Ethnicity Estimate 2019 White Paper

Catherine A. Ball, Jake K. Byrnes, Daniel Garrigan, Eurie Hong, Keith Noto, Josh Schraiber, Alisa Sedghifar, Shiya Song, Barry Starr, David Turissini, Yong Wang (in alphabetical order)

Summary:

The AncestryDNA science team has developed a fast, sophisticated, and accurate method for estimating the historical origins of customers' DNA going back several hundred to over 1,000 years. Our newest approach improves upon our previous version in the number of possible regions that a customer might be assigned (from 43 to 60) as well as an increase in accuracy to both regions assigned and the percentage assigned to each region. We have added many new regions as well as made improvements to the composition of our reference panel, resulting in more accurate estimates overall. Given the cutting-edge nature of this type of science, we will continue to refine our approach and improve estimates.

The basic idea behind ethnicity estimation involves comparing a customer's DNA to the DNA of people with long family histories in a particular region or group, what we call the reference panel, and looking for segments of DNA that are most similar. If, for example, a section of a customer's DNA looks most similar to DNA in the reference panel from people from Sweden, that section of the customer's DNA is said to be from Sweden, and so on. The end result is a portrait of a customer's DNA made up of percentages of the 60 ethnicities contained in the reference panel.

That is a short version of how AncestryDNA determines a customer's ethnicity estimate. The rest of the white paper will delve more deeply into

1. How the reference panel samples are chosen, their makeup, and how the panel is validated
2. How the algorithm that determines a customer's genetic ethnicity works and how it is validated

1. Introduction

Genetic ethnicity estimates that determine which populations in a reference panel are most similar to someone's DNA are a major component of the DNA Story provided by AncestryDNA. As its name suggests, DNA Story provides customers with insights into their past by analyzing their DNA.

AncestryDNA has employed a team of highly trained scientists with backgrounds in population genetics, statistics, machine learning, and computational biology to develop a fast, sophisticated, and accurate method for estimating genetic ethnicity for our customers. In this document, we describe the approach we use to estimate customers' genetic ethnicity. We will discuss the development of the reference panel we compare each customer sample against, the inference method we apply to estimate genetic ethnicity, and finally the extensive testing regimen we employ to assess the quality of our estimates.

Glossary

Admixed — Having ancestry from multiple populations.
Allele — A variant in the DNA sequence. For example, a SNP (defined below) could have two alleles: A or C.
Centimorgan (cM) — A unit of genetic length in the genome. Two genomic positions that are a centimorgan apart have a 1% chance during each meiosis (the cell division that creates egg cells or sperm) of experiencing a recombination event between them.
Chromosome — A large, inherited piece of DNA. Humans typically have 23 pairs of chromosomes with one copy of each pair inherited from each parent.
Genome — All of someone's genetic information; the DNA on all chromosomes
Genotype — A general term for observed genetic variation either for a single site or the whole genome.
Haplotype — A stretch of DNA along a chromosome
Hidden Markov model (HMM) — A statistical model for determining a series of hidden states based on a set of observations
Locus — A location in the genome. It could be a single site or a larger stretch of DNA.
Microarray — a DNA microarray is a way to analyze hundreds of thousands of DNA markers all at once.
Nucleotide — DNA is composed of strings of molecules called nucleotides (also called bases). There are four different types and they are usually represented by their initials: A, C, G, T.
Population — A group of people

Recombination — Before chromosomes are passed down from parent to child, each pair of chromosomes usually exchange long segments between one another and then are reattached in a process called recombination.
Single nucleotide polymorphism (SNP) — A single position (nucleotide) in the genome where different variants (alleles) are seen in different people.

2. Reference Panel

2.1 Calculating an Ethnicity Estimate

Two chromosomes from the same geographic region or the same population will share more DNA with one another than will two chromosomes from different regions or groups. So two pieces of DNA with a historical connection to Sweden will have more DNA in common than will a piece of DNA from Korea and a piece of DNA from Sweden. This is the basic premise behind the ethnicity estimate AncestryDNA provides to its members.

To create the ethnicity estimate, we compare a customer's DNA to a panel of DNA from people with known origins (referred to as the reference panel) and look to see which parts of the customer's DNA are similar to those from people represented in groups in the reference panel. If, for example, a section of a customer's DNA is most similar to the reference panel samples from Senegal, then we identify that section of the customer's DNA as coming from Senegal.

The accuracy of our ethnicity estimate depends on the quality of our reference panel. Because of this, AncestryDNA has invested a significant amount of effort in developing the best possible set of reference samples.

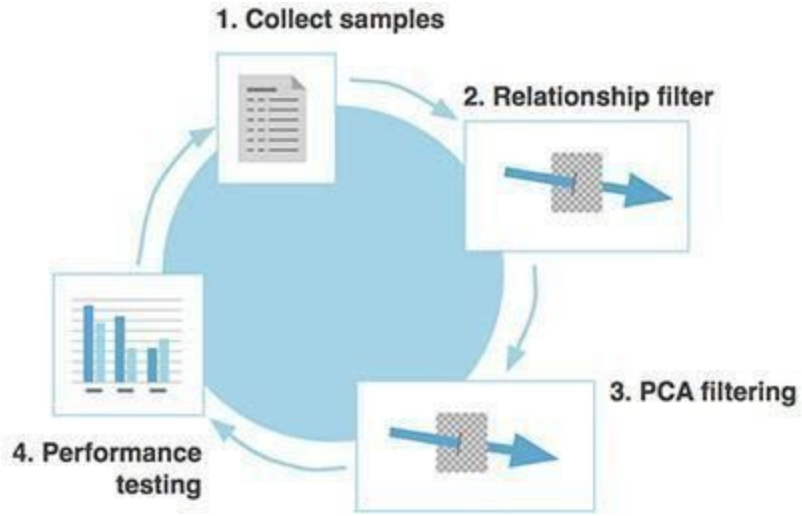

Figure 2.1: Reference Panel Refinement Cycle. *Schematic of the ethnicity estimation reference panel refinement cycle. In* ***step 1*** *we select candidate reference samples from published data, the AncestryDNA customer list, and the AncestryDNA proprietary reference collection. For AncestryDNA samples we rely on pedigree data to select those with deep ancestry from a single population. In* ***step 2*** *we filter out pieces of DNA between closely related samples from the candidate list. In* ***step 3*** *we use principal component analysis (PCA) to remove samples that show a disagreement in pedigree and genetic origin. We also use PCA to guide the identification of population groups. In* ***step 4*** *the panel is performance tested using numerous metrics and compared to the previous release. The final result is a high-quality, well-tested reference panel. The entire procedure is cyclic, and AncestryDNA will continue to make improvements to the panel with the goal of providing the most accurate ethnicity estimation possible with the data available.*

The rest of section 2 describes the steps taken to develop our current reference panel, including sample selection, quality control, and testing. The ethnicity update that we describe here is not only an update of the reference panel from our 2018 version but also increases the number of global regions from 43 to 60.

2.2 Who should be included in the reference panel?

Identifying the best candidates for the reference panel is key to providing the most accurate ethnicity estimate possible from a customer's DNA sample. Under perfect circumstances, we would construct our reference panel using DNA samples from people who lived hundreds of years ago. Unfortunately, it is not yet possible to reliably sample historical populations in this way. Instead, we must rely on DNA samples collected from people alive today and focus on those who can trace their ancestry to a single geographic location or population group.

When asked to trace familial origins, most people can only reliably go back one to five generations, making it difficult to find individuals with knowledge about more distant ancestry. This is because as we go back in time, historical records become sparse, and the number of ancestors we have to follow doubles with each generation.

Fortunately, knowing where someone's recent ancestors were born is often a sufficient proxy for much deeper ancestry. In the recent past, it was much more difficult and thus less common for people to migrate large distances. Because of this, the birthplace of a person's recent ancestors often represents the location of that person's deeper ancestral DNA.

AncestryDNA Reference Panel Candidates

In developing the most recent AncestryDNA ethnicity reference panel, we began with a candidate set of close to 97,000 samples. First, we examined over 1,000 samples from 52 worldwide populations from a public project called the Human Genome Diversity Project (HGDP) (Cann *et al*. 2002; Cavalli-Sforza 2005), over 1,800 samples from 20 populations from the 1000 Genomes Project (McVean *et al.*, 2012), and over 900 samples from 91 populations from the Human Origins dataset (Lazaridis et al. Nature 2014) Second, we examined samples from a proprietary AncestryDNA reference collection as well as AncestryDNA samples from customers who had previously consented to research. Most of the candidates were selected from the last two groups only after their family trees confirmed that they had a long family history in a particular region or within a particular group. A small number of candidates were selected without a deep family tree, but these passed the rigorous vetting process outlined below. Although it was not possible to confirm family trees for HGDP, Human Origins, and 1000 Genomes Project samples, these datasets were explicitly designed to sample a large set of distinct population groups representing a global picture of human genetic variation.

Reference Panel Candidates from Admixed Populations

In some parts of the world many indigenous people also have ancestry from multiple continents. For example, people of Amerindian descent in North and South America may have some ancestry from Europe and Africa. When creating reference panel regions reflecting geographic regions for the Americas and Oceania, we wanted to use only the parts of the genome with ancestry from the indigenous populations. We did this by looking at our previous ethnicity assignments and choosing only the segments of DNA (or windows) where both chromosomes had assignment to an ethnicity region corresponding to

the indigenous population. So, whereas most of our regions use DNA from the entire genome of each candidate, for regions from admixed populations we only use a fraction of each person's genomes. The ethnicity regions where we employ this approach are Indigenous Americas-North, Indigenous Americas-Mexico, Indigenous Americas-Yucatan, Indigenous Puerto Rico, Indigenous Haiti & Dominican Republic, Indigenous Cuba, Indigenous Americas–Central, Indigenous Americas-Andean, Indigenous Americas–Colombia & Venezuela, Indigenous Americas-Southeast, Samoa, Tonga, Polynesia, Melanesia, and Guam.

2.3 Reference Panel Quality Control

For each sample, we analyzed a set of approximately 300,000 SNPs that are shared between the Illumina OmniExpress platform and the Illumina HumanHap 650Y platform, which was used to genotype HGDP samples. After samples with large amounts of missing data were removed, we filtered out those which were likely to degrade the performance of the reference panel. Samples were typically removed because they were closely related to another reference sample or the underlying genetic information about a sample's origins disagreed with the family tree data.

When we perform genetic ethnicity estimation, we are interested in computing the probability that a particular segment of DNA, an observed haplotype, came from each possible source population in the reference panel (see Section 4 below). In other words, what are the odds that this particular stretch of DNA came from Sweden? Or France? Or any of the other regions we test?

To do this, we need to estimate the frequency of this haplotype in each population, and this requires that people in the reference panel not be closely related. This is because DNA segments shared as a result of recent ancestry, as identified through identity by descent (IBD), do not represent independent haplotypes in a population, so retaining them can distort the estimates of population haplotype frequencies. This is why we remove such segments for candidates that share more than a certain amount of IBD DNA (20 cM). Details about our approach for detecting shared segments of IBD DNA can be found in our AncestryDNA Matching white paper (https://www.ancestry.com/corporate/sites/default/files/AncestryDNA-Matching-White-Paper.pdf).

