

BITS :: Call for Abstracts 2024 - Oral communication

<i>Type</i>	Oral communication
<i>Session</i>	Bioinformatics AI, Models and Tools
<i>Title</i>	BacExplorer - Bacteria Functional Annotation and Mutation Analysis Pipeline
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Motivation

Every year millions of deaths are caused by infections. In particular, Antimicrobial resistance (AMR) is one of the top global public health and development threats. Bacteria, equipped with virulence factors and antimicrobial resistance genes, adeptly evade the body's defenses, causing illness and posing significant threats. Therefore, in combating this critical issue, prompt identification of bacterial sensitivity to antibiotics and understanding the mechanisms of resistance acquisition are imperative. The traditional method of bacterial cultivation followed by an antibiogram has long been the gold standard. However, in recent years, the proliferation of Next Generation Sequencing (NGS) analysis has revolutionized research, offering insights not only into antibiotic resistance but also various bacterial processes through annotations. Several powerful tools have emerged to aid in this endeavor, such as Tormes, Bactopia, rMAp, Bacpipe, and Campype, each with its unique strengths and limitations. As the demand for robust bioinformatics software for genome annotation grows, three critical elements have become evident: (i) the necessity for a comprehensive and swift automated sequencing pipeline encompassing multiple bioinformatics tools, (ii) the integration of efficient data management systems, and (iii) the development of interactive graphical interfaces capable of organizing users and presenting results in meaningful and accessible formats.

Methods

To accomplish all these tasks, we developed BacExplorer(Fig 1A). Developed in bash and R, this tool generates an interactive HTML report, streamlining the annotation process. Compatible with both fastq and fasta inputs, including short and long reads, BacExplorer harnesses various databases for comprehensive AMR analysis, including AMRfinder plus, arg-annot, Megares, CARD, Resfinder, and more, facilitating a thorough examination of resistance genes. BacExplorer's AMR and Virulence analyses are enhanced by heatmaps, illustrating the presence/absence of identified genes and clustering samples based on mutations. Additionally, it offers insights into MLST, plasmids, and organism-specific analyses like spa-type for *Staphylococcus aureus*. One of BacExplorer's standout features is its ability to enable users to scrutinize specific resistance gene mutations through manual curation or user uploads. Furthermore, the upcoming development of a Desktop App using Electron will extend accessibility to non-expert users.

Results

BacExplorer represents a significant advancement in simplifying bacterial annotation by leveraging existing annotation databases.

The interactive report (Fig 1B) streamlines the interpretation of annotation results, facilitating a quicker and more accessible understanding. It encompasses various sections, including: i) MLST (Multi-Locus Sequence Typing): which allows the bacterial identification; ii) Antimicrobial Resistance: drawing from 6 different databases for a comprehensive analysis of AMR genes. This section features a gene heatmap for sample clustering, enhancing visualization; iii) Virulence factors: utilizing 2 databases and heatmaps to highlight virulence-related genetic elements; iv) Plasmids: for plasmids identification; v) Optional sections: tailored for specific bacteria such as *S.aureus* and *K. pneumoniae* providing targeted insights genomic traits. Moreover, the report generates a separate excel output for point mutation analysis. This output provides information about resistance mechanisms, increasing the depth of analysis and facilitating informed decision-making.

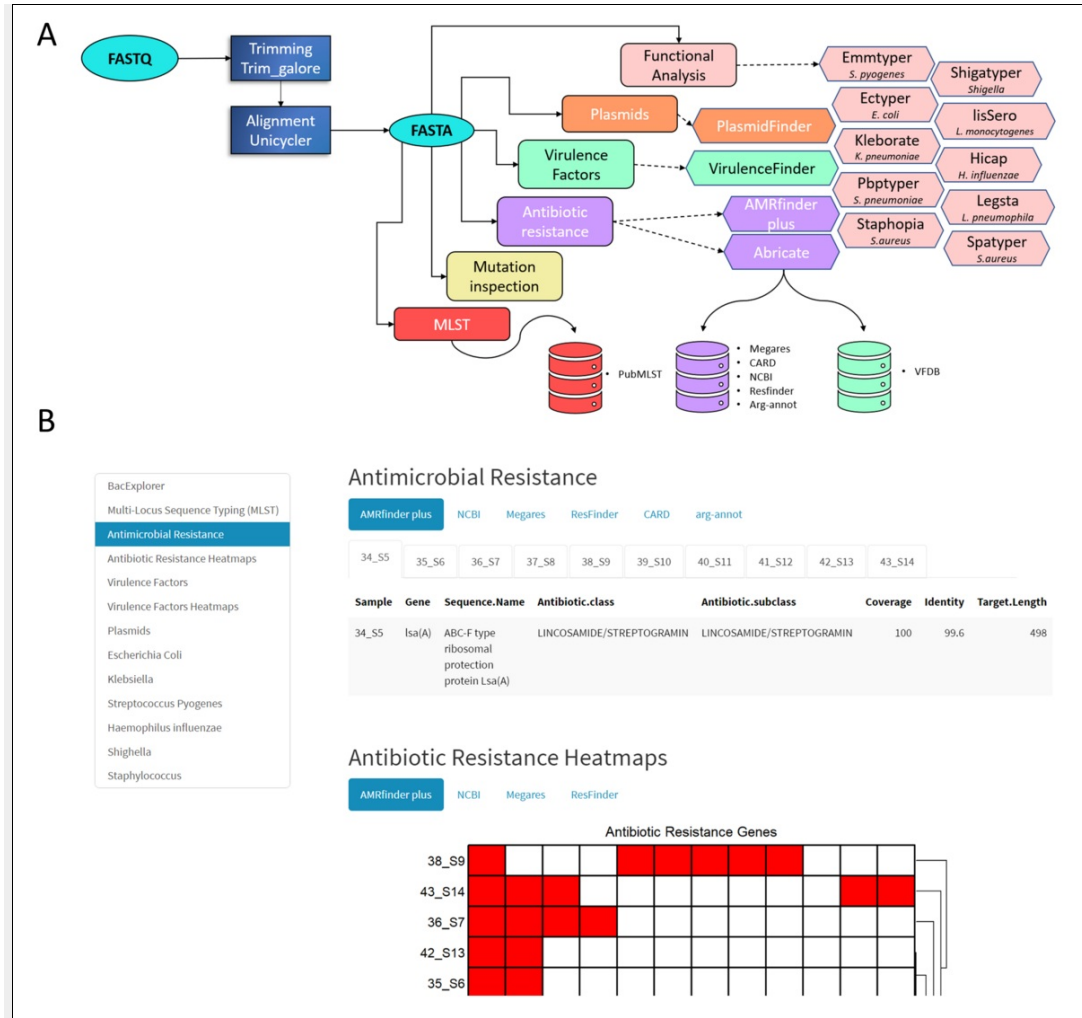
We can conclude that, by empowering microbiologists with enhanced knowledge of antibiotic resistance, the software accelerates and improves patients' care.

Info

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Figure



Availability -

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Summary

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