Hayman's analysis

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1 Abstract

Hayman's approach analyses a complete diallel (parents, F_1 and reciprocals) for gene action: an analysis of variance that separates additive, dominance, maternal and reciprocal effects; the variances V_r and covariances W_r of the arrays and their graph; the components D, H_1, H_2, F, h^2 and E; and tests of the additive-dominance model.

2 The analysis

```
h <-
  Hayman(
      y      = Yield
    , Rep    = Rep
    , Cross1 = Cross1
```

```
    , Cross2 = Cross2
    , data   = HaymanData
    )
knitr::kable(x = h$ANOVA, digits = 3)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Total	255	127716.027	NA	NA	NA
Rep	3	1036.192	345.397	3.001	0.032
Treatment	63	104923.873	1665.458	14.468	0.000
Additive	7	15218.571	2174.082	18.887	0.000
Non-Additive	28	88243.154	3151.541	27.378	0.000
b1	1	1367.594	1367.594	11.881	0.001
b2	7	13530.165	1932.881	16.791	0.000
b3	20	73345.396	3667.270	31.859	0.000
Maternal	7	310.737	44.391	0.386	0.910
Reciprocal	21	1151.411	54.829	0.476	0.976
Error	189	21755.963	115.111	NA	NA

Line b_1 tests the mean dominance deviation of the crosses from the parents (directional dominance), b_2 whether this deviation differs among parents, b_3 the remaining dominance. Maternal and reciprocal effects are not significant here.

3 Arrays: V_r and W_r

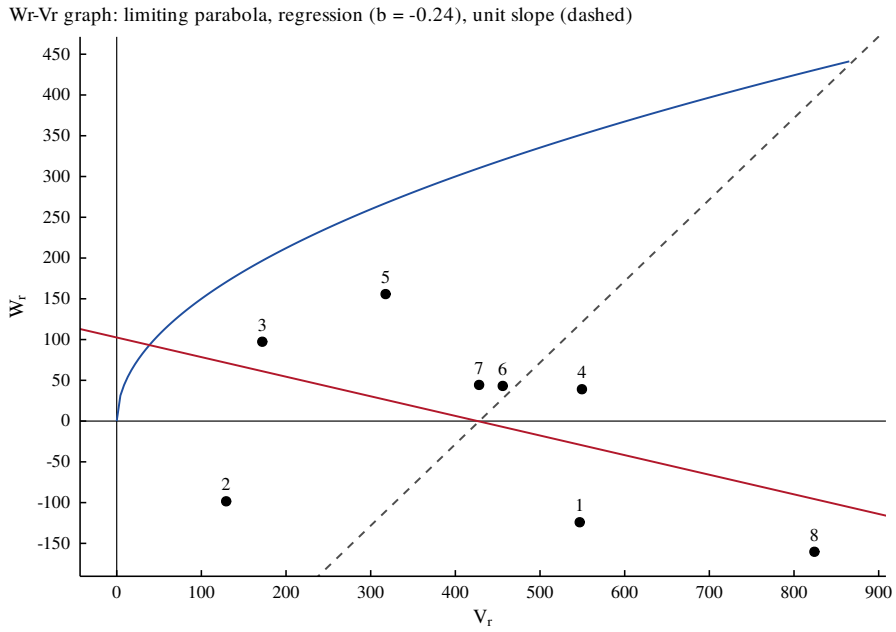
After averaging reciprocal crosses, array r (the progeny of parent r) has variance V_r and covariance W_r with the parents:

```
knitr::kable(x = h$Wr.Vr.Table[, c("Wr", "Vr", "Wr.Minus.Vr",
 ↪  "Wr.Plus.Vr", "Yr")], digits = 2)
```

Wr	Vr	Wr.Minus.Vr	Wr.Plus.Vr	Yr
-124.09	546.87	-670.97	422.78	85.65
-98.41	129.31	-227.72	30.90	98.26
97.33	171.95	-74.62	269.28	74.07
39.07	549.50	-510.43	588.57	91.64
155.78	317.59	-161.81	473.37	54.10
43.12	455.95	-412.83	499.08	100.39
44.36	428.02	-383.67	472.38	90.96
-160.30	824.10	-984.40	663.80	82.00

4 The W_r-V_r graph

```
plot(h)
```



Under the additive-dominance model the points lie on a line of unit slope (dashed) inside the limiting parabola $W_r^2 = V_r V_{0L0}$. Parents near the origin carry mostly dominant genes, parents far from it mostly recessive genes.

5 Tests of the model

```
knitr::kable(x = h$Tests, digits = 4)
```

	Statistic	Df	p.value
Uniformity of Wr - Vr (t^2)	4.2485	6	0.0849
b = 0 (t)	-1.3293	6	0.2321
b = 1 (t)	6.8569	6	0.0005

A significant t^2 or a slope that differs from 1 indicates epistasis or correlated gene distribution; the components below then need care. In this data set the slope is negative and differs from 1, so the additive-dominance model is not adequate.

6 Components of variation

```
knitr::kable(x = h$Components.of.Variation, digits = 3)
```

	Estimate	StdErr	t.value
E	29.677	74.009	0.401
D	195.287	222.026	0.880
F	406.984	524.628	0.776
H1	1856.573	510.406	3.637
H2	1516.416	444.053	3.415
h2	136.597	313.481	0.436

```
knitr::kable(x = h$Other.Parameters, digits = 3)
```

	Other Parameters
Mean degree of dominance sqrt(H1/D)	3.083
Proportion of genes H2/(4H1)	0.204
Dominant to recessive genes	2.021
r(Wr + Vr, Yr)	-0.155
r^2(Wr + Vr, Yr)	0.024
Gene groups h2/H2	0.090
Narrow-sense heritability	0.136

$\sqrt{H_1/D}$ above 1 indicates overdominance; $H_2/(4H_1)$ below 0.25 an unequal distribution of positive and negative alleles among the parents.

7 Summary

Hayman's analysis asks how genes act rather than which parents combine well; read the components only when the tests support the additive-dominance model.

8 References

Hayman, B. I. (1954). The theory and analysis of diallel crosses. *Genetics*, 39(6), 789–809.

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