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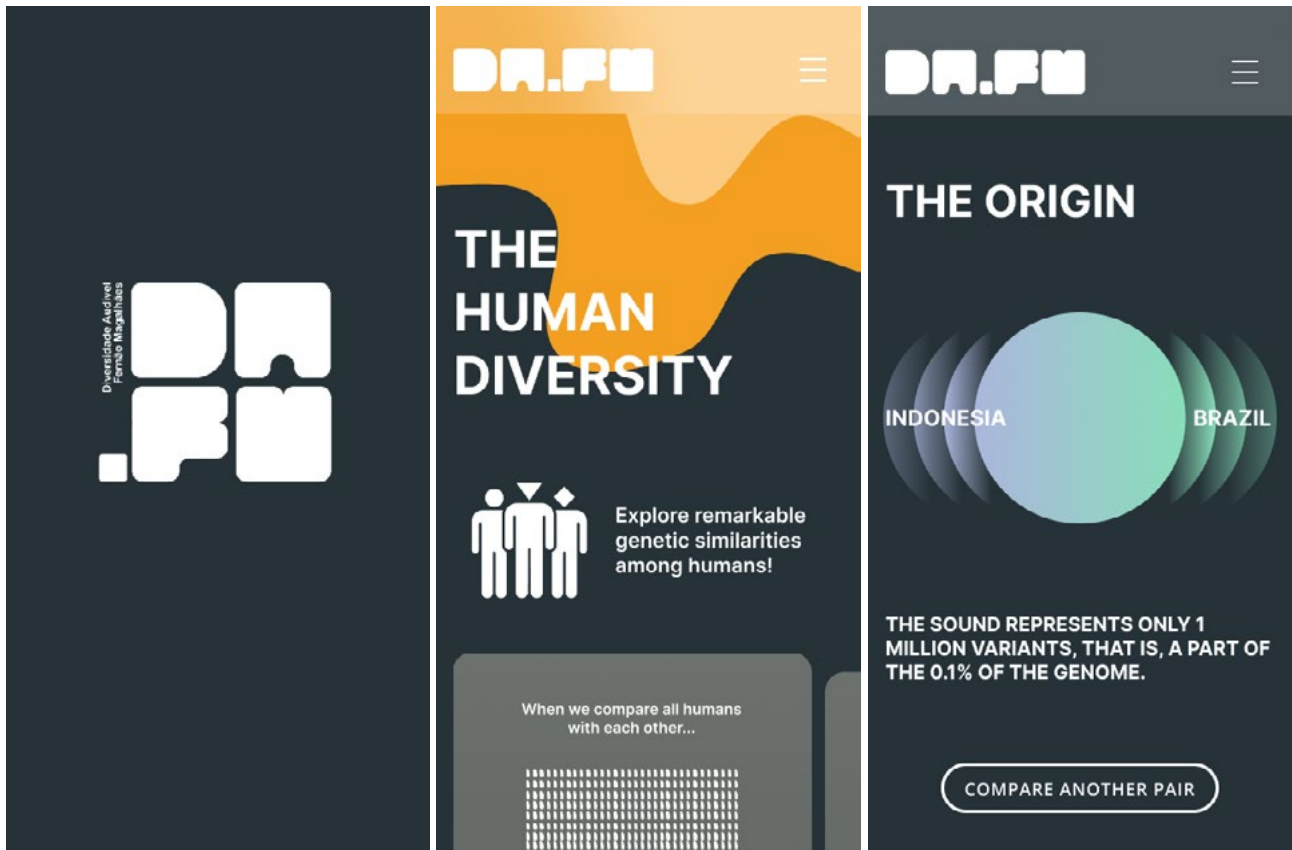
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More info at <https://ancestrytraveller.i3s.up.pt>

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Project “Human diversity along the Magalhães circum-navigation space: genetics, history and culture”



This app was developed in the scope of the project “Human diversity along the Magalhães circumnavigation space: genetics, history and culture”. Inspired by the circumnavigation voyage undertaken by Fernão Magalhães 500 years ago, this project focused on human diversity, linking genetics, history and culture. This first global journey was the starting point for exploring ancestry, an extremely complex, diverse concept often shrouded in contention. The result was several public activities and teaching resources.

