The genetic signature of evolutionary rescue
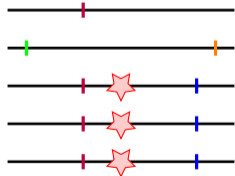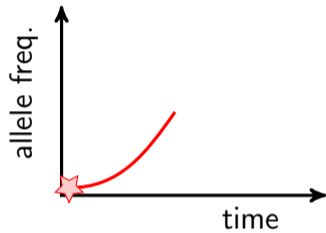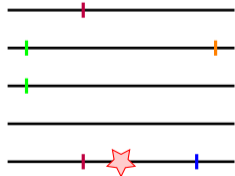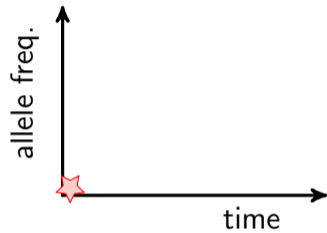
Matt Osmond & Graham Coop
Center for Population Biology, UC Davis

Sweeps & hitchhikers

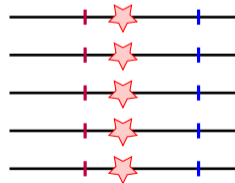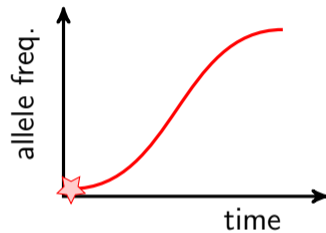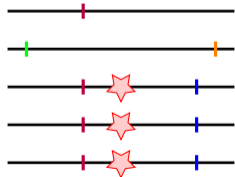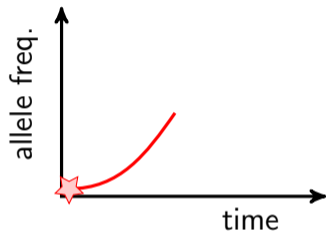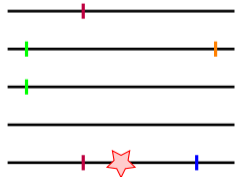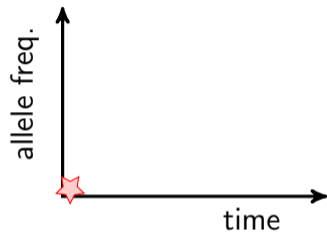# Sweeps & hitchhikers

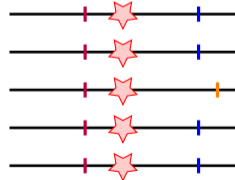# Sweeps & hitchhikers

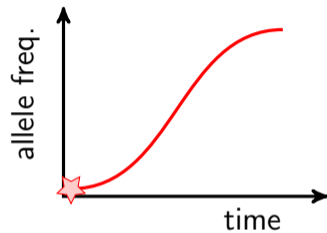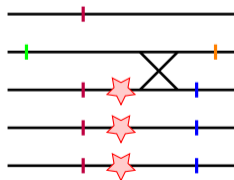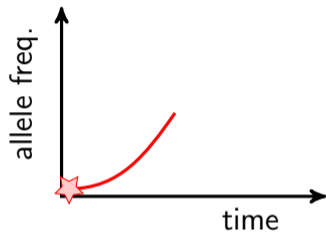
Maynard Smith & Haigh 1974, Kaplan *et al.* 1989

e.g., HIV drug resistance
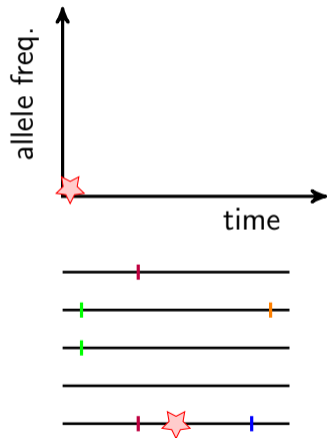
Recombination
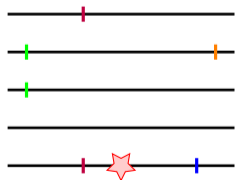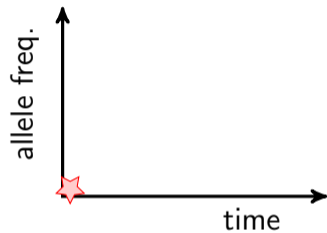
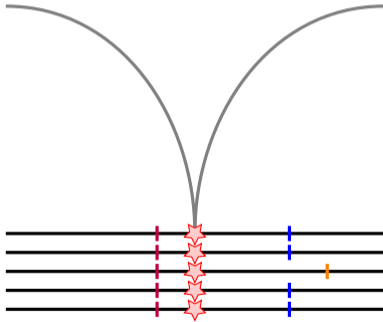# Genetic signatures
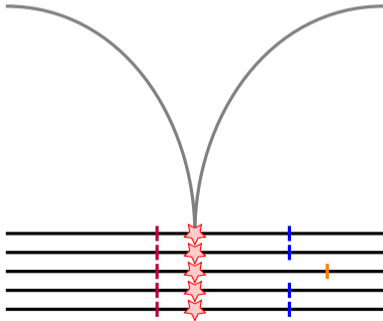
dips in diversity

Genetic signatures

dips in diversity

past

present

Genetic signatures

dips in diversity

past

present

Maynard Smith & Haigh 1974 *Gen. Res.*, Braverman *et al.* 1995 *Genetics*
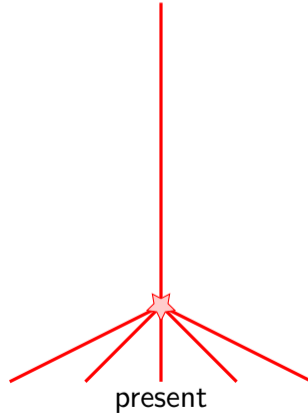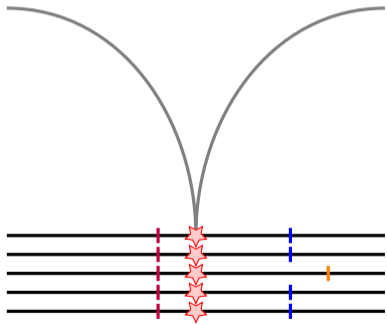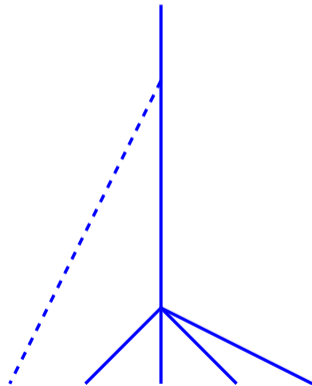
Genetic signatures

