

HOW DOES MATING SYSTEM AFFECT LINKED SELECTION IN CAPSELLA?

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BACKGROUND & MOTIVATION

Natural populations show a surprisingly narrow range of variation in genetic diversity in relation to their census size—much narrower than levels expected under neutrality [1]. A classic explanation for this is that linked selection acting on neutral sites will greatly reduce diversity levels genome-wide [2]. However, recent studies fail to support this hypothesis, except with regards to selfing species, where this contribution may be greater and help explain a larger deviation from neutral expectations [3]. This suggests that explicit comparative models of positive and negative linked selection may help gain new insights into the relative roles of demography and selection in reducing diversity in selfing lineages.

To investigate this, we explore the effects of linked selection on neutral diversity in the closely related obligate outcrossing *C. grandiflora* and the primarily selfing *C. rubella*, beginning with a look at how background selection affects neutral genetic diversity.

METHODS

- ▶ We use 182 *C. grandiflora* individuals from a single population in Greece, sequenced to high depth with Illumina
- ▶ The expected reduction in diversity due to background selection in a window k , $\pi/\pi_0 = e^{-G_k}$, was calculated using Rockman's [4] modification to Hudson & Kaplan's [5] equation, defined as

$$G_k = \sum_i \frac{u_i sh}{2(sh + P |M(x_{i+1}) - M(x_k)|)(sh + P |M(x_i) - M(x_k)|)}$$

where u_i is the deleterious mutation rate, P is the index of panmixia, M is the genetic map position, and k and i refer to the focal window and window i , respectively