Next, we remove samples from the reference panel candidate set when the genetic data about ethnicity disagrees with what that person has reported about their ethnicity–when underlying genetic information disagrees with the pedigree data. We identify these outliers using two approaches: (1) we identify clear

outliers using our previous ethnicity estimate version, and (2) we use principal component analysis (PCA). PCA is frequently used for exploratory data analysis in population genetics research (Jackson 2003). When applied correctly to genotype data, PCA can capture the genetic variation separating distinct populations (Patterson 2006).

We apply PCA to the samples that have made it through the previous screening processes and plot the early stages of the analysis, the “first four principal components,” as a series of scatter plots. We color each sample by their population of origin, determined by pedigree for Ancestry samples and by sample label for public samples (see Figure 3.3).

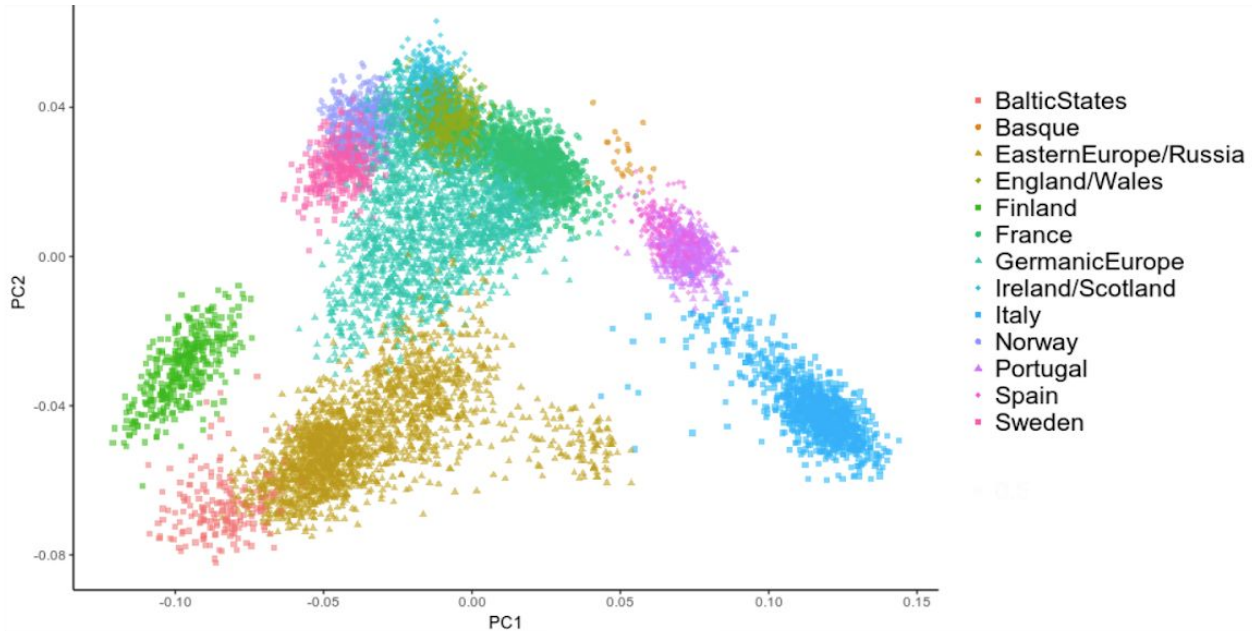

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Figure 2.2: PCA Analysis on European Panel Candidates. *Scatter plot of the first two components from a principal component analysis (PCA) of candidate European samples for the AncestryDNA reference panel. Visual inspection of PCA is useful for numerous aspects of data QC. First, it can be used to identify individual outliers, such as the EasternEurope/Russia samples (yellow triangles) that appear in the middle of the GermanicEurope (green triangles) cluster. It can also be useful for identifying poor sample grouping. Finally, it can reveal regions where there is limited genetic separation and clusters overlap (e.g. Ireland/Scotland and England, Wales & Northwestern Europe) and regions that can be further subdivided.*

Each population tends to form a cluster of points (each point is a sample) in the scatter plot. This is because points that are more genetically similar are closer in PCA space. Helpfully, these clusters of points tend to match geography as well because most people are genetically more similar to others from nearby. Furthermore, these plots quickly reveal outlier samples which are not near other samples from

the same population. For example, the yellow triangles in the green triangle cluster indicate samples with family trees from Eastern Europe, but their DNA is more similar to people from Germany. These are examples where the specified population of origin disagrees with the genetic origin represented in PCA space.

We visually inspect candidates for removal based on a scatterplot like the one in Figure 2.2. Because different collections of samples reveal different amounts of population structure, PCA and outlier removal are repeated for different subsets of data. We first remove outliers at the global level (all samples together), then at the continental level (e.g., outliers in a PCA using only European samples), then at the regional level (e.g., outliers in a PCA of all Scandinavian samples), and finally at the population level (e.g., outliers from a PCA of Norway).

2.4 Iterative Reference Panel Refinement

After removing PCA outliers, we divide our global reference panel into populations corresponding to distinct genetic clusters in the PCA plots. Before using the reference set to estimate ethnicities of AncestryDNA customers, we first determine its quality by measuring the performance of our ethnicity estimation on the reference set itself. How well does our ethnicity estimation do on samples that by definition are 100% of a single ethnicity?

To do this, we remove 5% of samples from the reference panel and estimate their ethnicity using the remaining 95% of samples as the new reference panel. We repeat this process 20 times, each time removing a different 5% of the panel and estimating their genetic ethnicities using the remaining 95%. We then look at the average predicted ethnicity for samples from each region in the reference set using the results of these cross-validation experiments. Figure 2.3 shows the results of this experiment as box plots.

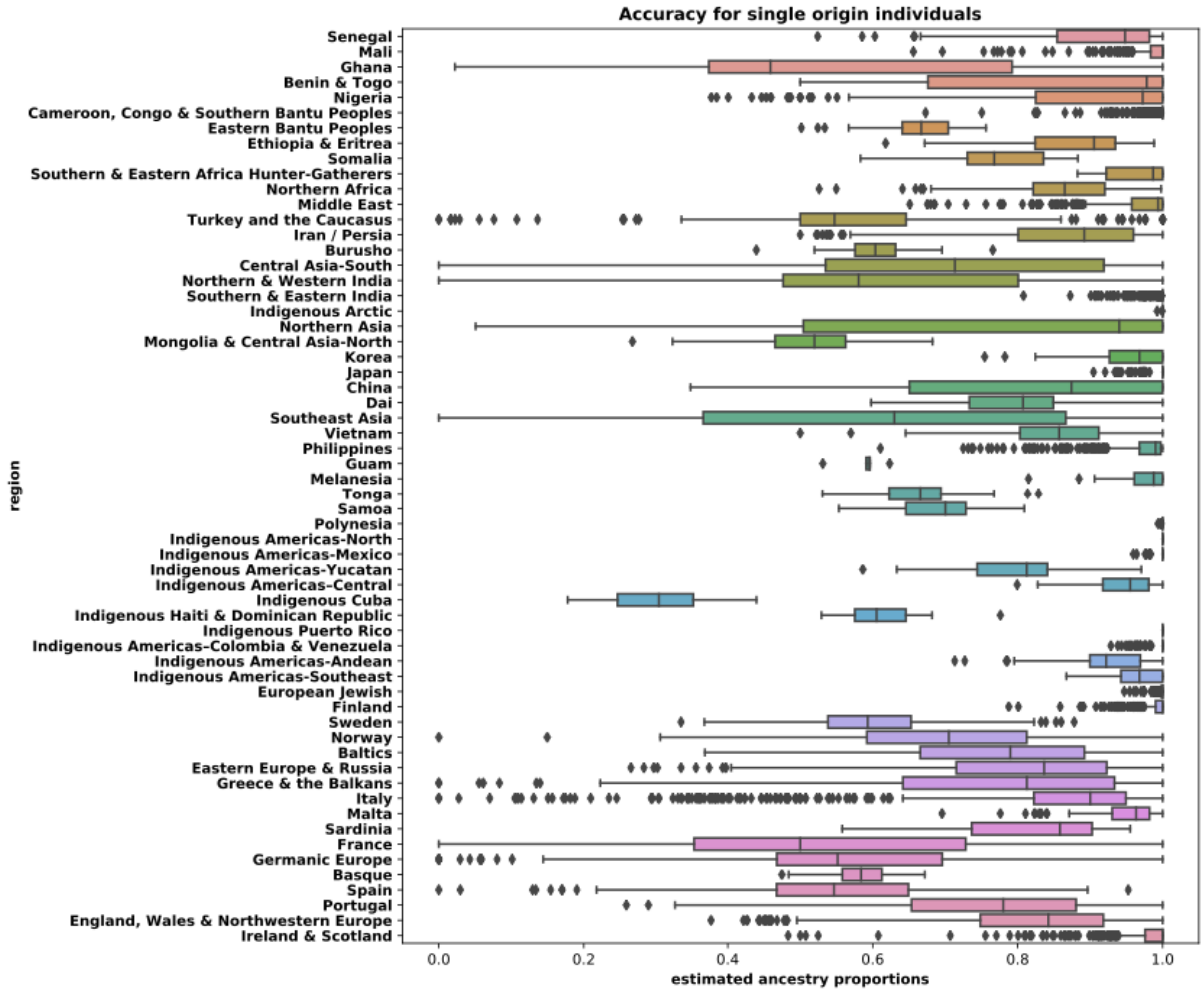


Figure 2.3: 20-fold cross-validation analysis of the Ethnicity 2019 reference panel. *Here we plot the results of an experiment in which 5% of samples are removed from the reference panel, and their ethnicity is estimated using the remaining (95%) panel samples. Each boxplot represents the distribution of estimated ethnicity for all samples from a given region (75%, 50%, and 25% percentiles of estimated ethnicity). For the majority of samples in each region, we predict on average 80.5% of the genetic ethnicity to be from the correct region. And for the most part, the other 19.5% comes from nearby regions. However, there are exceptions. In particular, our average prediction accuracy for samples for Indigenous Cuba and Mongolia & Central Asia-North are not quite as high. There are many factors affecting the accuracy of these numbers, most importantly the number of reference samples in the panel for each region and the genetic distinctness of each region.*

The purpose of this analysis is twofold. First, reference panel samples with extremely poor performance in the cross-validation analysis are removed, as they may poorly represent their ethnic group of origin.

Second, the cross-validation experiments allow us to demonstrate our ability to accurately estimate the ethnicities of our reference panel samples using our ethnicity estimation method (see section 3) and thus help us redefine population boundaries. For example, we may merge two populations if performance in the cross-validation experiment is poor in each group but is found to be better in a merged group.

After performing several rounds of reference panel refinement based on cross-validation experiments, we settled on dividing our latest reference panel into 60 global regions. These regions are described in further detail below.

2.5 Updated Reference Panel

The updated AncestryDNA ethnicity estimation reference panel contains 40,017 samples carefully selected as described to represent 60 global regions (Table 2.1), each with a unique genetic profile. As a comparison, our previous panel of 16,638 samples represented 43 distinct global regions.