dips in diversity past

negative Tajima's D

present

Maynard Smith & Haigh 1974 *Gen. Res.*, Braverman *et al.* 1995 *Genetics*
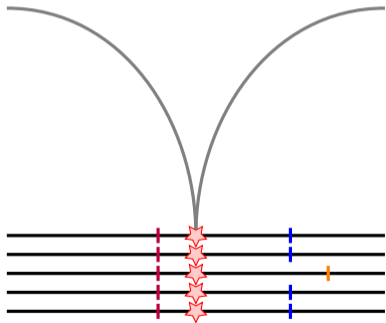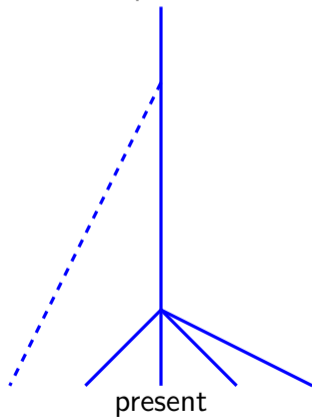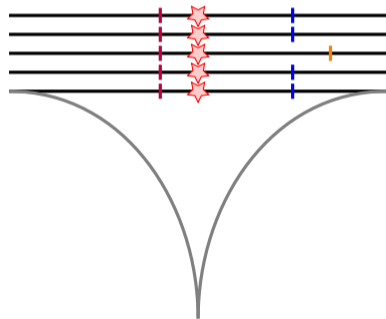
e.g., Malaria drug resistance

Frevert et al. 2005 *PLoS Biol.*, Margaret Shear

data from Nair *et al.* 2003 *MBE*
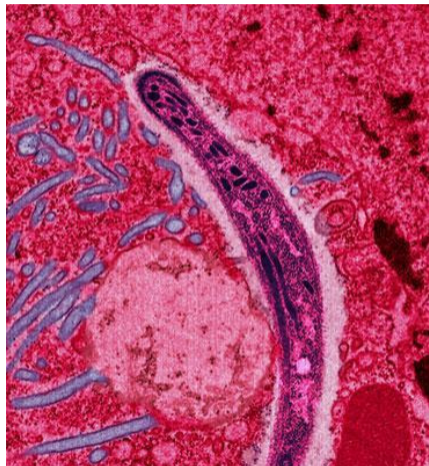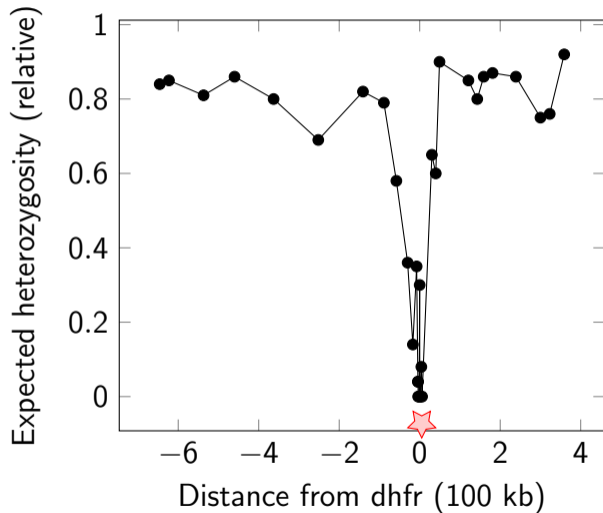
e.g., Drosophila insecticide resistance

genomic position
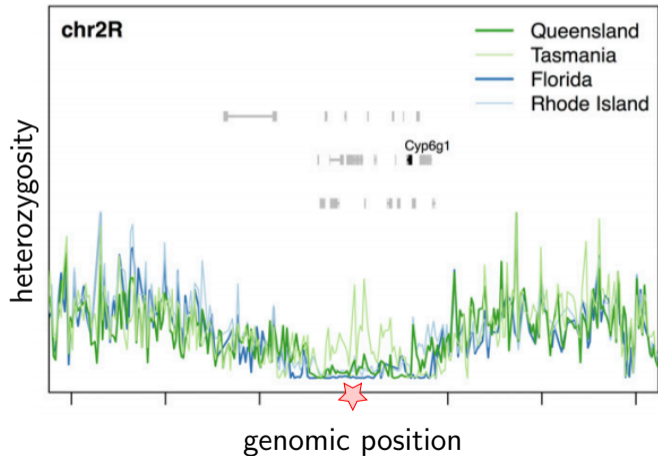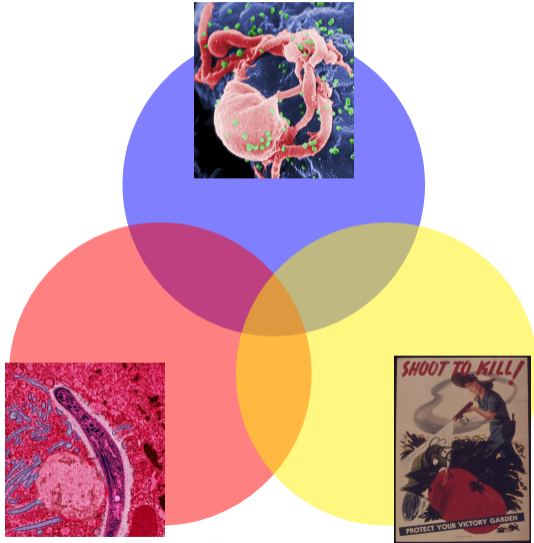
Very severe stress

