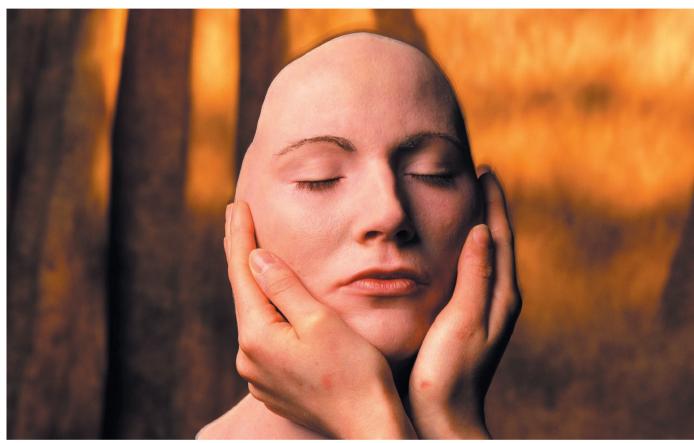
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A study claiming to be able to predict a person's face from their genome has drawn fire from experts.

GENOMICS

Experts pan study claiming DNA can predict facial traits

Risks of public access to genome data are misrepresented, say critics of Craig Venter paper.

BY SARA REARDON

A storm of criticism has rained down on a paper by genome-sequencing pioneer Craig Venter that claims to predict people's physical traits from their DNA. Reviewers and even a study co-author say that it overstates the ability to use a person's genes to identify the individual, which could raise

unnecessary fears about genetic privacy.

In the paper, published on 5 September in the *Proceedings of the National Academy of Sciences USA (PNAS)*, Venter and colleagues at his company Human Longevity, Inc. (HLI), based in San Diego, California, sequenced the whole genomes of 1,061 people of varying ages and ethnic backgrounds (C. Lippert *et al. Proc. Natl Acad. Sci. USA* http://doi.org/

ccxn; 2017). Using the genetic data, along with high-quality 3D photographs of the participants' faces, the researchers used an artificial-intelligence approach to find small differences in DNA sequences, called SNPs, associated with facial features such as cheekbone height. The team also searched for SNPs that correlated with factors including a person's height, weight, age and skin colour.

From a group of ten people randomly selected from HLI's database, the approach correctly identified an individual 74% of the time. The findings, according to the paper, suggest that law-enforcement agencies, scientists and others who handle human genomes should protect the data carefully to prevent people from being identified by their DNA alone. "A core belief from the HLI researchers is that there is now no such thing as true deidentification and full privacy in publicly accessible databases," HLI said in a statement.

But other geneticists, having studied the paper, say that in their opinion, the claim is vastly overblown. "I don't think this paper raises those risks, because they haven't demonstrated any ability to individuate this person from DNA," says Mark Shriver, an anthropologist at Pennsylvania State University in University Park. In a randomly selected group of ten people — especially one chosen from a data set as small and diverse as HLI's — knowing age, sex and race alone rules out most of the individuals, he says.

To demonstrate this, computational biologist Yaniv Erlich at Columbia University in New York City looked at the age, sex and ethnicity data from HLI's paper. In a study published on 7 September on the preprint server bioRxiv, he calculated that knowing only those three traits was sufficient to identify an individual out of a group of ten people in the HLI data set 75% of the time (Y. Erlich Preprint at bioRxiv http://doi.org/ccxp; 2017). Erlich contends that there was no need to know anything about the people's genomes. Furthermore, he says, HLI's reconstructions of facial structure from SNPs are not highly specific — they tend to look as much like an individual as

anyone of that person's sex and race.

Before it was published in *PNAS*, the paper had been submitted to *Science*, says Shriver, who reviewed the paper for that journal. He says that HLI's actual data are sound, and he is impressed with the group's novel method of determining age by sequencing the ends of chromosomes, which shorten over time. But he says that the study doesn't demonstrate

"It's important when we deal with privacy risks to get the facts right." that individuals can be identified by their DNA, as it claims to. "I think it totally misrepresents what they did and what they found," he says.

HLI said that its paper states that using multiple parameters, of which a person's face is only one, to identify someone is possible based on work with more than 1,000 genomes. "It heralds that prediction will become increasingly precise," says Heather Kowalski, an HLI spokesperson. HLI stated that it stands by its methodology and acknowledged that the sample set was small. It added that "the HLI team is working on rebuttal to criticisms by Yaniv in BioRxiv [sic]".

Shriver says that he and Erlich pointed out their concerns to the study authors in their reviews of the paper for *Science*. Both Shriver and Erlich say that the journal ultimately rejected the paper. (*Science* does not comment on unpublished studies.) The study was then submitted to *PNAS* under an option that allows a member of the US National Academies of Science, Engineering, and Medicine, such as Venter, to choose the reviewers. Two of them are information-privacy experts and

the remaining reviewer is a bioethicist. *PNAS* confirmed that Venter chose all three reviewers for the study. HLI declined to comment on the *PNAS* review process for the paper.

Jason Piper, a computational biologist and a paper co-author who now works at Apple in Singapore, agrees that the study misrepresents the findings. Piper adds that his contract with HLI waived his right to approve the manuscript before it was submitted, allowing the company to present his data as it saw fit. HLI responded by saying that "authors were given an opportunity to review and comment on the paper".

Piper has since criticized the study heavily on Twitter and says that, in his opinion, HLI has a potential conflict of interest in encouraging restricted access to DNA databases. HLI, a for-profit company, hopes to build the world's largest database of human genetic information.

"I think genetic privacy is very important, but the approach being taken is the wrong one," Piper says. It would be more useful to find a way to make genomic data public without allowing individuals to be identified, he says.

The company responded to criticisms of the paper by saying that "HLI stands by the protection of genome data and the promotion of modern solutions for data exchange". It added that the study was intended to spur discussion about how to share genetic information while protecting a person's privacy.

Still, Erlich is concerned that Venter's stature gives the paper extra weight in the eyes of policymakers, who may become overly concerned about DNA privacy. "New rules and regulations are based on papers like that," he says. "It's important when we deal with privacy risks to get the facts right."

POLICY

Researchers riled by lack of detail in Brexit science plans

UK government document fails to extinguish concerns over funding and migration.

BY DANIEL CRESSEY

ore than one year after UK citizens voted to leave the European Union, and close to three months into 'Brexit' negotiations, the British government has finally laid out how it would like to handle scientific relationships with the EU after it leaves the bloc next year. Many scientists are less than impressed.

In a document released on 6 September, the UK government pledges to "seek an ambitious

science and innovation agreement" in Brexit negotiations with the EU. But it simply sets out areas in which agreement will be sought, rather than making any specific proposals.

John Womersley, director-general of the European Spallation Source, a research facility in Lund, Sweden, says that although the aspirations in the document are welcome, the lack of detail means it will probably disappoint the scientific community more than reassure it. "I downloaded the document and I thought, hoped, expected, it would be too big for me to

digest in ten minutes. It was trivially easy to digest in ten minutes," he says.

Mike Galsworthy, of the Scientists for EU pressure group, says that the document makes "generally warm and happy noises" but contains nothing really new. "My anxiety is, specifically, we could have told you all of this two years ago," he says of its contents. "We have now wasted a quarter of the negotiation time and the government hasn't really put forward anything that really addresses the hard challenges."