Region	**Number of samples**
Baltics	147
Basque	31
Benin & Togo	287
Burusho	23
Cameroon, Congo & Southern Bantu Peoples	535
Central Asia–South	369
China	915
Cuba	3427
Dai	70
Eastern Bantu Peoples	91
Eastern Europe & Russia	1777
England, Wales & Northwestern Europe	1461
Ethiopia & Eritrea	55
European Jewish	450

Finland	408
France	998
Germanic Europe	2126
Ghana	109
Greece & the Balkans	354
Guam	57
Indigenous Americas–Andean	62
Indigenous Americas–Mexico	725
Indigenous Americas–North	2290
Indigenous Americas–Southeast	2966
Indigenous Americas–Yucatan	92
Indigenous Americas–Central	1008
Indigenous Americas–Colombia & Venezuela	2615
Indigenous Arctic	36
Indigenous Haiti & Dominican Republic	2868
Indigenous Puerto Rico	4803
Iran / Persia	577
Ireland & Scotland	560
Italy	1057
Japan	173
Korea	197
Mali	413
Malta	106
Melanesia	64
Middle East	467
Mongolia & Central Asia–North	58
Nigeria	522

Northern & Western India	413
Northern Africa	123
Northern Asia	43
Norway	402
Philippines	558
Polynesia	188
Portugal	627
Samoa	73
Sardinia	38
Senegal	114
Somalia	23
Southeast Asia	191
Southern & Eastern Africa Hunter-Gatherers	38
Southern & Eastern India	405
Spain	497
Sweden	414
Tonga	97
Turkey and the Caucasus	229
Vietnam	195
Total	**40,017**

Table 2.1: The Final AncestryDNA 2019 Ethnicity Reference Panel

We discuss more detailed tests of the performance of the 2019 ethnicity panel in Section 4. For details of the method AncestryDNA uses for genetic ethnicity estimation, see Section 3.

3. AncestryDNA Ethnicity Estimation

3.1 Introduction

After establishing and validating the reference panel, the next step is to estimate a customer's ethnicity by comparing over 300,000 single nucleotide polymorphisms (SNPs) from their DNA to those of the reference panel. We assume that an individual's DNA is a mixture of DNA from the 60 populations represented in the reference panel. This is illustrated in Figure 3.1, where, because of recombination, a customer inherits long stretches of DNA from his or her four grandparents who, in this example, come from four "single source" reference populations.

Because DNA is passed down from one generation to the next in long segments, it is likely that the DNA at two nearby loci in the genome were inherited from the same person and so the same population (for more details on DNA inheritance see our DNA Matching White Paper http://dna.ancestry.com/resource/whitePaper/AncestryDNA-Matching-White-Paper). This means we can get more accurate results by looking at multiple nearby SNPs together as a group, or haplotype, instead of looking at each SNP in isolation. Our updated method takes advantage of this to greatly improve our estimates.

We estimate a customer's genetic ethnicity by assuming that each segment of their genome comes from one of the 60 populations in the reference panel. We divide the customer's genome into 1,001 windows. We assume that each window is small enough that each of the two parental haplotypes present in the window came from exactly one population. We then combine information from all the windows to estimate what overall portion of the customer's genome came from each of the populations in the reference panel using a hidden Markov model (HMM).

As you can see in Figure 3.1, each window does not have to have a single ethnicity associated with it. Instead, it can have one from one parent and one from the other. For example, the first window has two different ethnicities represented by the colors green and red. Any ethnicity estimator that uses the technology AncestryDNA does to read DNA has to account for the possibility of two separate ethnicities in each window. In other words, it has to employ a model that looks at the DNA and can identify the DNA as a mix of red and green as opposed to just red or just green (or any of the other possible combinations).

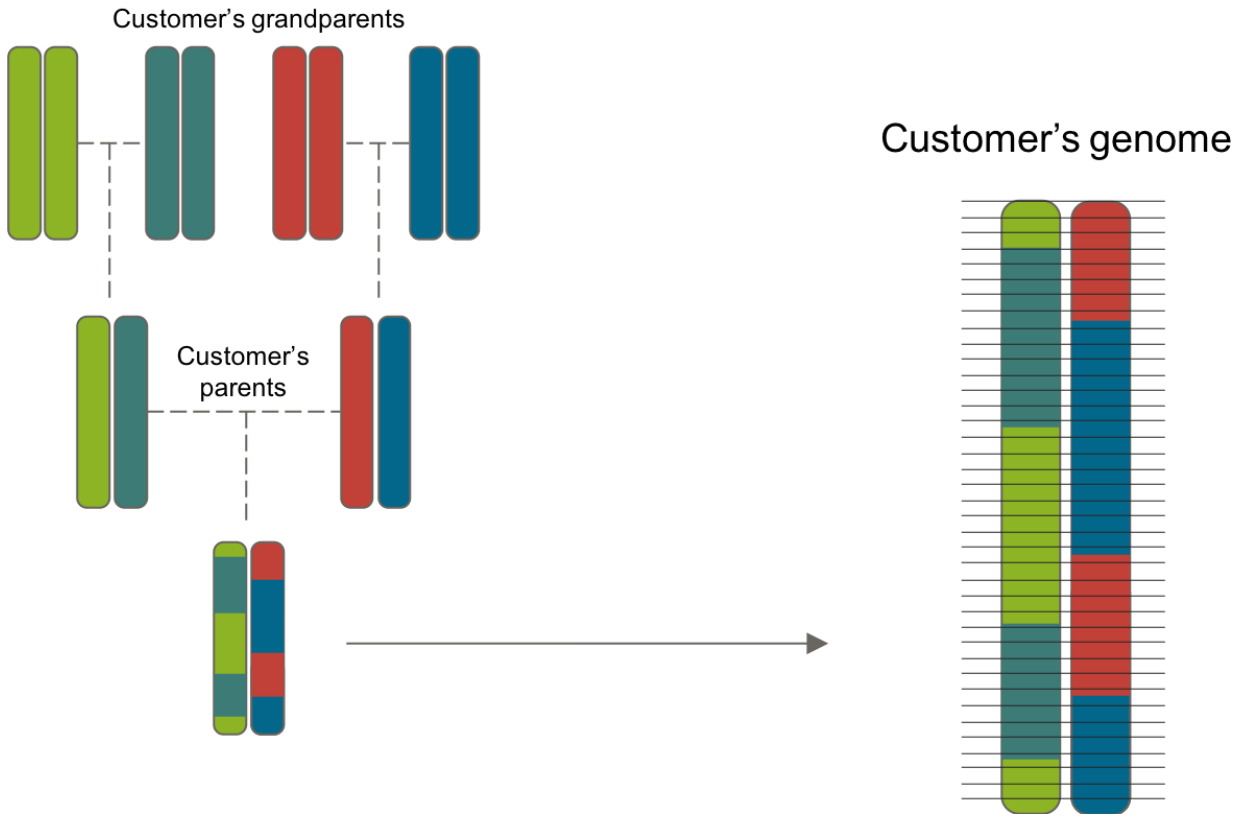


Figure 3.1: Inheritance of DNA from different populations. *On the left, we present a three-generation genetic family tree. For each individual, we show two vertical bars representing the two copies of a single chromosome present in each individual. These bars are colored by the reference population from which they inherited their DNA. Each of the four grandparents (solid bars, top row) has inherited 100% of their DNA from a single population that is different from the other three. The DNA is passed forward to the parents and finally to the customer, who, through the process of recombination and assortment, ends up inheriting a shuffled set of chromosomes from each parent. The colors show that the customer's DNA is a mixture of the DNA inherited from their four grandparents, with long stretches inherited from the same grandparent. On the right, we show that to obtain a customer's ethnicity estimate, we divide the customer's genome into small windows (represented by black horizontal lines). For each window we assign a single population to the DNA within that window inherited from each parent, one population for each parental haplotype. Each window gets a population assignment based on how well it matches genomes in the reference panel.*

3.2 Principles of a Hidden Markov Model

When we analyze DNA data, we do not know the population it comes from ahead of time. Instead, we observe a pair of alleles (often called a genotype) at each position (or SNP) in the DNA. One allele was inherited from Mom and the other from Dad.

Because the probability of a specific pair of alleles appearing at a certain position in the DNA varies for each of our 60 regions, we can use that information to tell us which region a stretch of DNA most likely came from. For example, if AA at a particular position is more common in people from Spain, someone with AA at that location might have a higher chance of having Spanish ancestry.

It is important to keep in mind that an AA at this particular position just makes it *more likely* the DNA comes from Spain. Plenty of people from Portugal, France, or even Korea might have AA at this position as well. The ethnicity estimate uses the probability at all positions within a window to determine where the DNA most likely came from. We infer the genetic ethnicity of each position using a statistical tool called a hidden Markov model (HMM) [Rabiner, 1989].

A customer's genome is a sequence of nucleotides—As, Ts, Cs, and Gs—strung together to make a chain. The precise nucleotide at any position depends on what population that segment of DNA has come from, but that information is not known. In determining ethnicity, an HMM statistically determines the most likely ancestral reference population from which a segment of DNA originates, its most likely "hidden state," based on a sequence of observations (in this case, the genotypes, or particular combination of SNPs).

We divide the customer's genome into 1,001 stretches of DNA called windows and determine the hidden state for each of them. Each window has two stretches of DNA, one from Mom and one from Dad, and they can either both be from the same ethnicity or from different ones. So the hidden state in this case is the ethnicity of each segment of DNA in the window.

HMMs have two components, called emission and transition probabilities. Emission probabilities tell us how likely it is that a stretch of DNA came from each of the 60 populations based on the observed sequence. The transition probability indicates how likely it is that there will be a change in the population identification from one window to the next. In other words, if in the DNA in the current window is from only Sweden, how likely is the DNA in the next window to also be from only Sweden?

This is a sensible model for human DNA because human genomes are organized linearly along chromosomes. Additionally, the nature of inheritance means that whole segments of the genome and, therefore, many consecutive nucleotides that Ancestry looks at along a chromosome, will have the same DNA ancestry.

3.3 Inferring Ethnicity Estimates from a Genome-Wide HMM

At AncestryDNA, we use microarrays to obtain DNA data from customer samples. We look at over 700,000 individual locations on the DNA (SNPs) and determine the nucleotides at each position. For example, we may see an A and a T at position 1, a G and a G at position 2, and so on. We use around 300,000 of these SNPs in the ethnicity estimate.

In working with data from arrays, it is important to remember that people have two copies of each of the 22 chromosomes that AncestryDNA reports data back on. One set of chromosomes comes from Mom and the other from Dad. This means there are two results for each position AncestryDNA analyzes, and those results must be interpreted to assign which DNA came from which set of chromosomes (this process is called phasing). AncestryDNA must consider what possible combinations of ethnicities might look like. For example, if one customer has a section of their DNA that came from Swedish ancestors from Mom's side of the family and Japanese ancestors on Dad's, the algorithm must be able to distinguish this from a second customer with Swedish and Nigerian ancestors.

We create a genome-wide HMM (illustrated in Figure 3.2) where each possible ethnicity combination (or hidden state) is represented by a pair of populations in a window of the genome, and changes between windows that are next to each other are unlikely to change the state. In other words, if in the preceding window the DNA from Mom and the DNA from Dad both came from Nigeria, then the next window is more likely to be the same.

