Title:
Transcriptomic characterization of \textit{in vivo}-like model of chronic infection

Description:
The physiology of bacteria in chronic infections, such as cystic fibrosis and non-healing wounds is far from being well-characterized. Our understanding of bacterial behavior and functioning during human infections remains superficial since most \textit{in vitro} experiments fail to mimic the complex host environment. Therefore, it is important to determine what differentiates current model systems from clinical conditions in order to develop \textit{in vitro} models to accurately simulate central aspects of the host environment and to better understand the biology of infections.

Recently, it has been shown that growing bacteria in alginate beads can mimic central aspects of \textit{in vivo} conditions, such as diffusion-limited bacterial growth forming dense bacterial aggregates. These aggregates are similar in size and morphology to \textit{in vivo} aggregates observed \textit{ex vivo} in cystic fibrosis lungs and chronic wounds. Though this model appears to closely resemble what is observed \textit{in vivo}, the resemblance to true chronic infection on a transcriptional level has yet to be characterized.

The master project will be focused on comparing the transcriptome of bacterial aggregates grown in the alginate bead model under different conditions to that of bacteria in infected human tissue using RNA-sequencing. The goal is to identify bacterial genes characteristic of a chronic infection by the help of machine learning and develop the alginate bead model to recreate the transcriptomic environment of bacteria during infection.

Required qualifications:
The student should be familiar with basic laboratory techniques, such as pipetting and reagent preparation. Some prior experience with programming and writing scripts (R, Python, and/or Unix) would also be beneficial, but not a requirement.

Responsible institution:
University of Copenhagen

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Allowed no of students per report (1-2):
1-2

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