- ▶ Scripts are available on github.com/tvkent/Capsella_LinkedSelection

DIVERSITY IS NEGATIVELY CORRELATED WITH FUNCTIONAL SITE DENSITY IN *C. GRANDIFLORA*

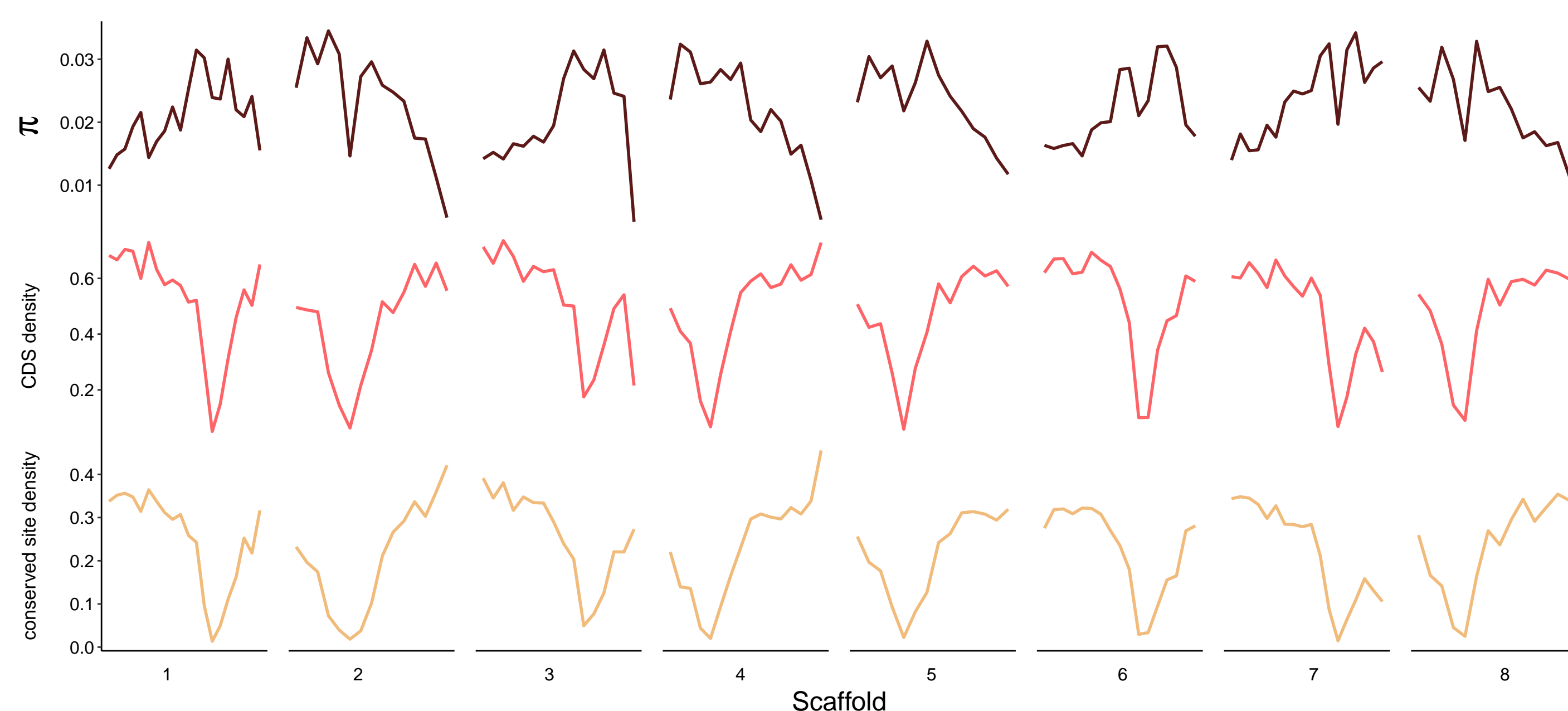


Figure 1: Genome wide neutral (4-fold degenerate) diversity (top), CDS density (middle), & conserved site density (bottom). Regions of very low gene & conserved site densities and high π are mostly in pericentromeric regions.

- ▶ Regions of high coding sequence (CDS) & conserved site densities correspond to regions of low neutral diversity (π)
- ▶ Gene dense, low neutral π regions tend to occur near the ends of chromosomes, with stronger effects further from pericentromeric regions
- ▶ Regions with high conserved site density are likely to be affected more strongly by linked selection (assuming adequate recombination), which could in part explain the loss of diversity observed in these regions

REFERENCES

[1] Corbett-Detig et al. (2015) PLoS Biol.; [2] Maynard Smith & Haigh (1974) Genet. Res. Camb.; [3] Coop (2016) biorxiv; Slotte [4] Rockman et al. (2010) Science; [5] Hudson & Kaplan (1995) Genetics; [6] Elyashiv et al. (2014) biorxiv

WEAK BACKGROUND SELECTION CONTRIBUTES TO DIVERSITY LOSS IN SELECT REGIONS OF *C. GRANDIFLORA*

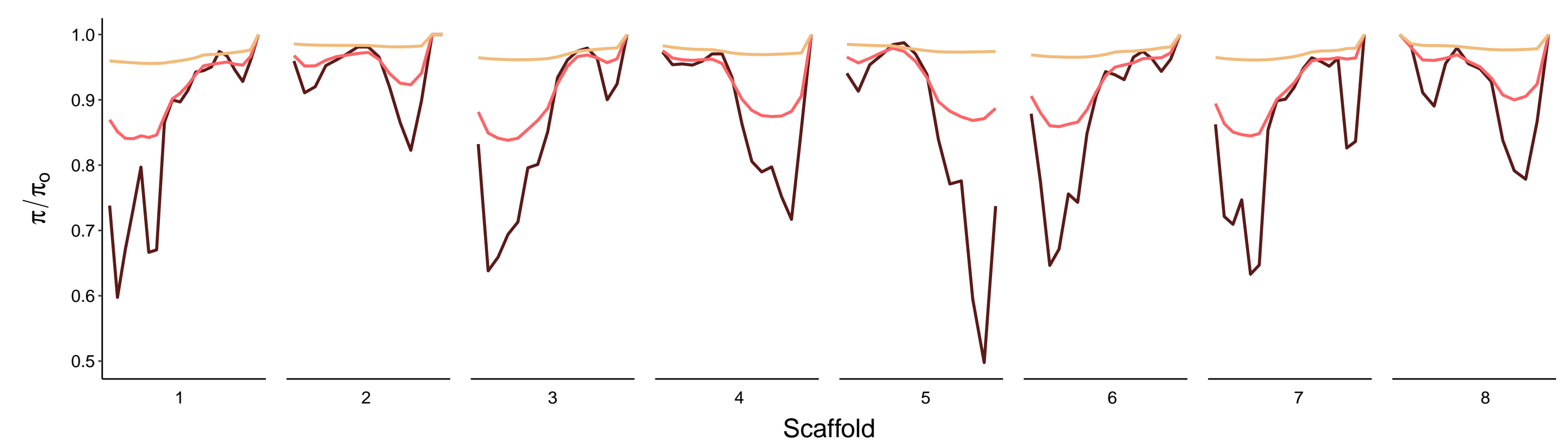


Figure 2: Predicted amount of diversity remaining after reduction due to background selection in *C. grandiflora*. Lines from top to bottom are for sh values of 0.5, 0.05, and 0.00005, respectively. $P=1$ for all, with the assumption that only the level of inbreeding is affecting panmixia

