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No major flaws in "Identification of individuals by trait prediction using whole-genome sequencing data"

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Abstract

In a recently published PNAS article, we studied the identifiability of genomic samples using machine learning methods [Lippert et al., 2017]. In a response, Erlich [2017] argued that our work contained major flaws. The main technical critique of Erlich [2017] builds on a simulation experiment that shows that our proposed algorithm, which uses only a genomic sample for identification, performed no better than a strategy that uses demographic variables. Below, we show why this comparison is misleading and provide a detailed discussion of the key critical points in our analysis that have been brought up in Erlich [2017] and in the media. We also want to point out that it is not only faces that may be derived from DNA, but a wide range of phenotypes and demographic variables. In this light, the main contribution of Lippert et al. [2017] is an algorithm that identifies genomes of individuals by combining DNA-based predictive models for multiple traits.

A perfect oracle.

Erlich [2017] sets out to find a simple baseline for the problem of identification of genomic samples treated in Lippert et al. [2017]. His strategy was to categorize subjects into one of 6 ethnicities by 2 genders by 10 bins for age in increments of 7 years, *i.e.*, a total of 120 groups. Identity of an individual is predicted by random sampling of a single subject from the same group. Although this setting is a relevant baseline when assessing identifiability

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in a database that is associated with demographic information not protected by HIPAA, this approach assumes a-priori knowledge of age, ethnicity and gender for each subject. Thus, the setting is different from the one in Lippert et al. [2017], where the only available material and information is the genomic sample. In the latter setting, any other phenotypic and demographic variables, including the aforementioned age, ethnicity and gender, are not assumed to be present, but instead have to be predicted from the genomic sample. In the Lippert et al. [2017] setting, the Erlich [2017] result could be seen as an upper bound, that is, the result that could be achieved in an experiment where one had an oracle that allowed perfect prediction of these traits.

In reality, predictions of any phenotypes and demographic data will have limited accuracy. So the final identification results for a model using real predictions will be less accurate than for a model which assumes that all information is provided in advance, such as the Erlich [2017] model. For example, Lippert et al. [2017] report a mean absolute error for prediction of age from a genomic sample of 8.0 years. Also, a person's ethnicity is not a perfect representation of a person's genetic ancestry, especially in strongly admixed populations such as African Americans or Latinos, where differences in ancestry are continuous. Even for gender, we only achieved an accuracy of 99.6% when predicting the value from the genome, as reported in Supplemental Information (SI) Appendix of Lippert et al. [2017].

The "Full" model (see Table 2) of Lippert et al. [2017] operates under true biological variability and uncertainty. It also includes noise from environmental contributions and technical imprecision in the collection of traits. Therefore, the comparison with the numbers from the Erlich [2017] oracle in Figure 1 of Erlich [2017] is not informative.

Only gender, ethnicity and age?

A question that had been raised is if predictions are only driven by gender, ethnicity and age. Lippert et al. [2017] evaluated this in detail on demographically homogeneous populations. To do so, Lippert et al. [2017] repeated identification experiments in gender and ethnicity stratified groups for Europeans and African Americans—the two most frequent ethnicities in the cohort. The results of this analysis are shown in Table 1 and SI Appendix, Figure S31, of Lippert et al. [2017].

The only demographic variable contained in the Erlich [2017] model that is not accounted for by means of stratification is age. Within gender and ethnicity stratified pools of size 10, the "Age" model selected the correct phenotypic set out of a pool—a task we call "select" (s_{10})—with accuracies between 0.16 and 0.22. The model correctly matched pools of genomes to pools of phenotypic sets—a task we call "match" (m_{10})—with accuracies between 0.14 and 0.21. Detailed definitions of s_{10} and m_{10} are provided in Lippert et al. [2017]. These values are comparable to the "Age" model on the full cohort (see Table 2 in Lippert et al. [2017]). For the "Full" model, we have obtained s_{10} values between 0.24 and 0.31 in the stratified analyses, representing consistent gains between 6% and 13% over "Age", the third variable included in the Erlich [2017] analysis. Consequently, the models

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provide quantifiable information beyond sex, gender and age.

No face value?

