

One Health and epidemiologic methods: in the same neighborhood?



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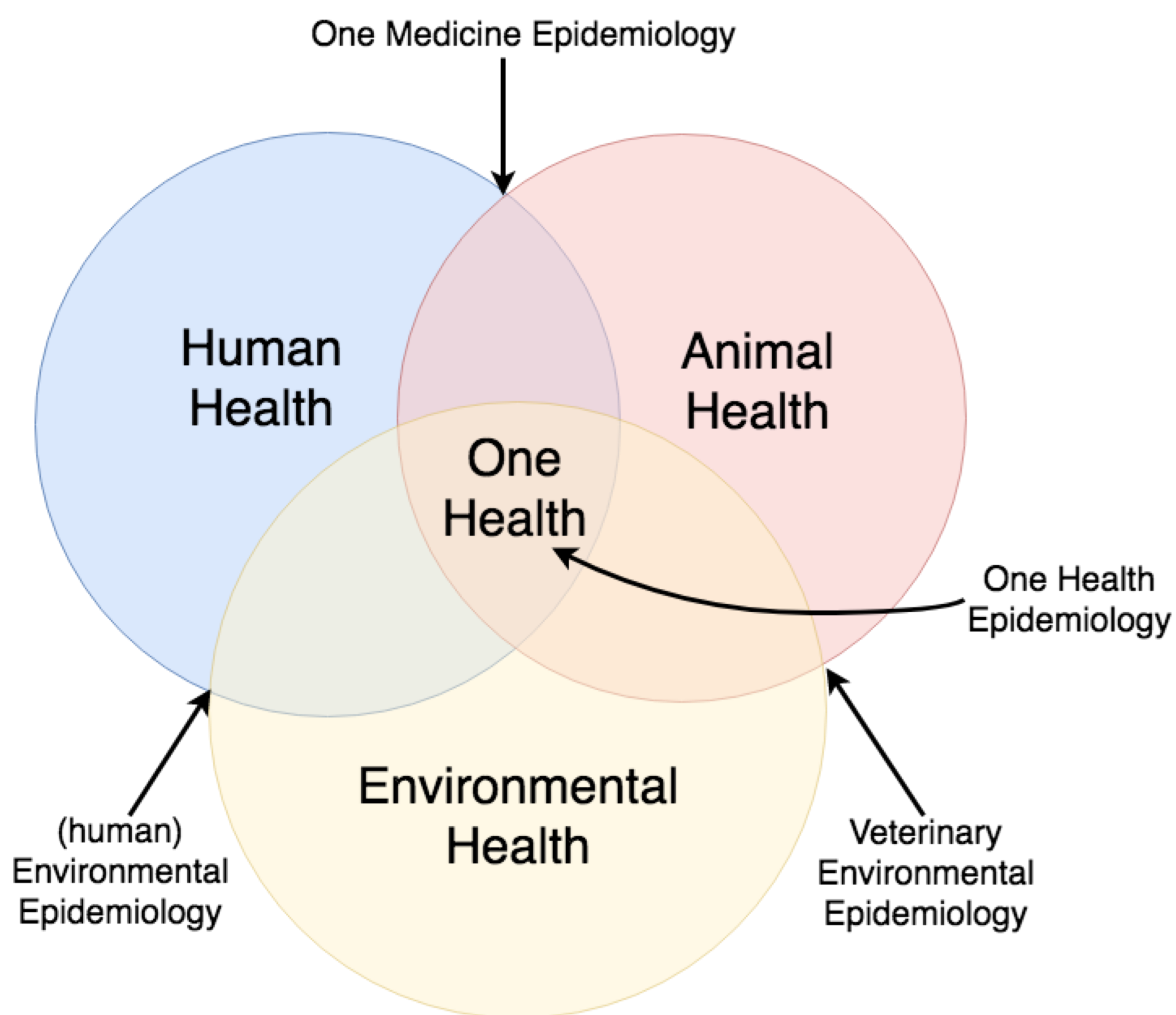


Figure 1: One Health conceptual model, adapted from: Davis et al. Checklist for One Health Epidemiological Reporting of Evidence (COHERE). One Health. 4 (2017), pp. 14-21.