Frevert et al. 2005 *PLoS Biol.*, Margaret Shear

Very severe stress
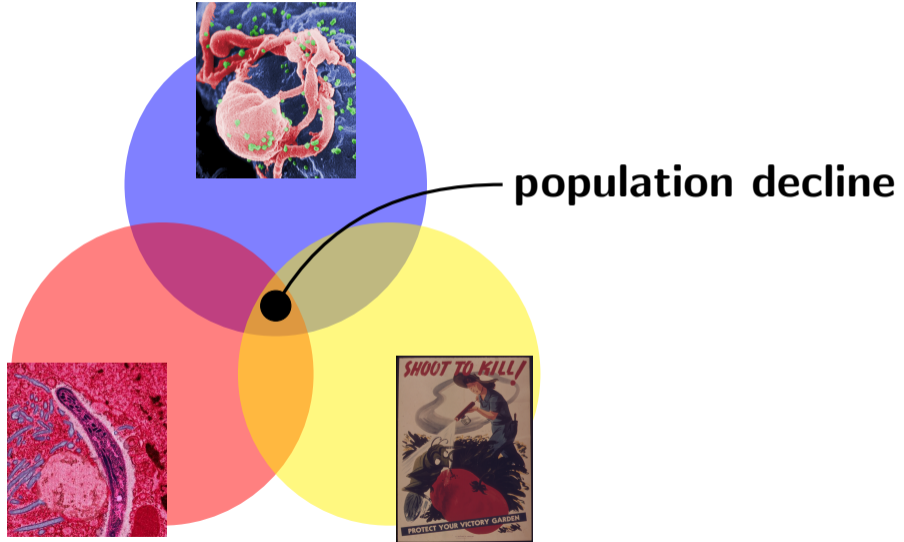
population decline

Evolutionary rescue

Evolutionary rescue

Gomulkiewicz & Holt 1995 *Evolution*

Evolutionary rescue
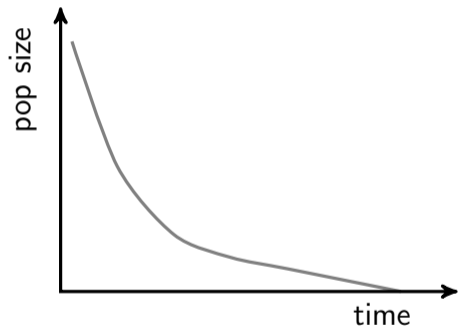
Evolutionary rescue
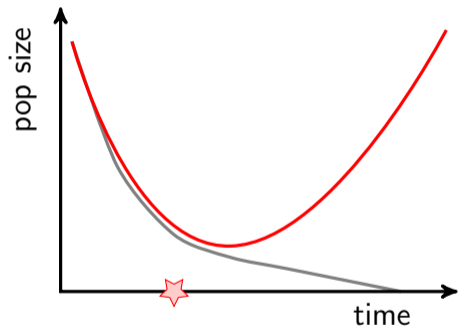
Gomulkiewicz & Holt 1995 *Evolution*   Wei *et al.* 1995 *Nature*
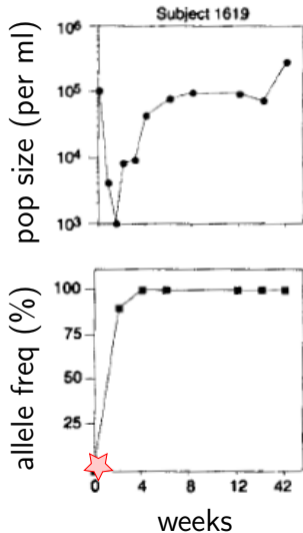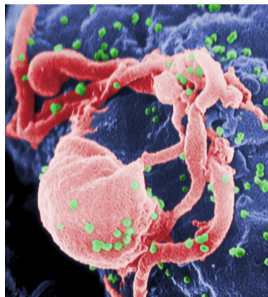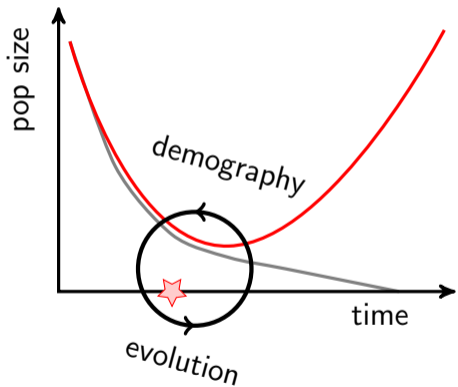
What genetic signatures does evolutionary rescue allow?

The model

The model

absolute fitness

1 — replacement

$1 - d$

aa   Aa   AA

genotype

The model

The model
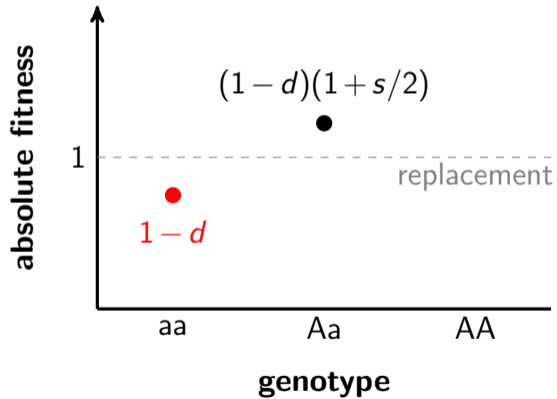
The model
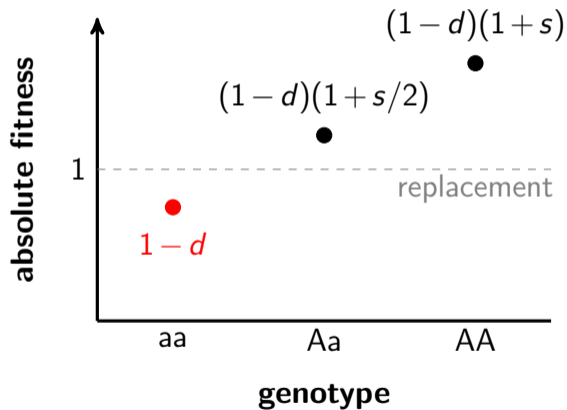
$d = 0.05,\ s = 0.2$
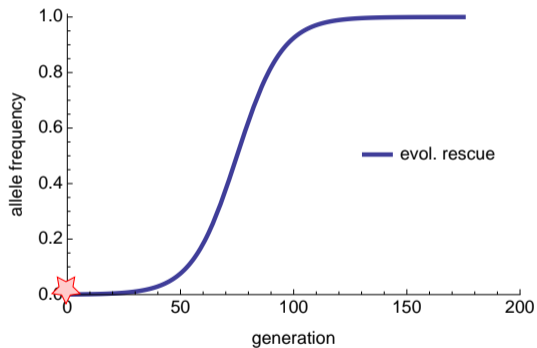
Dynamics │ rescue

