Evolutionary Patterns in Historical Genomes from Britain

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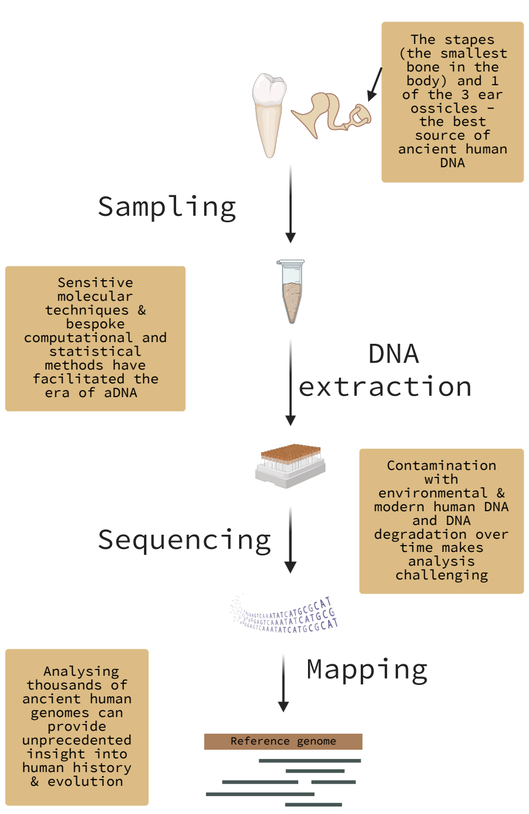
1/ What is ancient DNA (aDNA) & how do we obtain it?



2/ Why focus on Late and Post Medieval Britain?

Bridging past and present to refine our understanding of modern British ancestry

Strong local archaeology networks contributing samples & interpretations

Impact of infectious disease and selection on immune-related genes

Demographic shifts due to urbanisation and industrialisation

Confirm or revise historical records and gain social & cultural insight

3/ What have we learned?

Large-scale ancient genomic study with implications for population & medical genetics and history

Genetic disease detection and kinship analysis offer insight into cultural practices in past societies

Clusters of "distant relatives" between sites in Northwest England and Scotland suggest short-range mobility and fewer long-distance connections

This approach can highlight diseases to which people with higher PRS values would be more susceptible in the presence of environmental triggers

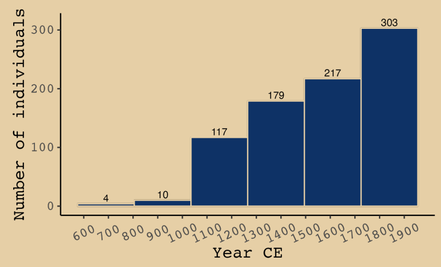
Future work can uncover additional adaptations and the physiological mechanisms underlying these findings

Using genomics to piece together a more complete narrative of how people lived, moved, adapted and survived in one of the most transformative periods of British history

