Response to heterogeneity of Tests and Platforms in economic evaluations: Synthetic model adoption; derivatives of transferable practice.

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With reference to:

Economic evaluation of genomic/genetic tests: a review and future directions: Published online by Cambridge University Press: 01 August 2022; Janet Bouttell, Robert Heggie, Karin Oien, Amy Romaniuk, Harper VanSteenhouse, Stephan von Delft and Neil Hawkins

Dear Colleagues,

As noted by the authors at the time of publishing; attempts to resolve heterogeneity in economical evaluation continue to elude many parties. One proposition, drawn from carpentry, is put forth for the community for discussion.

During construction of oak-framed homes, the wood inevitably shapes and warps. To calculate the stresses and optimal positions for tenon and mortise joints, a hypothetical ‘perfect’ line is mapped across the wood (plumb line). Calculation of angles and fit occur from this and the oak is then formed accordingly. This brings together imperfect items to work in their ideal manner e.g., natural

bow would have convexity face towards the sky to bear the load when used in a truss to absorb weight bearing of the roof, whilst ignoring the evident imprecisions.

Proposition: Economic evaluation community should devise a model for optimal conditions irrespective of real-world constraints e.g., ignore local geography, legacy infrastructure etc., or select across the national picture for the most efficient components to create benchmark figures.

For pathology/sequencing laboratories that are resident/proximal to secondary care: Assume maximal efficiencies in delivery (or baseline of realism e.g., 1hr logistical transport costs, semi-busy road, median fuel costs etc.). Expanding this illustration further; assume the lab design had no impediments to delivery, storage of materials/consumables were most cost-effective, configurations of assessment pre-mapped to standardised ideal (standardised operating procedure), all platforms reverted to the lowest median cost to access/run, and all costs-per-sample are presumptively made upon 'at-scale savings' etc. This model creates the theoretical ideal (plumb line) upon which all current real-world designs are benchmarked against, thus creating a figure that can assign a quantitative efficiency. One would assume all laboratories and healthcare providers to be inefficient compared to the ideal, but the extent (difference) could allow for an adjustment in calculation i.e., introduce handicap to modelling calculations.

The benefit from this approach:

i) Provides reflective questioning for the current models existing in real-world i.e., why are they so inefficient and what unique actions/processes/circumstance afford the most efficient?

ii) Allows for any model to factor the difference from a base line calculation. Crudely put, the ideal model is the new zero and all measurements are now taken from this and not relative measurements against one another.

As such, we may find that introduction of ‘genomic solutions’ are indeed cost-effective, but not in the proposed host/current configuration. This would mitigate against the loss of those HTA inadvertently deemed ‘cost-ineffective’ or assigned ‘uncertainty’ by providing decision-makers a contextual starting point:

The proposed solution may be effective and economical if efficiencies at key components (when contrasted against the hypothetical model) are met within the newly proposed design. No inefficiencies should exceed the median of most inefficient real-world providers.