Introduction and Background

- Communication between the epidemiologic methods and One Health communities is limited → **little attention to One Health epidemiologic methods.**
- One Health research questions are commonly complex, with **parallels to neighborhood exposures research**: study designs commonly result in **clustering** and rely on **distal causes**, and exposure is commonly the result of **self-selection.**
- Methods for correlated data are inconsistently applied, flawed and post hoc model selection methods are common, and other forms of bias are often overlooked.
- We demonstrate the potential for epidemiologic and causal inference methods to strengthen the validity of One Health research through application to a livestock exposure-human health question.

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Methods

Study design: cross-sectional.

Study setting: agropastoralist communities, Uganda

Exposure: cattle herd size (self-reported).

Outcome: human tuberculosis (TB) skin test (mm; TST).

Analyses:

- Linear regression with robust standard errors (SE): assumption of independent (uncorrelated) outcomes (naïve model).
- Generalized estimating equation (GEE): allows for violation of independence assumption. Exchangeable working correlation structure, robust SE.

Hypothesis: due to the poor control of zoonotic TB in Uganda, the association will be positive

Findings

A One Health DAG (merged human DAG and veterinary DAG) is presented in Figure 2. The minimum sufficient adjustment set is {recent cattle purchases, herd health}.

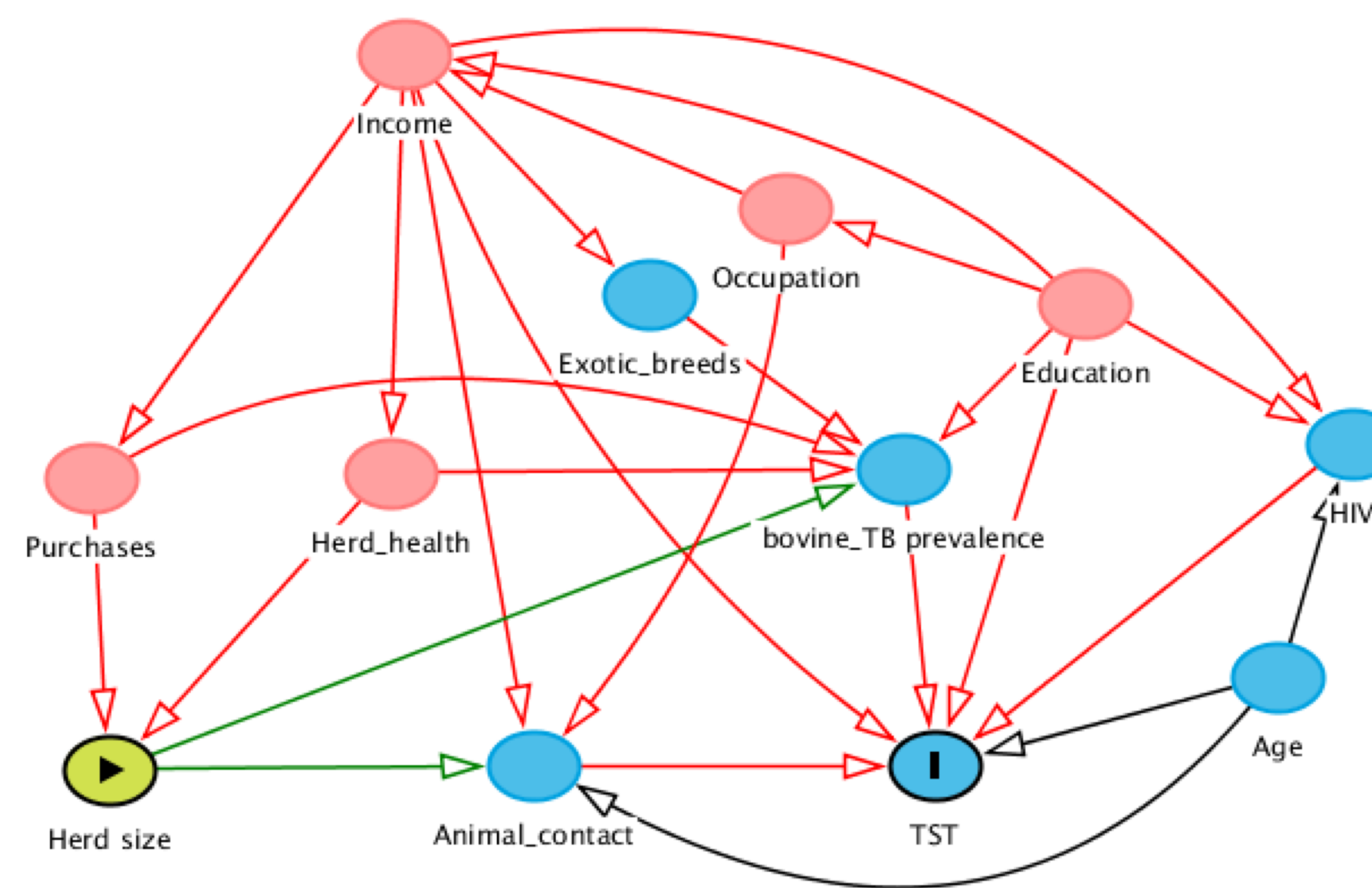


