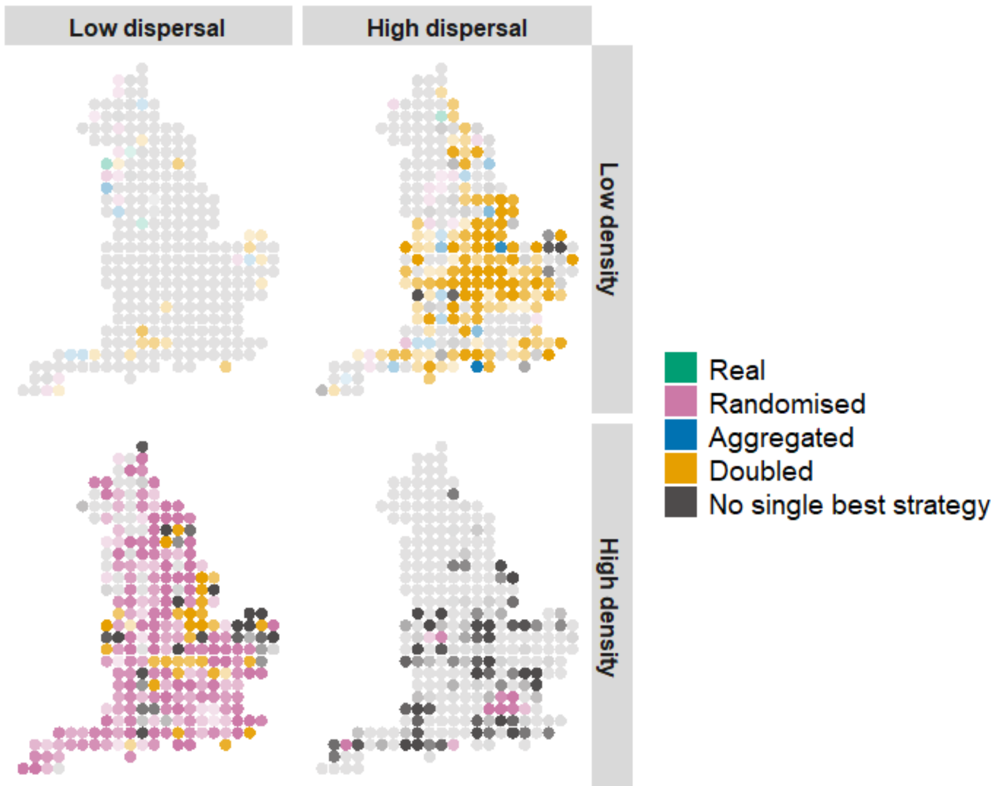

Figure A5: The best scenario for facilitating range expansion for each of the species types. Color illustrates the best scenario and transparency illustrates the magnitude of the benefit of the best scenario when compared to the 'no margins' baseline.

