Downloaded from orbit.dtu.dk on: Apr 24, 2024

DTU Library

# Genomic Epidemiology

**Lund, Ole; Thomsen, Martin; Bellod Cisneros, Jose Luis; Ahrenfeldt, Johanne; Tetzschner, Anna Maria Malberg; Leekitcharoenphon, Shinny; Kaas, Rolf Sommer; Lukjancenko, Oksana; Aarestrup, Frank**

*Published in:*
Book of Abstracts. DTU's Sustain Conference 2015

*Publication date:*
2015

*Document Version*
Publisher's PDF, also known as Version of record

Link back to DTU Orbit

*Citation (APA):*
Lund, O., Thomsen, M., Bellod Cisneros, J. L., Ahrenfeldt, J., Tetzschner, A. M. M., Leekitcharoenphon, S., Kaas, R. S., Lukjancenko, O., & Aarestrup, F. (2015). Genomic Epidemiology. In *Book of Abstracts. DTU's Sustain Conference 2015* Article Q-7 Technical University of Denmark.

**General rights**
Copyright and moral rights for the publications made accessible in the public portal are retained by the authors and/or other copyright owners and it is a condition of accessing publications that users recognise and abide by the legal requirements associated with these rights.

- Users may download and print one copy of any publication from the public portal for the purpose of private study or research.
- You may not further distribute the material or use it for any profit-making activity or commercial gain
- You may freely distribute the URL identifying the publication in the public portal

If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.

# Genomic Epidemiology

Ole Lund*[1], Martin Thomsen[1], Jose L. Bellod Cisneros [1], Johanne Ahrenfeldt [1], Anna Maria Malberg Tetzschner[1], Shinny Leekitcharoenphon[2], Rolf Sommer Kaas[2], Oksana Lukjancenko[2], Frank Aarestrup[2]

1: DTU Systems Biology; 2: DTU Food;

*Corresponding author email: make-link-to-mail@dtu.dk

WGS holds the promise to revolutionize surveillance and diagnostics of infectious diseases due to its high resolution. It may be used across many areas such as monitoring food, environment, clinical, veterinary, wildlife, etc., for all known pathogens, i.e., viruses, bacteria, fungi, parasites, etc. A major obstacle is how to create a robust and simple to use system that will allow its adaptation within the relevant labs. A goal would be to establish a Web-based system, allowing users to upload sequence and meta data for several isolates in one batch up- load, and have several analysis made on each isolate: assembly, species typing, MLST typing (for bacteria), resistance gene finding, virulence prediction, and gene finding. Furthermore the system should allow single nucleotide poly- morphism (SNP) based comparison of the uploaded isolates with all previously uploaded isolates.

The Center for Genomic Epidemiology (CGE) has, over the last 4 years, worked on developing a system for surveillance and diagnostics of infectious diseases. This system has been running since 2012 (genomicepidemiology.org). So far, more than 150,000 isolates have been analyzed. This has demonstrated that online analysis of WGS information is possible. This means it should be possible to create a unified portal so that all area and pathogen data can be compared, enabling us to trace back all infections. The work will in the coming years be continued in the context of the COMPARE project.