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**Calculating Expected Phenotypic Differences.**

1. Formulas

The formal relation between the combined or total within and between group heritability, heritability between groups, and genetic and phenotypic differences is given by Defries (1972a), McClearn and Defries (1973), Loehlin, Lindzey, & Spuhler (1975), Cheverud (1985), Jensen (1998):

(1)

where is the between group heritability, is the combined or total heritability, *r* is the genetic intraclass correlation, and *t* is the phenotypic intraclass correlation, which is equivalent to the square of the point biserial correlation (i.e., *r*pbs2). This formula can be expressed in terms of within groups heritability, . In this case:

(2)

where is the average of the heritabilities within both groups. Equations (1) & (2) are simplified, but can be expanded to include gene-environment covariance (COVGE) (Defries, 1972b). In this case, the between group heritability is not but is equal to:

+ *h*G \* *e*G \* *r*AGEG

where hG and eG are the square root of the between groups heritability and between group environmentality, respectively, and *r*AGEG is the gene-environment correlation between groups. Thus,

in the case of positive COVGE, equations (1) and (2) will underestimate genetic differences between groups (McClearn and Defries, 1973). This formula can be further expanded to include dominance (e.g., Wright, 1952). See the exchange between Defries and Jensen (Jensen, 1972; also: Jensen, 1998) for when narrow or broad-sense within groups heritability is more appropriate. Here we will work with the simplified equation.

The intraclass correlations (*r* and *t*) can be interpreted in terms of one-way analysis of variance (Loehlin, Lindzey, & Spuhler, 1975), where:

(3)

where MSb represents the mean square between groups and MSw represents the mean square within groups. ICCs are equivalent to , which can be converted into Cohen’s d with the following equation:

or, equivalently, (4)   
where Cohen’s *d* is:

(5)

and *M*1 and *M*2 are the means for group 1 and group 2, respectively and SDpooled is the pooled standard deviation. Alternatively, can be converted into a point-biserial correlation, and this can be converted into Cohen’s *d* with the following equation:

*r*pbs = or, equivalently, *d* = (6)

For diploid populations, *r*, the genetic intraclass correlation, in equation (1) and (2), is:

*r* = 2Fst / (1+ FIT) (7)

where Fst is the fixation index, or the between group variance in allele frequencies, and FIT  is the overall level of inbreeding in the total population (Hamilton, 1971; Cheverud, 1985; Whitlock, 2004).

Contrary to what is often thought, the upper bounds of Fst is typically < 1 (Hedrick, 2005;

Alcala & Rosenberg, 2017; Alcala & Rosenberg, 2019). Fst is mathematically constrained by heterozygosity and the frequency *M* of the most frequent allele. (For typical Humans SNPs, the upper bounds is around .70; e.g., Xu, Huang, Qian, & Jin, 2008; Alcala & Rosenberg, 2017).Thus, Fst is not on the variance scale of 0 to 1. In light of this, Hedrick (2005) proposed a standardized metric; similarly, Alcala & Rosenberg (2017) proposed the ratio Fst/Fst\_max, which ranges from 0 to 1.

To correct for the mathematical constraints and place Fst on a variance metric, we can follow (Alcala & Rosenberg, 2017) and create corrected value, Fst \_c:

Fst \_c = Fst  / Fst \_max (8)

The corresponding corrected genetic intraclass correlation, rc , is:

*rc* = 2 Fst\_c/ (1+ FIT) (9)

There are other concerns with common Fst estimators, given assumptions about population structure (Ochoa & Storey, 2021). These assumptions can lead to underestimations of the coefficient of relatedness, which *r* represents (DeFries, 1972a), in context to admixture (Ochoa & Storey, 2019). However, we will proceed with Weir and Cockerham's estimator.

Now, equation (2) can be rearranged to solve for *t* (the phenotypic variance).This gives:

(10)

Based on equation (10), one can solve for the expected gap, where environments are equal, which is done by setting to 1. This gives the following:

(11)

Using equation (1), with the total heritability instead of within groups heritability, (11) is simply:

(12)

Equation (12) can be related to the equation for expected differences given by Turkheimer (1991, eq. 6), where:

P1observed = + and P2observed = + (13)

and P1  and P2 are the standardized observed phenotypic values for group 1 and group 2, respectively and and are the standardized genetic and environmental values for the respective groups.

When (and thus = 1), then:

P1 – P2 = )

And so, in terms of standardized phenotypic (dp expected) and genetic (dg) differences:

*dP expected*  = \* *dg* (14)

With formula (6), we can convert the standardized differences (dp and dg) into point-biserial correlations, yielding:

(15)

Squaring both sides, recaptures equation (12), since the genetic intraclass correlation (*r*) and the phenotypic intraclass correlation (*t)* are equivalent to the square of the point biserial correlation. From the above, it can also be seen that the or the “genotypic gap” is equal to √ \* dobserved, where the √ can be interpreted as the correlation between phenotype and genotype between groups, i.e.:

(16)

This is because we can rewrite equation (1) as:

(17)

Taking the square root of both sides, gives:

(18)