- ▶ With an obligately outcrossing mating system, *C. grandiflora* may only experience relatively large effects of background selection (surpassing 30% neutral diversity loss) in gene-dense regions when negative selection is very weak ($sh = 0.00005$)
- ▶ In these regions of high conserved site density (30-40%), it is likely that negative selection pressure on average is higher than that which causes drastic diversity loss due to background selection, however, the diversity loss due to background selection should be non-trivial
- ▶ It is possible that background selection is a moderate contributor to neutral diversity loss in gene-dense regions, but not genome-wide, although explicit model fitting needs to be done

HOW MIGHT SELFING CHANGE THIS IN *C. RUBELLA*?

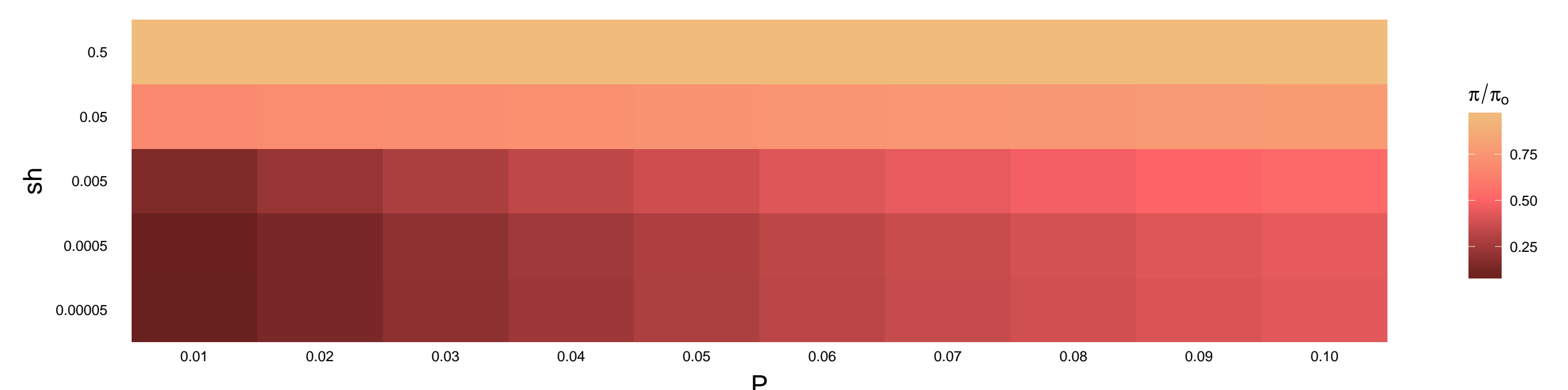


Figure 3: Predicted amount of diversity remaining after reduction due to background selection in *C. rubella*. Selection on the y axis and expected range of panmixia on the x axis, with heat corresponding to the reduction in neutral diversity

- ▶ With strong negative selection pressure, the increased level of selfing expected in *C. rubella* will not change the reduction in neutral diversity due to background selection compared to the same level of selection in *C. grandiflora*
- ▶ With increasingly weaker negative selection, the expected selfing rate in *C. rubella* is expected to result in a dramatic loss in neutral diversity due to background selection
- ▶ Under weak to moderate negative selection, *C. rubella* is expected to be strongly affected by background selection, with a larger genome-wide loss than seen in *C. grandiflora*

FUTURE DIRECTIONS

- ▶ We will be fitting a model of background selection to both species, using the predicted values presented here
- ▶ We will also be fitting the joint model of positive and negative linked selection presented in Elyashiv et al. 2014 [6]
- ▶ We will be exploring the consequences of diversity loss due to linked selection in selfing species and how they differ from their outcrossing relatives & forward simulating background selection in *C. rubella*

