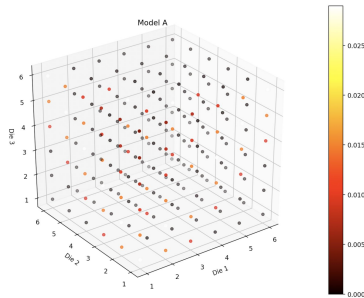


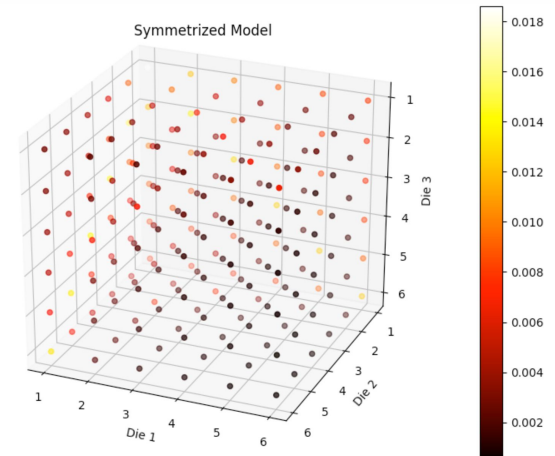
A New Approach to Epidemic Model Creation

Inspired by de Finetti's Theorem:

1. Models can be symmetrized
2. Symmetric models can be decomposed into mixtures of independent and identically distributed models



Symmetrizing operator



$$Prob_{E=sym(B)}(z, y, z) = \frac{1}{3} \left\{ \frac{0.02}{1 + |xy - z|} + \frac{0.02}{1 + |xz - y|} + \frac{0.02}{1 + |yz - x|} \right\}$$

Advantages:

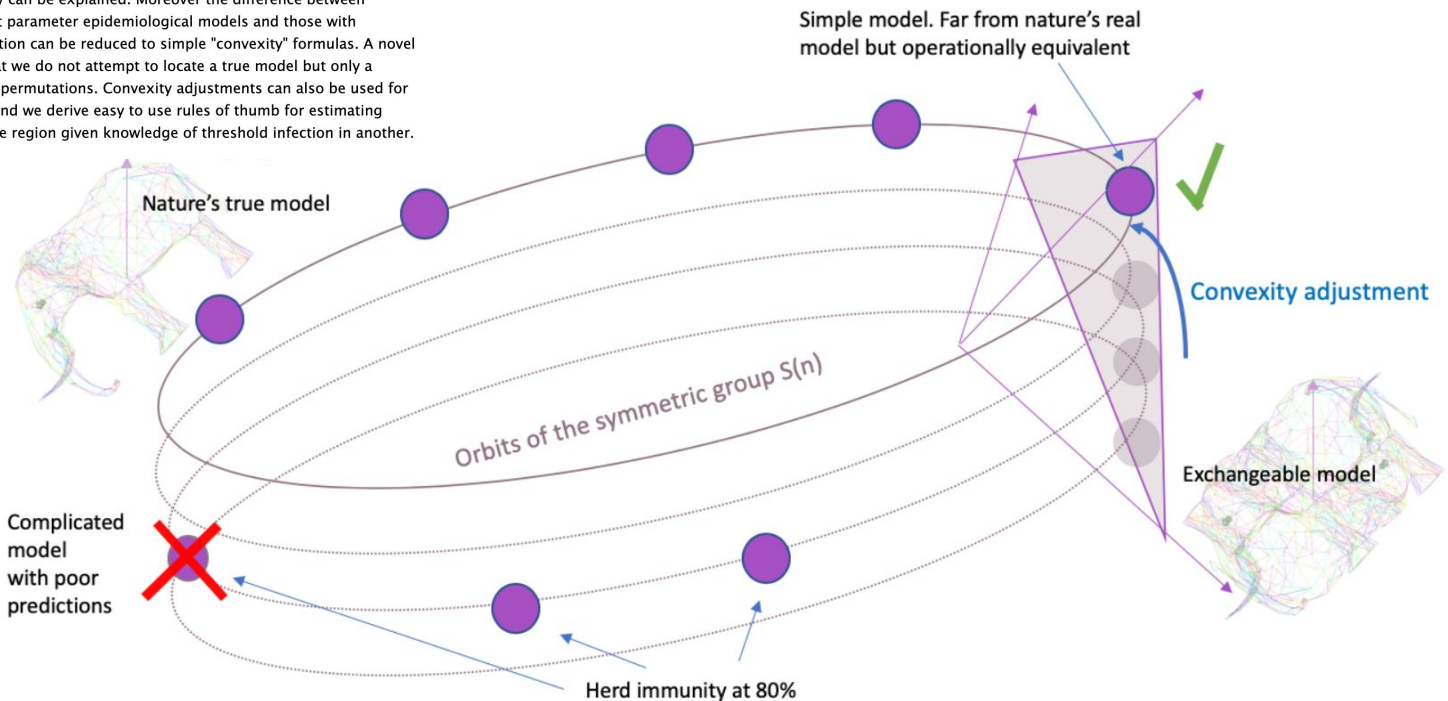
- Leaves unchanged most actionable intelligence
- Much smaller model search space: $1/n!$
- Basis of IID models
- Can use convexity adjustments to find the right one

Solves the Herd Immunity Paradox for Sweden (easily)

Addressing the Herd Immunity Paradox Using Symmetry, Convexity Adjustments and Bond Prices

Peter Cotton

In constant parameter compartmental models an early onset of herd immunity is at odds with estimates of R values from early stage growth. This paper utilizes a result from the theory of interest rate modeling, namely a bond pricing formula of Vasicek, and an approach inspired by a foundational result in statistics, de Finetti's Theorem, to show how the modeling discrepancy can be explained. Moreover the difference between predictions of classic constant parameter epidemiological models and those with variation and stochastic evolution can be reduced to simple "convexity" formulas. A novel feature of this approach is that we do not attempt to locate a true model but only a model that is equivalent after permutations. Convexity adjustments can also be used for cross sectional comparisons and we derive easy to use rules of thumb for estimating threshold infection level in one region given knowledge of threshold infection in another.



Details at www.microprediction.com/blog