Much of the public discussion concentrates on face prediction. The analysis in Lippert et al. [2017] involves a combination of many phenotypic predictors, including but not limited to models derived from facial images. From facial images we derived skin color, eye color, 3D structural landmark distances, as well as 3D shape and 3D color. As images provide rich phenotypes, it is not surprising that the "3D Face" model, which consists of the shape and color components used to render faces, achieves relatively high s_{10} of 58% and m_{10} of 64% (see Table 2 in Lippert et al. [2017]). Yet, the paper does not claim that it is rendering a face from the genome that allows identification of a genomic sample, but rather a combination of many phenotypic predictors, one of which is face prediction. Indeed, when adding additional traits on top of "3D Face", accuracy gradually increases: The "All Face" model, consisting of a combination of all traits derived from the face, increases s_{10} by 4% and m_{10} by 7%. Adding the demographic variables age, ethnicity and gender ("All Face + Demogr.") yields additional performance increases of over 10%. This is close to the "Full" model, which also includes the remaining phenotypes not derived from facial images and has s_{10} of 0.74 and m_{10} of 0.83.

Figure S11 in the SI Appendix of Lippert et al. [2017] shows a visualization of the predicted faces for all individuals in the cohort who consented to have their images shown. For Europeans, which were genetically less heterogeneous than other ethnicities, these predicted faces are generally very similar to each other. The effect is most prominent for European males, where renderings of predicted faces look almost identical. Correspondingly, re-identification accuracies using the visualized "3D Face" variables, are consistently lower on the gender-stratified European cohorts than on the gender-stratified African American cohorts, and lowest on European males, where we obtained $s_{10} = 0.13$ and $m_{10} = 0.14$ (see Table 1B). These values are better than random, which implies that even visually similar predictions carry quantifiable information. As clearly stated in the abstract of our original work, the main contribution of Lippert et al. [2017] is not identification by face prediction, but rather an "algorithm that integrates *multiple* predictions to determine which genomic samples and phenotype measurements originate from the same person."

Age can be predicted at minimal cost.

Erlich [2017] inaccurately points out that the approach for age prediction in Lippert et al. [2017] is expensive. His reasoning is that our approach for telomere length estimation, one component of age prediction, made use of 512 repeatedly sequenced NA12878 DNA reference samples[1] to determine an optimal threshold to classify sequencing reads as telomeric.

[1] `http://jimb.stanford.edu/giab/`

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NA12878 sequences are a regular byproduct of any large genomics facility, as NA12878 reference DNA is routinely used as quality controls in sequencing [Zook et al., 2016]. Therefore, the resources used to determine this parameter, which only has to be determined a single time, are readily available. The fact that sequencing costs are going down rapidly, renders it unlikely that cost will remain a barrier, even for smaller sequencing facilities. The full result of our analysis is included in the SI Appendix, Figure S1A of Lippert et al. [2017] and may be applied and re-used in other studies. Otherwise, every sample in our study has been sequenced only once at a depth of 30X, and Ding et al. [2014] as well as SI Appendix, Figure S2 of Lippert et al. [2017] show that a minimum depth of as low as 2.5X is sufficient to determine telomere length. To conclude, telomere length prediction adds insignificant overhead to a routine whole genome sequence.

Let's face it!

Our work is a proof of concept done with a small set of individuals that presents a strategy for identification of genomic data using predictive modeling. While facial images provide rich data from which to build phenotypic models, it is important to notice that it is not only faces that may be derived from the genome. The genome codes for a vast number of heritable phenotypes. For many of these, larger data sets of genomic and phenotypic data will improve prediction accuracy. The genome also provides information about demographic variables, such as gender, ethnicity, and age, plus others not treated in this study, such as surnames [Gymrek et al., 2013]. Lippert et al. [2017] presents an algorithm that enables optimal combination of any number of such phenotypic and demographic prediction models. Each of these models contributes additional identifying information. Gradual improvements derived from larger data sets and better models are central to the success of machine learning applications.

