

Machine learning-based analysis of mass spectrometry data for rapid diagnosis of respiratory viruses in saliva samples

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I am developing a data analysis workflow involving machine learning technologies like recurrent and convolutional neural networks as well as classification systems, for the rapid and reliable identification and quantification of viral proteins in mass spectrometry data from human saliva samples. The goal is to implement this workflow in high-throughput quantitative testing for respiratory viral infections, including advanced features such as parallel testing for different viruses and early detection of viral mutations.

Primary author: DOERNER, Simon (FS-CS (CSSB-Geschaefsstelle))

Presenter: DOERNER, Simon (FS-CS (CSSB-Geschaefsstelle))