The state in a given window is a pair of populations, where each ethnicity in the pair can be different (e.g., red and green in window 1 of the third row of Figure 3.2) or the same (e.g., green and green in window 1 of the top row of Figure 3.2). Each population pair assignment has a probability of appearing (or the "observed genotypes") in the window (emission probability).

We also account for the probability of changing population assignments between adjacent windows (transition probability). Essentially this means that if you are, for example, Sweden/Sweden in one window, there will need to be very strong evidence from the observed DNA data that the neighboring window has a different population assignment. By applying these probabilities to the whole genome, we can obtain a sequence of population assignments along a customer's genome.

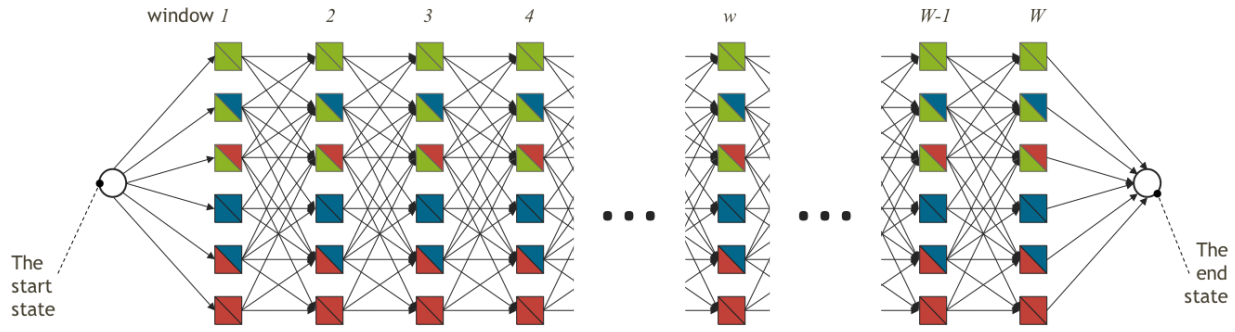


Figure 3.2: An illustration of the genome-wide HMM for three populations. The genome is divided into *W* windows, and we model transitions from a given window *w*, to the adjacent window *w+1*. Here, the possible (hidden) states for a window are represented by colored squares, with different colors representing different population assignments. Boxes with two different colors represent mixed ancestry in the window. Arrows between boxes represent transitions, and each box/state emits the customer's observed genotype with a probability that was pre-computed in the previous step. Transitions that do not result in a change in state/colors between two windows are more likely than those that do. Only transitions that result in at most one color/population change are allowed.

3.4 Transition Probabilities

Transition probabilities are really just the odds that an ethnicity will change from one window to the next. Ancestry only considers a transition to the window that is immediately adjacent, so the only things that determine the transition probability are the state at the current window and the state it transits to at the next window. This "memoryless" property is a key feature of an HMM.

We do not allow transitions between states where both populations are different because from a biological perspective, it is very unlikely that there would be a change in the same window in both the set of DNA from Mom and the set of DNA from Dad. This greatly reduces the number of possible transitions and the complexity of the HMM.

The exception to this rule is when there is a transition from the end of one chromosome to the beginning of the next. In these cases, changes are much more likely than they are within the same chromosome because the DNA in different chromosomes are not connected. This is accomplished by forcing a silent state between chromosomes, which makes sense because there is no connection between two chromosomes. The transition probability from a silent state to a given pair of population assignments is simply given by the genome-wide probability of any position of the genome having that population

assignment. In other words, there is no information from a previous window to affect the interpretation of a window that immediately follows a silent state. We estimate this value as part of the HMM. Initially, this value is set to be the same for every population pair, and is learned during the iterations of the HMM as each sample is processed.

3.5 Emission Probabilities

Determining how likely the DNA in a window came from a population (the emission probability) is a complicated process and is described in more detail in the appendix.

Briefly, our approach includes the following steps:

I. **Define the windows.** DNA is inherited in long stretches of contiguous DNA within chromosomes referred to as haplotypes. Working with these blocks of DNA can be more informative than working with individual positions within the DNA. We do not know the exact haplotype boundaries, which differ between people, but we can achieve a good approximation by dividing the genome into 1,001 small windows. Each window covers one section of a single chromosome and is small enough (*e.g.,* 3-10 centimorgans) that both the maternal and paternal haplotype, the DNA from Mom and the DNA from Dad, in a given window are likely to each come from a single, though not necessarily the same, population.

II. **Create the haplotype models.** Next we need to compare a customer's haplotype within a window to those in our reference panel to assess how likely it is to have come from each population. For example, how likely are both segments of DNA in a haplotype to come from Sweden vs. one from Sweden and one from France, and so on through all of the possibilities. To do this we first need to create a haplotype model. We do this by constructing a *BEAGLE* [Browning, 2007] haplotype cluster model for each window using hundreds of thousands of haplotypes (see Matching white paper for more on this). Since we start with unphased customer genotype data, data in which maternal and paternal haplotypes are not distinguished, the model accounts for all possible haplotypes given a set of genotypes, and each state in a haplotype cluster model represents a cluster of similar haplotypes.

III. **Annotate the reference panel.** We want to identify the haplotype clusters in our model that are associated with each population in the reference panel. Because we are confident in the geographic origin of members of the reference panel, we are able to calculate the probability that a haplotype from a given population is represented by a particular haplotype cluster. These

values are used to compute the emission probabilities in the genome-wide HMM that assigns ethnicity.

IV. **Compare the test sample to the reference panel to assign population labels using an HMM.** To do this, we compute the likelihood that the pair of haplotypes present in each window of a test sample come from the populations in the reference panel. For each window, both haplotypes may come from the same population or from different populations, and the resulting emission probabilities are calculated for all possible combinations.

HMMs are used in a number of existing approaches for estimating ancestral proportions [Maples 2013]. The key part of our method is step III, where we use rich haplotype models in each window, annotated with population labels from the haplotypes in our reference panel, to assign a likelihood over all population labels to the haplotypes in our test sample. It is worth noting that our method lends itself to high-throughput ethnicity estimation, as steps (I) through (III) above–learning the haplotype models from a large training set and then annotating them with the reference panel populations–need only be carried out once.

3.6 HMM Model

We use HMMs because they can effectively consider all possible ethnicity assignments to all windows in the genome and do so efficiently. Ancestry runs our HMM on a customer's DNA to find the most likely sequence of ethnicities along the DNA. In more technical terms, the algorithm takes the "Viterbi" path, the sequence of hidden states that returns the highest probability. The final ethnicity proportions the customers receive are calculated by counting the proportion of the Viterbi path (weighted by recombination distance) that are assigned to a particular population in the reference panel. For example, a customer with the sequence Sweden/Sweden, Sweden/Sweden, Sweden/Sweden, France/Sweden, France/Sweden (and an incredibly small genome!) would be 20% France and 80% Sweden, given the five windows have identical size.

Because these proportions are estimates, we need a way to determine the confidence surrounding these values. To do this, we randomly sample 1,000 non-Viterbi paths, or paths that might not be the most likely (but are still likely). In each of the 1,000 runs, a given window is assigned a population pair with a probability that depends on the assignment, within the same run, of the previous window and the predetermined transition and emission probabilities. These 1,000 values are used to provide a confidence range on the reported Viterbi estimate.

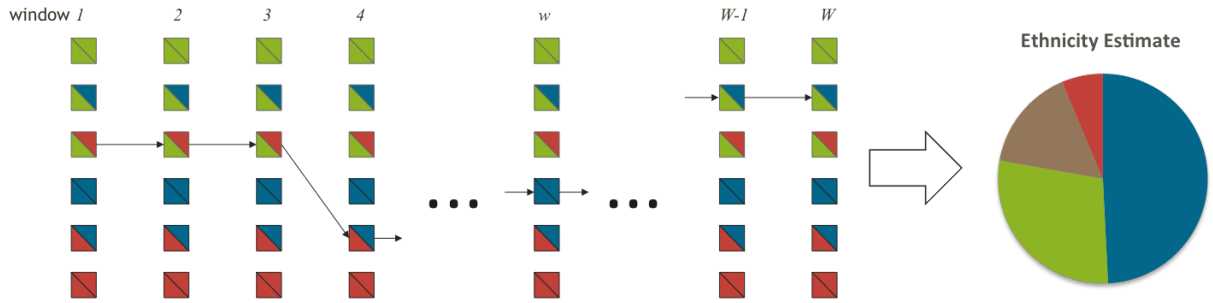


Figure 4.6: Illustration of the Viterbi path, represented by arrows, through the HMM that determines an ethnicity estimate.

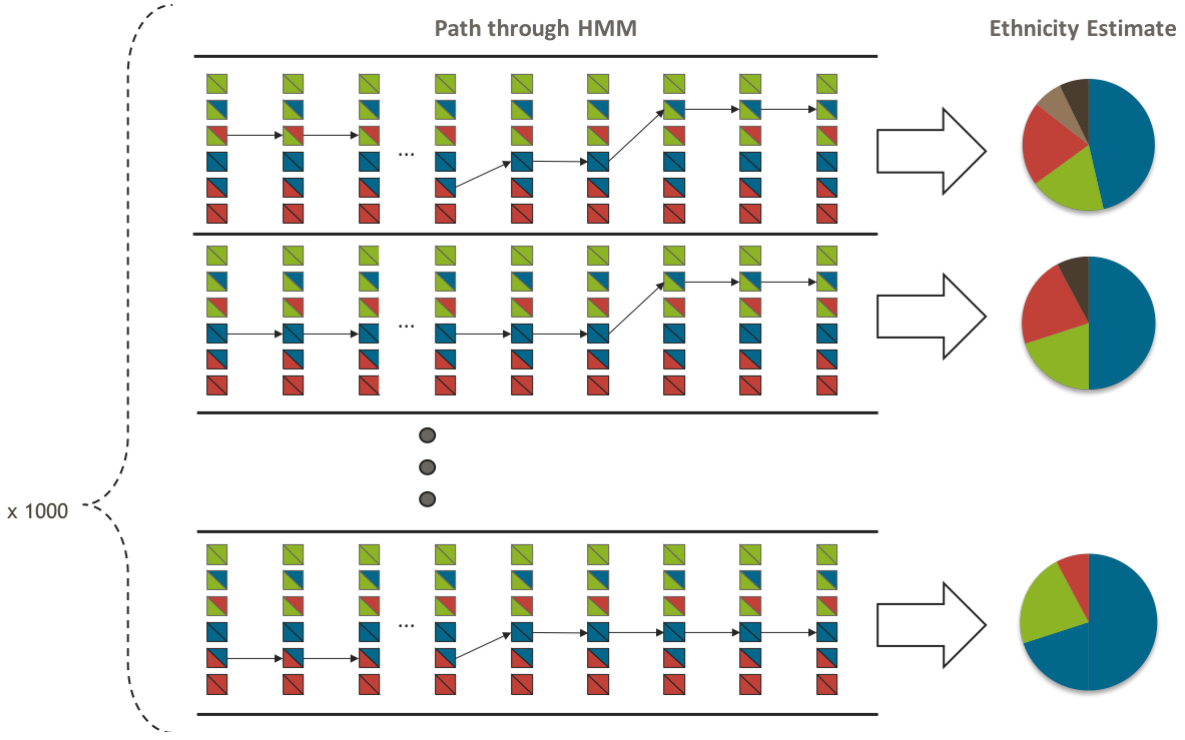


Figure 4.7: Illustration of our stochastic path-sampling process.