In the current public debate of our work, it is useful to separate the scientific results and the importance/implications of these results. For the former, the question is whether we did correctly what we set out to do. Hopefully we did. For the latter, the question is whether the ideas, methods or results turn out to be important. This discussion showed that it is a sensitive topic triggering a sometimes emotional debate. We definitely welcome a constructive debate on the topic of genomic privacy, a topic that is of relevance for policy and for genomic sciences: "Although sharing of genomic data is invaluable for research, our results suggest that genomes cannot be considered fully deidentifiable and should be shared by using appropriate levels of security and due diligence." [Lippert et al., 2017] As the community relies on the availability of genomic data to decode the genetic causes of disease, we should openly face this challenge and discuss potential implications for personal privacy. We also would like to emphasize the importance of advanced genome privacy protection strategies[2] for enhancing data exchange.

[2] `https://genomeprivacy.org`

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African

		2	5	10	20	50
Male						
Full	Match	0.82	0.48	0.29	0.18	nan
	Select	0.74	0.47	0.28	0.16	nan
All Face + Demogr.	Match	0.8	0.47	0.29	0.15	nan
	Select	0.75	0.42	0.27	0.17	nan
All Face + Add'l	Match	0.74	0.47	0.28	0.17	nan
	Select	0.7	0.44	0.27	0.15	nan
All Face	Match	0.77	0.47	0.28	0.16	nan
	Select	0.71	0.42	0.28	0.15	nan
3D Face	Match	0.76	0.39	0.22	0.15	nan
	Select	0.67	0.37	0.23	0.14	nan
Landmarks	Match	0.69	0.33	0.17	0.093	nan
	Select	0.64	0.34	0.18	0.086	nan
Eyecolor	Match	0.68	0.34	0.16	0.09	nan
	Select	0.63	0.34	0.17	0.082	nan
Skincolor	Match	0.62	0.32	0.17	0.098	nan
	Select	0.6	0.3	0.18	0.096	nan
Ethnicity	Match	0.5	0.21	0.12	0.054	nan
	Select	0.5	0.2	0.1	0.052	nan
Age	Match	0.71	0.37	0.21	0.095	nan
	Select	0.67	0.37	0.22	0.098	nan
Gender	Match	0.4	0.28	0.12	0.17	nan
	Select	0.38	0.28	0.17	0.1	nan
Voice	Match	0.67	0.34	0.17	0.072	nan
	Select	0.61	0.32	0.16	0.082	nan
Height/Weight/BMI	Match	0.59	0.28	0.17	0.089	nan
	Select	0.57	0.28	0.17	0.099	nan
Random	Match	0.5	0.2	0.1	0.05	0.02
	Select	0.5	0.2	0.1	0.05	0.02

A

European

		2	5	10	20	50
Male						
Full	Match	0.72	0.4	0.23	0.11	nan
	Select	0.67	0.37	0.24	0.13	nan
All Face + Demogr.	Match	0.74	0.41	0.2	0.12	nan
	Select	0.7	0.38	0.24	0.13	nan
All Face + Add'l	Match	0.69	0.35	0.2	0.088	nan
	Select	0.68	0.36	0.2	0.13	nan
All Face	Match	0.7	0.38	0.19	0.1	nan
	Select	0.68	0.36	0.2	0.11	nan
3D Face	Match	0.58	0.26	0.14	0.082	nan
	Select	0.56	0.25	0.13	0.073	nan
Landmarks	Match	0.61	0.24	0.13	0.053	nan
	Select	0.57	0.25	0.12	0.07	nan
Eyecolor	Match	0.73	0.32	0.16	0.085	nan
	Select	0.7	0.34	0.19	0.11	nan
Skincolor	Match	0.54	0.22	0.1	0.053	nan
	Select	0.51	0.19	0.087	0.032	nan
Ethnicity	Match	0.55	0.2	0.086	0.05	nan
	Select	0.5	0.2	0.1	0.05	nan
Age	Match	0.61	0.29	0.14	0.085	nan
	Select	0.6	0.28	0.16	0.085	nan
Gender	Match	0.42	0.26	0.17	0	nan
	Select	0.36	0.29	0.2	0	nan
Voice	Match	0.56	0.23	0.11	0.047	nan
	Select	0.53	0.22	0.12	0.065	nan
Height/Weight/BMI	Match	0.56	0.21	0.098	0.052	nan
	Select	0.52	0.19	0.092	0.05	nan
Random	Match	0.5	0.2	0.1	0.05	0.02
	Select	0.5	0.2	0.1	0.05	0.02