One of the outcomes of this endeavour was an art and science exhibition, which explored various concepts of human genetics and how they connect. **“Audible Diversity”**, included in this app, was part of the **exhibition**.

The app was later expanded to provide a global and synthesized overview of some of the basic concepts explored in the project, namely the human genome, human diversity, the journey of human expansion and the first global voyage.

Human Genome

DNA (deoxyribonucleic acid) is composed of four nucleotide bases - adenine (A), cytosine (C), guanine (G) and thymine (T) - that repeat thousands upon thousands of times, depending on the size of the genome.

The bases pair in a specific way (A-T; C-G) and this complementarity allows the formation of the DNA double-strand, forming a double helix structure. In total, the human genome includes sequences that encode information in the form of another molecule (proteins, transport RNAs, micro RNAs - designated areas of coding DNA) and areas with other functions (e.g., regulatory) or of unknown function (non-coding DNA).

The human genome is composed of two copies of 23 DNA molecules. The 23 molecules contain approximately 3.1 billion bases, of which only 3.1 million (0.1%) correspond to variable positions. These variable regions are responsible for genetic diversity among all individuals.

RESOURCES:

1. Video **"What is DNA and How Does it Work?"**

This video covers basic concepts about DNA, its workings and its structure.

2. Video **"DNA Structure and Replication"**

This video describes the amazing DNA molecule and how it replicates in our cells.

Human Diversity

The human genome contains about 3.1 billion base pairs, distributed across 23 chromosomes. The genetic variation between two humans is about 0.1%.

The diversity of today's populations, which have gone through countless natural phenomena and cultural changes, leads to the misperception that we are more different from each other than we really are. This stems from the fact that we are a young species. Other mammals, such as wild boars or cats, show a diversity 4 times greater than that of humans. Even chimpanzees, the species closest to us and whose population is very small, have a genetic diversity of almost 0.2%, twice that of ours.

Countering this phenomenon is the diversity increase resulting from our long history of miscegenation. Despite social, historical and cultural conflicts, when we take an ancestry test, we are faced with the enormous contribution of migrations, prehistoric and historical, to our genetic heritage.

In addition, genetic variation around the world is distributed in a continuum; there are no sharp boundaries between human population groups. Research results show that about 85% of all human genetic variation exists within human populations, whereas only 15% of variation exists between populations.

RECURSOS:

1. Video **"Are We All Related?"**

This video uses mathematics and genetics to show us that we all come from the same family and share ancestors.

2. Information on human genetic diversity from the **"National Human Genome Research Institute"**: This organization is among the foremost authorities in the field of genomics. On its website, you can find general information on the topic and educational resources for teachers and students.

3. Video **"The DNA Journey"**

This video, produced by a travel company, went viral. They invited 67 people from all over the world to take an ancestry test. The result? They found that they had a lot more in common than they had figured.

Human expansion

Humanity's first great journey was the expansion of modern humans (*Homo sapiens*) across the globe. With Africa as a starting point 300,000 – 200,000 years ago, only about 70,000 years ago did a small group of modern humans successfully migrate out of Africa, taking advantage of the favourable conditions to expand over the immense land mass. The expansion took place quickly in evolutionary terms and was made in waves of small groups that expanded and multiplied in the new territories reached. One of the genetic effects of this expansion process completed by small founding groups was the decrease of populations' genetic diversity the farther they were from the original region.

RESOURCES:

1. Video **"Why Human Ancestry Matters: Crash Course Big History 205"**

This video is a brief narrative of modern humans' expansion from their origin in Africa 300-200 thousand years ago. The contents narrated here are similar to those depicted in our exhibit **"A journey through human genetic diversity"**.

2. Video **"Map Shows How Humans Migrated Across the Globe"**

Short video showing how the first humans spread from East Africa across the globe.

3. We suggest you use **3D Globe**, a didactic tool devised in this project's scope, and its instructions. This globe contrasts two great voyages: the voyage of human expansion, and the first circumnavigation by Magalhães and Elcano.

4. We suggest the **game Populations** to explore how humanity's great voyage influenced the variability of current populations and basic concepts of population genetics. The game was also developed in the scope of this project and introduces knowledge about population genetics in a playful way, simulating how diversity can evolve over time as a result of different phenomena while also exploring the risks of low diversity.