4. Assessing Ethnicity Estimation Performance

After developing and optimizing both the estimation process and the reference panel, the final step is to determine how well they perform together at assigning ethnicity. Basically, we see how close our process gets to the right answer through rigorous testing using a wide variety of test cases with known ethnicity.

4.1 Cross-Validation

We evaluate the performance of the ethnicity estimation process by running it on two different test cases where we know what the correct answer should be: single-origin individuals (including synthetic single-origin individuals) from the reference panel and synthetic individuals with mixed ethnicities. We gauge its effectiveness by seeing how close we get to the true ethnicity.

Reference panel groups: Our reference panel has two types of reference groups. In the first, people have a long family history in a single region with no influx of other individuals to that region. They represent a typical person from that region and by definition, have 100% of the region they represent in their DNA. The second group is a little more complex. This group represents indigenous peoples who also have ancestors from a different region. An example would be people from Mexico who may have Native American, European, and African ancestors. We are able to include only the parts of their DNA that are Native American (or indigenous) to the reference panel.

Single-origin individuals: We use two different sets of single origin individuals in our cross validation studies. The first are those for whom we utilize their entire genome as a reference for a particular region. By definition these individuals in our reference panel each have 100% of a single ethnicity.

This approach does not work for the reference panel regions where we used the indigenous DNA of admixed individuals. For these reference panel regions, primarily from the Americas and Oceania, we created synthetic single origin individuals by piecing together genotype sequences that represented indigenous ancestry from multiple individuals. These synthetic single origin individuals are then used to evaluate the accuracy of our method.

We evaluate our process by running 20-fold cross-validation experiments using these single-origin individuals from our reference panel. For example, if we had 100 people in each reference panel group, we would take 5 from each of the 60 groups and run the algorithm on these 300 samples using the remaining 5,700 individuals as the reference group. Then a

different 5 would be taken from each group and the process repeated 20 times so that every individual in the reference panel is tested.

Overall we observe that the updated process correctly assigns an average of 80.5% of the genetic ethnicity to the correct region for single-origin individuals from our reference panel (Figure 2.3). We predicted nearly 100% of the genetic ethnicity from the correct region for the following groups:

- European Jewish
- Indigenous Americas--North
- Indigenous Puerto Rico
- Indigenous Americas--Mexico
- Indigenous–Arctic
- Polynesia
- Japan
- Indigenous Americas–Colombia & Venezuela
- Eastern & Southern India
- Cameroon, Congo & Southern Bantu Peoples
- Finland
- Mali
- Ireland & Scotland
- Melanesia
- Philippines
- Middle East
- Indigenous Americas--Southeast
- Africa South-Central Hunter-Gatherers

For some regions, such as Indigenous Cuba, Mongolia, France, and Spain, the numbers are not as high, with average assignment of 30%, 51%, 53%, and 55% to the correct region, respectively. However, even if the prediction accuracies fall short of 100% for some regions, the remaining ethnicity is still assigned to nearby regions. For example,individuals from Mongolia might get some assignments to Northern Asia; individuals from Spain might get some level of assignment to Portugal (see Figure 4.2).

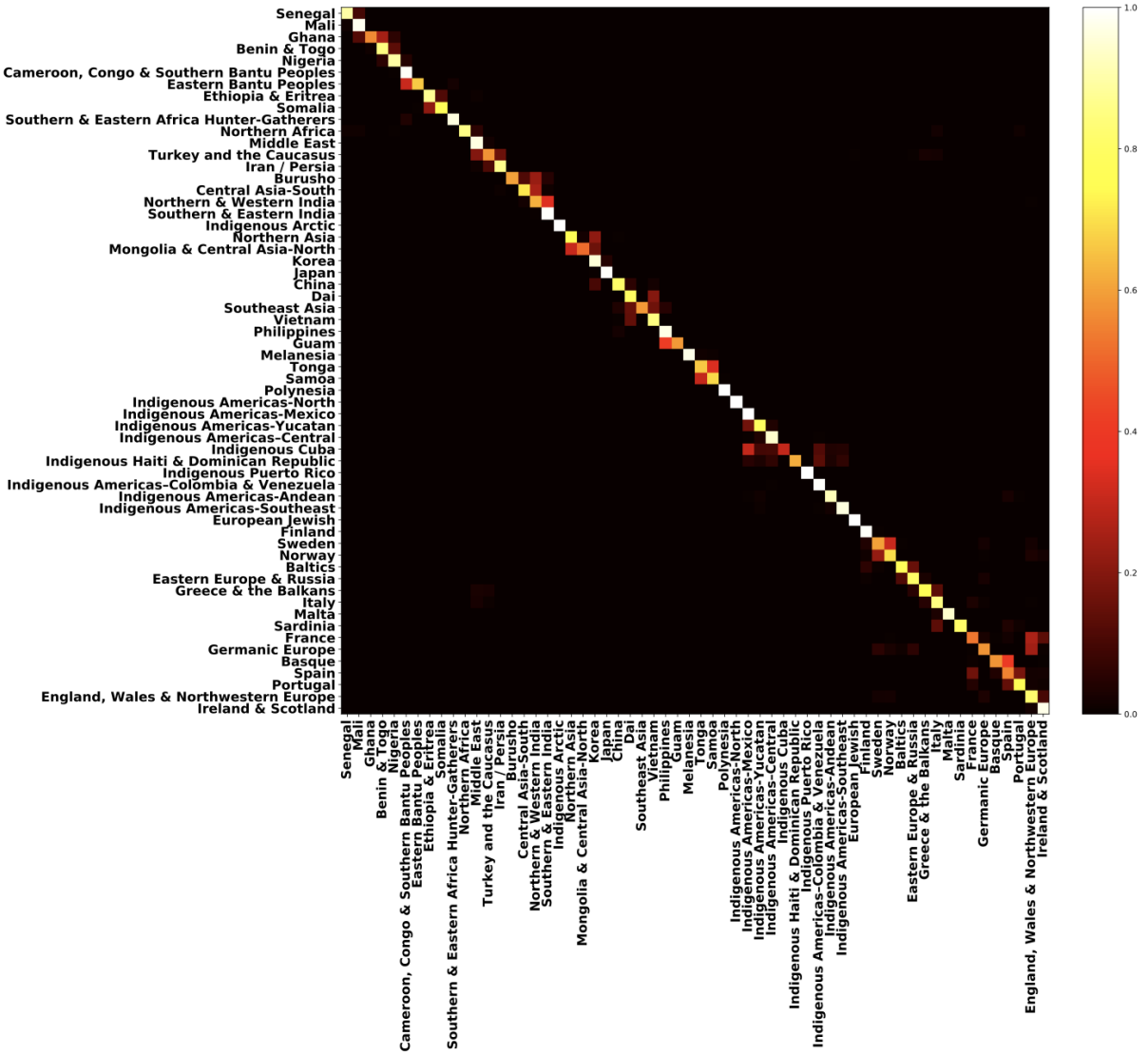


Figure 4.2: Average estimated ethnicities for single-origin individuals from each population. In this graph, each row represents single-origin individuals from the population listed. Each column represents each of the possible 60 ethnicities that the single-origin individual might be assigned to. The graph is set up such that the matching individual and his or her ethnicity are aligned along the diagonal line. If the algorithm worked perfectly, there would be only white boxes along the diagonal—white represents 100% origin from that population. Any boxes that are not on the diagonal represent misassigned populations. This graph also shows that certain ethnicities can be confounded by other ethnicities. For example, individuals with 100% Spanish ethnicity can be assigned to France and Portugal.

Synthetic individuals with mixed ethnicities: We also evaluated the accuracy of ethnicity estimates for “synthetic” individuals of mixed ethnicity origins. These test cases are simulations we construct with known mixtures of ethnicities. Each synthetically admixed individual can have as few as 2 or as many as 20 ethnicity regions, with various proportions. Since the true ethnicity

proportions are known, we can calculate precision and recall for each ethnicity region. Precision and recall are two important factors in evaluating our estimation process.

Precision can be thought of as how much of the reported ethnicity is true. For example, if our process predicts an individual has 40% Northern Africa, but only 30% really is, then the process has a precision of 0.75 for Northern Africa ethnicity. Mathematically, precision is expressed as the amount of correctly identified ethnicity divided by the estimated value for that region.

Recall can be thought of as how much of the true ethnicity is called by the process. Keeping with our Northern Africa ethnicity, imagine that an individual has 50% Northern Africa ancestry, but the algorithm predicts 40%. In this case, the process has a recall of 0.8 for Northern Africa ethnicity.

Table 4.1 : Precision/Recall for each region calculated from ethnicity estimates of synthetic individuals with mixed ethnicities.

Region	**Precision**	**Recall**
Baltics	0.43	0.81
Basque	0.48	0.65
Benin & Togo	0.84	0.88
Burusho	0.87	0.52
Cameroon, Congo & Southern Bantu Peoples	0.9	0.98
Central Asia-South	0.89	0.7
China	0.95	0.84
Dai	0.46	0.84
Eastern Bantu Peoples	0.96	0.7
Eastern Europe & Russia	0.87	0.81
England, Wales & Northwestern Europe	0.58	0.81
Ethiopia & Eritrea	0.91	0.93
European Jewish	0.93	0.98

Finland	0.87	0.97
France	0.65	0.52
Germanic Europe	0.79	0.64
Ghana	0.88	0.54
Greece & the Balkans	0.58	0.65
Guam	0.69	0.63
Indigenous Americas-Andean	0.93	0.9
Indigenous Americas-Mexico	0.92	0.97
Indigenous Americas-North	0.98	0.99
Indigenous Americas-Southeast	0.95	0.92
Indigenous Americas-Yucatan	0.72	0.86
Indigenous Americas–Central	0.94	0.91
Indigenous Americas–Colombia & Venezuela	0.94	0.96
Indigenous Arctic	0.98	0.99
Indigenous Cuba	0.67	0.16
Indigenous Haiti & Dominican Republic	0.88	0.66
Indigenous Puerto Rico	0.98	0.99
Iran / Persia	0.87	0.68
Ireland & Scotland	0.59	0.97
Italy	0.77	0.68
Japan	0.88	0.96
Korea & Northern China	0.62	0.92
Mali	0.92	0.97
Malta	0.91	0.89

Melanesia	0.97	0.98
Middle East	0.81	0.85
Mongolia & Central Asia-North	0.91	0.53
Nigeria	0.91	0.92
Northern & Western India	0.73	0.71
Northern Africa	0.93	0.79
Northern Asia	0.74	0.72
Norway	0.63	0.74
Philippines	0.97	0.95
Polynesia	0.98	0.99
Portugal	0.86	0.56
Samoa	0.82	0.87
Sardinia	0.58	0.82
Senegal	0.92	0.93
Somalia	0.86	0.87
Southeast Asia	0.97	0.59
Southern & Eastern Africa Hunter-Gatherers	0.91	0.97
Southern & Eastern India	0.77	0.89
Spain	0.75	0.42
Sweden	0.57	0.66
Tonga	0.88	0.86
Turkey and the Caucasus	0.46	0.56
Vietnam	0.68	0.86

We found that most ethnicity regions have precision and recall that are both higher than 60%, especially several regions that perform extremely well:

