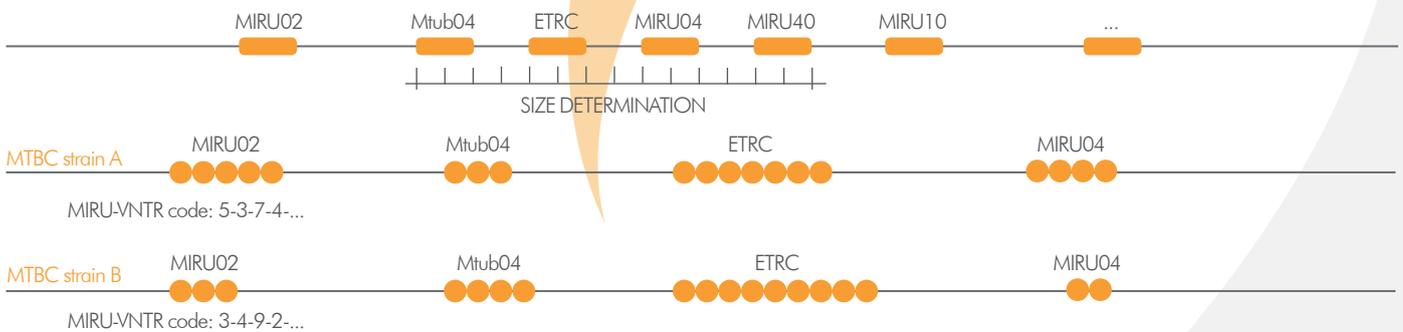


MYCOBACTERIAL INTERSPERSED REPETITIVE UNIT-VARIABLE NUMBER OF TANDEM REPEAT TYPING (MIRU-VNTR)

What is MIRU-VNTR typing?

Mycobacterial interspersed repetitive unit-variable number of tandem repeat (MIRU-VNTR) typing is a method for fast and high-resolution genotyping of *Mycobacterium tuberculosis* isolates. The method distinguishes the *M. tuberculosis* strains by the difference in the number of copies of tandem repeats at specific regions of the *M. tuberculosis* genome.



MIRU-VNTR loci are selected that are both sufficiently and complementary discriminatory. Conserved primers are designed outside the tandem repeat for each VNTR. The size of bp of each PCR-amplicon is the sum of the size of the tandem repeat plus the offsets at both ends.



A set of 24 MIRU-VNTR loci has been reported to have a high discriminatory power for *Mycobacterium tuberculosis* isolates (Supply et al. 2006). The nomenclature of the different genotypes based on this set of MIRU-VNTR loci is maintained at the MIRU-VNTRplus server. The nomenclature is split up in two sets of type designations: MtbC15 and MtbC 9, corresponding to a core set of 15 (most discriminatory) VNTRs, and 9 additional VNTRs respectively. The MtbC 15-9 type is defined by a combination of both types.

MIRU typing in BioNumerics

The MIRU-VNTR application creates a database environment for the import and analysis of MIRU-VNTR data, making it an easy to use typing application. Synchronization with the MIRU-VNTRplus server is possible with a single click, while new types are assigned automatically.

YOUR ADVANTAGES



WHY USE **BioNumerics** FOR YOUR MIRU-VNTR typing?

- ✓ Easy MIRU-VNTR setup
- ✓ Flexible import options
- ✓ High throughput, detailed reporting
- ✓ Impressive set of analysis tools

Easy MIRU-VNTR setup



The MIRU-VNTR setup in the BioNumerics database is automatically defined after installation of the MIRU-VNTR application. The 24 VNTRs managed by the MIRU-VNTRplus database are added to the MLVA management window, with their theoretical VNTR bin predictions based on each VNTR's repeat length, tolerance and offset.

Custom mappings can be defined to accommodate for deviations in fragment size determination. Distribution plots for individual VNTRs are useful to assess the deviation from theoretical copy numbers and define or refine the VNTR mappings.

Flexible import options



In case of raw chromatogram files (Applied Biosystems and Beckman), BioNumerics can parse pool, strain and dye information from the file names and file content using an import template defined by the user. In case of GeneMapper or Beckman peak table files, this information is parsed from the tab-delimited peak table.

The processing of capillary electrophoresis runs, including peak detection and normalization, can be completed in seconds in the integrated curve processing window.

NOTE:

The MIRU-VNTR plugin is a free add-on. The minimal configuration consists of the "Fingerprint Data", "Character Data" and "Tree and Network Interference" modules. Please contact us for more information.

High throughput, detailed reporting



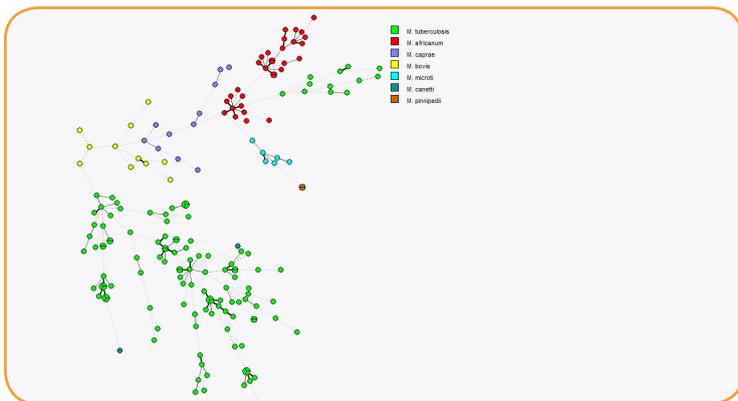
BioNumerics is able to process thousands of MIRU-VNTR runs, creating reports listing unresolved VNTRs, multiple peaks found, and any other problems. Reports can highlight errors, absolute deviations from the expected values and negative and positive deviations. The MIRU-VNTR repeat numbers are stored in integer-type character sets where each MIRU-VNTR represents one character.

Impressive set of analysis tools



MIRU-VNTR data can be analyzed as categorical characters (each different copy number is a different allele) or as quantitative characters. In the latter case, the larger the difference between copy numbers, the less related the organisms are considered.

Population modelling networks can be calculated using the finest and most comprehensive cluster analysis application available today, applying micro-evolutionary criteria as priority rules and displaying branch significance support indication. The Minimum Spanning Tree algorithm applied on multi-locus VNTR data in BioNumerics has proven to be invaluable for epidemiological study and population genetics of bacterial populations.



CONVINCED? INTRIGUED? TRY IT FOR YOURSELF!

www.bionumerics.com

Scan the QR codes to access each step



1. Make sure you have a **BioNumerics** license (also see note above).



2. Watch tutorial movies or download sample data for use in **BioNumerics**.

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