Figure A6. Conditions of IFM simulations which result in extinction

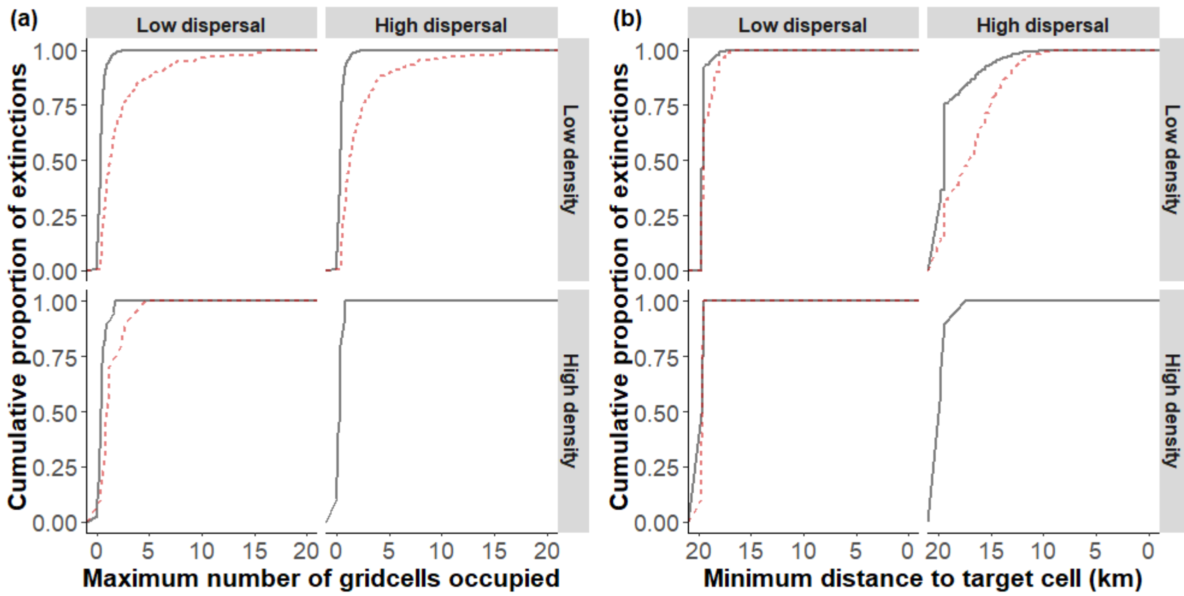

Figure A6: Cumulative proportion of extinctions within Incidence-Function Model (IFM) simulations related to (a) the maximum number of gridcells (500 m) which are ever occupied within the simulation and (b) the minimum distance between occupied cells and the target cell (edge of landscape) at the timestep (generation) before extinction occurs. Solid black line indicates simulations under the 'no set-aside strips' scenario. Dashed red line indicates simulations under the 'current set-aside strips' scenario.

Figure A7. Impact on range expansion of varying the carrying capacity of set-aside strip habitat

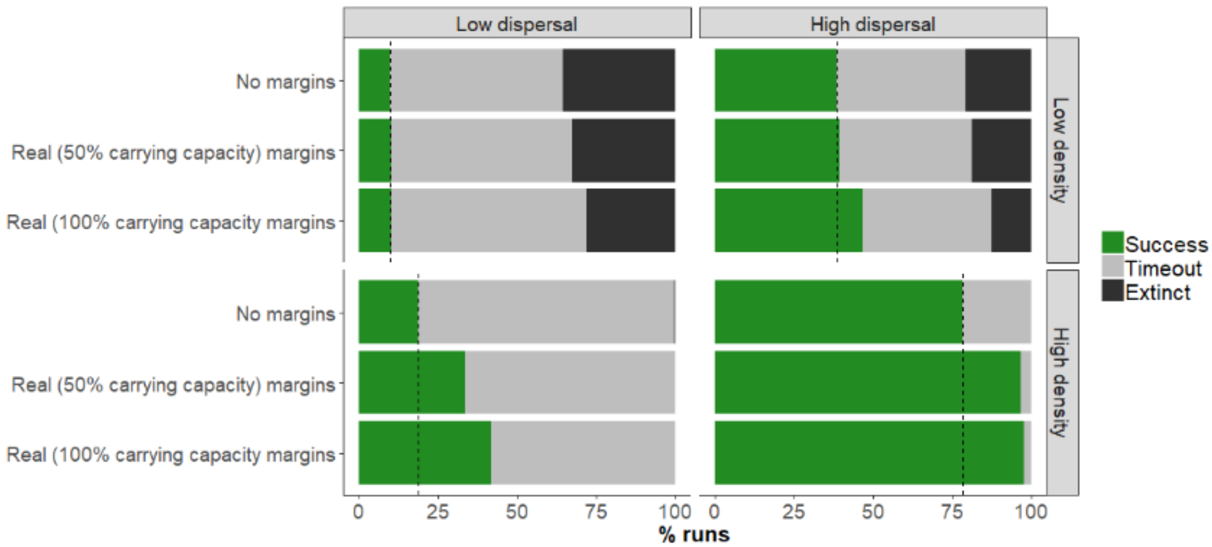

Figure A7: Range expansion simulations assuming full and half carrying capacity in set-aside strip patches for each of the four species types. The outcome of each run was classified as either an extinction (the metapopulation went globally extinct), a timeout (the metapopulation survived the 200 generations of the simulation but failed to colonize the 'target' cell) or a success (the metapopulation successfully colonized the 'target' cell). Each species type was simulated 10,680 times under each scenario (267 landscapes x 8 directions x 5 repeats). Dashed lines indicate baseline proportion of successful simulation runs when no set-aside strips are present.