First global voyage

The first global voyage encircles the vast “archipelago” of continents and was undertaken between 1519 and 1522. Fernão Magalhães and Juan Sebastián Elcano undertook a sea voyage and, for practically the whole duration, their course went through the southern hemisphere. This journey goes in the opposite direction to the human expansion, which started 70,000 years ago and was carried out mainly by land. Many of this second voyage’s landmarks were, at the time, vital and dynamic commercial points and a meeting ground of different cultures and lineages. After all, many generations of modern humans have built, destroyed and rebuilt geographies, cultures and knowledge. It was this voyage, however, that proved global sea travel was possible.

EXPLORATION PROPOSAL:

To further explore the voyage of Fernão Magalhães and Juan Sebastián Elcano we suggest:

1. The **Magalhaes2020 app**, produced by the newspaper Expresso, which goes through Magalhães’ whole journey.
2. Reading **“Series: Encounters, equivocations, and extensions of memory: legacies of the circumnavigation voyage”**, written by researchers in our project to offer a critical insight into the history of the voyage trailed by Magalhães and Elcano.
3. Using the **3D Globe**, a didactic tool created for this project, and its instructions. We propose that you use the globe together with the **Population Education’s interactive tool**. This app lets you explore the evolution of the population in correlation with historical events. Students can go over historical events that occurred during the period spanning the circumnavigation voyage, which took place between 1519 and 1522. By exploring the events happening, say, between 1500 and 1550, students can then discuss geopolitical circumstances between the Iberian Peninsula and the destination, the Maluku Islands.

DA.FM (Audible Diversity)

Among humans, the genome varies only 0.1%, a result of the alteration of bases in the enormous DNA sequence. Today we are able to ascertain practically all the regions where two individuals may have a different base. Therefore, to characterise their ancestry, it is not necessary to sequence the entire genome, but rather to characterise which bases are present in these variable regions.

To understand this process, it is important to understand what a SNP is: **Single nucleotide polymorphism**.

SPN, or single nucleotide polymorphism, is a variation between individuals at the position of a single nucleotide in a DNA sequence.

If more than 1% of a population does not have the same nucleotide at a specific position in the DNA sequence, then this variation can be classified as an SNP.

SNPs occur throughout DNA, including non-coding regions (in which DNA does not encode proteins). On average, they occur almost once in every 1,000 nucleotides, meaning that an individual's genome comprehends about 4 to 5 million SNPs.

Most SNPs do not affect health or development, but some of these genetic differences help predict an individual's response to certain medications, susceptibility to environmental factors, and risk of developing diseases.

RECURSOS:

1. **Video "Genetics 101: What are SNPs?"** This video is the result of a collaboration between Khan Academy and 23andMe, and it explains what SNPs are and how they can be used to understand similarities and differences between individuals.

In research, different methods are used to detect genetic variability. Some are designed to detect only known variants. It may be important, for instance, to learn whether a person has inherited a particular variant that will impact their health. Should that be the case, a specific DNA test can be performed to determine if the person carries this variant. Other methods allow DNA analysis to detect the presence of a large number of known variants; **microarray tests** are one such method, in which hundreds of thousands of SNPs can be detected at once.

The microarray is like a "chip" that contains thousands of dots with individual strands of DNA; some are fragments of the normal gene and others are the genetic variants of interest. The DNA from the sample binds to the DNA on the chip. If you have a specific variant, the DNA binds to the spot on the chip with that variant.

Subsequently, the data are compared with reference databases containing variants associated with different population groups. If you have a variant only found in Europeans or Africans, then it is very likely that you have ancestors in that geographic region. The genome tested is compared with the reference database to identify which variants are present and a report is compiled based on this analysis. The ancestry information in the report will always depend on the reference database used.

RECURSOS:

1. More **information on DNA microarray**
Wikipedia page with detailed information on the functioning of DNA microarray, its types and uses.
2. Article "**The limits of ancestry DNA tests, explained**"
Video article that explains how ancestry tests work and introduces some questions about how we understand your data and results.

The "**Audible Diversity**" app starts from individual data of genetic profiles (about 1 million variants) of 15 individuals from 5 geographical points related to the Fernão Magalhães' expedition. Through musical translation, we can sonically perceive the analysis of genetic variability. The adopted sonification method was audification, which compares the results of each individual's specific genetic data. The level of genetic variability is symbolized across the sound spectrum whenever we compare two individuals. Lower values of genetic variability are represented by low-intensity sounds; conversely, an elevated genetic variability translates into more intense sounds, together with a faster rhythmic pattern.

