

MLVApus.net: Database and Analysis Tool for Polyphasic Bacterial Typing with MLVA and SNP Data

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Abstract

Background: Molecular typing of bacteria is essential for epidemiological purposes such as investigating the spreading of specific genotypes or for outbreak detection. Recently, typing using multiple locus variable number of tandem repeat analysis (MLVA) and single nucleotide polymorphisms (SNP) gained increased interest, in particular, because these methods create reproducible and portable results and are especially useful for monomorphic bacteria. Several online-accessible databases containing MLVA- or SNP-data for clinical strains exist already. However, all of these databases are limited to the analysis of data of a single typing method. Therefore, it was our aim to design an expandable database application for multiple typing data of various pathogens.

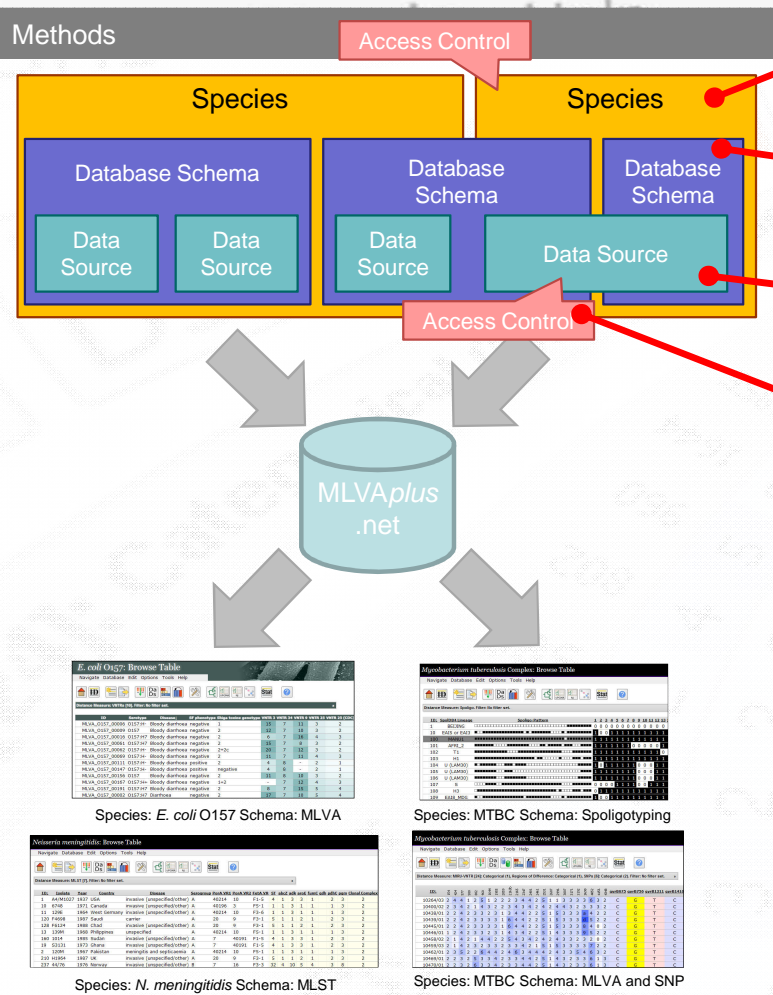
Methods: MLVApus.net is a web-based application implemented in Java that can be accessed with any standard web browser. The user interface pages are generated by the JavaServer Faces technology. For data storage and retrieval, a MySQL database system is used.

Results: The MLVApus.net application allows users to create online-accessible databases for a combination of MLVA, SNP and other categorical data. Access rights for each database can be modified to grant read and write access to the public or to specific users only. Users can upload strain data to the server and, if authorized, store this data in the database. The available analysis features include polyphasic distance calculation based on a weighted combination of different typing data, drawing and exporting of graphs based on UPGMA-, neighbor-joining, and minimum spanning tree algorithms. Currently, MLVApus.net hosts datasets with MLVA and SNP data for *Mycobacterium tuberculosis* complex strains and MLVA data for *Escherichia coli* EHEC O:157 strains.

Conclusion: MLVApus.net is a powerful tool for analysis of bacterial strains based on different categorical typing data. Furthermore, it can be used to provide easy access to extendable strain collections for the scientific community. The application is free and open to all users and can be accessed at

<http://www.mlvaplus.net>

Methods



A species, e.g. *E. coli*, MTBC, *Neisseria meningitidis*. Each Species can have multiple Database Schemas and multiple Data Sources. Visibility can be limited to specific users.

Database Schema. Defines the columns of the data table, e.g. for a specific typing method. Columns can differ in data types, value ranges and visual styles.

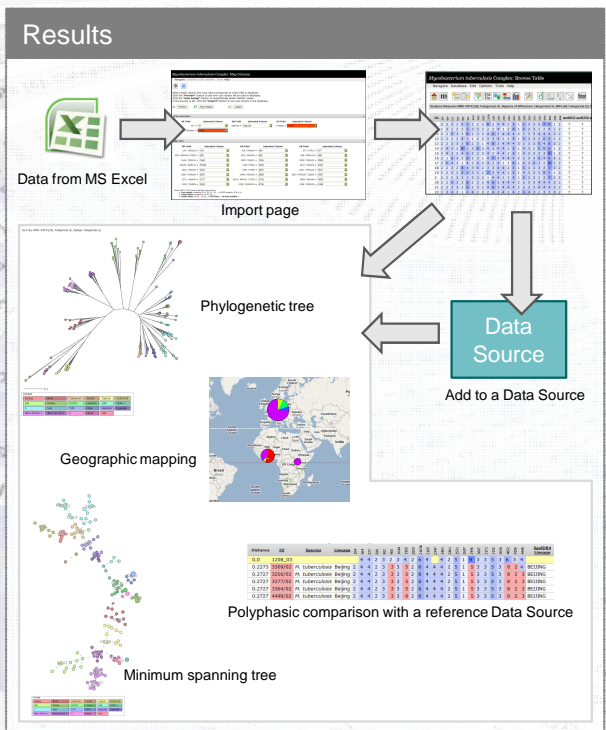
Contains the strain data. A Data Source can be shared between Database Schemas. Visibility and/or write access can be limited to specific users.

Access Control for Species and Data Sources allows to limit access to specific users.
 → for Species: visibility
 → for Data Sources: visibility/write access

Data Types

- Text
- Numbers
- Date
- VNTR
- SNP
- Binary
- Susceptibility
- Other categorical (e.g. MLST)

Results



Conclusion

MLVApus.net is a generalization of the web-application MIRU-VNTRplus [1,2]. It was designed to allow the rapid creation of online databases for user-defined species and typing methods. MLVApus.net can be used to create non-expanding public or private online reference databases or extendable online strain databases for public or private strain collections.

References:
 [1] Allix-Béguec C, Harmsen D, Weniger T, Supply P, Niemann S. Evaluation and user-strategy of MIRU-VNTRplus, a multifunctional database for online analysis of genotyping data and phylogenetic identification of *Mycobacterium tuberculosis* complex isolates. J Clin Microbiol 2006; 46:2950-9
 [2] Weniger T, Krawczyk J, Supply P, Niemann S, Harmsen D. MIRU-VNTRplus: a web tool for polyphasic genotyping of *Mycobacterium tuberculosis* complex bacteria. Nucl Acids Res 2010, in press