B

		2	5	10	20	50
Female						
Full	Match	0.8	0.5	0.32	0.21	0.11
	Select	0.72	0.46	0.31	0.2	0.099
All Face + Demogr.	Match	0.79	0.51	0.3	0.19	0.11
	Select	0.73	0.46	0.29	0.18	0.097
All Face + Add'l	Match	0.77	0.46	0.29	0.18	0.085
	Select	0.71	0.43	0.27	0.18	0.087
All Face	Match	0.74	0.4	0.25	0.15	0.069
	Select	0.69	0.39	0.24	0.14	0.077
3D Face	Match	0.71	0.36	0.21	0.11	0.054
	Select	0.65	0.34	0.21	0.11	0.045
Landmarks	Match	0.64	0.32	0.15	0.075	0.029
	Select	0.6	0.29	0.16	0.077	0.027
Eyecolor	Match	0.68	0.32	0.18	0.11	0.054
	Select	0.63	0.32	0.18	0.1	0.052
Skincolor	Match	0.56	0.24	0.14	0.064	0.027
	Select	0.55	0.23	0.12	0.044	0.019
Ethnicity	Match	0.47	0.2	0.11	0.053	0.023
	Select	0.5	0.2	0.099	0.048	0.021
Age	Match	0.69	0.36	0.2	0.11	0.058
	Select	0.67	0.37	0.21	0.12	0.048
Gender	Match	0.5	0.25	0.14	0.11	0.02
	Select	0.52	0.23	0.14	0.075	0
Voice	Match	0.68	0.35	0.21	0.11	0.057
	Select	0.64	0.34	0.19	0.11	0.047
Height/Weight/BMI	Match	0.57	0.26	0.12	0.064	0.031
	Select	0.54	0.24	0.12	0.05	0.022
Random	Match	0.5	0.2	0.1	0.05	0.02
	Select	0.5	0.2	0.1	0.05	0.02

C

		2	5	10	20	50
Female						
Full	Match	0.8	0.52	0.31	0.17	nan
	Select	0.78	0.49	0.3	0.19	nan
All Face + Demogr.	Match	0.82	0.51	0.32	0.17	nan
	Select	0.79	0.49	0.32	0.2	nan
All Face + Add'l	Match	0.84	0.52	0.29	0.17	nan
	Select	0.79	0.5	0.3	0.16	nan
All Face	Match	0.85	0.51	0.29	0.12	nan
	Select	0.79	0.48	0.29	0.15	nan
3D Face	Match	0.71	0.34	0.19	0.097	nan
	Select	0.66	0.34	0.19	0.11	nan
Landmarks	Match	0.6	0.31	0.15	0.09	nan
	Select	0.61	0.28	0.17	0.077	nan
Eyecolor	Match	0.77	0.39	0.21	0.097	nan
	Select	0.77	0.39	0.24	0.13	nan
Skincolor	Match	0.52	0.29	0.14	0.092	nan
	Select	0.53	0.27	0.18	0.09	nan
Ethnicity	Match	0.54	0.2	0.1	0.065	nan
	Select	0.5	0.2	0.1	0.05	nan
Age	Match	0.69	0.33	0.16	0.075	nan
	Select	0.66	0.33	0.18	0.075	nan
Gender	Match	0.36	0.32	0.1	0	nan
	Select	0.32	0.32	0.2	0	nan
Voice	Match	0.67	0.34	0.19	0.12	nan
	Select	0.65	0.31	0.15	0.078	nan
Height/Weight/BMI	Match	0.61	0.25	0.15	0.087	nan
	Select	0.58	0.24	0.13	0.078	nan
Random	Match	0.5	0.2	0.1	0.05	0.02
	Select	0.5	0.2	0.1	0.05	0.02

D

Table 1: Select and match results stratified by sex and ethnicity. Shown are different numbers of pool sizes from two to 50 within (A) African American males, (B) European males (C) African American females, (D) European females. "nan" values indicate that the size of the test sample sets were too small due to stratification. For a detailed list of models and data involved in any experiment, see Table 2.