Brief description of population ancestry from the 5 analysed locations:

- PORTUGUESE

Portuguese ancestry is diverse, shaped by millennia of events on the Iberian Peninsula. The first inhabitants were hunter-gatherers who arrived in the region 40,000 years ago. During the last Ice Age, the Peninsula served as a climate refuge, ensuring the survival of human populations that later migrated to other parts of Europe. The introduction of agriculture 7,500 years ago also contributed to the diverse genetic profile, maintaining a strong hunter-gatherer component. About 5,500 years ago, migrants from the Russian and Ukrainian steppes arrived on the Peninsula, partially replacing the existing male population. Starting in the first millennium BC, the Celts began to reach the Iberian Peninsula and especially influenced the North. During the Roman period, interactions and migrations intensified, adding Jewish and North African influences to the peninsula. After the fall of the Roman Empire, Germanic tribes such as Suebi and Visigoths settled in the Iberian Peninsula, leaving their genetic traces. Between the 8th and 12th centuries, the Muslim conquest brought Moorish and Jewish genetic contributions. During the Middle Ages, Jewish migrations as well as trade and slavery with sub-Saharan Africa increased Sephardic genes. Minor influences include Viking settlements between the 9th and 11th centuries, especially in the Douro and Minho regions, and pre-Roman Phoenician and Greek influences in the southern coastal areas. Today's Portuguese ancestry therefore reflects a complex mix of cultures and genetic origins and remains one of the most genetically diverse regions in Europe.

- BRAZILIANS

The Brazilian population is one of the most heterogeneous in the world, with three main components – European, African and Native American - and boasts extensive miscegenation, the result of more than 500 years of interactions between different ethnic groups. Indigenous peoples were the first inhabitants of Brazil, whose diversity left a significant mark on the current population. The arrival of Europeans, mainly Portuguese, starting in the sixteenth century, introduced a genetic mixture with native populations, predominantly among European men and indigenous women. For centuries, Brazil was one of the major destinations of the transatlantic slave trade, and millions of West Africans - mainly from Guinea, Congo, Angola, Mozambique and Nigeria - were taken there. The genetic and cultural contribution of these Africans is profound and influences many aspects of contemporary Brazilian society. In the late 19th and early 20th centuries, Brazil also received large waves of immigrants from various parts of the world, including Italians, Germans, Japanese, Syrians, and Lebanese. The genetic makeup in Brazil reveals a diverse geographical distribution, reflecting each region's occupation history. In the Northeast, which witnessed the arrival of larger contingents of African slaves, African ancestry is predominant. In the South, including Rio de Janeiro, an intense European migratory flow in the 18th and 19th centuries contributed to the highest proportion of European ancestry in the country, up to 81.8%. Due to its geographic isolation and the Amazon, the Northern region was occupied at a later stage, with a high prevalence of indigenous populations.

- INDONESIANS

The ancestry of Indonesia reflects the complex history of migrations and cultural interactions in the archipelago, presenting two main ancestral genetic components – Papuan and Asian. The Papuan component, which originates from early modern humans in Sunda and Sahul (ancient landmasses in the region during periods of glaciation), reaches its highest frequency in eastern Indonesia but it is essentially absent west of the Wallace line, which separates the distinct Sunda and Sahul faunas. The Asian genetic component, the most frequent, had its origin possibly via Taiwan, about 5,500 years ago, and it is associated with the Neolithic expansion of Austronesian speakers. The expansion of agricultural practices has significantly influenced the genetic variability of local populations, facilitating interactions and cultural exchanges with neighbouring Southeast Asian groups. The sea routes connecting Indonesia with other parts of Asia, such as India, China, and even the Middle East, played a crucial role in introducing new genetic and cultural elements. However, the impact of miscegenation in Indonesia tends to be less pronounced than in other regions of the world. The Indonesian population's genetic diversity mainly reflects Asian influences and maintains a distinct genetic identity within Southeast Asia.