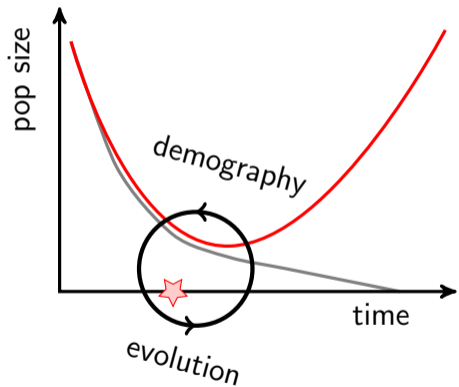
$d = 0.05$, $s = 0.2$

Dynamics │ rescue
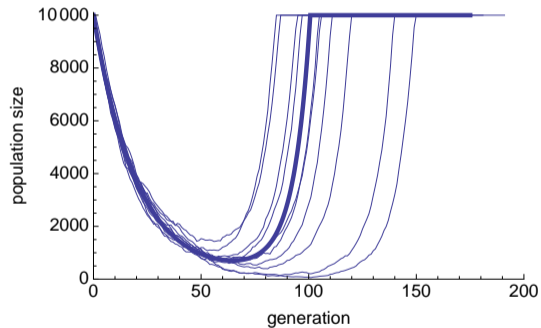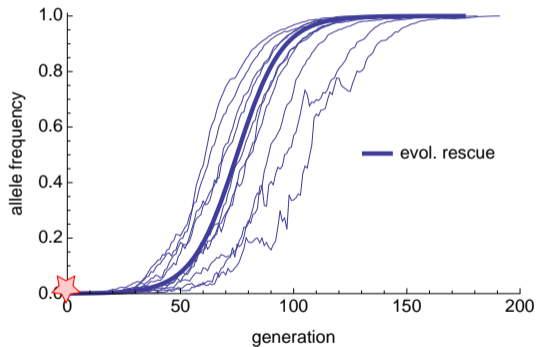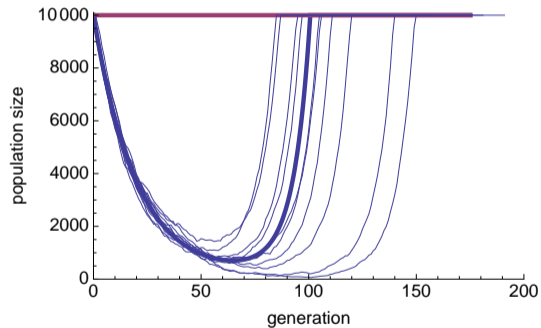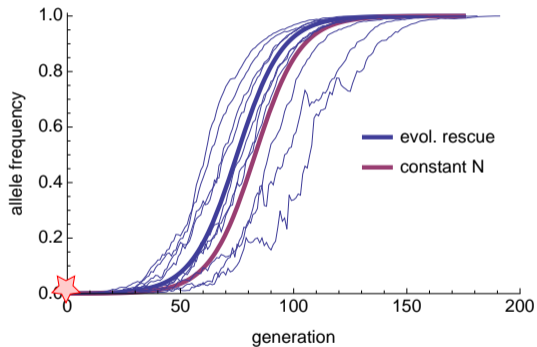
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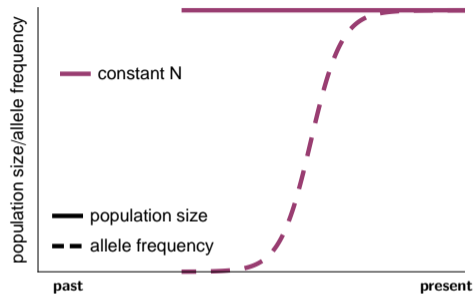
$$d = 0.05, \ N(0) = 10^4$$

The coalescent | rescue
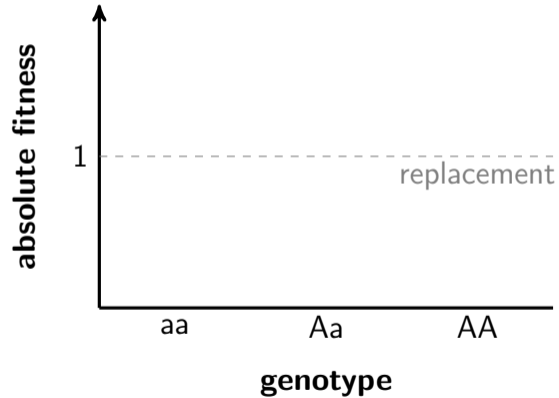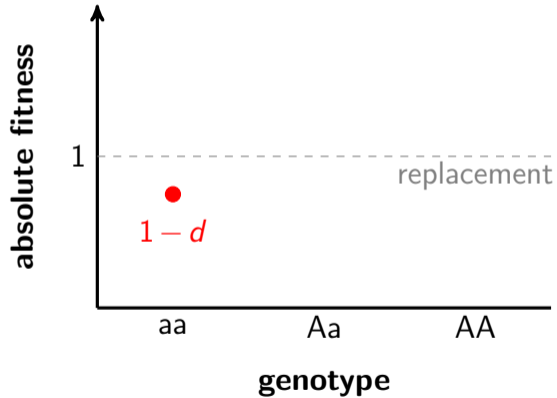

$$p_{\mathrm{coal}}(k,t) = \binom{k}{2}\frac{1}{N(t)p(t)}$$

$$p_{\mathrm{rec}}(k,t) = k\frac{r}{2}[1-p(t)]$$

$$d = 0.05,\ N(0) = 10^4$$

The coalescent │ rescue

population size/allele frequency
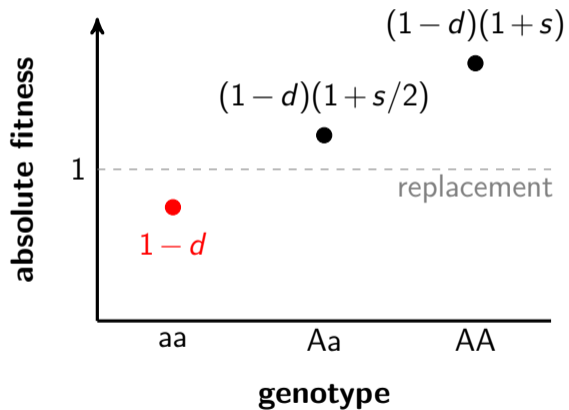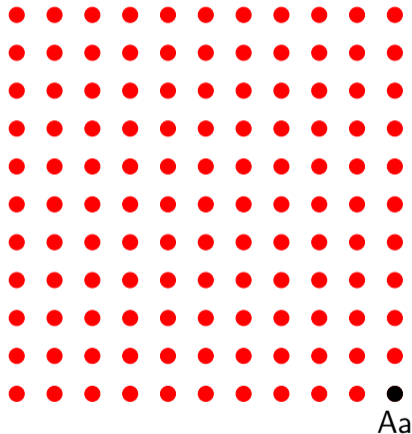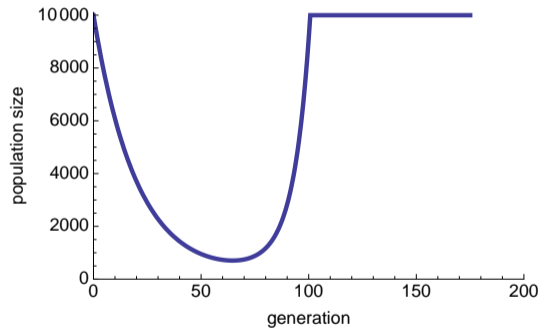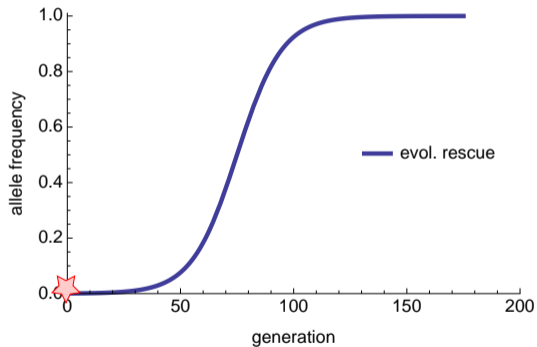
— constant N

