

# Estimating dispersal from adult abundance and recruitment

*Tarik C. Gouhier*

*July 29, 2015*

## Model overview

The goal is to determine how to estimate the parameters (mean, variance) of a normal dispersal kernel  $D$  from spatial patterns of recruitment and abundance across years. The model should consist of three successive stages: Larval production ( $L_{x,t}$ ), recruitment ( $R_{x,t}$ ) and adult abundance ( $A_{x,t+1}$ ) at location  $x$ . Below I describe each stage of the model along with the data available.

## Larval production

Larval production  $L_{x,t}$  at each site  $x$  depends on adult abundance  $A_{x,t}$  and environmental conditions  $E_{x,t}$  such that:

$$L_{x,t} = f(A_{t,x}, E_{t,x}) = p_{t,x} \cdot A_{t,x} \cdot E_{t,x}$$

Where  $p_{t,x}$  represents the average larval production per unit of adult abundance. It's fine for  $f$  to be linear initially. In reality, this function is probably unimodal with respect to environmental conditions  $E$ . Larvae  $L_{x,t}$  then disperse according to a kernel that can be approximated by a normal distribution. Although we cannot track how larvae travel up and down the coast, we do have access to the larvae that end up arriving at each site.

## Recruitment

Recruitment  $R_{x,t}$  represents all the larvae that arrive at a given site  $x$  at time  $t$ . This quantity depends on the number of larvae that are produced across the coastline  $L_{x,t}$  at time  $t$  and then get dispersed according to our normal dispersal kernel  $D$  whose parameters we seek to estimate. Using Yi's original model, this kernel could be expressed as:

$$D = L_{x,t} \cdot e^{-\frac{(d_{x,i} - \mu_d)^2}{\sigma_d^2}}$$

Summing the larvae produced across all sites  $i$  and recruiting to site  $x$  based on environmental conditions  $E_{x,t}$  yields recruitment  $R_{x,t} = g(L_{\cdot,t}, E_{x,t})$  such that:

$$R_{x,t} = k + \log \left( \sum_{i=1}^N L_{i,t} \cdot e^{-\frac{(d_{x,i} - \mu_d)^2}{\sigma_d^2}} \right) + \beta \cdot E_{x,t} + \epsilon$$

Where  $\beta$  is a vector of parameters and  $E_{x,t}$  is a  $N$ -site by 3 matrix containing measurements of sea surface temperature, upwelling and chl-a.

## Adult abundance

The final step is to model adult abundance  $A_{x,t+1}$  as a function of recruitment  $R_{x,t}$ . The temporal lag is due to the fact that larvae take at least one year to contribute to “adult abundance” (they’re technically still juveniles). Larval survival into adulthood depends on a host of factors including species interactions and environmental conditions. If we focus exclusively on environmental conditions and ignore species interactions for now, we can model adult abundance  $A_{x,t+1} = h(R_{x,t}, E_{x,t+1})$  such that:

$$A_{x,t+1} = b \cdot R_{x,t} \cdot E_{x,t+1}$$

I’m really unsure about the form of function  $h$  here. We should use model selection to compare linear and more complex relationships (e.g., quadratic).

## Getting the recruitment data

Unfortunately, the recruitment data was not collected at the same locations as the adult abundance data. Hence, we need to interpolate the recruitment data using cubic splines prior to merging it with the adult abundance data. The clunky code below does just that.

```
# 2-D interpolation
library(akima)
# Load adult data
load('pisco.RData')
# Load recruitment data
recruits <- read.csv("intertidal_recruitment.csv")
# Extract adult abundance of mussels (species M. californianus) in the mid zone
adults <- subset(data.mid.zone, speciesnum == 75)
# Get unique sites for surveys of adult mussels
sites.adults <- unique(subset(adults, select = c("lat", "lon")))
# Sort by latitude and longitude
sites.adults <- sites.adults[order(sites.adults$lat, sites.adults$lon), ]
# Number of sites for adults
nsites <- nrow(sites.adults)
# Aggregate recruitment data by year for mussels only
recruits <- aggregate(mytilus.rec ~ lat + lon + year, FUN = mean,
                      na.rm = TRUE, data = recruits)
# Sort recruitment data
recruits <- recruits[order(recruits$lat, recruits$lon), ]
# Get unique years for recruitment
recruits.years <- unique(recruits$year)
recruits.interp <- matrix(nrow = nsites * length(unique(recruits$year)),
                        ncol = 4)
colnames(recruits.interp) <- c("year", "lon", "lat", "mytilus.rec")

# Loop performs 2D interpolation of recruitment data for each unique year
# and then extracts only the locations where we have adult abundance
k <- 1
for (y in recruits.years) {
  sub <- subset(recruits, year == y)
  tmp <- interp(x = sub$lon, y = sub$lat, z = sub$mytilus.rec,
               xo = sites.adults$lon, yo = sites.adults$lat,
               linear = FALSE, extrap = TRUE)
```

```

# Get recruitment at sites where we have abundance only
rec <- diag(tmp$z)
# Get rid of nonsensical negative recruitment values
rec[rec < 0 ] <- 0
recruits.interp[k:(k + nsites - 1), ] <- cbind(y, tmp$x, tmp$y, rec)
k <- k + nsites
}
# Merge adult abundance and interpolated recruitment data
adults.recruits.merged <- merge(adults, recruits.interp)
write.csv(file = "adults.recruits.merged.csv",
          adults.recruits.merged, row.names = FALSE)

```