

## Ralph & Coop: patchy selection

Let's start with the more obvious:

- eq. 56 is wrong, as easily seen with  $\Theta = 0$

in this case  $\sin \Theta = 0$  and  $\cos \Theta = 1$

$$\Rightarrow \left( \left( 1 - \frac{r_0}{r} \cos \Theta \right)^2 + \frac{r_0^2}{r^2} \sin^2 \Theta \right)^{1/2} - 1 = 1 - \frac{r_0}{r} - 1 = -\frac{r_0}{r}$$

eq 56 has an extra 2, which results from a wrong expansion of

$$\sqrt{1+x} \simeq 1 + \frac{x}{2} \dots \Rightarrow \text{eq 57-61 are also wrong}$$

- time in transit

One can obtain these results by a simple saddle point approximation

$$\begin{aligned} P(\text{getting to } x \text{ in time } t) &= P(\text{diffusion to } x \text{ in time } t) \times P(\text{surviving}) \\ &= \frac{1}{(2\pi\sigma^2)^{1/2}} e^{-\frac{x^2}{2\sigma^2 t} - st} \end{aligned}$$

the exponent is minimal when  $\frac{x^2}{2\sigma^2 t^2} = s \Rightarrow t^* = \frac{x}{\sigma\sqrt{2s}}$

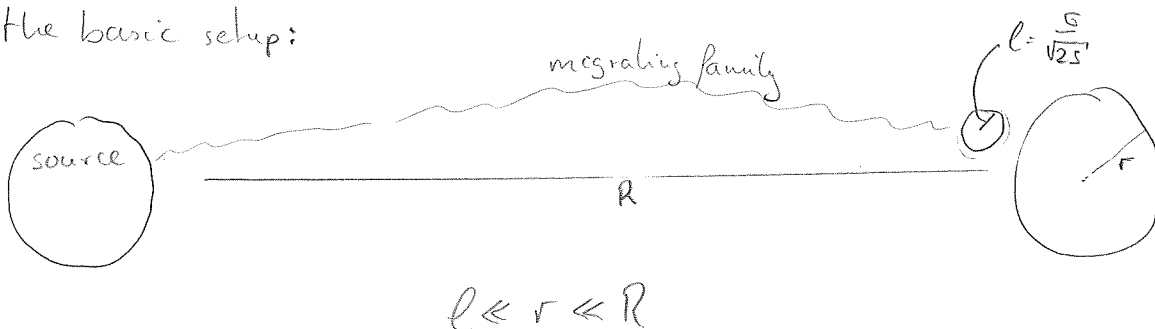
this gives your eq 17

the variance is simply the inverse of the second derivative of the exponent

$$\frac{1}{\text{var}[t]} = \frac{x^2}{\sigma^2 t^{*3}} = \frac{s}{x(2s)^{3/2}}$$

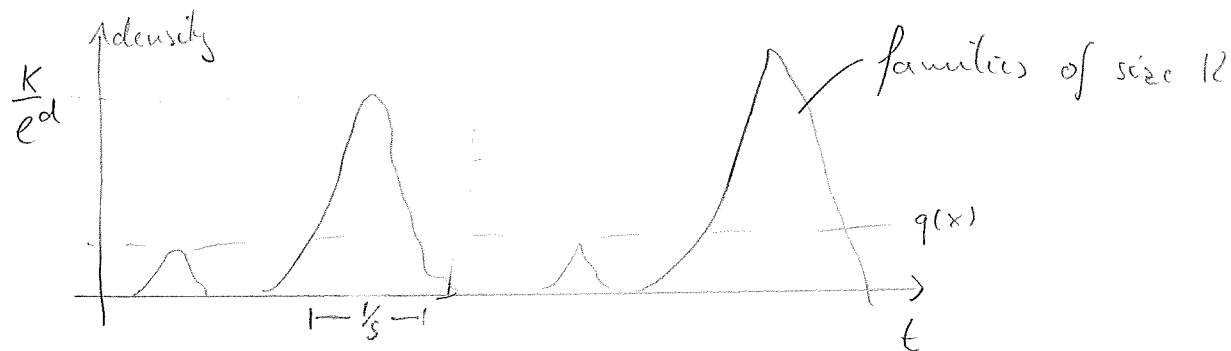
- now to the thornier issues of dimension, geometry & fluxes

the basic setup:



the average migrant density is  $q(x) \sim e^{-x \cdot \frac{\sqrt{2s'}}{s}} = e^{-x/l}$

but fluctuates far from the source as



local density of a family:  $\frac{K}{\ell^d}$

note that the distribution of family sizes  $\sim \frac{e^{-sK}}{K}$  similar to that of deleterious alleles.

Families of size  $K$  live for  $K$  generations, such that they contribute  $K^2$  to the time averaged density.  $q(x)$  is hence dominated by the largest families  $K \sim s^{-1}$ , but families reach this size only with prob.  $s$

$$q(x) = \frac{\lambda_{arr}}{\ell^d} s K^2 \approx \frac{\lambda_{arr}}{\ell^d} s^{-1} \quad \text{where } \lambda_{arr} \text{ is the rate for families to overlap with } x$$

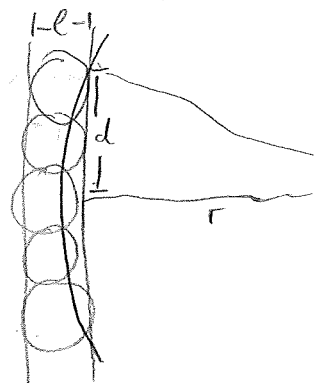
$$\lambda_{arr} \approx q(x) s \ell^d \quad \text{note that the dimensions work out?}$$

To calculate  $\lambda_{mig}$ , we need the approximate number of equivalent locations for seeding of successful migrants.

since  $q(x) \sim e^{-x/l}$ , they need to be within the same distance from the source to approx  $\sim l$

the number of  $\ell^d$  balls scales as  $\sqrt{\frac{\ell}{\ell}}$  in  $d=2$

$$\Rightarrow \lambda_{mig} \sim s q(R) s \ell^d \sqrt{\frac{\ell}{\ell}} (1 - e^{-R/l})$$



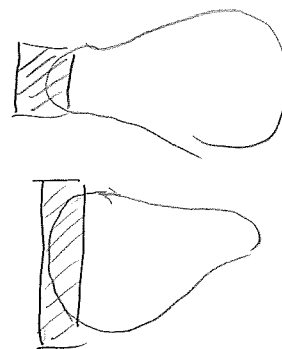
it is worth noting that this reduces correctly to

$$J_{\text{avg}} = p_e \int_A dx \rho q(x) \quad \text{in the limit } p_e \ll s$$

(the integral is dominated by a stripe of width  $l$  and height  $\sqrt{e\tau}$ )

more importantly,  $J_{\text{avg}}$  depends on the geometry of the sink patch:

$J_{\text{avg}}$  for the lower is larger since it can absorb migrants from a much larger cross-section.



## • fluxes.

It might be worth noting that the flux of individuals is implicit in the equation for the average density:

$$\partial_t q(r) = 0 = \frac{\sigma^2}{2} \frac{\partial}{\partial r^2} q(r) + \frac{\sigma^2(d-1)}{2r} \frac{\partial}{\partial r} q(r) - sq(r)$$

$$= \underbrace{\frac{1}{r^{d-1}} \frac{\partial}{\partial r} \left[ \frac{\sigma^2 r^{d-1}}{2} \frac{\partial}{\partial r} q(r) \right]}_{\text{flux}} - sq(r)$$

divergence of flux = local death.