— population size
- - allele frequency

past   present

$$p_{\mathrm{coal}}(k,t) = \binom{k}{2}\frac{1}{N(t)p(t)}$$

$$p_{\mathrm{rec}}(k,t) = k\frac{r}{2}[1-p(t)]$$

$k = 2$

coalesce first

recombine first

$d = 0.05,\ N(0) = 10^4$

The coalescent │ rescue

$$p_{\text{coal}}(k, t) = \binom{k}{2} \frac{1}{N(t)p(t)}$$

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The coalescent │ rescue

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The coalescent │ rescue

$$p_{\text{coal}}(k, t) = \binom{k}{2} \frac{1}{N(t)p(t)}$$

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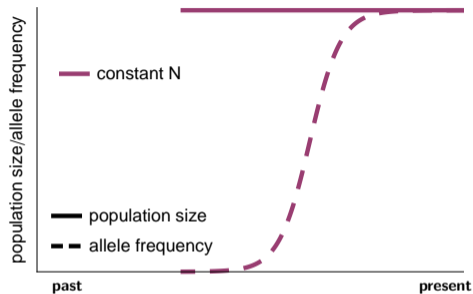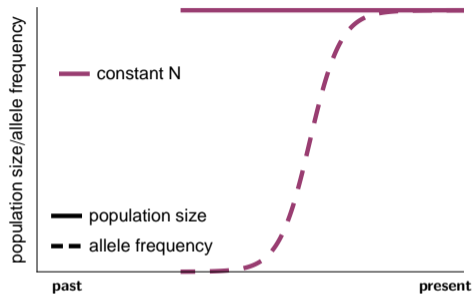
$k = 2$

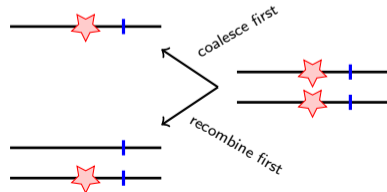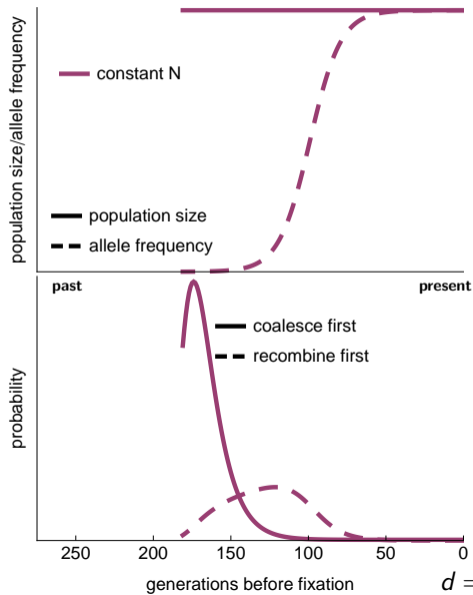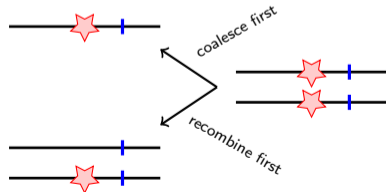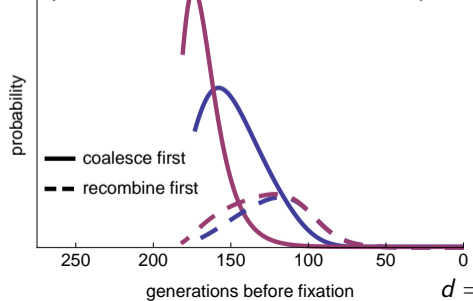coalesce first