- Indigenous-Arctic
- Polynesia
- Indigenous-Puerto Rico
- Indigenous Americas-North
- Philippines
- Melanesia
- Indigenous Americas-Southeast
- Indigenous Americas-Andean
- Indigenous Americas–Central
- Indigenous Americas–Colombia & Venezuela
- Indigenous Americas-Mexico
- Southern & Eastern Africa Hunter-Gatherers
- Nigeria
- Cameroon, Congo & Southern Bantu Peoples

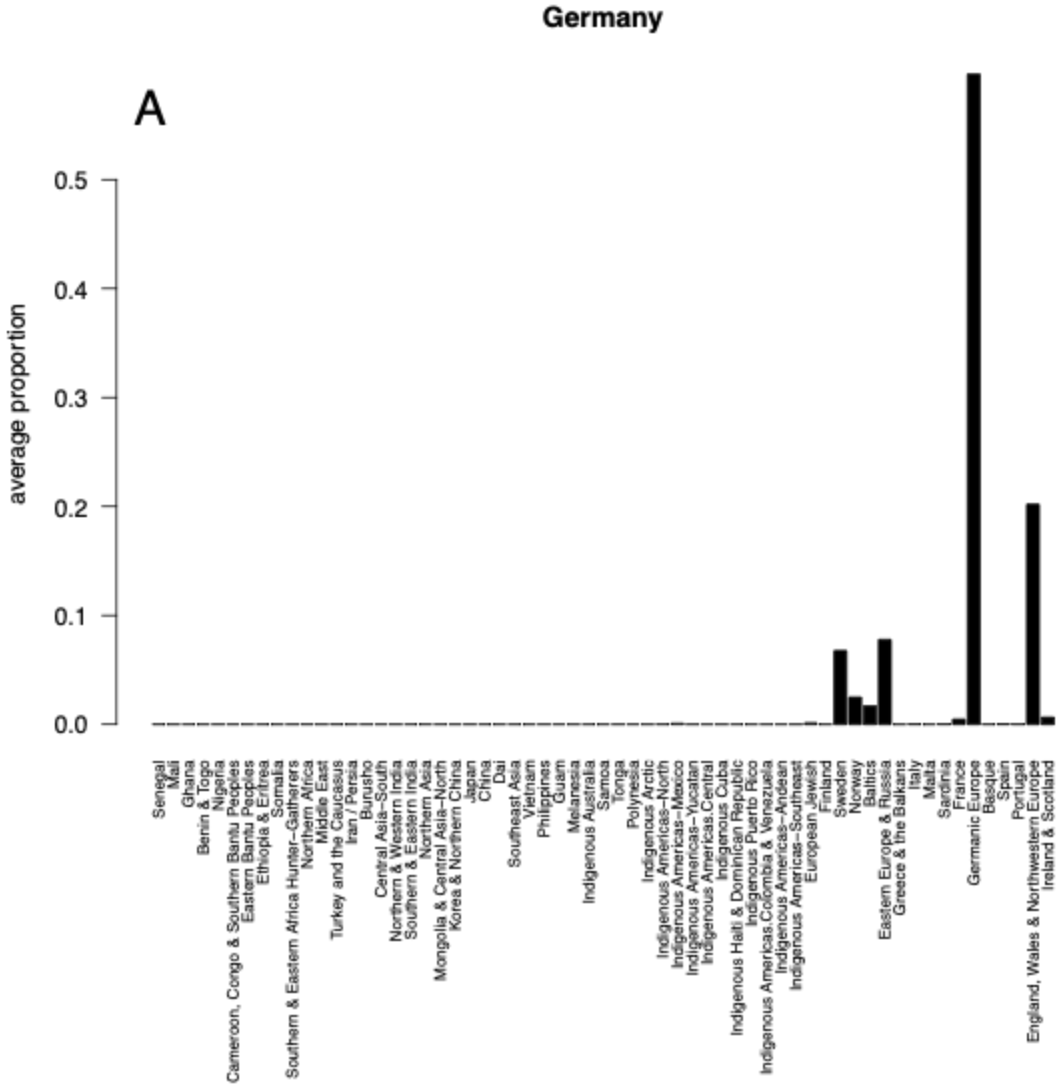
Some regions, such as Indigenous Cuba and Spain have relatively lower recall, 16% and 42% respectively, while some regions, such as Baltics, Turkey & the Caucasus, and Dai have relatively lower precision, 43%, 46%, and 46% respectively.

4.2 Region Assessment

Analyzing samples from individuals whose known ancestors are from only one of our ethnicity regions also allows us to measure how much overlap exists between regions and help our customers interpret their results. To find these individuals, we use customer-created family trees and look for customers who have consented to research who have all of their ancestors from the same country. Ideally, we'd use people with all of their grandparents from the same country, but due to low numbers for some countries we sometimes use parents.

Customers who are not in the reference panel and have deep trees tracing back to a single country are expected to have high assignments to the ethnicity associated with that country, and this is what we generally find. For example, Figure 4.3A shows the average ethnicity assignments for 194 customers with all four grandparents born in Germany. As you can see, while most of their ethnicity is from Germany, other regions do appear in small but significant amounts. These analyses help ensure that ethnicity estimates for people from a region agree with expectations.

However, not everyone receives an estimate that follows the average for each country, and it's often useful to look at individual results to understand why. Figure 4.3B shows the average ethnicity estimates for people with all four grandparents from Japan.



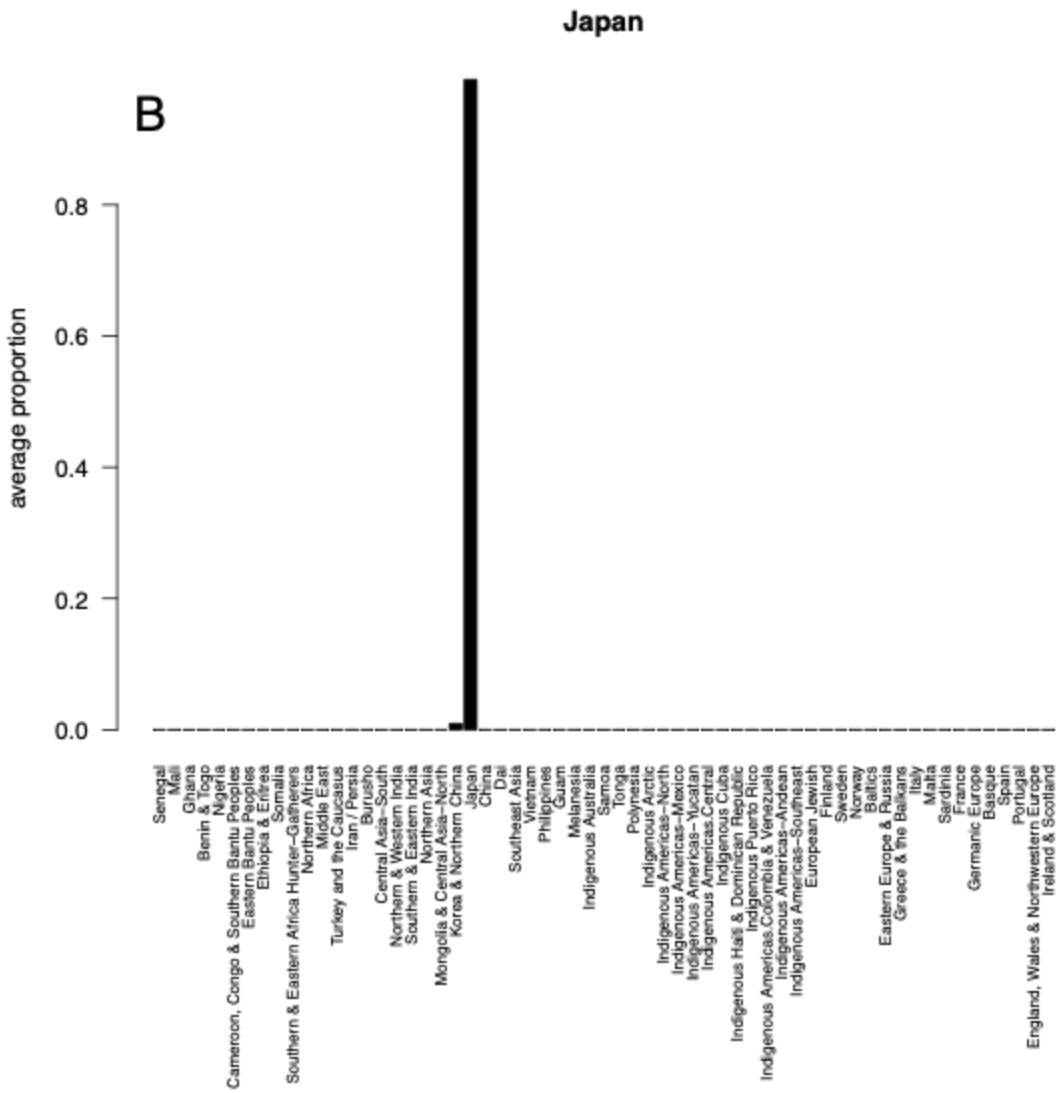


Figure 4.3 Average ethnicity assignments based on grandparental birth location. *Average ethnicity assignments for customers with all four grandparents born in the same country. (A) Germany, (B) Japan*

We also use the maps like the one shown in Figure 4.4 to ensure that ethnicity estimates make sense geographically. The geographic distribution of ethnicity estimates within a country can often help make sense of otherwise surprising results. For example, as you can see in Figure 4.4, there is a high level of Ireland and Scotland ancestry in the Brittany region of France. This makes sense because the Ireland and Scotland assignment is the result of Celtic peoples who lived both there and in Brittany. In fact, the Celtic

language Breton is traditionally spoken there. Higher Ireland and Scotland estimates in Wales also likely reflect the history of Celtic migration in that region.

