Bacterial whole genome-based phylogeny: construction of a new benchmarking dataset and assessment of some existing methods - DTU Orbit (29/10/2017)

**Background**

Whole genome sequencing (WGS) is increasingly used in diagnostics and surveillance of infectious diseases. A major application for WGS is to use the data for identifying outbreak clusters, and there is therefore a need for methods that can accurately and efficiently infer phylogenies from sequencing reads. In the present study we describe a new dataset that we have created for the purpose of benchmarking such WGS-based methods for epidemiological data, and also present an analysis where we use the data to compare the performance of some current methods.

**Results**

Our aim was to create a benchmark data set that mimics sequencing data of the sort that might be collected during an outbreak of an infectious disease. This was achieved by letting an E. coli hypermutator strain grow in the lab for 8 consecutive days, each day splitting the culture in two while also collecting samples for sequencing. The result is a data set consisting of 101 whole genome sequences with known phylogenetic relationship. Among the sequenced samples 51 correspond to internal nodes in the phylogeny because they are ancestral, while the remaining 50 correspond to leaves. We also used the newly created data set to compare three different online available methods that infer phylogenies from whole-genome sequencing reads: NDtree, CSI Phylogeny and REALPHY. One complication when comparing the output of these methods with the known phylogeny is that phylogenetic methods typically build trees where all observed sequences are placed as leafs, even though some of them are in fact ancestral. We therefore devised a method for post processing the inferred trees by collapsing short branches (thus relocating some leaves to internal nodes), and also present two new measures of tree similarity that takes into account the identity of both internal and leaf nodes.

**Conclusions**

Based on this analysis we find that, among the investigated methods, CSI Phylogeny had the best performance, correctly identifying 73% of all branches in the tree and 71% of all clades. We have made all data from this experiment (raw sequencing reads, consensus whole-genome sequences, as well as descriptions of the known phylogeny in a variety of formats) publicly available, with the hope that other groups may find this data useful for benchmarking and exploring the performance of epidemiological methods. All data is freely available at: https://cge.cbs.dtu.dk/services/evolution_data.php.
Scopus rating (2012): SJR 2.181 SNIP 1.225 CiteScore 4.61
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 2.271 SNIP 1.197 CiteScore 4.38
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 2.109 SNIP 1.038
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 2.181 SNIP 1.015
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 2.067 SNIP 1.005
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.846 SNIP 1.04
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.431 SNIP 0.895
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 1.994 SNIP 0.894
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 1.852 SNIP 0.617
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 1.909 SNIP 0.561
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 1.342 SNIP 0.532
Scopus rating (2001): SJR 0.132 SNIP 0.016
Original language: English
Phylogeny, Evolution, Benchmark, WGS
Electronic versions:
DOIs:
10.1186/s12864-016-3407-6

Bibliographical note
This article is distributed under the terms of the Creative Commons Attribution 4.0 International License (http://creativecommons.org/licenses/by/4.0/), which permits unrestricted use, distribution, and reproduction in any medium, provided you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons license, and indicate if changes were made. The Creative Commons Public Domain Dedication waiver (http://creativecommons.org/publicdomain/zero/1.0/) applies to the data made available in this article, unless otherwise stated.
Source: PublicationPreSubmission
Source-ID: 128124692
Publication: Research - peer-review › Journal article – Annual report year: 2017