Probably Chelsea
By Heather Dewey-Hagborg

Probably Chelsea consists of thirty different possible portraits of Chelsea Manning algorithmically-generated by an analysis of her DNA. Genomic data can tell a multitude of different stories about who and what you are. *Probably Chelsea* shows just how many ways your DNA can be interpreted as data, and how subjective the act of reading DNA really is.

I first got to know Chelsea Manning by reading her DNA. Before we ever exchanged a letter or text message she mailed me her cheek swabs and hair clippings, and I extracted her DNA, sequenced pieces of it and analyzed them to create her portrait.

Three years earlier I had created a system for algorithmically-generating 3d faces based on DNA data. In my artwork *Stranger Visions* I profiled DNA from forensic artifacts I found in public, like cigarette butts and chewed up gum, and then computationally generated 3d models representing what these strangers might look like based on genomic research. I 3d printed the models at life size in full color.

For the first portrait I made of Chelsea in 2015 I used the same system, input her genomic data, and generated two versions of her face: one androgynous and one "female." Placing these two portraits side by side I made apparent the reductionism of pinning someone's gender to simplistic readings of genetic sex—a routine practice in DNA forensics.

Probably Chelsea pushes this even further by presenting thirty different variations on Chelsea's portrait, suspended as a crowd at an assortment of human heights in the center of the gallery. The form of the installation was inspired by conversations Chelsea and I had about the limits of DNA profiling, along with the incredible mass movement that advocated for her release from prison. We have so much more in common genetically than difference. *Probably Chelsea* evokes a kind of DNA solidarity; on a molecular level we are all Chelsea Manning.

Unfortunately, genomic reductionism has become increasingly common. Police departments can now purchase "DNA mugshots" based on little more than a few microliters of DNA.[1] These pictures, presented as objective, neutral, and certain, rely heavily on reductionist concepts of genetic sex and ancestry, and subjective renderings of how these appear. The scientific reality, however, is complex, multiple, contingent, and probabilistic. There is no certainty in reading sex and ancestry from DNA, and often the guesses that are made are little better than a coin flip.

There are 6 billion base pairs in the human genome, most of which are shared among all of us. Most variations between people are in non-coding regions, i.e. the spaces in between our genes that have no known function. Meanwhile, it is becoming increasingly clear that the influence of the environment alters gene expression, turning genes on and off in various levels and combinations. So what can a genome tell us?

It can give us clues, or probabilities of phenotypes. It can relate people to their families and recent ancestors. And it can connect to an archaeology of deep human and evolutionary history. But not with certainty; always only as probabilities. DNA can tell many stories, and as with all data, it lends itself to multiple interpretations.

One of the first things I analyzed in Chelsea's genome was her mitochondrial DNA (mtDNA). MtDNA is inherited more or less unchanged from mother to child. Small mutations which occur in hyper variable regions of the DNA are passed down across generations and have been used to trace ancestry as a form of genetic archaeology.[2]

Groups that share the same mutations are called haplogroups and they are classified with letters and numbers. Chelsea's Haplogroup is J. The specific mutations in her DNA sub-sequence have been found in the Middle East, Europe, the Caucasus, North East Africa, Central Asia, and even in ancient Egyptian mummies.[3] Based on this fragment of DNA alone it is easy to imagine all kinds of possible stories for Chelsea.

Her mitochondrial DNA has special significance as it represents both a female lineage, perhaps an unlearning of patriarchy buried in our cells, as well as an intimate connection to so many global populations. It points to a deep history, but also the limits of our knowledge and the limits of our data; the limits of viewing DNA as "code" or some ultimate truth of identity. This complexity is true for nearly every phenotype. Most genetic variations only predict the likelihood of phenotypic traits, but they determine nothing.

Chelsea's mitochondrial DNA is special and at the same time it is totally ordinary. Other DNA variations tell similarly complex stories. For example, the GG variant of her rs12913832 polymorphism, which is often considered synonymous with blue eyes in Northern Europeans, is also found in Hispanic, African American, and South Asian populations, with varying phenotypes. So the same exact data can be read in different ways. This variant might predict she is *most likely* to have blue eyes and be of European ancestry, but there is still a good chance she could have brown eyes and she might not have much or any European ancestry at all.[4]

Even biological or genetic sex, commonly considered to be simple and straight forward turns out to be amazingly complex. Genetic pathways related to secondary sexual characteristics and hormone production are scattered around the genome on various chromosomes and many remain unknown. These phenotypes vary on a spectrum, are mutable and show the limits of efforts to use DNA to predict gender.[5]

Each genomic variation is a piece of data, a new clue and another possible story. As more data is put together some things become more probable, and some less, but there is never certainty and there are always alternate possible narratives. *Probably Chelsea* portrays these alternate narratives and represents a sampling of the many stories Chelsea's DNA can tell.

[1] Parabon Nanolabs. "Parabon Snapshot DNA Phenotyping." http://snapshot.parabon-nanolabs.com/.

[2] Wesley M. Brown, "Polymorphism in Mitochondrial DNA of Humans as Revealed by Restriction Endonuclease Analysis." *Proceedings of the National Academy of Sciences of the United States of America* 77, no. 6 (June 1980): 3605–9.

[3] Verónica Fernandes, Petr Triska, Joana B. Pereira, Farida Alshamali, Teresa Rito, Alison Machado, Zuzana Fajkošová, et al. "Genetic Stratigraphy of Key Demographic Events in Arabia." PLOS ONE 10, no. 3 (March 4, 2015): e0118625. doi:10.1371/journal.pone.0118625.
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[4] Marcus and Novembre, Visualizing the Geography of Genetic Variants. 2016. http://popgen.uchicago.edu/ggv/?data=%221000genomes%22&chr=15&pos=28365618

[5] Sarah S. Richardson, Sex Itself: The Search for Male and Female in the Human Genome. Chicago; London: University of Chicago Press, 2013.