

mitoBench & mitoDB: Novel interactive methods for population genetics on mitochondrial DNA



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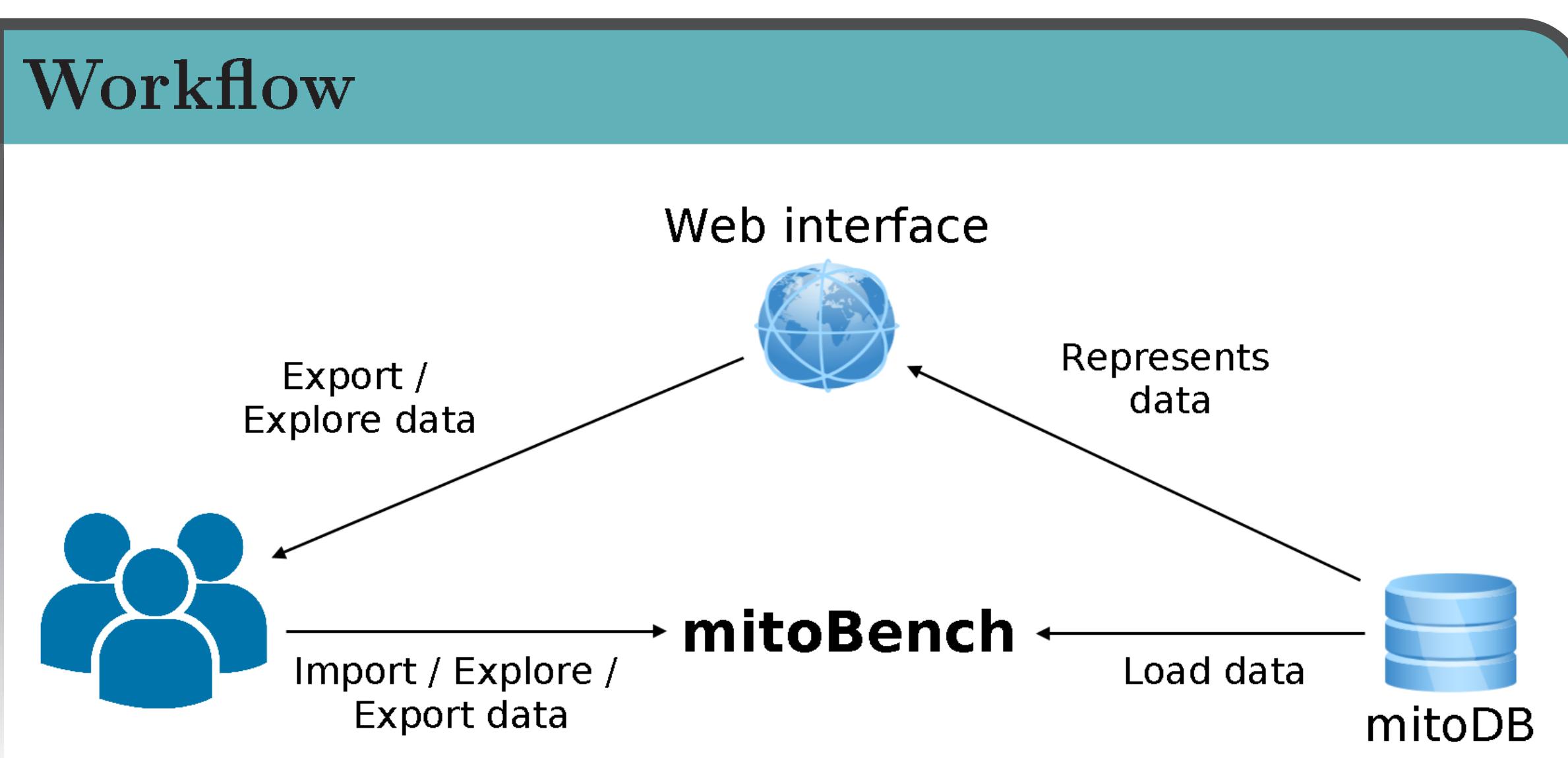


