Solving the Problem of Comparing Whole Bacterial Genomes across Different Sequencing Platforms - DTU Orbit (28/12/2018)

Whole genome sequencing (WGS) shows great potential for real-time monitoring and identification of infectious disease outbreaks. However, rapid and reliable comparison of data generated in multiple laboratories and using multiple technologies is essential. So far studies have focused on using one technology because each technology has a systematic bias making integration of data generated from different platforms difficult. We developed two different procedures for identifying variable sites and inferring phylogenies in WGS data across multiple platforms. The methods were evaluated on three bacterial data sets and sequenced on three different platforms (Illumina, 454, Ion Torrent). We show that the methods are able to overcome the systematic biases caused by the sequencers and infer the expected phylogenies. It is concluded that the cause of the success of these new procedures is due to a validation of all informative sites that are included in the analysis. The procedures are available as web tools.

General information
State: Published
Organisations: Comparative Microbial Genomics, National Food Institute, Division of Epidemiology and Microbial Genomics, Department of Systems Biology, Center for Biological Sequence Analysis, Immunological Bioinformatics
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Number of pages: 8
Publication date: 2014
Peer-reviewed: Yes

Publication information
Journal: PLOS ONE
Volume: 9
Issue number: 8
Article number: e104984
ISSN (Print): 1932-6203
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 3.01 SJR 1.164 SNIP 1.111
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.11 SJR 1.236 SNIP 1.101
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 3.32 SJR 1.427 SNIP 1.136
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 3.54 SJR 1.559 SNIP 1.148
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 3.94 SJR 1.772 SNIP 1.153
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 4.15 SJR 1.982 SNIP 1.156
Web of Science (2012): Impact factor 3.73
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 4.58 SJR 2.425 SNIP 1.233
Web of Science (2011): Impact factor 4.092
ISI indexed (2011): ISI indexed no
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1