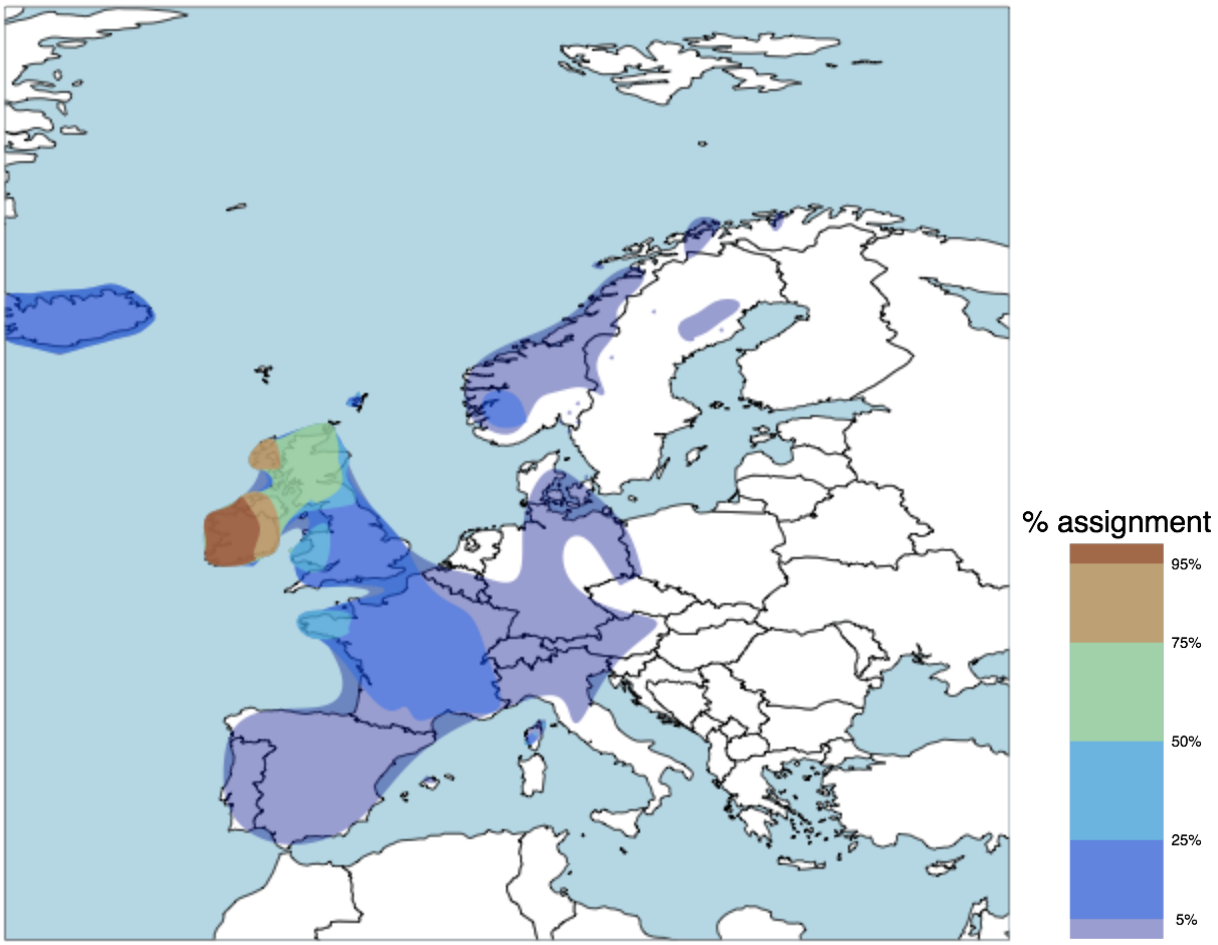
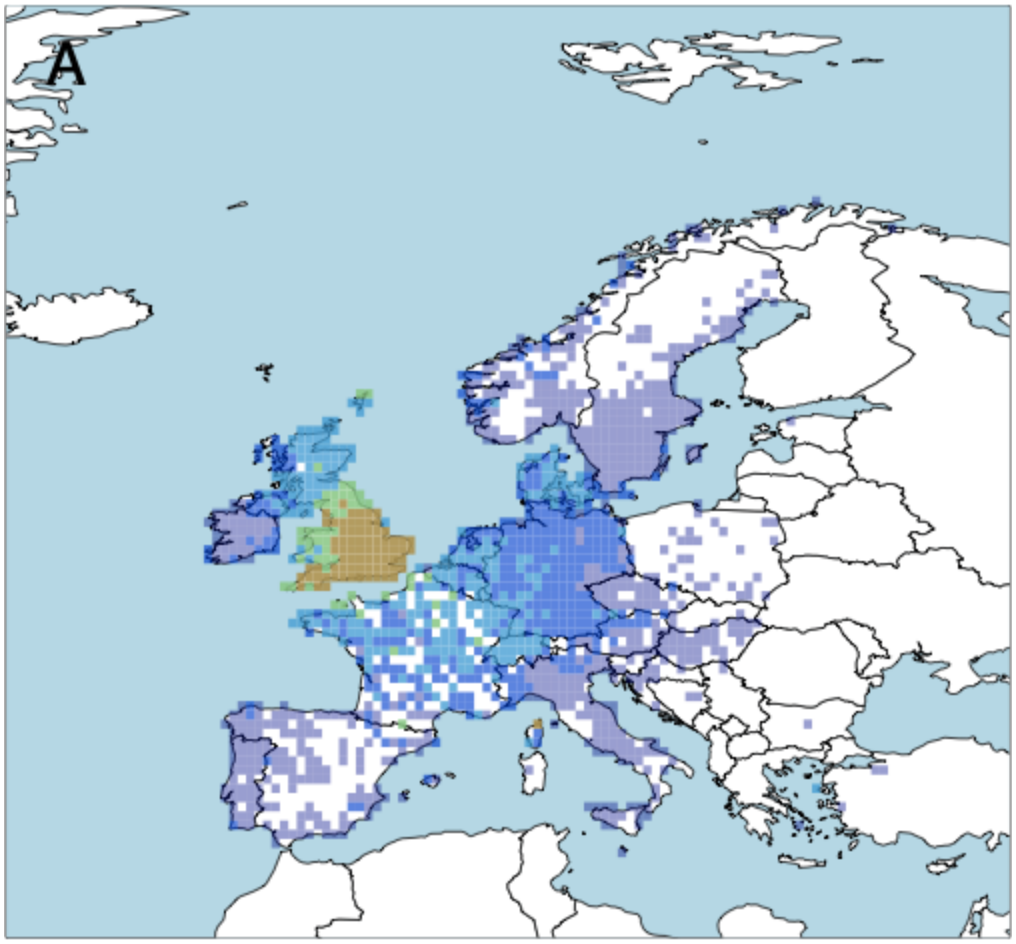


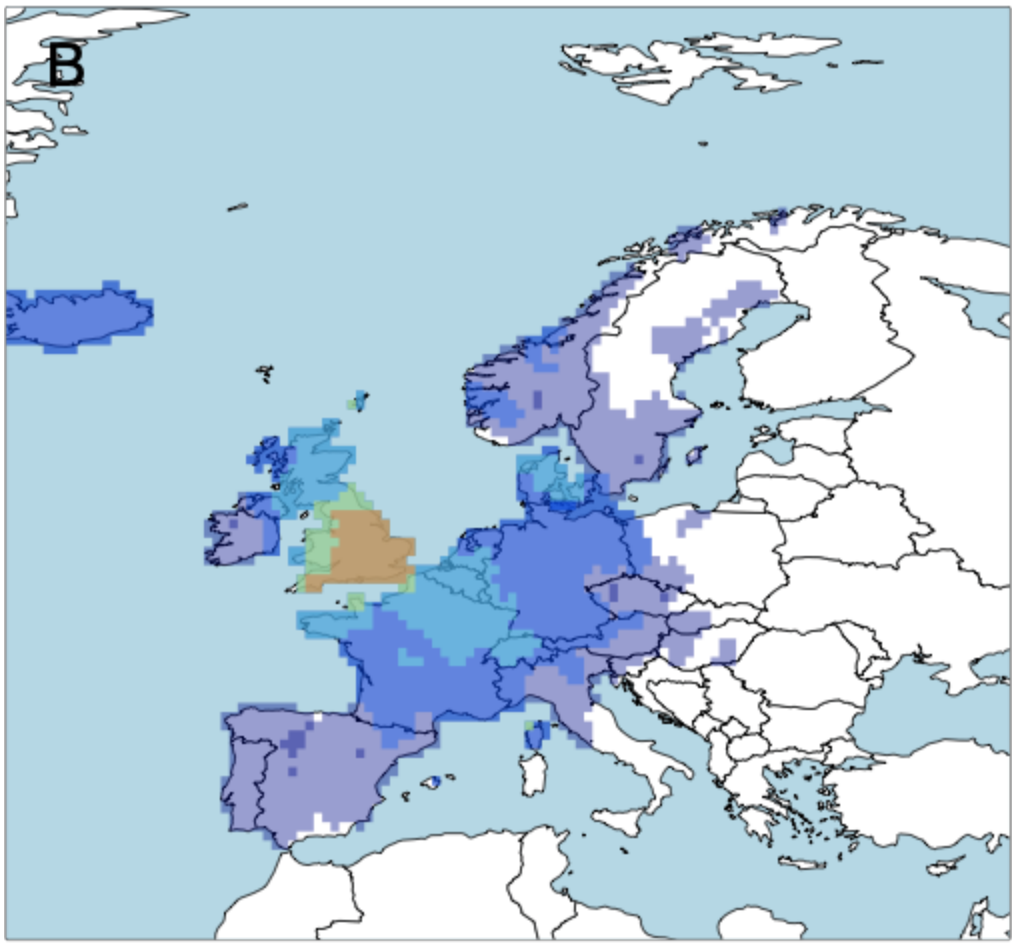
Figure 4.4 ***Map of average Ireland and Scotland estimates.*** *High estimates outside of Ireland in Scotland, Wales, and Brittany (as shown in light blue and green) likely reflect historic migrations of Celtic people.*

These analyses help us understand the genetic diversity of the regions and allow us to better communicate these results to our customers (e.g., even if all of a customer's ancestors are German, the customer can expect to have some amount of genetic ethnicity from adjacent regions). These analyses also aid us in prioritizing future developments for further ethnicity estimation updates.

4.3 Regional Polygon Construction

Because we use 60 populations in our reference panel, we divide the globe into 60 overlapping geographic regions/groups. Each region represents a population with a unique genetic profile. Where possible, we use the known geographic locations of our samples to guide where the regional boundaries should be. Figure 4.5 shows an example of the information used to define regional polygons.

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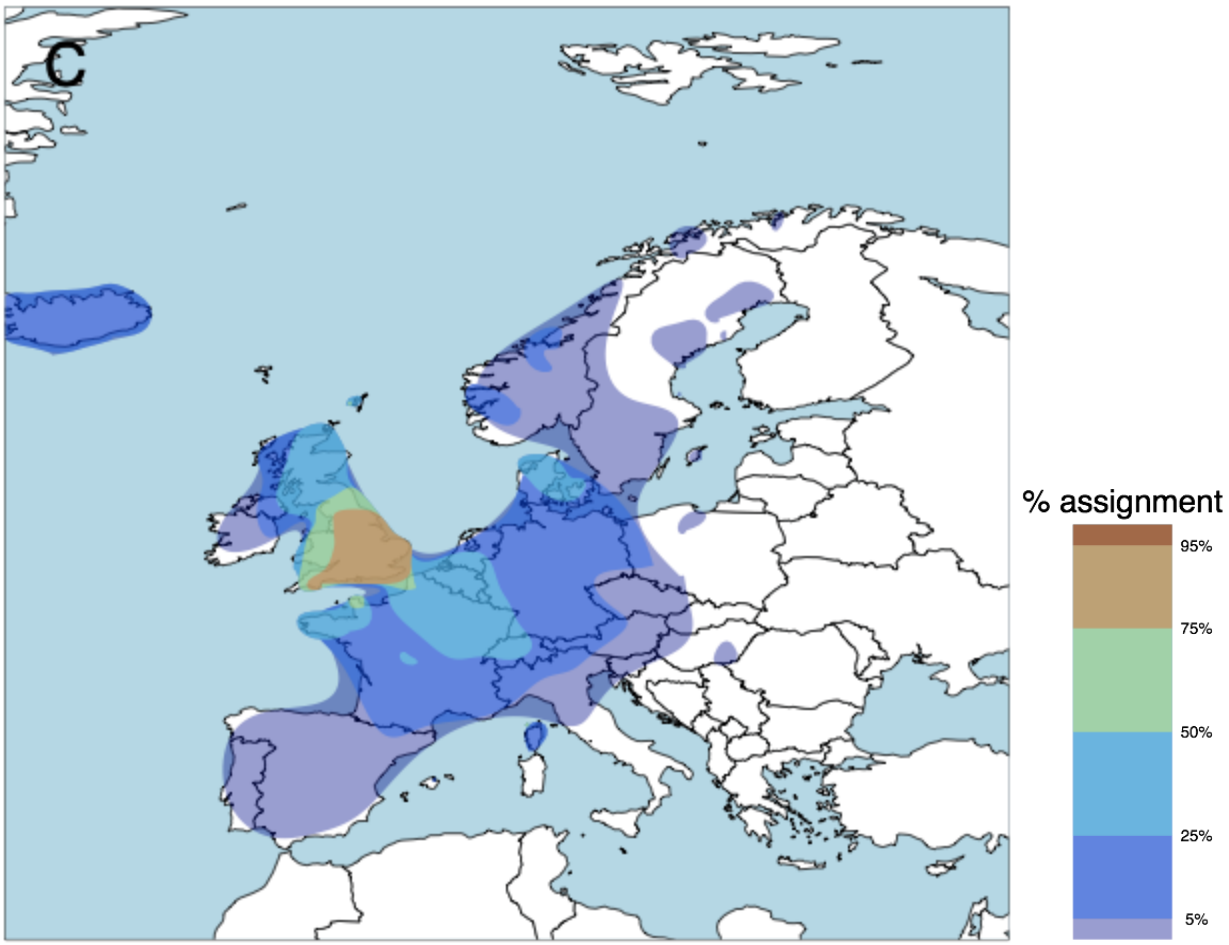