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Motivation & Goals

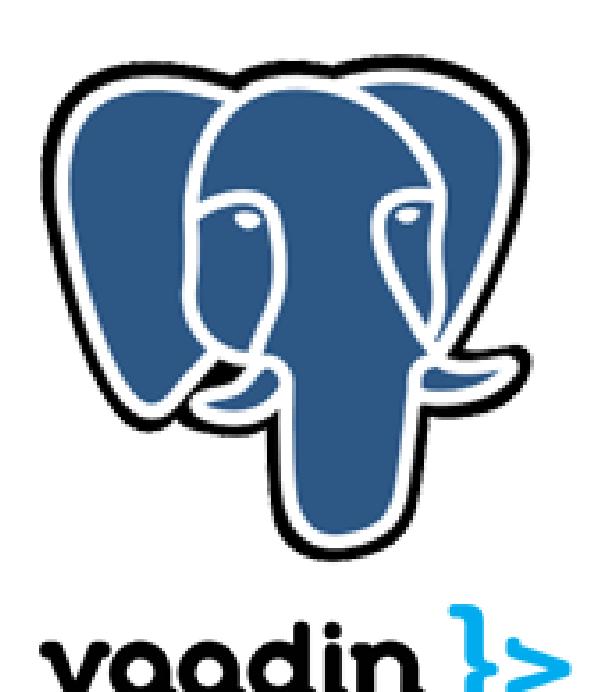
- Mitochondrial DNA (mtDNA) is often the only proxy available to study extinct populations and their relationship with modern populations
- Tools for the analysis typically rely on different file formats → requiring manual interaction with the data for downstream analysis
- mitoBench: workbench to ease file conversions, methods to interactively analyze and visualize human mitochondrial data
- mitoDB: database for human mitochondrial genomes to provide a central reference that can be easily accessed via the workbench and a web-frontend

Workflow



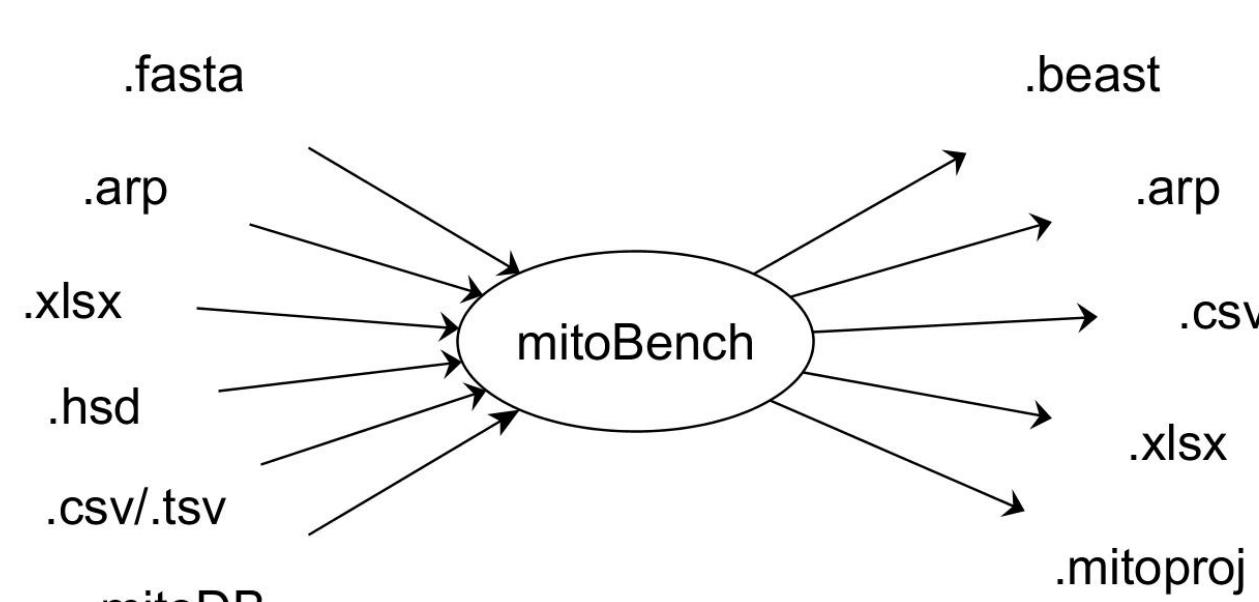
mitoDB

- Database: Providing meta-information (Location, language, Sequence data, ...)
- Web-Frontend: Browsing data, searching for locations, quick look at database contents
- Data Upload: Little curation - Users can rate samples in the web based on their experiences with data
- Access: Web-Frontend (exporting) and mitoBench (export + analysis)



mitoBench

File conversions



⇒ connect the workbench with existing analysis methods/resources such as BEAST¹, Arlequin², PhyloTree³ and others

Data grouping

- group data based on shared features (e.g. time period, location)
- user defined grouping
 - ⇒ allows analysis of Haplogroup distribution between different groups

