

## Reply to "Internet-Based Solutions for Analysis of Next-Generation Sequence Data"

Norelle L. Sherry, Timothy P. Stinear and Benjamin P. Howden

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## Reply to “Internet-Based Solutions for Analysis of Next-Generation Sequence Data”

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Bacterial genome sequencing is an evolving technology that will soon be applied to routine medical microbiology. In our recent publication, we noted the lack of user-friendly tools for genome analysis (1). We thank M. V. Larsen from the Centre for Genomic Epidemiology (Denmark) for alerting us to their Web-based tools (2) that are starting to fill this void, which were not published at the time we analyzed our genome sequence data. We have reanalyzed our data using *de novo* assembled genomes (in FASTA file format) to compare to our more labor-intensive methods and found them easy to use for identifying resistance genes (3) and to perform rapid MLST analysis (4). The robustness of the data output does appear to be dependent, not surprisingly, on the quality of the partial genome assembly.

As with any technology moving from the research to the diagnostic setting, there will certainly be gaps in expertise and experience during the implementation of genome sequencing in the diagnostic laboratory. Freely available, user-friendly resources such as these will certainly begin to bridge this crucial gap.

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