- EAST TIMORESE

Timor-Leste, in Southeast Asia, has a genetic and cultural heritage influenced by Asian, Pacific and, more recently, European peoples. The first inhabitants of Timor-Leste were the Austronesian peoples who spread across Southeast Asia and the Pacific. These migrants, possibly from Taiwan some 4,000 to 5,000 years ago, brought agriculture, navigation technology, and new languages, leaving a significant mark on the genetic makeup of today's inhabitants. In addition to the Austronesian heritage, the Timorese also have a significant genetic contribution from the Papuan peoples, descendants of the first modern humans to occupy the Sunda and Sahul region, which covered New Guinea and Australia, more than 40,000 years ago. In Timor-Leste, this ancestry is most evident in mountainous regions and more isolated areas, reflecting the complex history of migration and genetic mixing. With the arrival of European explorers in the 16th century, first the Portuguese and then the Dutch, a new chapter in the history of Timor-Leste began. The Portuguese presence, which lasted more than 400 years, bore cultural, linguistic and, to a lesser extent, genetic influences. The genetic diversity observed in Timorese is a testament to the multifaceted history of migration and human interaction in the region.

- CAPE VERDEAN

African people were the first dwellers of the Cape Verde islands, in particular those of Senegambian and Guinean origin, who were brought onto the archipelago as slaves during the 15th and 16th centuries. These African groups significantly contributed to the genetic composition of the present Cape Verdean population. Besides their African heritage, Cape Verdean people were also influenced by Europeans due to Portuguese colonization, beginning in the 15th century. Portuguese settlers brought not only their culture and language but also European genes that mixed with the local population throughout centuries. This mixture resulted in a unique genetic diversity, thus Cape Verdeans' wide range of physical and genetic traits.

Recent genetic studies have shown that Cape Verdeans are an outstanding example of how diverse historical and cultural influences can shape a unique genetic makeup. This rich ancestry tapestry mirrors Cape Verde's multifaceted history and human interactions over the centuries.

EXPLORATION PROPOSAL:

1. Discuss with students:

- Why are recent and/or poorly mixed populations less diverse?
- Why are ancient and very mixed populations more diverse?
- Why do individuals from populations with more distinct ancestry have greater comparative variability?

2. Use the app to compare two Timorese, two Brazilians and two other individuals from different populations. Taking into account the information previously provided about these populations' ancestry, discuss the sounds you heard and potential meanings.

3. How does DNA reveal our ancestry?

Explore how DNA can be used to identify family history and geographic origins.

4. What are genetic markers?

Explain how different DNA markers indicate diseases, physical characteristics or ancestral lineages.

5. What are the limitations of DNA testing for ancestry?

Ponder on the inaccuracies and biases that the results may elicit, as well as the influence of mixed populations and the lack of complete data for all regions of the world. The article "[The limits of ancestry DNA tests, explained](#)" may be useful.

6. How does being knowledgeable about ancestry influence our identity? Discuss the importance of understanding ancestry and how this information can shape your self-perception.

7. What are the social and cultural implications of discovering an unexpected ancestry? Discuss how the discovery of lineages different than expected may impact identity and worldview.

8. How does ancestry connect with culture and history? Explore the role of genetics in understanding migrations, interactions between cultures, and the formation of ethnic and national identities.

9. How does the study of genetics add to preserving cultural and biological diversity? Discuss the importance of protecting human genetic diversity and the challenges of preserving different ethnic groups' culture and history.

10. Use the **website “Sapiens Teaching”** as a complementary tool to explore these topics. This teaching tool focuses on the intersection of pedagogy, ethnography and anthropology, and it includes discussion guides, activities and reflections.

- **Guided page exploration**

Divide students into small groups and assign different sections of the page to each group. Give each group a specific task, such as identifying and explaining historical research methods, discussing key concepts, or analysing case studies presented on the page. Ask each group to present their findings, thus promoting information and perspective exchange.

- **Discuss in the classroom**

Use open-ended questions to prompt debate, such as “What methods are most effective to study history?” or “How do historical concepts influence our understanding of the past?”. Organise debates on the relevance and application of different historical methods and concepts in contemporary studies.

- **Do interactive activities:**

Ask students to apply a specific historical method to a case study provided on the page, and review their findings and conclusions. Have students create a collaborative timeline that includes the discussed historical methods and the contexts in which they were applied.

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