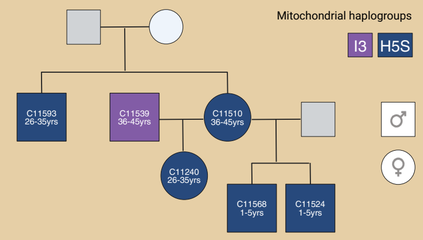
830 ancient genomes

55 archaeological sites

1000 CE - present day

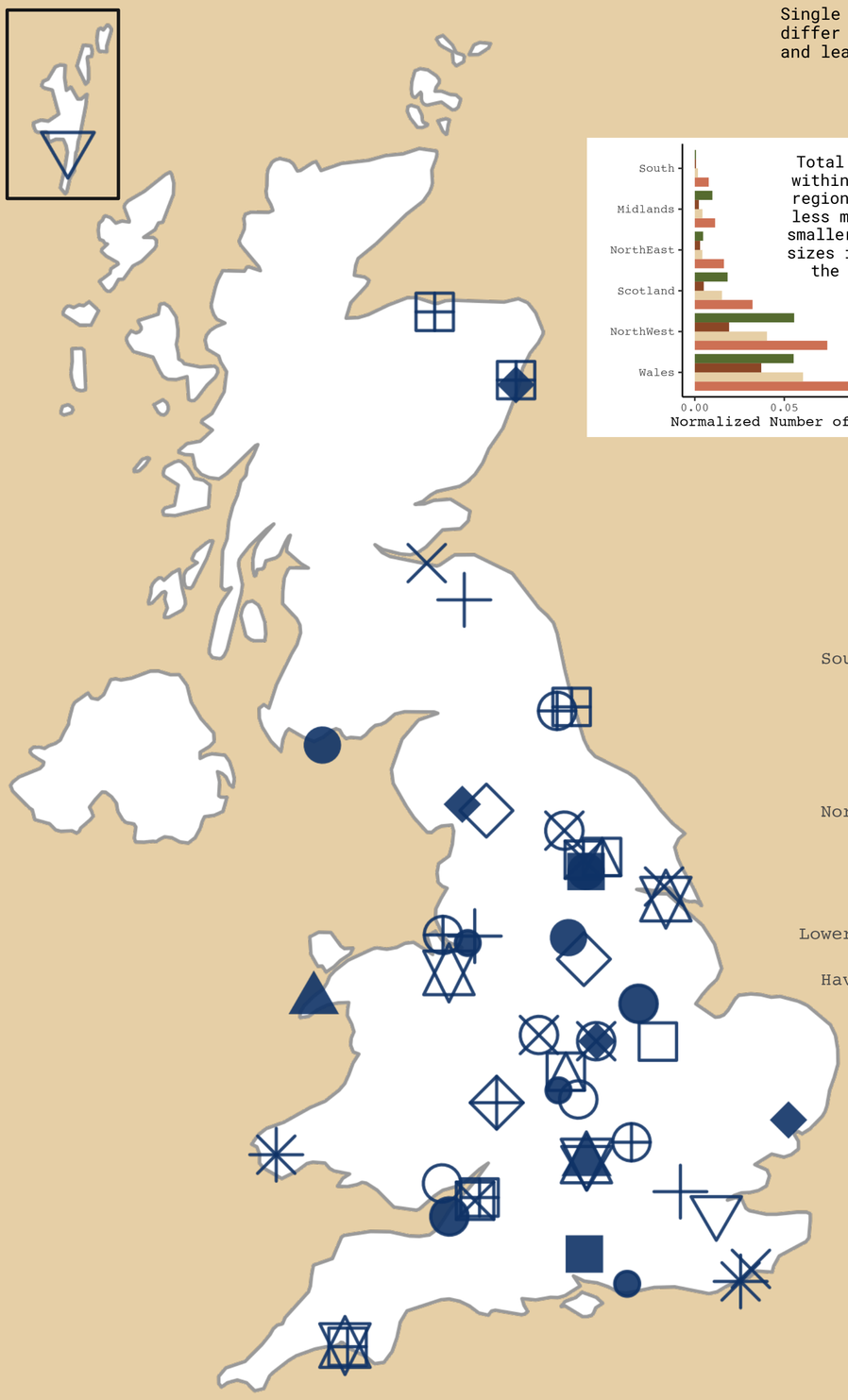


Temporal distribution of genomes produced and analysed in the present study. This is a 20x increase in the number of available genomes from Late and Post Medieval Britain, representing people that lived in larger cities (like London and Edinburgh) as well as smaller villages, hospitals or friaries (like the deserted settlement of Lower Radbourne and the Winchester Leper Hospital). Spatial distribution is shown in the map below.

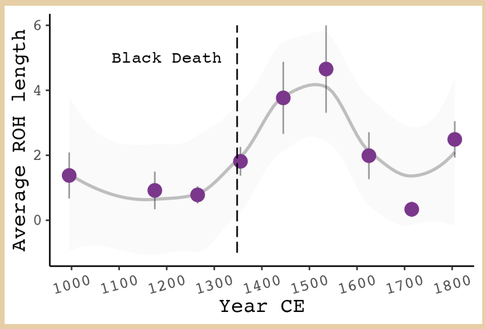


Using ancient DNA we can reconstruct family trees based on the degree of genetic relatedness between individuals, their mitochondrial and Y haplogroups (these are inherited exclusively from the mother and the father, respectively) and osteological estimates of age at death.This is an example of one such tree, where a woman was buried with her husband, brother, and daughter, as well as with two sons from a different partner.

