

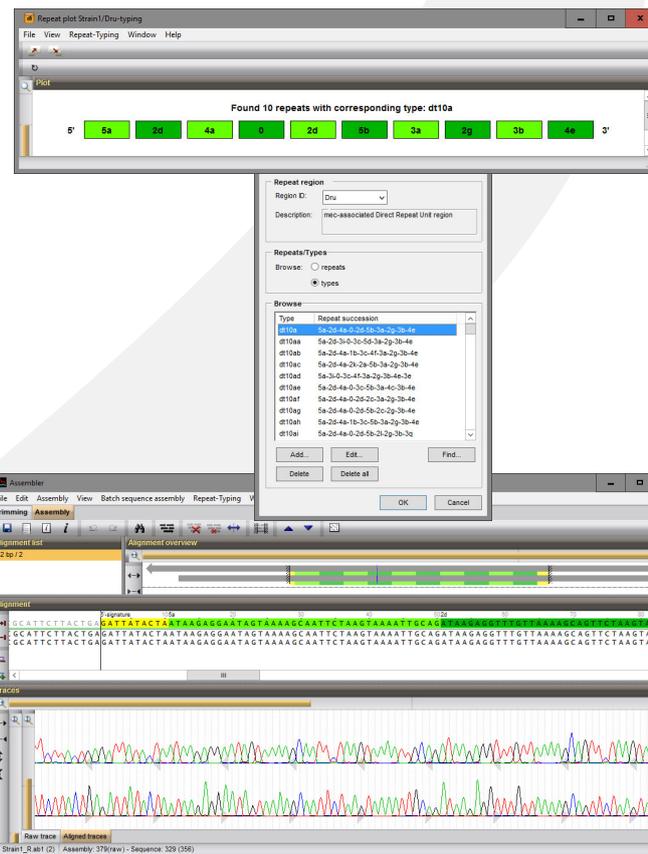
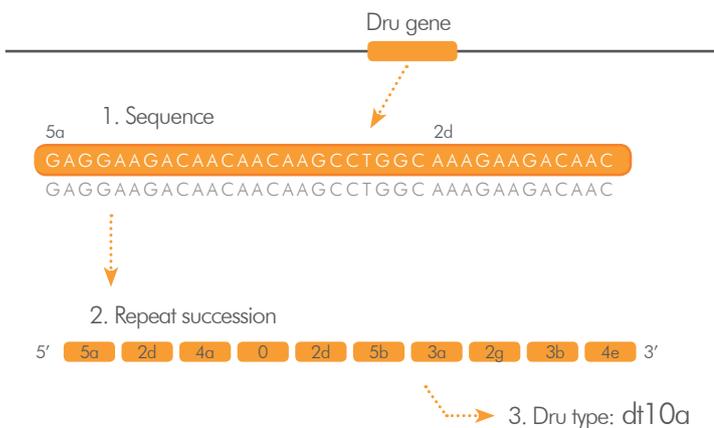
POLYMORPHIC VNTR SEQUENCE TYPING

What is polymorphic VNTR sequence typing?

Variable-Number of Tandem Repeats (VNTRs) are well known for their high mutation rate and therefore widely used for subtyping. Some VNTRs, however, exhibit polymorphism in their individual repeat sequences. By sequencing the polymorphic repeat region, each newly determined repeat variant can be assigned a unique repeat code. The repeat succession for a given strain in turn, determines that strain's VNTR type.

Polymorphic VNTR regions have been explored in various infectious bacteria for quick, portable, and inexpensive subtyping in hospital and outbreak settings. The best known example is undoubtedly spa typing, which is widely used for subtyping of *Staphylococcus aureus*. Because of the specificity of spa typing in terms of standardization, server synchronization and various other settings, a separate spa typing plugin is available in BioNumerics.

Dru typing of a polymorphic VNTR in *S. aureus*



VNTR sequence typing in BioNumerics

The Polymorphic VNTR typing plugin and spa typing plugin offer the same functionality, with the main difference being that the Polymorphic VNTR plugin offers the ability to be customized, making it more of a research tool that allows (and requires) the user to define the plugin's settings. This way, multiple polymorphic VNTRs can be defined, compared and analyzed in a combined way for the same organism.

YOUR ADVANTAGES



WHY USE **BioNumerics** FOR VNTR TYPING?

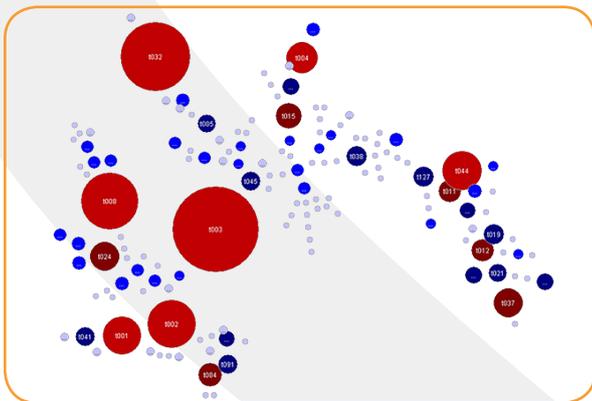
- ✓ Easy database setup
- ✓ Automated import/assembly of traces
- ✓ Fast assignment of repeats and types
- ✓ Impressive set of analysis tools

Easy database setup



BioNumerics allows you to define the VNTRs to be used, the trimming positions for each VNTR, the database fields, synchronization of repeats and settings for assembly. Optionally, the files or server URL(s) for repeat and repeat succession types can also be defined.

- Sequence and character experiments are created for the VNTR sequences and repeat successions, respectively.
- Start and stop trimming positions are stored in the assembly template but can be changed by the user whenever appropriate.
- Base calling quality control settings (PHRED based) can be applied if required by an upload server.
- Information fields are created for repeat successions and VNTR types.
- Server URLs for repeats and types can be defined and changed anytime by the user if the server's URL changes.
- BioNumerics automatically downloads the repeat and type definitions at installation, and optionally, each time at database startup.



Automated import/assembly of traces



Automated import and assembly of batches of sequencer trace files from various sources (Applied BioSystems, Beckman, Amersham, FASTA). File names are parsed into strain and gene information.

Consensus sequences are automatically trimmed using start and stop signatures and placed in the right direction. When the batch assembly is finished, an overview report is shown, listing the status of each assembly. Assembly problems can be cleaned up interactively while visualizing the aligned traces and the base differences with the nearest existing repeats.

Fast assignment of repeats and types

Repeat successions types are instantly identified using the synchronized database, or can be uploaded to a server for identification. New (non-existing) repeat successions, can be defined manually.

Impressive set of analysis tools

Calculate population modelling networks in the finest and most comprehensive cluster analysis application available today, using Minimum Spanning Trees or other phylogenetic clustering methods. Calculate and display partitioning for clonal complexes and use BioNumerics' rich set of statistics tools.

NOTE:

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



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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