

Two Remarks on the Inference of “Macro” Genetic Effects

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Model Uncertainty

Empirical work attempting to uncover the mechanisms underlying differences between aggregate populations (in particular for economic growth) is plagued by issues of model specification.

1. Parametric forms
2. Theoretical disagreements
3. Exchangeability

Among the lessons from relatively unsuccessful efforts, model uncertainty must be addressed in order to produce sturdy evidence.

Suppose one wants to calculate a genes-related measure. A frequentist produces an estimate of the measure; a Bayesian produces a posterior probability) given available data d and the choice of a model m :

$$G(d|m)$$

I propose shifting the focus from $G(d|m)$ for a given m to considering what information is contained about deterrence is present for data d and a model space M which consists of a space of candidate models.

One can calculate a “model-space” based genes-related measure via

$$G(d|M) = \sum_m G(d|m) \mu(m|d)$$

This is just Bayes rule.

Moments of Posterior Density

expected value

$$EG(d|M) = \sum_m EG(d|m) \mu(m|d)$$

variance

$$\begin{aligned} \text{var } G(d|M) = \\ \sum_m \text{var } G(d|m) \mu(d|m) + \sum_m (EG(d|m) - EG(d|M))^2 \end{aligned}$$

$\sum_m (EG(d|m) - EG(d|M))^2$ measures uncertainty generated by lack of knowledge of correct model.

Does It Matter?

1. Few growth mechanisms have proven robust
2. Claims of deterrence effect to capital punishment turn out to be extremely fragile

One Outstanding Problem: Posterior Probabilities

$$\Pr(m|d) \propto \Pr(d|m)\Pr(m).$$

The posterior probabilities reflect both the evidentiary support for each model, as reflected in $\Pr(d|m)$, as well as the researcher's prior beliefs about the models, $\Pr(m)$.

What priors have been used?

1. Uniform (standard)
2. Dilution (George)
3. Hierarchical (Brock, Durlauf, and West: Durlauf, Kourtellos, and Tan)

Current research by Adrian Raftery and others has considered links between model space priors and behavior of posteriors.

DKT are working on IV and model averaging.

Identification of Individual, Social Effects, and Group Level Genetic Effects

Canonical Model

$$\omega_{it} = \tau y_{gt} + \gamma x_{it} + \delta \sum_j c_{ij} x_{jt} + \varphi \sum_j a_{ij} \omega_{jt} + \xi_{it}$$

ω_{it} = outcome

y_{gt} = group-level influence

x_{it} = individual-level influence

C, A = sociomatrices for effects of characteristics and choices.

Errors uncorrelated with y_{gt} , x_{it}

Are parameters identified? Answer: no, unless one has prior information on sociomatrices C and A . Blume, Brock, Durlauf, Jayaraman delineate.

Can genes be incorporated? Error may contain a group-specific component

$$\xi_{it} = \alpha_g + \varepsilon_{it}$$

Are the values of α_g identified? Yes, if original model is identified. The group differences are a form of y_g

However

1. No information exists in covariance structure of errors about α_g .

Leads to one reason why some economists are skeptical about use of heritability calculations to say something about group differences,

2. Group-level fixed effects obviously can arise from many sources.

Seems natural place to consider how genomic data can pin down causes.

In typical application of this class of models, self-selection on unobservables must be addressed. BD, BBDJ approach: use Heckman-style control functions.

Not clear it matters, for course, for ethnic groups, although may not be quite as trivial as one would guess.

Note it matters in other contexts (apologies to Harpending, I choose two of his references, Daly and Wilson and Putnam).