recombine first

$d = 0.05, \ N(0) = 10^4$

The coalescent │ rescue
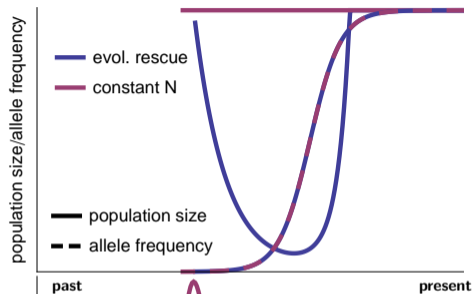

$$p_{\text{coal}}(k, t) = \binom{k}{2} \frac{1}{N(t)p(t)}$$

$$p_{\text{rec}}(k, t) = k\frac{r}{2}[1 - p(t)]$$

$k = 2$

less recombination in rescue
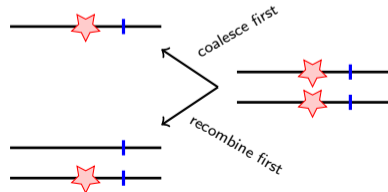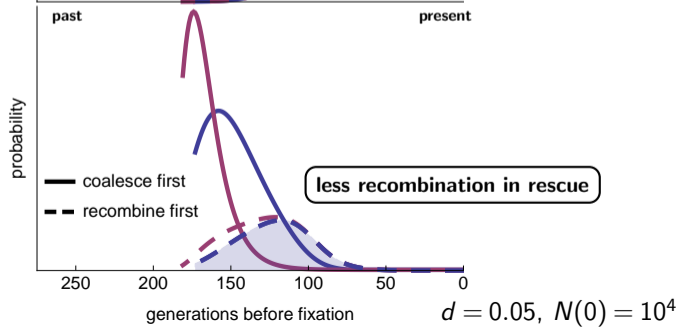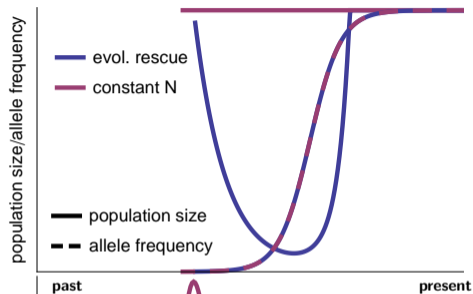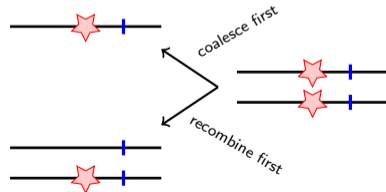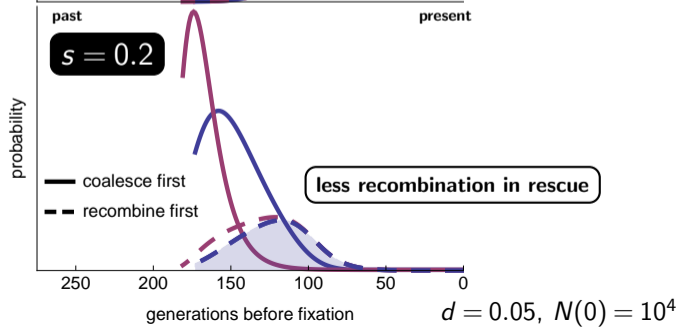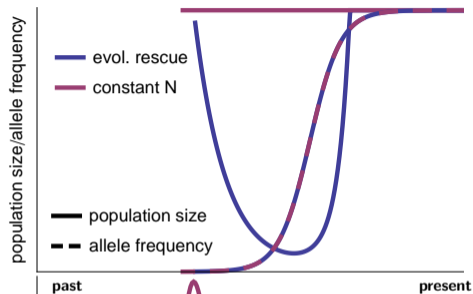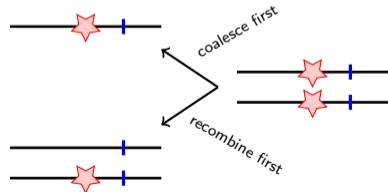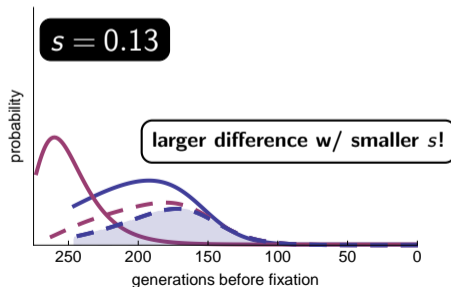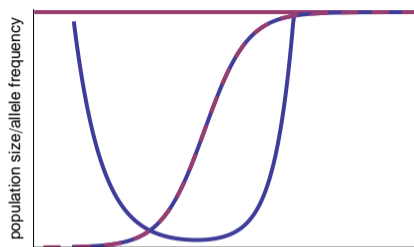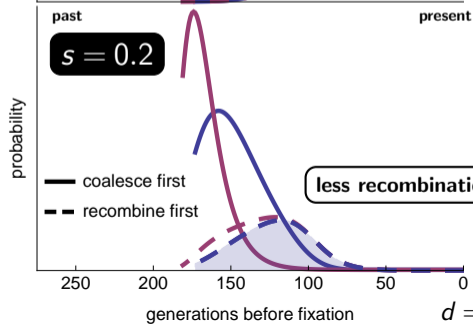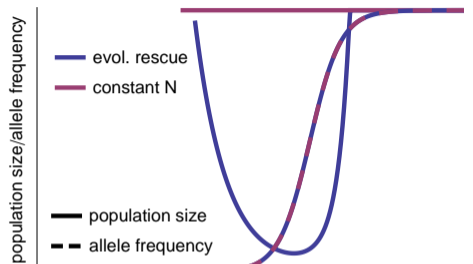
$d = 0.05, \; N(0) = 10^4$

The coalescent | rescue

population size/allele frequency

- evol. rescue
- constant N

— population size
- - allele frequency

past   **present**

$s = 0.2$

probability

— coalesce first
- - recombine first

less recombination in rescue

250   200   150   100   50   0
generations before fixation

$s = 0.13$

larger difference w/ smaller s!

250   200   150   100   50   0
generations before fixation

$d = 0.05, \; N(0) = 10^4$

Dips in diversity | rescue
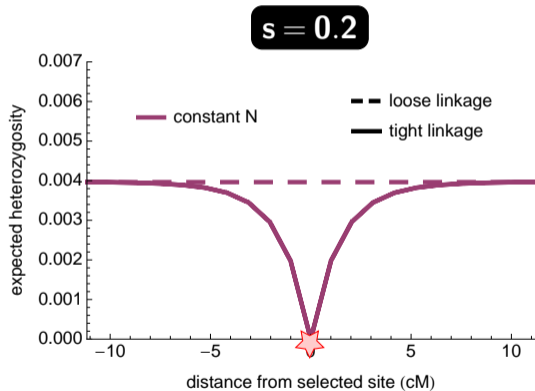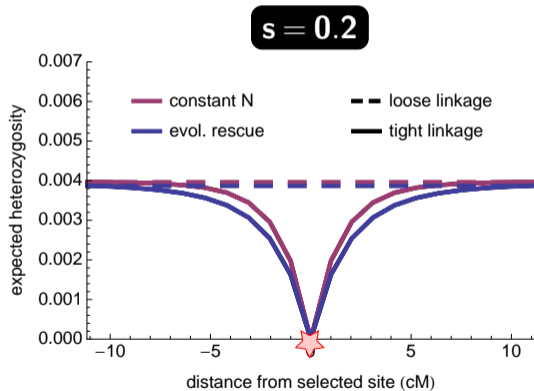
Dips in diversity | rescue

$d = 0.05, \ N(0) = 10^4$

Dips in diversity | rescue

$s = 0.2$

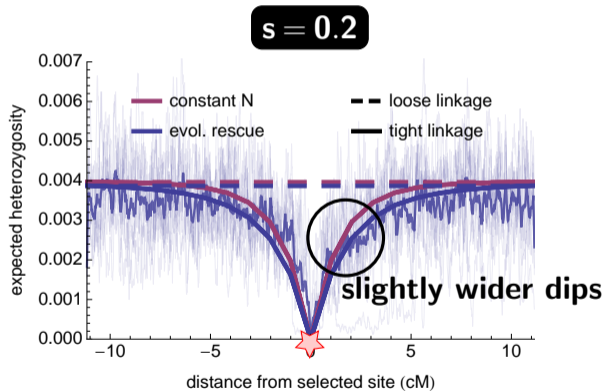constant N — loose linkage
evol. rescue — tight linkage

expected heterozygosity

distance from selected site (cM)