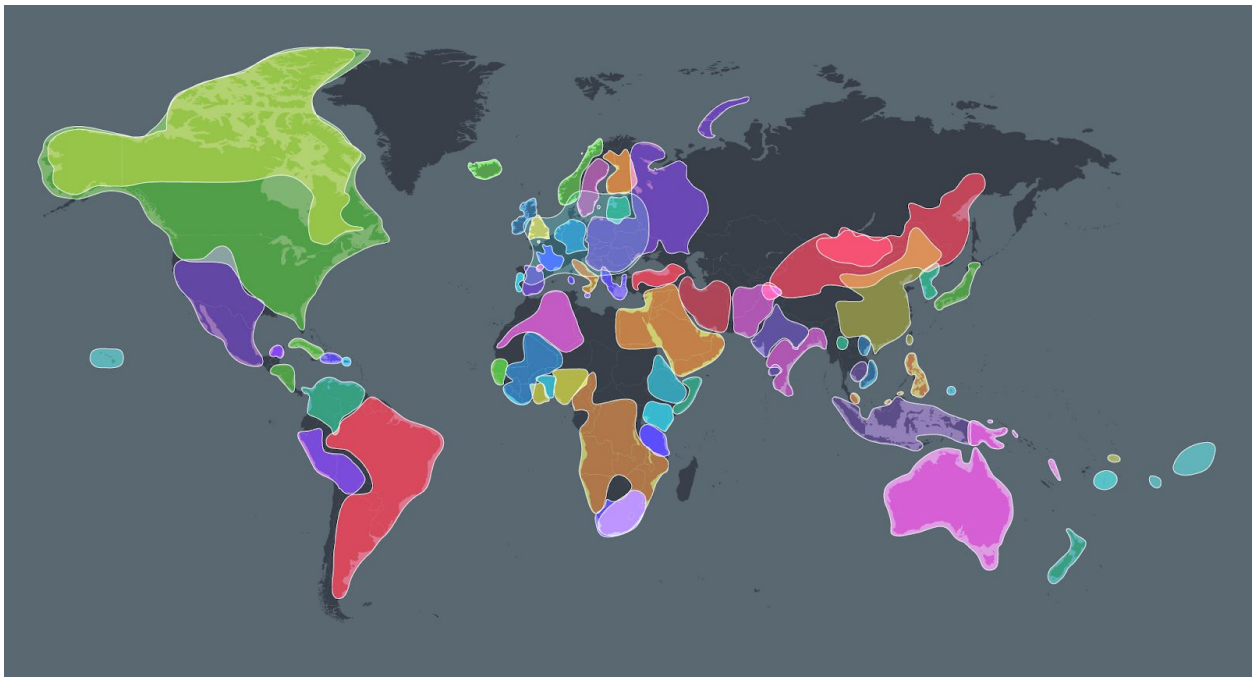
Figure 4.5: Using geographical sample locations to draw regional polygons. *Panel A shows the distribution of the England, Wales & Northwestern Europe ethnicity predicted for a set of samples with geographic information. Samples are assigned to grids of 0.5 degrees longitude by 0.5 degrees latitude based on the average birth location of their ancestors' grandparents. The color of each grid squarepoint on the map represents the average England, Wales and Northwestern Europe ethnicity of samples from each grid. Panel B shows the maps after filling in missing regions and smoothing the results. The information is processed with kernel smoothing to create the outlines representing the ancestry regions shown to customers, as shown in panel C.*

In Figure 4.5A, we show the amount of ethnicity assigned to the England, Wales and Northwestern Europe region for a subset of reference samples with known geographic locations. Figure 4.5B shows the results after imputing values to fill in gaps and applying smoothing methods to make the plot less spotty. It is clear from the plot that there is a gradient of ethnicity in this region that is centered in England that quickly tapers off in surrounding regions. For example, the next level of concentration, represented by green in the image, is in areas surrounding England, such as Wales, France, and Belgium. The ethnicity gradient continues to diminish as represented in purple with the borders reaching as far away as Italy, Switzerland, Sweden, and Ireland. Where possible, this information is applied directly to the drawing of

regional boundaries (Figure 4.5C) that appear on the maps presented as part of the AncestryDNA product experience.

These polygons appear as nested regions with increasing depth of shading. The reddish brown regions represent the regions with the highest average assignments and are the most likely physical locations of a customer's ancestors. The blue/purple regions have lower average levels and represent other possible locations of origin that are less likely. Each set of polygons is accompanied by a detailed account of the history of the region.

The map below shows polygons for all 60 ethnic groups based on the second tier of the polygons, constructed as described above.



4.4 Reporting uncertainty of estimated values

Ethnicity estimates are not an exact science. The percentage AncestryDNA reports to a customer is the most likely percentage within a range of percentages. In this section, we discuss how we calculate this

range. It is important to keep in mind that here at AncestryDNA we continue to build upon our previous work to offer ever more accurate results to our customers.

So, for example, we might report someone as 40% England, Wales and Northwestern Europe with a confidence range of 30-60%. This means that they are most likely 40% England, Wales and Northwestern Europe but they could be anywhere between 30% and 60% England, Wales and Northwestern Europe.

As discussed in section 3, we run a genome-wide Viterbi estimate on a customer's DNA sample and report that back as the customer's most likely ethnicity estimate. From this we are able to get transition probabilities that we can then use to generate new ethnicity estimates that while likely, are not the most likely. The range is based on 1,000 of these sampled paths. For example, if a window has an 80% chance of being from England and Wales, then it has a 20% chance of being from some other region. The confidence interval captures these sorts of lower chances across a customer's DNA.

We devised a way, using the 1,000 sampled estimates, to estimate the confidence interval surrounding the Viterbi estimate reported to the customer. Our objective when defining this approach was to maximize the probability that the reported range contains the true ancestry proportion (**recall**), while also maximizing **precision** by maintaining a fairly narrow range.

We take the mean and standard deviation of the 1,000 sampled estimates and use these to calculate a confidence range surrounding the Viterbi estimate. When calculating this range, we take into account the value of the Viterbi estimate and the population for which we are calculating the range.

We can test our process for calculating the range using the same synthetic admixed individuals used for the cross-validation studies to determine how often it correctly gets the known ethnicity percentage within the range. In other words, how often does the range overlap the known ethnicity. We find that the algorithm performs very well for some populations and less well for others. Since we know the true ethnicity, we can incorporate correction factors specific for each population to maximize the probability that the true ethnicity falls within the range.

5. Future Ethnicity Estimation Refinement

While AncestryDNA is extremely proud of the updates in this release of its genetic ethnicity estimation process, we will continue to improve the product over time. The availability of new data, the development

of new methodologies, and the discovery of new information relating to patterns of human genetic variation will all necessitate future improvements to the product.

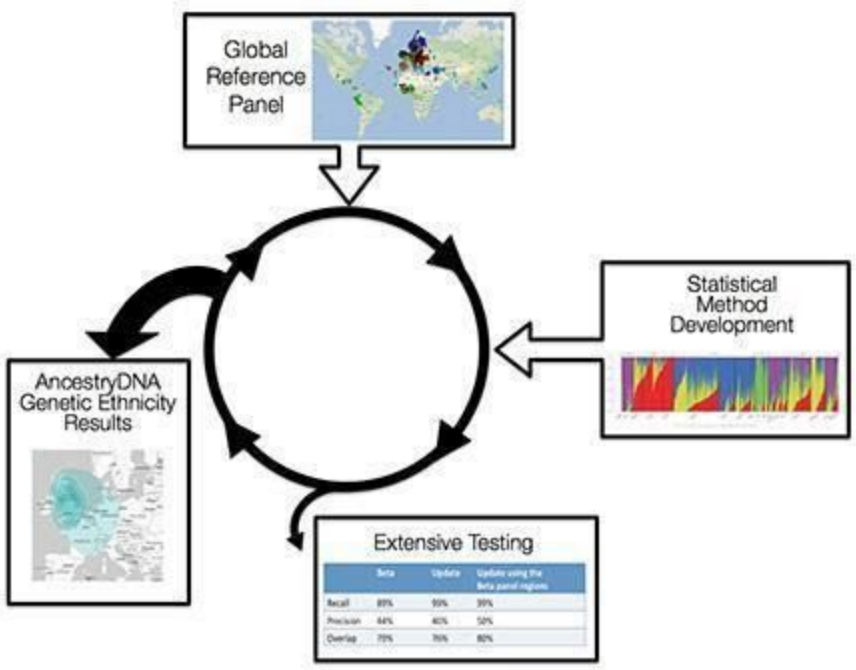


Figure 5.1: *Ethnicity Improvement Cycle.*

Each of the steps above represents a critical part of our ethnicity estimation procedure and development. Currently, we are working to further expand our global reference panel for future ethnicity updates. We have already begun genotyping and analyzing samples for a future update which will provide finer-grained estimates of ethnicity. We have also begun a new diversity initiative to gather DNA samples from underrepresented regions around the world in order to expand the number of regions we can report back to customers.

Simultaneously, we are also working to improve our algorithms for ethnicity estimation. Future ethnicity updates will include an improvement to our statistical methodology that will more fully leverage information in genetic data to reveal even more information about population history. Along the way, we always perform thorough testing, involving analyses like those described above. These tests inform the focus of our improvements, and help to refine our improvements as necessary.

Each new release of genetic ethnicity estimation will represent a step forward in our ability to give our customers a complete description of their genetic ancestry and inform them about their ancient genetic

origins. We hope that, like the entire team at AncestryDNA, our customers will look forward to these future developments.

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