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| Genetic and Population Analysis  Haplotracker: Tracing the movement of Haplogroups on a Map  Nikhilesh Vasanthakumar1\*  1Department of Biology, Box 118, 22100, Lund University, Sweden.  \*To whom correspondence should be addressed.  Abstract  **Motivation:** Understanding the migratory patterns of ancient human populations is important to unravelling human history and evolution and can provide crucial insights on how certain groups of populations moved, mixed and diversified over time.  **Results:** Haplotracker tool is an easy-to-use interactive web-based application that allows easier access to visualizing the Haplogroup data for those interested in Population genetics and migration patterns.  **Availability:** Haplotracker uses Python and hosted using streamlit.It is available at **https://nikhilesh-vasanthakumar-haplotracker-haplogroup-tracker-wqf8g7.streamlit.app/** and the source code is available at **https://github.com/Nikhilesh-Vasanthakumar/Haplotracker**  **Contact:** ni2651va-s@student.lu.se  **Supplementary information:** Supplementary data are available at *Bioinformatics* online. |

# Introduction

Haplogroups are genetic lineages or groups of people who share a common ancestor and have inherited similar genetic variations, known as haplotypes. Haplogroups are named using letters of the alphabet, with subdivisions denoted by numbers and letters.Haplogroups are maternally or paternally inherited from only one parent thus enabling unique identification. The distribution of haplogroups varies across different populations, reflecting the history of human migration and population movements over time.

The study of haplogroups has important applications in genetic genealogy, anthropology, and population genetics, as it can provide insight into the evolution and diversity of human populations.

The Haplotracker is an interactive web-based application **https://nikhilesh-vasanthakumar-haplotracker-haplogroup-tracker-wqf8g7.streamlit.app/** designed to provide easy access to this information and help visualize the movement of the haplogroups in history on the map based on ancient DNA dataset for Eurasia.

# Methods

HaploTracker is a web-based application developed using Python v3.9 and hosted on Streamlit. The tool relies on several Python libraries, including Pandas (v1.5.3), Plotly (v5.13.1), Streamlit (v1.20.0), Pillow (v9.4.0), plotly-express (v0.4.1), and openpyxl (v3.1.2). These libraries were used to implement the application's core functionalities, such as data visualization, mapping etc. HaploTracker uses data obtained from an Excel file provided, which serves as a database for the processed ancient DNA data. By leveraging these tools and resources, HaploTracker enables users to explore their selected haplogroup data.

# Features

HaploTracker works by integrating genetic and geographic data to visualize the distribution of human genetic variations. The tool allows users to filter a large database of genetic data based on their input, and display the relevant haplogroups on a map of their choosing. To use HaploTracker, the user starts by selecting the mode of operation which could be “MtDna”, “MtDNA-Female”,”MtDNA-Male” and “Y-Chromosome”, the user then can select multiple haplogroups they wish to visualize, and choose the type of map on which they want to view them. HaploTracker then filters the database and displays the selected haplogroups on the chosen map, allowing the user to explore geographical distribution of their chosen haplogroups.The user can also at any point hover over the points to find out its latitude, longitude, Modern-day country and the “age from 2020”.

The user can then select a haplogroup to generate a static trace plot of its distribution. The user can then play this animation to visualize the movement of the haplogroup over time and space, providing insights into the migration patterns and population histories of the selected group..After which, the user is able to select which haplogroup they wish to animate and this creates a map which contains a static trace plot.The user can play this animation to visualize it.

Haplotracker being a web application makes it easily accessible, scalable and allows for collaborative features such as user accounts and real-time updates, but it may also be dependent on a reliable internet connection, have limited processing power, be vulnerable to security risks, have a potentially inferior user experience compared to a standalone program.

# Discussion

Haplotracker being a web-based application provides easy access to haplogroup data and to visualize the human genetic variation distribution.The tool allows user flexibility to choose any number of Haplogroups to visualize limited only by the dataset. HaploTracker filters the database and displays the selected haplogroups on the chosen map, allowing the user to explore the geographical distribution of their chosen haplogroups.

One of the key features of HaploTracker is its ability to generate a static trace plot of the distribution of a selected haplogroup. The user can then animate this plot to visualize the movement of the haplogroup over time and space, providing insights into the migration patterns and population histories of the selected group.

HaploTracker can be a valuable tool for a wide range of users interested in studying haplogroups and their movements over time. For genetic genealogists, HaploTracker can be scaled to input user given data which can help in tracing their family trees by visualizing the geographic spread of their haplogroups. Anthropologists can use HaploTracker to investigate the migration patterns and history of human populations in different regions of the world. Population geneticists can use it to study the genetic diversity and evolution of different populations and to identify potential genetic markers associated with disease susceptibility or other traits.

Furthermore, HaploTracker can provide insights into the genetic makeup of human populations and the history of human migrations, which can be useful in various fields such as forensics, biogeography, and archeology. In summary, HaploTracker can be an invaluable resource for researchers and enthusiasts interested in the evolution and diversity of human populations.

One limitation is that Haplotracker is dependent on the accuracy of the ancient DNA dataset for Eurasia that is used as a database. Any inaccuracies or errors in the data can affect the results generated by the tool.

There are some known bugs which include the styles.css file not loading

in the streamlit website and the Play button for the animation being merged with the background. Additional bugs may be reported by the users as and will be solved over time.

There are several potential improvements that can be made for the app including adding a module to receive in user processed data or receive the data which can be processed to create a database for Haplotracker. Possible integration with machine-learning algorithms to predict the haplogroups based on genetic data alone. Haplotracker could also be further integrated with existing online databases to expand the tools scope.

# Conclusion

In conclusion, the HaploTracker application is a useful tool for visualizing and analyzing haplogroups and their geographic distribution. The application's ability to animate the movement of haplogroups over time provides insights into human migration patterns and population histories. HaploTracker can be beneficial to researchers and enthusiasts in various fields, including genetic genealogy, anthropology, and population genetics. While the tool has limitations and known bugs, there is great potential for further development and improvement, including integration with machine-learning algorithms and other online databases. Overall, HaploTracker is a valuable resource for studying the diversity and evolution of human populations, and its continued development could lead to significant improvements and has the potential to further advance our understanding of human population genetics and migration patterns.

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**Fig. 1. Relation between τ and *t*.** This example has only two continuous Steppers, S1 and S2.

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**Table 1.**Benchmark results of the cascade oscillators model

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| |S| | Predicted cost | Timing | Predicted speed | Speed |
| 1 | S219.20(100%) | 68m43s | 1.00 | 1.00 |
| 2 | 29.10+219.10(~50%) | 35m13s | 2.00 | 1.95 |
| 4 | 219.20(100%) | 68m43s | 1.00 | 1.00 |
| 10 | 29.10+219.10(~50%) | 35m13s | 2.00 | 1.95 |
| 20 | 219.20(100%) | 68m43s | 1.00 | 9.5 |

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Acknowledgements

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*Conflict of Interest:* none declared.

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