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	Label	Target	Phenotype Source	Genome Source
Demogr.	Gender	Gender	= self-reported Gender	= Sex (∼ XY)
	Age	Age	= self-reported Age	∼ Telomeres + XY
	Ethnicity	Ethnicity	= self-reported Ethnicity	∼ Genome PCs
Add'l	Height/Weight/BMI	Height	= measured Height	∼ SNPs + Genome PCs + Sex (∼ XY) + Age (∼ Telomeres, XY)
		Weight	= measured Weight	∼ SNPs + Genome PCs + Sex (∼ XY CCN) + Age (∼ Telomeres, XY)
		BMI	= Weight/Height^2	∼ SNPs + Genome PCs + Sex (∼ XY) + Age (∼ Telomeres + XY)
	Voice	Voice i-vectors	= Voice i-vectors	∼ SNPs + Genome PCs + Sex (∼ XY) + Age (∼ Telomeres + XY)
		Gender	∼ Voice i-vectors	= Sex (∼ XY)
		Age	∼ Voice i-vectors	∼ Telomeres + XY
		Ancestry	∼ Voice i-vectors	= Ancestry
All Face	Eyecolor	Eyecolor	= measured Eyecolor	∼ SNPs + Genome PCs
	Skincolor	Skincolor	= measured Skincolor	∼ SNPs + Genome PCs
	Landmarks	Landmarks	= manual annotation	∼ SNPs + Genome PCs + Sex (∼ XY) + Age (∼ Telomeres + XY)
		Gender	∼ Landmarks	= Sex (∼ XY)
		Age	∼ Landmarks	∼ Telomeres + XY
		Ancestry	∼ Landmarks	= Ancestry
	3D Face	Shape PCs	= Shape PCs	∼ Genome PCs + Sex (∼ XY CCN) + Age (∼ Telomeres + XY)
		Color PCs	= Color PCs	∼ Genome PCs + Sex (∼ XY) + Age (∼ Telomeres + XY)
		Gender	∼ Shape PCs + Color PCs	= Sex (∼ XY)
		Age	∼ Shape PCs + Color PCs	∼ Telomeres + XY
		Ancestry	∼ Shape PCs + Color PCs	= Ancestry
Together	All Face	3D Face ∪ Landmarks ∪ Eyecolor ∪ Skincolor		
	All Face + Add'l	3D Face ∪ Landmarks ∪ Eyecolor ∪ Skincolor ∪ Voice ∪ Height/Weight/BMI		
	All Face + Demogr.	3D Face ∪ Landmarks ∪ Eyecolor ∪ Skincolor ∪ Ethnicity ∪ Age ∪ Gender		
	Full	3D Face ∪ Landmarks ∪ Eyecolor ∪ Skincolor ∪ Voice ∪ Height/Weight/BMI ∪ Ethnicity ∪ Age ∪ Gender		

For each embedding, "Label", all "Target" variables that are compared are listed. Each "Target" variable is predicted from a "Phenotype Source" and a "Genome Source". "=" refers to use of observed values and "∼" refers to predictive models learned from data. For model covariates that are inferred from a model involving other variables, we show the model in parentheses. The embeddings under "Together" are unions of other embeddings. "Gender" is self reported gender. "Sex" is the genetic sex. "Ethnicity" is self-reported ethnicity. "Genome PCs" refers to 1,000 PCs inferred from common variation. "Ancestry" refers to five-region genomic ancestry proportions (AFR, EUR, EAS, AMR, CSA). "Telomeres" refers to estimated telomere length. "XY" refers to estimated CCNs for the sex chromosomes. "Voice i-vectors" refer to the voice i-vector embedding of voice samples. "Landmarks" refers to the XYZ values of 36 landmark locations (see SI Appendix, Table S1 in Lippert et al. [2017]). "Eyecolor" refers to RGB values of eyecolor estimated from the images. "Skincolor" refers to RGB values of facecolor estimated from the images. "Shape PCs" refers to the 3D image embedding of face shape. "Color PCs" refers to the 3D image embedding of face texture.

Table 2: List of models used for Identification.