

# Estimating Viability



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Symbol	Definition
$n_{11}$	number of individuals with <i>homozygous</i> ( $p$ ) genotype
$n_{12}$	number of individuals with <i>heterozygous</i> genotype
$n_{22}$	number of individuals with <i>homozygous</i> ( $q$ ) genotype
$w_{11}$	fitness of <i>homozygous</i> ( $p$ ) genotype
$w_{12}$	fitness of <i>heterozygous</i> genotype
$w_{22}$	fitness of <i>homozygous</i> ( $q$ ) genotype

Genotype	$A_1A_1$	$A_1A_2$	$A_2A_2$
Number in zygotes	$n_{11}^{(z)}$	$n_{12}^{(z)}$	$n_{22}^{(z)}$
Viability	$w_{11}$	$w_{12}$	$w_{22}$
Number in adults	$n_{11}^{(a)} = w_{11}n_{11}^{(z)}$	$n_{12}^{(a)} = w_{12}n_{12}^{(z)}$	$n_{22}^{(a)} = w_{22}n_{22}^{(z)}$

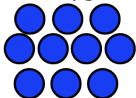
$$w_{ij} = \frac{n_{ij}^{(a)}}{n_{ij}^{(z)}}$$

Genotype	$A_1A_1$	$A_1A_2$	$A_2A_2$
Relative viability	$\frac{w_{11}}{w_{12}}$	1	$\frac{w_{22}}{w_{12}}$

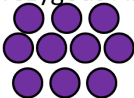
# Diagrammatic example

“Zygote”

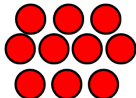
Homozygous A1



Heterozygous A1/A2



Homozygous A2



“Adult”

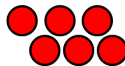
Absolute fitness = 0.20



Absolute fitness = 0.40



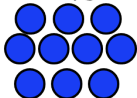
Absolute fitness = 0.60



# Diagrammatic example

“Zygote”

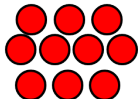
Homozygous A1



Heterozygous A1/A2



Homozygous A2



“Adult”

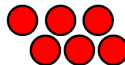
Relative fitness = 0.50



Relative fitness = 1.00



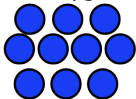
Absolute fitness = 1.50



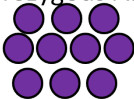
# Diagrammatic example

“Zygote”

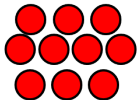
Homozygous A1



Heterozygous A1/A2



Homozygous A2

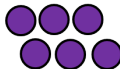


“Adult”

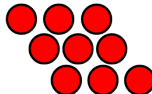
Absolute fitness = 0.30



Absolute fitness = 0.60



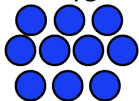
Absolute fitness = 0.90



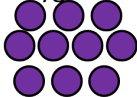
# Diagrammatic example

“Zygote”

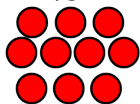
Homozygous A1



Heterozygous A1/A2



Homozygous A2

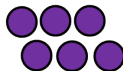


“Adult”

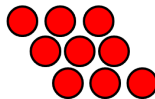
Relative fitness = 0.50



Relative fitness = 1.00



Relative fitness = 1.50





## Numerical example

Genotype	$A_1A_1$	$A_1A_2$	$A_2A_2$
Number in zygotes	208	372	243
Viability	$w_{11}$	$w_{12}$	$w_{22}$
Number in adults	147	206	92

$$w_{ij} = \frac{n_{ij}^{(a)}}{n_{ij}^{(z)}}$$

## Numerical example

Genotype	$A_1A_1$	$A_1A_2$	$A_2A_2$
Number in zygotes	212	372	243
Viability	0.71	0.55	0.38
Number in adults	147	206	92