Supplementary tables

Table A1. Set-aside strip option codes (Environmental Stewardship Scheme)

Scheme	Code	Option Type	Option
ELS	EE1	Buffer strips	2m on cultivated land
ELS	EE2	Buffer strips	4m on cultivated land
ELS	EE3	Buffer strips	6m on cultivated land
ELS	EE4	Buffer strips	2m intensive grassland
ELS	EE5	Buffer strips	4m intensive grassland
ELS	EE6	Buffer strips	6m intensive grassland
ELS	EE12	Buffer strips	Supplement to add wildflowers to field corners and buffer strips on cultivated land
ELS	EF4	Arable land	Nectar flower mixture
ELS	EF11	Arable land	Uncropped cultivated set-aside strips for rare plants
ELS	EK1	Grassland outside the Severely Disadvantaged Areas (SDAs)	Take field corners out of management
HLS	HE10	Arable land	Floristically enhanced grass buffer strips (non-rotational)
OELS	OE1	Buffer strips	2m on rotational land
OELS	OE2	Buffer strips	4m on rotational land
OELS	OE3	Buffer strips	6m on rotational land
OELS	OE4	Buffer strips	2m organic grassland
OELS	OE5	Buffer strips	4m organic grassland
OELS	OE6	Buffer strips	6m organic grassland
OELS	EE12	Buffer strips	Supplement to add wildflowers to field corners and buffer strips on cultivated land
OELS	OF4	Arable land	Nectar flower mixture

OELS	OF11	Arable land	Uncropped cultivated set-aside strips for rare plants
OELS	OK1	Grassland outside the Severely Disadvantaged Areas (SDAs)	Take field corners out of management

Table A2. GLMM model results

*Table A2: Summary of fixed effects from generalized linear mixed effects model: logit(success/failure) ~ log(% SNG cover + 1) * % set-aside strip cover * species type ($p < 0.05$*, $p < 0.01$**, $p < 0.001$***).*

Fixed effect	Coefficient	SE	z value	p
log(% SNG cover + 1)	12.670	1.785	7.099	<1.26e-12***
% set-aside strip cover	10.868	3.182	3.415	0.000638***
species2	16.353	2.791	5.858	4.68e-09***
species3	13.844	2.778	4.984	6.22e-07***
species4	24.668	2.840	8.685	<2e-16***
log(% SNG cover + 1): % set-aside strip cover	-5.370	1.307	-4.109	3.97e-05***
log(% SNG cover + 1) : species2	-3.093	1.737	-1.780	0.075014
log(% SNG cover + 1) : species3	-5.713	1.717	-3.328	0.000873***
log(% SNG cover + 1) : species4	-2.916	2.022	-1.442	0.149165
% set-aside strip cover : species2	-1.405	2.935	-0.479	0.632078
% set-aside strip cover : species3	9.715	2.937	3.308	0.000939***
% set-aside strip cover : species4	45.536	6.753	6.743	1.55e-11***

Species1 corresponds to the low density, low dispersal species type (density = 1,000 km^{-2}; mean dispersal = 0.5 km).

Species2 corresponds to the low density, high dispersal species type (density = 1,000 km^{-2}; mean dispersal = 2 km).

Species3 corresponds to the high density, low dispersal species type (density = 100,000 km^{-2}; mean dispersal = 0.5 km).

Species4 corresponds to the high density, high dispersal species type (density = 100,000 km^{-2}; mean dispersal = 2 km).