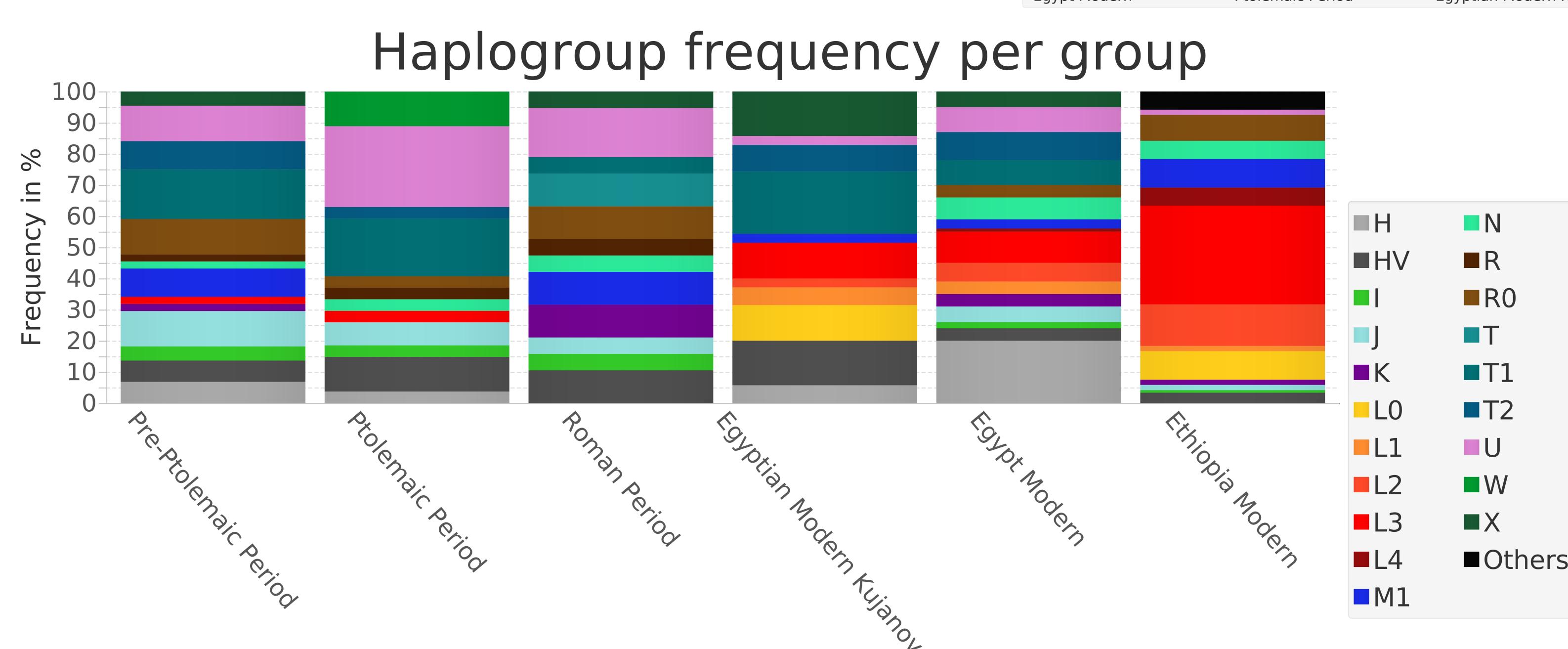
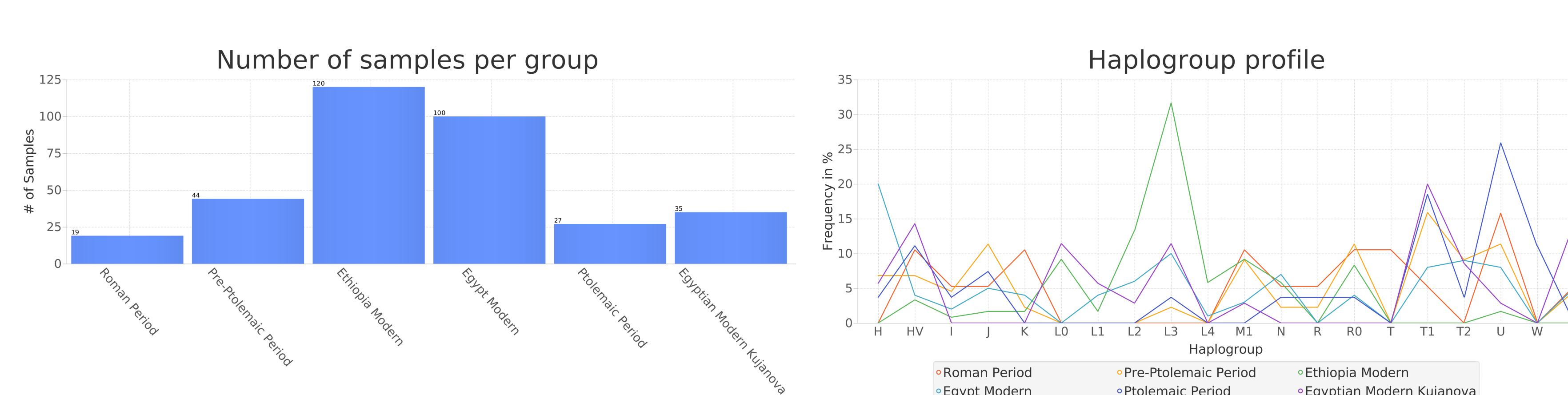
Data filtering / Statistics

- Haplogroup filtering / frequencies
- Mutation filtering / frequencies

Exemplary study

Analysis of 90 ancient Egyptian mummies⁴

→ Did Haplogroup frequencies change over time?