And from equation (15), we see that the left hand is equal to

Equation 1 and 2 can be rewritten to solve for , the between group environmentality. This is just 1- , thus:

(19)

To note, while, and sum to 1, the expected differences on account of genes and environment, when expressed in standard deviations, will not sum to the phenotypic gap. This is because standard deviations are a linear measurement, and do not express differences in variance units (Jensen, 1998). Rather, to add the effects, one has to take the square root of the sum of the squared differences. The formula is:

*d* phenotypic = (20)

For example, in a case where the phenotypic differences is 1 (*t* = .20), the within groups heritability is .50, and r = .20, = .5 and . By equation (14), the effect owing to environment will be = .71 SD or 10.6066 IQ points. And the effect owing to genes will be the same; this is also the expected difference given by equation (9). The phenotypic differencesis recovered with equation (19), as = 15.

From the above, it is obvious that is not equal to the real-world percentage of the differences which, owing to genes, would remain when the environments were equalized. The inference makes the r2 interpretative fallacy (Hunter & Schmidt, 2004), which results because variance-explained does not represent a linear relation between x and y. Rather expected percentage genetic, in the ordinary sense, is given by:

Percentage genetic expected = / dobserved (21)

Example:

Using the Education SNP Fst values in Table 1, calculate the expected differences owing to genes for Africans and Europeans, assuming an within groups heritability of .5.

Table 1. Fst Values for the 10k MTAG eduSNPs by 1000 Genomes Population Pairs.

\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Population\_1 | Population\_2 | Edu\_Fst |  | Edu\_Fit |
| AFR | EAS | 0.1402 |  | 0.1470 |
| AFR | EUR | 0.1090 |  | 0.1153 |
| AFR | SAS | 0.1018 |  | 0.1125 |
| AFR | AMR | 0.0984 |  | 0.1160 |
| EAS | EUR | 0.0964 |  | 0.1030 |
| AMR | EAS | 0.0714 |  | 0.0899 |
| EAS | SAS | 0.0626 |  | 0.0741 |
| EUR | SAS | 0.0342 |  | 0.0451 |
| AMR | SAS | 0.0296 |  | 0.0528 |
| AMR | EUR | 0.0226 |  | 0.0412 |

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*Note*: AFR = African, EAS = East Asian, SAS = South Asian, Eur = European, and AMR = admixed American (Mexican, Puerto Ricans, Colombian, and Peruvian) populations.

For Africans (AFR) and European (EUR), the MTAG SNPS the Fst = .1090. By equation (7), *r* = 2(.1090)/(1+.1153) = .1955. Given a *=* .5, then texpected from equation (9) is:

texpected  =    .5   \*        =    .1083

Given equations (3) and (4), this equals *d* = 0.70 or a 10.46 point difference on a metric with a standard deviation of 15.

Using *rc* from equation (9), instead, *r* = 2(.1090/.70)/(1+.1153) = .2792. The texpected is:

texpected  =    .5   \*        =    .1623

This equal *d* = .88 or a 13.20 point difference.

Since estimates of h2 and H2 may vary, and since there may be disagreement on how to correct Fst , one can provide a table for the different possibilities, given Fst = .1090. This is shown in Table 2.

Table 2. BGH and Expected Variance and IQ point difference Given Different Values of *r* and H2.

\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| H2 | Fst | *r* | *t*\_observed | BGH | *t*\_expected | *d*\_expected | Expected IQ point difference | Cohen's Interpretation |
| 0.20 | 0.1090 | 0.1955 | 0.2000 | 0.194 | 0.0463 | 0.4409 | 6.61 | Medium |
| 0.35 | 0.1090 | 0.1955 | 0.2000 | 0.340 | 0.0784 | 0.5833 | 8.75 | Medium |
| 0.50 | 0.1090 | 0.1955 | 0.2000 | 0.486 | 0.1083 | 0.6971 | 10.46 | Medium |
| 0.65 | 0.1090 | 0.1955 | 0.2000 | 0.632 | 0.1364 | 0.7949 | 11.92 | Large |
| 0.80 | 0.1090 | 0.1955 | 0.2000 | 0.778 | 0.1628 | 0.8818 | 13.23 | Large |
|  |  |  |  |  |  |  |  |  |
| H2 | Fst | *r\_c* | *t*\_observed | BGH | *t*\_expected | *d*\_expected | Expected IQ point difference | Cohen's Interpretation |
| 0.20 | 0.1090 | 0.2792 | 0.2000 | 0.310 | 0.0719 | 0.5567 | 8.35 | Medium |
| 0.35 | 0.1090 | 0.2792 | 0.2000 | 0.542 | 0.1194 | 0.7364 | 11.05 | Medium |
| 0.50 | 0.1090 | 0.2792 | 0.2000 | 0.775 | 0.1623 | 0.8802 | 13.20 | Medium |
| 0.65 | 0.1090 | 0.2792 | 0.2000 | 1.007 | 0.2011 | 1.0035 | 15.05 | Large |
| 0.80 | 0.1090 | 0.2792 | 0.2000 | 1.240 | 0.2366 | 1.1133 | 16.70 | Large |

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