

Accepted Manuscript

A Primer on Microbial Bioinformatics for non-bioinformaticians

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PII: S1198-743X(17)30709-7

DOI: [10.1016/j.cmi.2017.12.015](https://doi.org/10.1016/j.cmi.2017.12.015)

Reference: CMI 1157

To appear in: *Clinical Microbiology and Infection*

Received Date: 15 June 2017

Revised Date: 13 November 2017

Accepted Date: 22 December 2017

Please cite this article as: Carriço JA, Rossi M, Moran-Gilad J, Van Domselaar G, Ramirez M, A Primer on Microbial Bioinformatics for non-bioinformaticians, *Clinical Microbiology and Infection* (2018), doi: 10.1016/j.cmi.2017.12.015.

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Keywords: Microbial Bioinformatics, High Throughput Sequencing, Genomic Epidemiology, Microbial Typing, Bioinformatics software

Abstract

Background: Presently, the bottleneck in the deployment of High Throughput Sequencing (HTS) technology is the ability to analyse the increasing amount of data produced in a fit-for-purpose manner. The field of Microbial Bioinformatics is thriving and quickly adapting to the technological changes, which creates difficulties for non-bioinformaticians to follow the complexity and increasing jargon of this field.

Aims: This review is directed towards non-bioinformaticians who wish to gain understanding of the overall microbial bioinformatic processes from the raw data obtained from the sequencers to the final outputs.

Sources: the software and analytical strategies reviewed are based on the personal experience of the authors.

Content: The bioinformatic processes of transforming raw reads to actionable information in a clinical and epidemiological context will be explained. We will review the advantages and limitations of two major strategies currently applied: read mapping, which is the comparison with a pre-defined reference genome and *de novo* assembly, the unguided assembly of the raw data. Finally, we will discuss the main analytical methodologies and the most frequently used freely available software and its application in the context of bacterial infectious disease management.

Implications: HTS technologies are overhauling outbreak investigation and epidemiological surveillance while creating new challenges due to the amount and complexity of data

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