**Dominance Effects**

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Previously, genotypic value was decomposed into additive (*u*) and residual (*r*) components, where the latter has zero covariance between different individuals. To model the dominance component of *r*, let us revisit the theory of average effects for a single locus. Let denote the maternal and paternal genes, respectively, at a locus with *m* alleles. The genotypic value of genotype is denoted , and its frequency at panmictic equilibrium is the product of the allele frequencies: . Using notation from factorial experiments, the regression of the genotypic value on allele dosage is

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|  | [1] |

where *i* is the **additive effect** of gene *i* and the residual is the **dominance effect** (a.k.a. the dominance deviation) for genotype *ij*. At panmictic equilibrium, the covariance between additive and dominance effects is zero, which leads to the following decomposition of variance:

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| Additive variance =  Dominance variance = | [2] |

For the case of two alleles (*B*/*b*), there are three diploid genotypes (*BB*, *Bb*, *bb*) and each has a corresponding dominance effect. Let *p* denote the frequency of the *B* allele and .

For the additive effects, we proceeded by defining the allele substitution effect . The analogous quantity for dominance effects is

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|  | [3] |

There is no accepted name for the parameter in the literature, so I will call it the **dominance substitution effect**. From Eq. 3 we can see that it is the difference of the two possible allele substitution effects for dominance. Just as the solution for the additive effects can be written succinctly in terms of , the same is true for the dominance effects:

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|  | [4] |

Under this parameterization, the expression for dominance variance (Eq. 2) becomes

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|  | [5] |

If *X* denotes the dosage of allele *B* and *v* is the dominance deviation for an individual with genotype *X*, then Eq. 4 is equivalent to

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|  | [6] |

Eq. 6 defines a dominance genotype *V* that is a **quadratic** function of allele dosage. This can be compared with the analogous expression for breeding value involving the centered genotype *W*, which is a **linear** function of allele dosage.

**Estimating Dominance with Markers**

In earlier lectures, non-additive effects were modeled as i.i.d. Now we will consider the covariance between dominance effects based on Eq. 6. Let **X** denote the *n* x *m* matrix of allele dosages for a population of *n* individuals with *m* bi-allelic markers. Let **W** denote the matrix of centered genotypes (computed by subtracting the mean for each marker from the allele dosage) and **V** is the matrix of dominance genotypes computed according to Eq. 6.

Decompose the genotypic value into additive, dominance, and residual effects:

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|  | [7] |

In Eq. 7, is the vector of allele substitution effects for the markers, and is the vector of dominance substitution effects (Eq. 3). Assuming that both vectors are i.i.d. random effects,

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|  | [8] |

then the additive and dominance values are multivariate normal:

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|  | [9] |

Although I am no longer using a subscript *m*, both the additive (**A**) and dominance (**D**) relationship matrices in Eq. 9 will be estimated from the markers. The expression for the additive relationship matrix,

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|  | [10] |

was derived previously by considering the variance of the additive values. The corresponding expression for the dominance values is (see Eq. 5)

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|  | [11] |