Dips in diversity | rescue
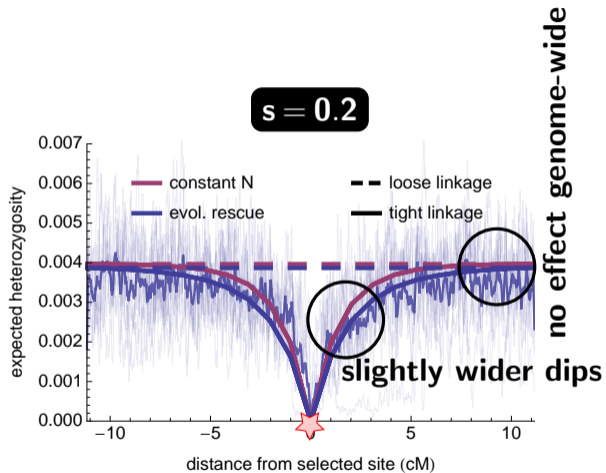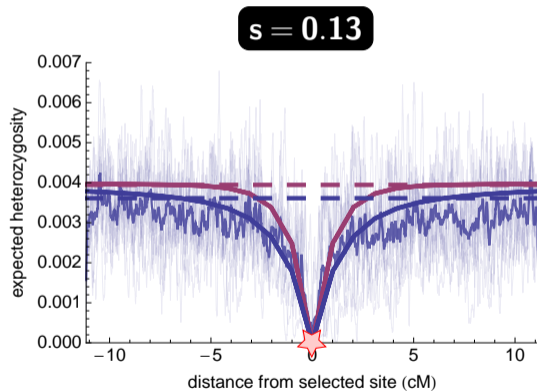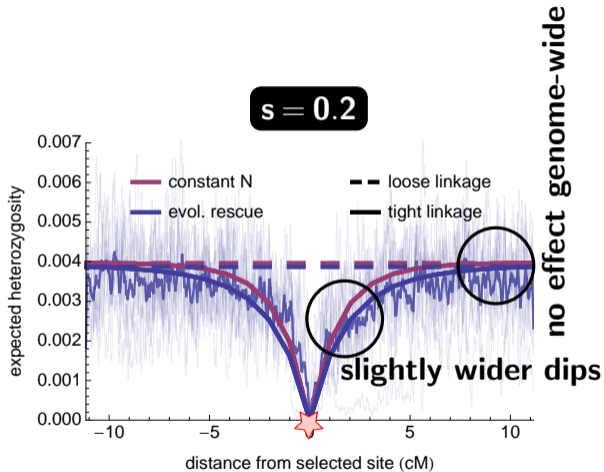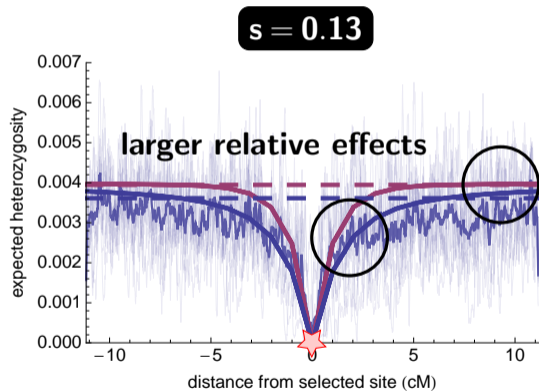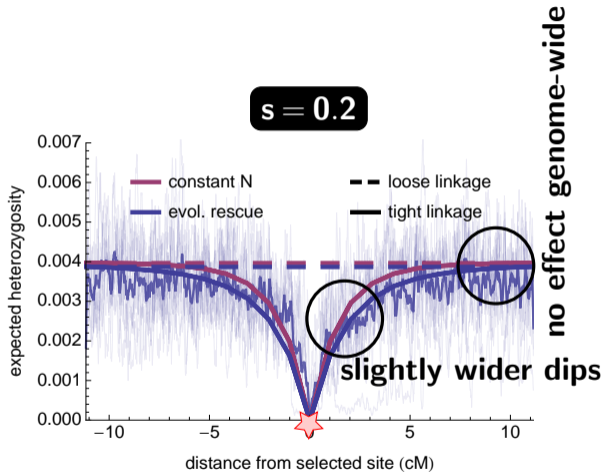
Dips in diversity │ rescue

Dips in diversity | rescue

Dips in diversity │ rescue

$d = 0.05$, $N(0) = 10^4$

Tajima's D | rescue

$s = 0.2$

evol. rescue
constant N

distance from selected site (cM)

Tajima's D

$d = 0.05$, $N(0) = 10^4$

Simulations in SLIM 3; Haller & Messer 2019, Haller *et al.* 2019

Tajima's D | rescue

$s = 0.2$

no effect near sweep

evol. rescue
constant N

Tajima's D

distance from selected site (cM)

Tajima's D | rescue

$s = 0.2$

detects bottleneck

no effect near sweep

- evol. rescue
- constant N

Tajima's D

distance from selected site (cM)
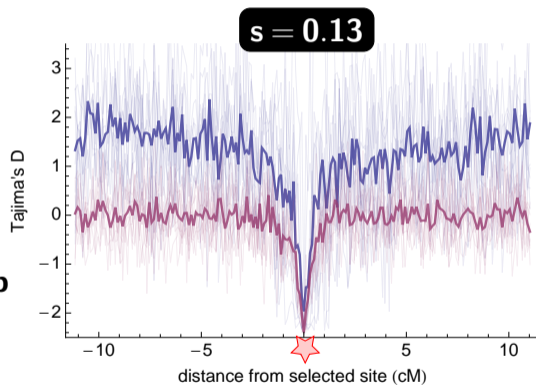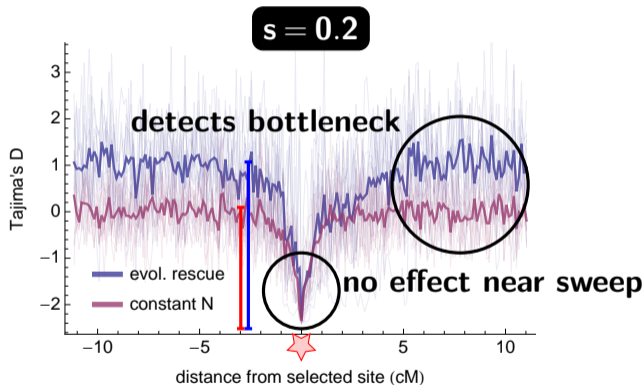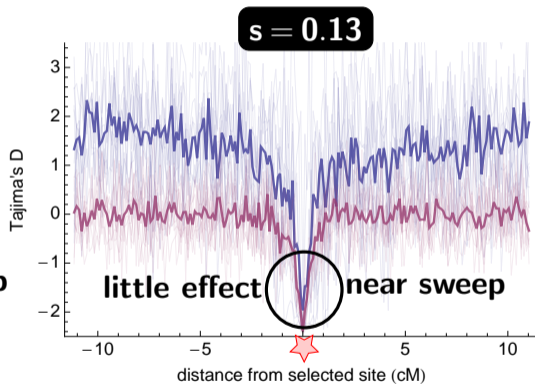
Tajima's D | rescue
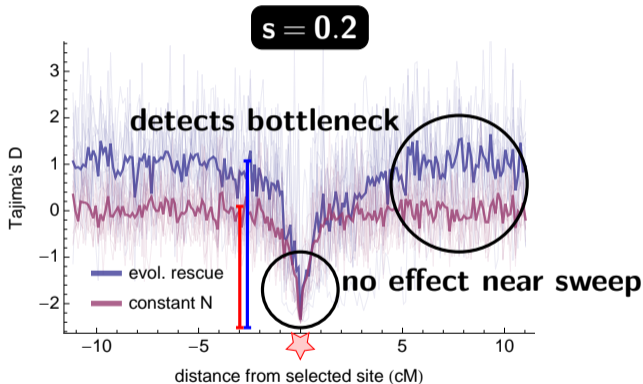
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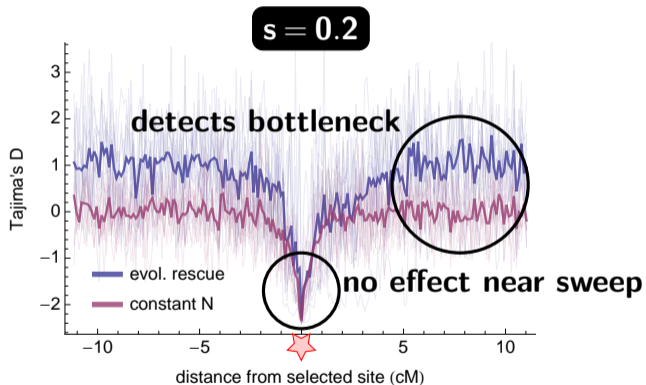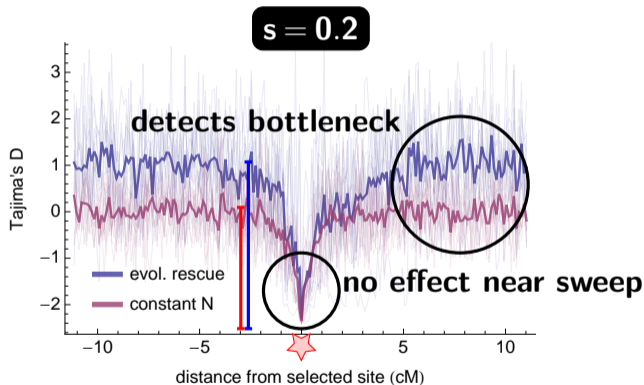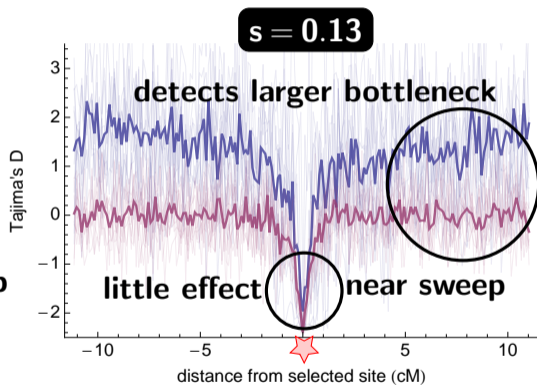