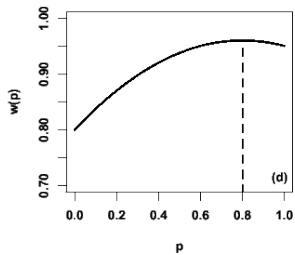
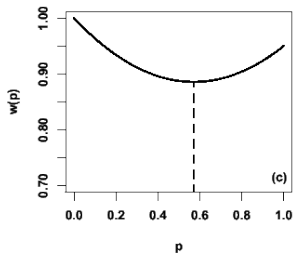
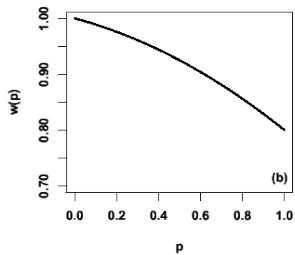
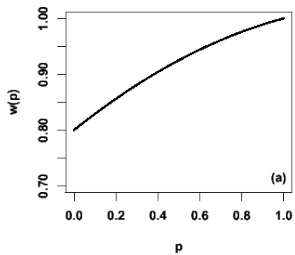
$$w_{ij} = \frac{n_{ij}^{(a)}}{n_{ij}^{(z)}}$$

Genotype	$A_1A_1$	$A_1A_2$	$A_2A_2$
Relative viability	$\frac{w_{11}}{w_{12}}$	1	$\frac{w_{22}}{w_{12}}$

Genotype	$A_1A_1$	$A_1A_2$	$A_2A_2$
Relative viability	$\frac{0.71}{0.55}$	1	$\frac{0.38}{0.55}$

Genotype	$A_1A_1$	$A_1A_2$	$A_2A_2$
Relative viability	1.29	1	0.69

Pattern	Description
Directional	$w_{11} > w_{12} > w_{22}$ or $w_{11} < w_{12} < w_{22}$
Disruptive	$w_{11} > w_{12}, w_{22} > w_{12}$
Stabilizing	$w_{11} < w_{12}, w_{22} < w_{12}$



Genotype	$A_1A_1$	$A_1A_2$	$A_2A_2$
Relative viability	1.29	1	0.69



## Project 3

Project 3 looks at the peppered moth, *Biston betularia* and two of its morphs, *typica* and *carbonaria*



## Kettlewell (1955)

		<i>typica</i>	<i>carbonaria</i>
Dorset	Released	486	473
	Recaptured	62	30
Birmingham	Released	137	447
	Recaptured	18	123

# Dorset



# Birmingham



# Questions

1. What are the **absolute** viabilities of *typica* and *carbonaria* in each location?
2. What is the viability of *typica* **relative** to *carbonaria* in each location?
3. If you assume that the fitnesses remain constant and that viability selection is the only evolutionary force acting on the populations, what will the long-term outcome of selection in each location be?
4. How confident are you in your answer to #3?
5. Is the fitness of *typica* relative to *carbonaria* in either location consistent with the corresponding relative fitness estimate that Haldane obtained?

How do we do this in a Bayesian context?

1. Estimate absolute viabilities.
2. Apply formula to calculate relative viabilities..

JAGS code for non-destructive sampling:

$$n.11.adult \sim dbin(w.11, n.11.zygote)$$
$$n.12.adult \sim dbin(w.12, n.12.zygote)$$
$$n.22.adult \sim dbin(w.22, n.22.zygote)$$

# Hints

- ▶ Model the number of survivors for each phenotype separately in each population. Assume that the number of survivors is drawn from a binomial distribution with a probability equal to its absolute viability and a sample size equal to the number of moths released.
- ▶ Use uniform priors on the absolute fitnesses: `dunif(0, 1)`.
- ▶ Estimate the relative fitnesses within JAGS so that you get both the posterior mean and 95 % credible intervals.
- ▶ Make the estimates separately for each location.



# References

- ▶ Kettlewell, Henry Bernard Davies. "Selection experiments on industrial melanism in the Lepidoptera." *Heredity* 9 (1955): 323-342.