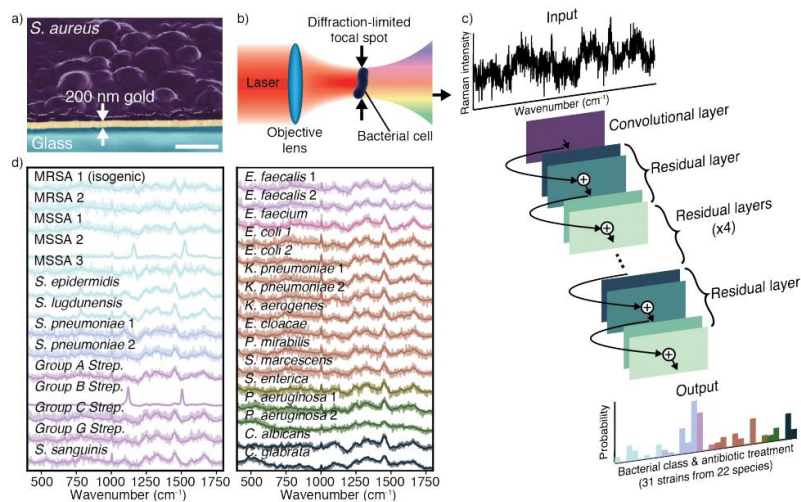




TOWARDS AN AUTOMATED IDENTIFICATION OF THE MICROBIAL "RAMANOME"

Background

Raman spectroscopy is an optical technique, which is used to characterize vibrational, rotational and other low-frequency modes in a single cells. It returns a biochemical fingerprint that gives a quantitative description concerning the molecules that are present. Recently, Raman spectroscopy has sparked the interest of microbiologists. Each bacterial population has its own unique Raman fingerprint, also called the "Ramanome" [1]. This fingerprint incorporates information coming from different kinds of molecules such as lipids, proteins and carbohydrate, and this type of data turns out to be very sensitive. In other words, bacterial subpopulations can be identified with high resolution using algorithms specifically designed for this kind of data [2]. Likewise, the amount of data is increasing, and so-called *deep learning* approaches have been proposed to automatically analyze Raman data [3].



Scope of the thesis

A number of challenges arise concerning the analysis of Raman data, which will be tackled in this thesis. The goal of this thesis is to develop a predictive model, which is able automatically classify bacterial cells according to its taxonomy based on a Raman fingerprint. One possible research avenue would be to compare *deep learning* approaches with more traditional machine learning methods, and evaluate their added value. Having experience in Python or R is a plus, but not a prerequisite.

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BACKGROUND

All

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