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

Anaïs Fopma (6199356)

Supervisors: Prof. dr. Stef van Buuren, Dr. Gerko Vink & Mingyang Cai

Programme: Methodology and Statistics for the Behavioural, Biomedical and Social Sciences

Word count: 747

Date: 15 October 2021

1. Introduction

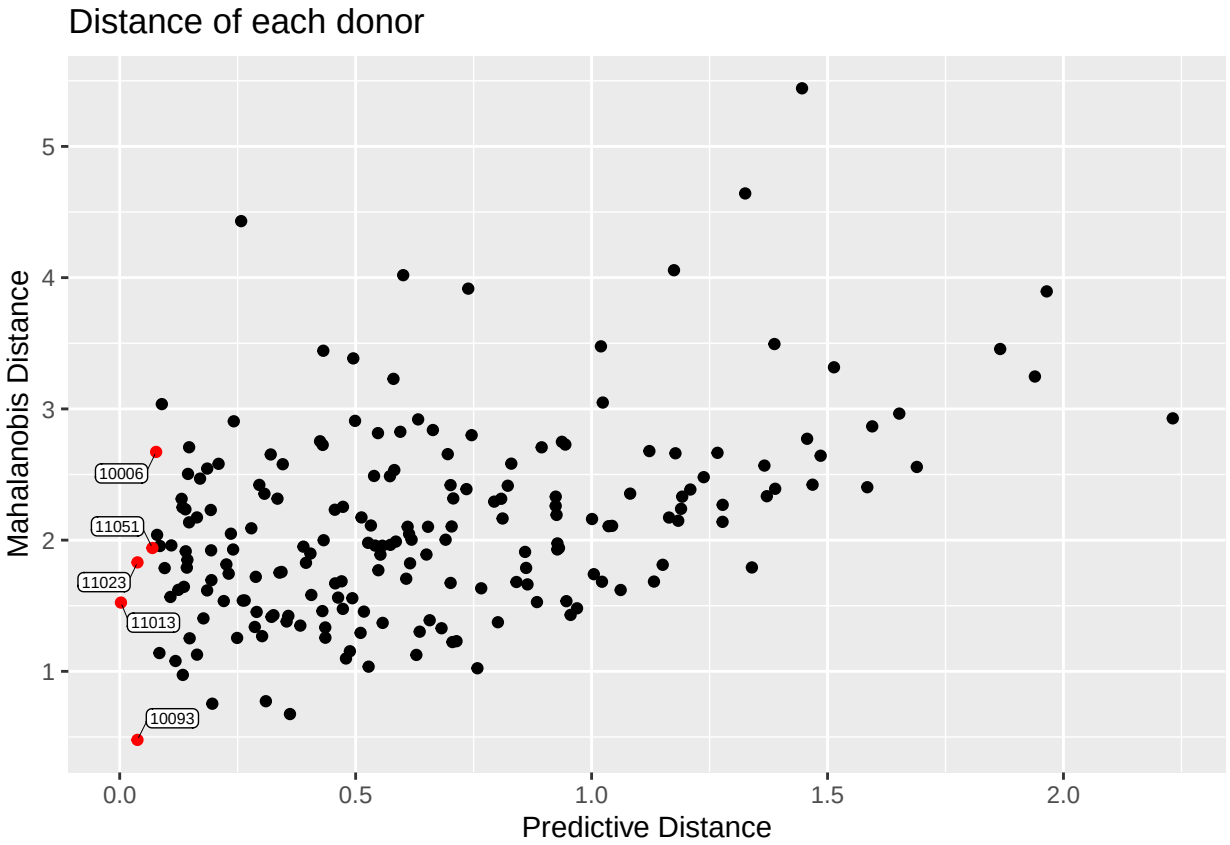
Growth curve modelling is a technique used to predict the future development of a child. It has important practical implementations, as it can provide answers to questions health professionals, parents, and insurance companies may have.[1] These are questions such as: 'Given what is known about the child, how will it develop in the future?' and 'In the case of inhibited growth, will development be normal after intervention?'[1] Curve matching[1] is a growth curve modelling approach that is currently used for this purpose. Its aim is to predict the growth of a target child by using the data of a number of donors (older children) that are most similar to the target. 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 do we obtain good matches? The current approach uses predictive mean matching (PMM). 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.[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. To illustrate this, the first combination is illustrated in the figure below. We have the growth data of 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 with the corresponding subject id's. We can see that 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.



In the simulation study, the methods to be evaluated are the three different blended distance measures. These are compared to each other and to the predictive distance. This results in a total of four methods to be applied to the simulated data. For these data, we will sample different simulated data sets from populations with varying variance covariance structures. Performance of each method 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] will be used for PMM. The preferred journal for publication is Statistics in Medicine. Approval by the FETC has been obtained.