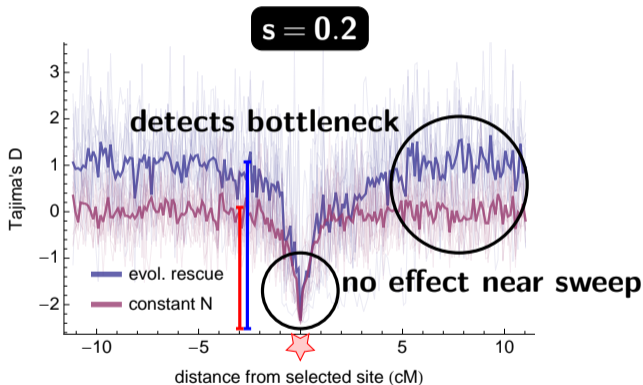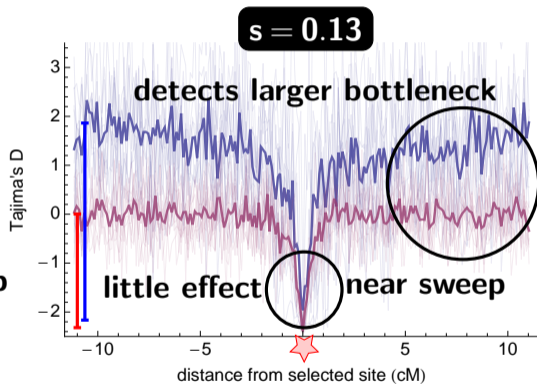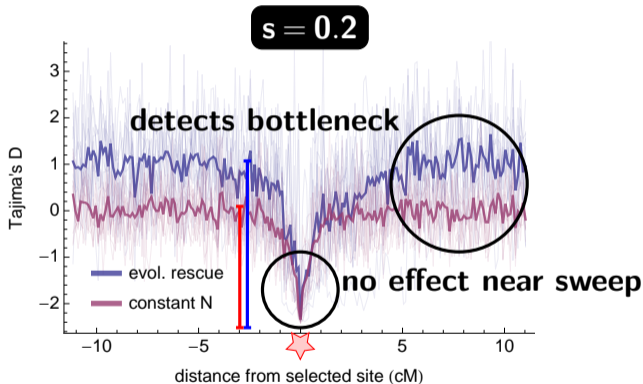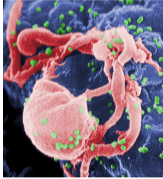$d = 0.05$, $N(0) = 10^4$

Tajima's D | rescue

$d = 0.05$, $N(0) = 10^4$

Tajima's D | rescue

$d = 0.05$, $N(0) = 10^4$

Simulations in SLIM 3; Haller & Messer 2019, Haller *et al.* 2019

Osmond & Coop   14
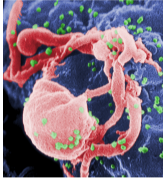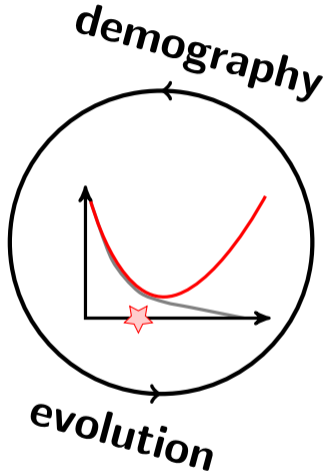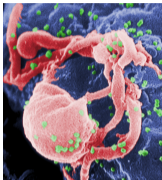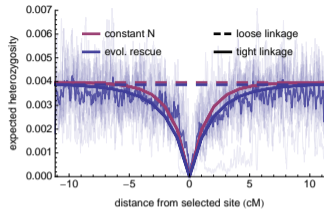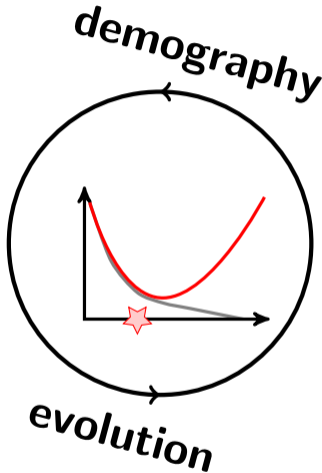
$d = 0.05$, $N(0) = 10^4$

strong stress $\implies$
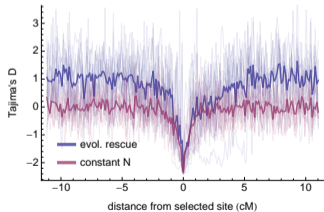
strong stress $\implies$

strong stress $\Longrightarrow$ demography / evolution $\Longrightarrow$ **genetic patterns**

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