



Twigstats

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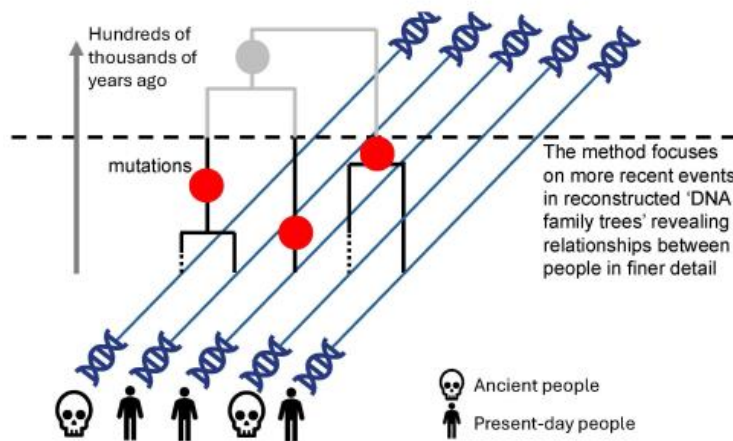
Why in News?

The new **genetic analysis tool, Twigstats**, has significantly improved the precision of tracing individual-level ancestry using **ancient [Deoxyribonucleic acid \(DNA\)](#)** samples from northern and **Central Europe**, dating from **500 BC to 1000 AD**.

What is Twigstats?

- **About:** Twigstats is an **advanced analytical tool** developed for **genetic studies**, particularly focused on **ancestry analysis** with high precision.
 - It is designed to **enhance the understanding of population dynamics** by utilizing **genetic data, archaeological findings, and historical context**.
- **Working:** Twigstats reconstructs genetic family trees by **analyzing shared genetic mutations between individuals**.
 - It **uses recent [mutations](#) to trace ancestry** and establish connections between people from different time periods, **linking modern DNA with that of ancient populations**.
- **Key Features:**
 - **Time-Stratified Ancestry Analysis:** Twigstats uses a **time-stratified approach** to analyze genetic data, enhancing accuracy by studying how ancestry and populations evolved across historical periods
 - **Integration of Genetic Techniques:** The tool combines **haplotypes (shared DNA segments), rare variants**, and **[Single Nucleotide Polymorphisms \(SNPs\)](#)** to offer a comprehensive understanding of ancestry and population structure which provides **deeper insights into demographic transitions** across time, enhancing the accuracy of genetic analysis.
 - **Compatibility with R:** It utilizes **statistical languages R and C++** to assist researchers in analyzing genetic data with greater precision.

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What are the Techniques Used for Genetic Analysis?

- **Single Nucleotide Polymorphisms (SNPs):** SNP is a laboratory method used to **find differences in a DNA sequence** where **one nucleotide (A, C, G, or T) varies between individuals** at certain points.
 - It is widely used to reconstruct genetic histories and ancestry models from ancient genetic material (aDNA).
 - SNP analysis requires **high-quality DNA samples** and faces challenges with **closely related ancestral groups**.
- **Haplotypes Method:** The study involves **combinations of genetic markers** that are **inherited together on the same chromosome**.
 - This technique helps researchers **understand disease patterns and population genetics**, offering insights that might be missed by analyzing individual markers alone.
 - It focuses on **haplotypes**, which are groups of alleles inherited together.
- **Genealogical Tree Inference:** This method is used to **trace the ancestry and genetic relationships** of individuals by **constructing family trees or genealogical trees**.
 - It **analyzes both modern and ancient genomes** to understand population structure and demographic changes.

UPSC Civil Services Examination, Previous Year Questions (PYQs)

Q1. With reference to agriculture in India, how can the technique of 'genome sequencing', often seen in the news, be used in the immediate future? (2017)

1. Genome sequencing can be used to identify genetic markers for disease resistance and drought tolerance in various crop plants.
2. This technique helps in reducing the time required to develop new varieties of crop plants.
3. It can be used to decipher the host-pathogen relationships in crops.

Select the correct answer using the code given below:

- (a) 1 only
- (b) 2 and 3 only

(c) 1 and 3 only
(d) 1, 2 and 3

Ans: (d)

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