# Introduction

Metagenomic sequencing data has increased the understanding of the role of the microbiome and given insight into a variety of (bacterial) communities. Korem *et al.* (2015) used the pattern of metagenomic sequencing read coverage around the origin of replication (oriC) to gain insight into the growth dynamics of gut microbiota. Detecting the oriC in bacteria can hence be of great importance for metagenomic analysis. With the oriC being the starting point of bacterial replication, its detection can facilitate the analysis of certain motifs and features around this location or simply be used as a starting point for gene annotation.

A frequently used indicator of the oriC is the so-called skew which is based on the strand asymmetry between the leading and lagging strand. The leadings strand usually is rich in guanine (G) and adenine (A) whereas a higher content of cytosine (C) and thymine (T) can be found in the lagging strand (Touchon and Rocha, 2008). The putative location of the oriC is then indicated by a minimum of the GC skew (G-C)/(G+C) or a maximum in the AT skew respectively. Even though the GC skew is frequently used, the AT skew is able to cover for less pronounced regions in the GC skew (Grigoriev, 1998).

Another measure used for oriC prediction is the DnaA motif. DnaA is the key protein in the initiation of replication. It binds to clusters of DnaA boxes that accumulate around the oriC. The DnaA motif is nine base pairs long and is highly conserved with the consensus sequence

“*TT TNCACA*” (Blaesing *et al*., 2017). Detecting the location of these clusters of DnaA boxes can therefore improve the prediction of a putative oriC.

This project tries to identify putative oriC locations of four different bacteria species (*Escherichia coli, Vibrio cholerae, Salmonella enterica, Thermotoga petrophila*). The approximate region of the oriC is identified using GC and AT skews. In this region, the DnaA motif clusters are then located to further specify the region.

# Material and Methods

## Data

Reference Sequences were downloaded from NCBI Assembly database.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Organism | Family | DnaA Box |  |  |
| Escherichia coli | Enterobacteriaceae |  |  |  |
| Vibrio cholerae | Vibrionaceae |  |  |  |
| Thermotoga petrophila | Thermotogaceae |  |  |  |
| Salmonella enterica | Enterobacteriaceae |  |  |  |

## Skew Diagrams

First the GC-skew minimum was calculated for reference strains of the bacterial families of *Enterobacteriaceae* and *Vibrionaceae* to obtain an overview of the values to be expected. In the next step the minimum was determined for 10 strains of the four species *Escherichia coli*, *Salmonella enteritidis*, *Vibrio cholerae*, and *Thermotoga petrophila*. Since only one complete genome of *T. petrophila* was available, other Thermotoga *subspecies* were considered too. Determined GC minima were then compared to the minima given in the DoriC database.

The DnaA motifs were analysed by profile alignment in a +/- 2000 window around the determined GC minimum. Motifs with a score >= 10 were counted and compared to the number of motifs at the oriC as given in the DoriC database (Not yet done).

## Motif Finding

position-specific scoring matrix (PSSM) calculated

PSSM score for each position of the OriC region sequences

## Meme

Meme (Multiple Em for Motif Elicitation)

Command-Line version of MEME Suite

## 

# Results

# Discussion

Z-curve method would likely improve the OriC localization.[[1]](#footnote-0)

# Literature

Blaesing, F., Weigel, C., Welzeck, M. and Messer, W. (2017) Analysis of the DNA‐binding

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1. "Identification of replication origins in archaeal ... - NCBI." <https://www.ncbi.nlm.nih.gov/pubmed/15876567>. Aufgerufen am 7 Jan.. 2020. [↑](#footnote-ref-0)