Figure 2: Directed Acyclic Graph depicting the herd size-human TST relationship. Income, occupation, education, HIV, and age are collected on each participant. Bovine TB prevalence is the proportion of the participant's herd testing positive on TST, exotic breeds is the proportion of the herd that are exotic breeds or exotic x local crossbreeds, and purchases indicates recent purchases of new stock. The minimal sufficient adjustment set is purchases and herd health.

Complete data: 548 individuals, 162 households, 50 villages.

- Estimated ICCs: 0.222 (household), 0.195 (village).
- Model results: Figure 3. Herd size is parameterized as 10 head for both models

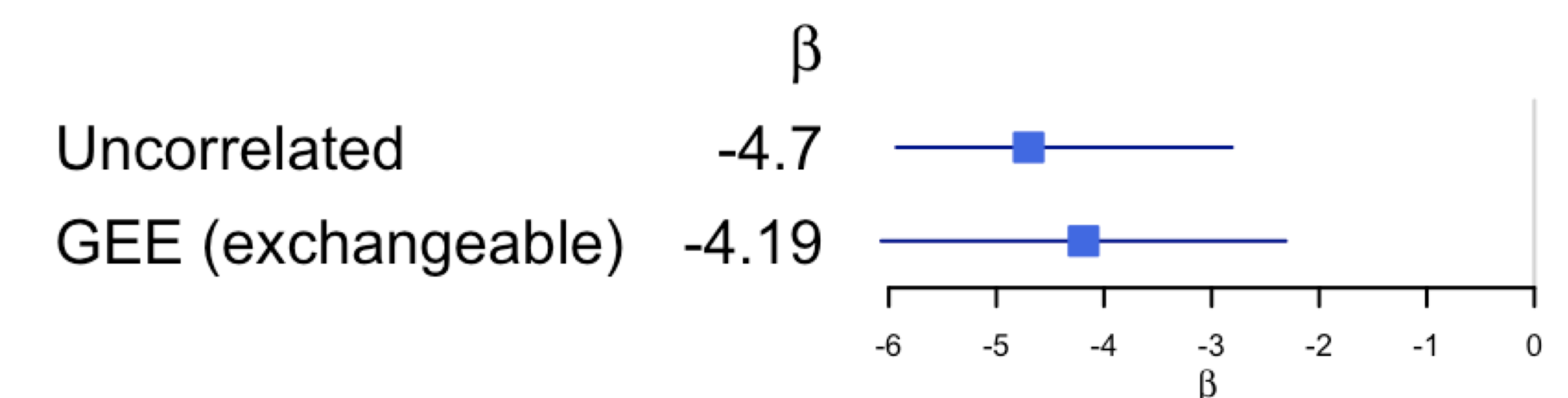


Figure 3: Forest plot of model results. Both models use robust SE.

Conclusions

- TST results cluster both within households and within villages; failure to account for this biases SE estimates.
- The herd size effect is distal to the animal contact and bovine TB prevalence effects, violating consistency.
- Threats to exchangeability likely drive the unexpected negative herd size – TST effect: herd size arises through self-selection mechanisms such as income and stock purchases, and control of such mechanisms requires adjustment for variables not commonly collected in epidemiologic studies, including a latent variable.

Statistical models should be informed by **One Health DAGs** and consideration of **clustering**. Further methods development, including measurement of **latent variables**, estimation of **distal effects**, and adequate adjustment for **self-selection**, could draw on learnings from neighborhood effects research.



Figure 4: When your measure of socioeconomic status can give you TB

