

# LONG DNA-SEQUENCE READS FOR MICROBIAL BIOAEROSOL SURVEILLANCE

Robert Maximilian Leidenfrost<sup>1</sup>, Dierk-Christoph Pöther<sup>2</sup>, Henriette Mietke<sup>3</sup>, Udo Jäckel<sup>2</sup> & Röbbbe Wünschiers<sup>1</sup>

<sup>1</sup> Mittweida University of Applied Sciences, Technikumplatz 17, 09648 Mittweida

<sup>2</sup> Federal Institute for Occupational Safety and Health, Nöldnerstr. 40-42, 10317, Berlin

<sup>3</sup> State Operating Company for Environment and Agriculture, Waldheimer Str. 218, 01683, Nossen

Regulation concerning occupational or environmental safety and health in Germany offers limited options with respect to risk assessment for airborne micro-biological agents based on molecular analysis. The knowledge to identify and quantify potentially harmful biological agents in bioaerosols is however required for risk assessment. Subsequently, there is a need for development and evaluation of new analysis methods. Here we evaluate long DNA-sequence reads for profiling microbial bioaerosols and their suitability for near-real time field investigation.

After nucleic acid extraction from a bacterial mock community, we compared a) full length reads vs. 16S analysis and b) Oxford Nanopore Technologies' high-accuracy vs. fast basecalling algorithm. We applied the workflow to a bioaerosol sample generated in an agricultural environment. Pitfalls encountered during processing thereof will be highlighted.