Healthy Aging Signal Research Impact Statement

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The work we have done has been very much exploratory and research oriented. It is not likely that it would be used in a way that would affect a large group of people without further improvement. However, contemplating its future use, what we have created are models that either predict chronological age from DNA methylation data, or classify individuals as "healthy" or "unhealthy" based on such data. We envision that the first type of model might be used in the future as a means to assess whether a given person's cellular aging is more or less rapid than their chronological age, and then based on this assessment, some therapeutic intervention might be recommended. If the model was off in a systematic way, say always over predicting age for a certain group of people, this could lead to recommendations for treatments that are not needed. Conversely, if the model always underpredicts age for some group, then some chances for effective treatment might be missed. Thus, it would be important that, whatever model was implemented medically, it be as accurate as possible for everyone. Similar issues apply to our healthy vs unhealthy classifier. If it were to consistently make poor classifications on some minority groups, then this too could lead to either interventions that are not needed, or a lack of interventions that are.

We might think about the possible subsets of the population that could be affected in such a way. Clearly, there are many having to do with life circumstances, however, it is most natural to first think about gender and race. In our data there was information about a person's race in only 30% of the samples. We did not think this was enough to include it as a feature in our models, so we do not know if our models are more or less accurate for one race over another. Certainly, this would need to be examined with a different and hopefully larger dataset before any model would be used medically. We did have information about sex for the samples in our data, and we have checked the effects of considering sex in our models. What we found was that adding this information had very little effect on the errors of our models when all samples were considered. However, we did find that our linear models are more accurate on females (MAE ~ 3.7 years) than on males (MAE ~4.0 years), but the difference is not systematic. That is, while the error is larger for males, there does not appear to be a bias toward over or under predicting for either group, so this may not be a problem. Still, this difference should be studied further with a larger dataset before any model is used clinically.