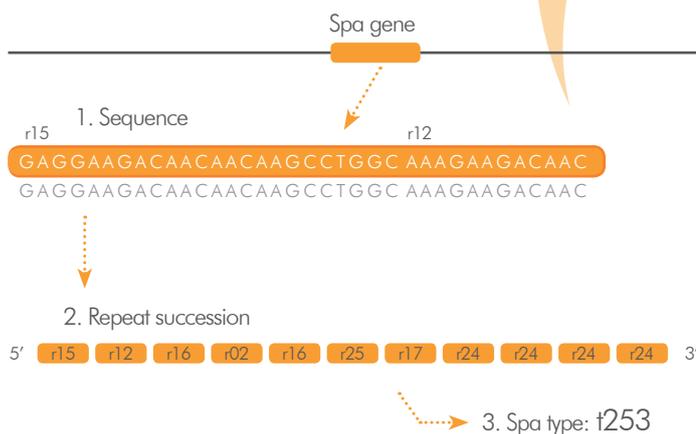


STAPHYLOCOCCUS AUREUS SPA TYPING

What is *spa* typing?

The *spa* typing technique uses the sequence of a polymorphic VNTR in the 3' coding region of the *S. aureus*-specific staphylococcal protein A (*spa*). Each new base composition of the polymorphic repeat found in a strain is assigned a unique repeat code. The repeat succession for a given strain determines its *spa* type. The individual repeat length for the *spa* VNTR is usually 24 bp, but exceptions of 21 to 30 bp exist.

Although *spa* typing is a single-locus typing technique, it offers a subtyping resolution comparable to more expensive and/or laborious techniques such as MLST and PFGE. The technique is widely used for subtyping of *S. aureus* in hospital and outbreak settings.



spa typing in BioNumerics

BioNumerics provides a fully automated workflow, from import of raw sequencer trace files to assignment of repeat codes and *spa* types. Any assembly issue or warning is reported during the workflow and can be addressed with a single mouse click. BioNumerics automatically synchronizes repeat and *spa* type signatures with the SeqNet/Ridom Spa Server and instantly acquires new *spa* types from the Spa Server. In collaboration with SeqNet and Ridom GmbH, BioNumerics thereby uses the authentication and quality control protocols required by the server database.

Furthermore, BioNumerics offers a rich databasing and analysis platform, where *spa* typing data can be clustered and analyzed together with other subtyping data such as MLST, PFGE and any other phenotypic, genotypic, epidemiologic and geographic data.

YOUR ADVANTAGES



WHY USE **BioNumerics**
FOR SPA TYPING?

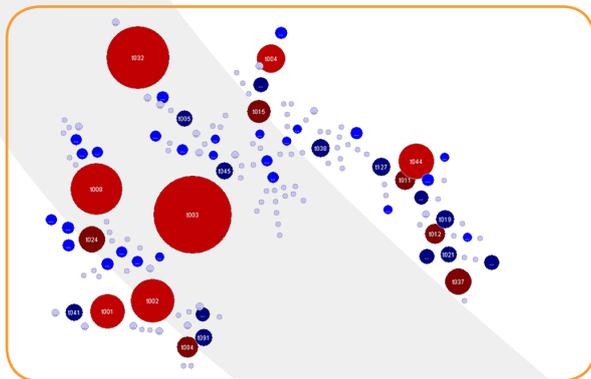
- ✓ Easy database setup
- ✓ Automated import/assembly of traces
- ✓ Synchronization with Spa server
- ✓ Impressive set of analysis tools

Easy database setup



BioNumerics is configured automatically to contain the experiment types, database fields and settings for *spa* typing:

- Sequence and character experiments are created for the *spa* sequences and repeat successions, respectively.
- Start and stop trimming positions are stored in the *spa* assembly template but can be changed by the user whenever appropriate.
- Base calling quality control settings (PHRED based) are predefined according to the SeqNet criteria but can be modified by the user if no synchronization with SeqNet is required.
- Information fields are created for repeat successions, *spa* types, and optionally Kreiswirth notation and clonal complex information.
- Spa Server URLs for repeats and types are predefined but can be changed 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

Automatic 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.

Synchronization with Spa Server



Repeat successions types are instantly identified using the synchronized database. For new repeat successions, the Spa Server automatically generates an *spa* type and returns the assignment to BioNumerics.

Impressive set of analysis tools

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

NOTE:

The *spa* 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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