Outlook

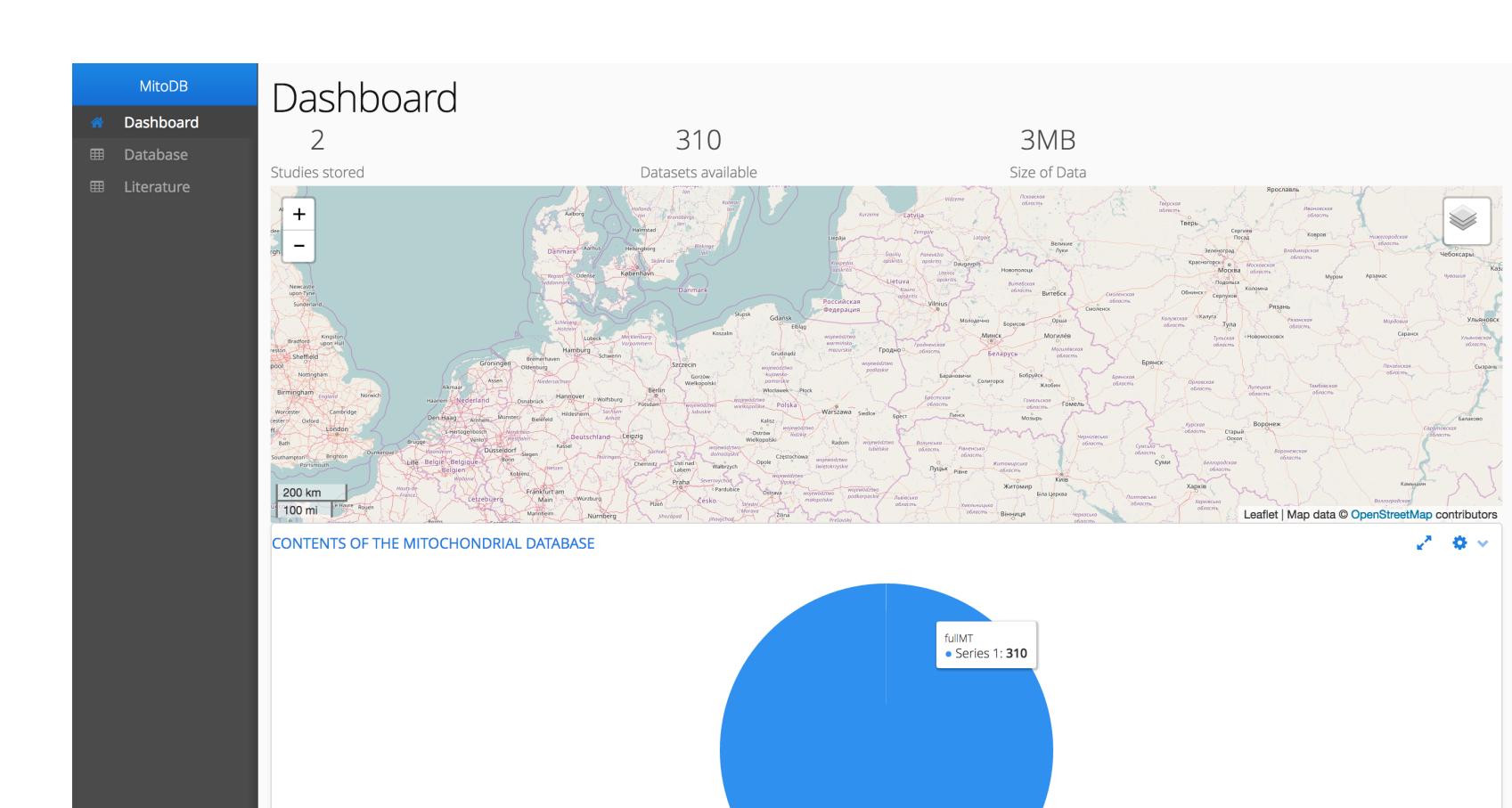
mitoBench

- Provide methods for downstream analysis (e.g. F_{ST} calculations, Founder Analysis)
- Offer more visualizations (e.g. geographical maps for origin of samples)



mitoDB & web interface

- Export/import functionality
- Web-based dashboard to explore database
- More public datasets: 1000G, GenBank, ...



References

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