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# Automatic sequential clustering in the context of integrated genomic surveillance

*Tuesday, October 14, 2025 3:00 PM (15 minutes)*

Integrated Genomic Surveillance (IGS) enables the surveillance of various, public health-relevant bacterial and viral pathogens. For bacterial species, the identification of genomic clusters represents the foundation for outbreak investigations and epidemiological studies. Providing well-defined genomic clusters therefore represents an essential task of IGS, in order to support the surveillance of relevant bacterial species by the federal and local health authorities in Germany.

For the automatic computation and definition of genomic clusters, a diverse set of challenges has been identified: the dependence on external data silos should be minimized, the clustering and its nomenclature should be robust over time and the clusters should represent meaningful groupings, even in the presence of samples with lower quality (e.g. missing data).

Within this work, these challenges are addressed and advantages as well as disadvantages of some possible solutions are highlighted and discussed. Finally, the current analytical approach and the software implementation utilized within the IGS project, termed Seqsi (SEQuential SIngle-linkage clustering), is presented.

## Keywords

Bioinformatics, Clustering, Genomics, Sequence Typing

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## Professional Status of the Speaker

Senior Scientist

## Junior Scientist Status

No, I am not a Junior Scientist.

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