Thesis proposal: A blended distance to define "people-like-me"

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1. Introduction

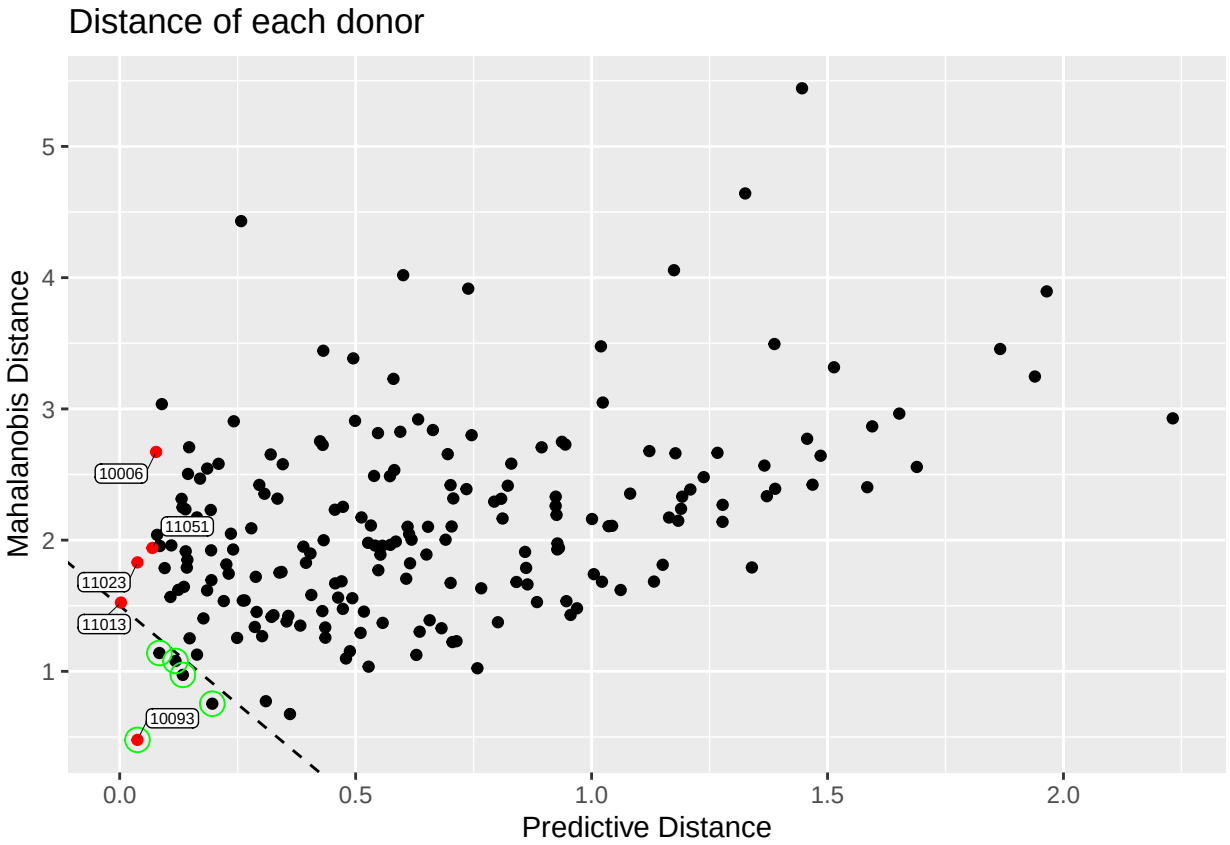
Growth curve modelling is a technique used to predict the future development of a child. It has important practical implementations and can provide answers to questions health professionals, parents, and insurance companies may have.[1] Such questions often focus on future development of a child or, in the case of inhibited growth, the child's potential development after intervention.[1] Curve matching[1] is a growth curve modelling approach that is currently used to answer these questions. Its aim is to predict the growth of a target child by using the data of a number of donors (children for which data is available) that are most similar to the target child. These donors are the so-called "people like me." In order to do this, we first need to define similarity and match the donors to the target. The key question is: How can good matches be obtained? The state-of-the-art techniques use predictive mean matching (PMM), wherein first a linear regression model is fitted on a donor database, which contains the data of all donors. Then, this model is used to predict the values for all donors and for the target at a certain point in the future, for example at 14 months. Finally, the distance between the predicted value of each of the donors and the predicted value of the target is calculated. This is the predictive distance. A number of donors with the smallest predictive distance are selected as the best matches. Their growth curves are then plotted and point estimates can be calculated by averaging the measurements.

PMM is known to be the state of the art in missing data imputation and has proven to be promising in growth curve matching as well.[1] However, there are two reasons to move beyond the predictive distance used in PMM and investigate alternative distance metrics. First, users of curve matching may find it difficult to select one particular future time point to base the matches on. Second, the predictive distance may make the matches look unconvincing. Since different profiles may lead to the same predicted value, the curves of some matches may be quite far from the curve of the target.

For these reasons, the practical use of curve matching can be improved by combining the predictive distance with alternative distance metrics that take into account historic similarity, thus creating a "blended distance" metric. It is expected that this may come at the cost of prediction accuracy, however. Therefore, the objective of this study is to investigate where to strike a balance between the predictive distance and alternative distances.

2. Strategy

A simulation study will be conducted to investigate the properties of three different blended distance measures. These blended distance measures consist of a combination of the predictive distance and the Mahalanobis distance, Fréchet distance, and Hamming distance, respectively. The first combination of the predictive distance and the Mahalanobis distance is illustrated in the figure below on 200 children from the SMOCC study.[2] The first subject is taken as the target, the 199 other subjects as the donors. In the figure, the Mahalanobis distance of each donor for the measurements during the first six months of growth is plotted against the predictive distance between each donor and the target. The five matches based on the predictive distance[3] are shown in red and labelled. Although these matches have a small predictive distance, some matches (especially subject 10006) have a large Mahalanobis distance. A blended distance would balance these two distance measures, such that the triangular donors (circled in green) are chosen.



In the simulation study, four methods will be applied to the simulated data: the predictive distance and the three blended distance measures. For these data, we will sample different simulated data sets from populations with varying variance covariance structures to be able to study the influence of data structures (e.g. high or low correlations) on the performance of the methods. Performance will be evaluated in terms of predictability (i.e. the explained variance, how well do the selected donors predict the growth of the target?) and proximity of the curves of the selected donors to that of the target.

After the simulation study, all methods will be applied to empirical data from the SMOCC study,[2] in order to evaluate performance on real data. R version 4.1.1 (2021-08-10)[4] will be used to perform the analyses. The *brokenstick*[5] package will be used for estimating the growth models, the *mice* package[6] for PMM. The preferred journal for publication is Statistics in Medicine. Approval by the FETC has been obtained.

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