References (including additional references)

1. Van Buuren S. Curve matching: A data-driven technique to improve individual prediction of childhood growth. *Annals of Nutrition and Metabolism*. 2014;65(2-3):227-233. doi:10.1159/000365398
2. Herngreen WP, Van Buuren S, Van Wieringen JC, Reerink JD, Verloove-Vanhorick SP, Ruys JH. Growth in length and weight from birth to 2 years of a representative sample of Netherlands children (born in 1988–89) related to socioeconomic status and other background characteristics. *Annals of human biology*. 1994;21(5):449-463. doi:10.1080/03014469400003472
3. Buuren S van. Broken stick model for irregular longitudinal data. *Journal of Statistical Software*. 2020;Submitted for publication:1-47.
4. Team RC. R: A Language and Environment for Statistical Computing. Published online 2021. https://www.R-project.org/
5. Buuren S van. Broken Stick Model for Irregular Longitudinal Data. https://github.com/growthcharts/brokenstick
6. Buuren S van, Groothuis-Oudshoorn K. Mice: Multivariate Imputation by Chained Equations in R. *Journal of Statistical Software*. 2011;45(3):1-67. https://www.jstatsoft.org/v45/i03/
7. Morris TP, White IR, Crowther MJ. Using simulation studies to evaluate statistical methods. *Statistics in Medicine*. 2019;38(11):2074-2102. doi:10.1002/sim.8086
8. Ashworth A, Shrimpton R, Jamil K. Growth monitoring and promotion: Review of evidence of impact. *Maternal & child nutrition*. 2008;4:86-117. doi:10.1111/j.1740-8709.2007.00125.x.
9. Berkey CS, Kent RL. Longitudinal principal components and non-linear regression models of early childhood growth. *Annals of human biology*. 1983;10(6):523-536. doi:10.1080/03014468300006751
10. Van Dommelen P, Van Buuren S. Methods to obtain referral criteria in growth monitoring. *Statistical methods in medical research*. 2014;23(4):369-389. doi:10.1177/0962280212473301
11. Onis M de, Onyango AW. WHO child growth standards. *The Lancet*. 2008;371(9608):204. doi:10.1016/S0140-6736(08)60131-2
12. De Onis M, Onyango A, Borghi E, Siyam A, Blössner M, Lutter C. Worldwide implementation of the WHO child growth standards. *Public health nutrition*. 2012;15(9):1603-1610. doi:10.1017/S136898001200105X
13. De Onis M, Wijnhoven TM, Onyango AW. Worldwide practices in child growth monitoring. *The Journal of pediatrics*. 2004;144(4):461-465. doi:10.1016/j.jpeds.2003.12.034
14. Wilde JA de, Dommelen P van, Buuren S van, Middelkoop BJ. Height of South Asian children in the Netherlands aged 0–20 years: Secular trends and comparisons with current Asian Indian, Dutch and WHO references. *Annals of human biology*. 2015;42(1):38-44. doi:10.3109/03014460.2014.926988
15. Hu Y, He X, Tao J, Shi N. Modeling and prediction of children's growth data via functional principal component analysis. *Science in China Series A: Mathematics*. 2009;52(6):1342-1350. doi:10.1007/s11425-009-0088-5
16. Hauspie RC, Cameron N, Molinari L. *Methods in Human Growth Research*. Vol 39. Cambridge University Press; 2004.
17. Ng K, Sun J, Hu J, Wang F. Personalized predictive modeling and risk factor identification using patient similarity. *AMIA Summits on Translational Science Proceedings*. 2015;2015:132.
18. Schönbeck Y, Van Dommelen P, HiraSing RA, Van Buuren S. Trend in height of Turkish and Moroccan children living in the Netherlands. *PLoS One*. 2015;10(5):e0124686. doi:10.1371/journal.pone.0124686
19. Straatmann VS, Pearce A, Hope S, et al. How well can poor child health and development be predicted by data collected in early childhood? *J Epidemiol Community Health*. 2018;72(12):1132-1140.
20. Zimmerman DL, Núñez-Antón V, Gregoire TG, et al. Parametric modelling of growth curve data: An overview. *Test*. 2001;10(1):1-73. doi:10.1007/BF02595823

21. Efron B, Hastie T. *Computer Age Statistical Inference*. Vol 5. Cambridge University Press; 2016.

22. Siddique J, Belin TR. Multiple imputation using an iterative hot-deck with distance-based donor selection. *Statistics in Medicine*. 2008;27(1):83-102. doi:10.1002/sim.3001