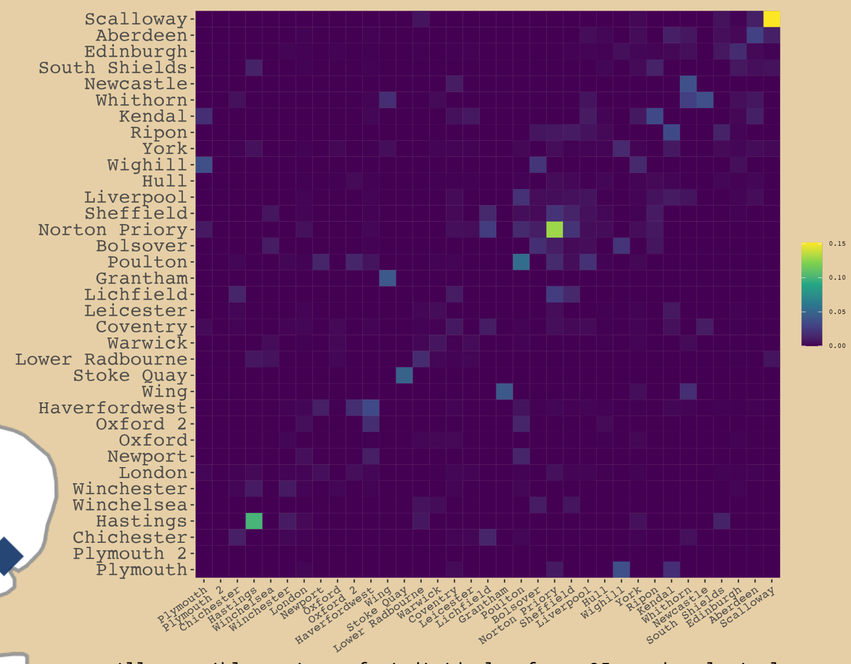
Mobility & Demography



Single Nucleotide Polymorphisms (SNPs - positions in the genome that differ between individuals) are useful to investigate mobility patterns and learn about the individuals we are studying & their own ancestors.



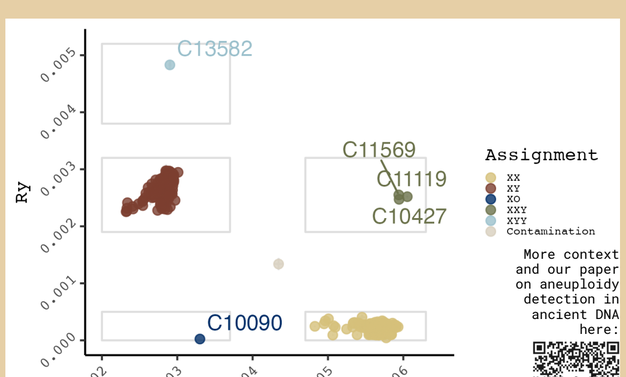
Population crash following the Black Death, as shown by increased Runs of Homozygosity (ROH)



All possible pairs of individuals from 35 archaeological sites were tested for Identical-By-Descent (IBD) segments, i.e. long stretches of DNA shared between individuals with a recent common ancestor. Overall, people shared more IBD with others from the same or neighbouring sites.

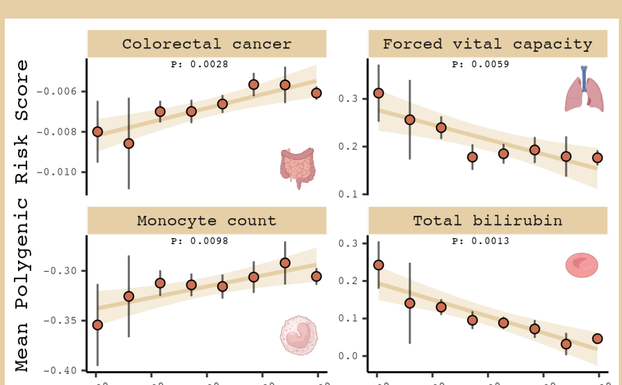
Health & Disease

Detection of aneuploidies



One individual with Turner syndrome (45,X0) was identified for the first time using ancient DNA, alongside individuals with Down, Klinefelter and Jacob's syndrome. These syndromes are examples of aneuploidies, where there are additional or missing chromosomes in someone's karyotype.

Disease risk through time



Polygenic Risk Scores (PRS) represent an individual's genetic "predisposition" or risk for a trait or a complex disease. A higher PRS value does not necessarily signify manifestation of the disease of interest and we can not predict whether a specific ancient individual might have suffered from it.

Four traits with PRS values showing significant increase or decrease in the last millennium, possibly as a response to changes in diet, infection or other environmental conditions.

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