

ODoSE: A Webserver for Genome-Wide Calculation of Adaptive Divergence in Prokaryotes

Michiel Vos,
 Tim A. H. te Beek,
 Marc A. van Driel,
 Martijn A. Huynen,
 Adam Eyre-Walker,
 Mark W. J. van Passel

Abstract

Quantifying patterns of adaptive divergence between taxa is a major goal in the comparative and evolutionary study of prokaryote genomes. When applied appropriately, the McDonald-Kreitman (MK) test is a powerful test of selection based on the relative frequency of non-synonymous and synonymous substitutions between species compared to non-synonymous and synonymous polymorphisms within species. The webserver ODoSE (Ortholog Direction of Selection Engine) allows the calculation of a novel extension of the MK test, the Direction of Selection (DoS) statistic, as well as the calculation of a weighted-average Neutrality Index (NI) statistic for the entire core genome, allowing for systematic analysis of the evolutionary forces shaping core genome divergence in prokaryotes. ODoSE is hosted in a Galaxy environment, which makes it easy to use and amenable to customization and is freely available at www.odose.nl.

Citation: Vos M, te Beek TAH, van Driel MA, Huynen MA, Eyre-Walker A, et al. (2013) ODoSE: A Webserver for Genome-Wide Calculation of Adaptive Divergence in Prokaryotes. PLoS ONE 8(5): e62447. doi:10.1371/journal.pone.0062447

Editor: Celine Brochier-Armanet, Université Claude Bernard - Lyon 1, France

Received: January 22, 2013; **Accepted:** March 21, 2013; **Published:** May 6, 2013

Copyright: © 2013 Vos et al. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

Funding: MWJvP is funded by the Netherlands Organization for Scientific Research (NWO) via a VENI grant. TtB and MAVd are funded by the BioAssist/BRS programme of the Netherlands Bioinformatics Centre, which is supported by the Netherlands Genomics Initiative. This work is part of the programme of BiG Grid, the Dutch e-Science Grid, which is financially supported by the NWO. MV is supported by investment from the European Regional Development Fund and the European Social Fund Convergence Programme for Cornwall and the Isles of Scilly to the European Centre for the Environment and Human Health. The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

Competing interests: MWJvP is a PLOS ONE Editorial Board member. This does not alter the authors' adherence to all the PLOS ONE policies on sharing data and materials.

Introduction

The immense genomic diversity of bacteria and archaea is rapidly being uncovered by next-generation sequencing methods. Much attention in comparative genomics studies is given to differences in gene content mediated by lateral gene transfer, gene duplication and gene loss, as related strains can differ markedly in gene content [1]. The accessory genome clearly is of profound importance to the physiology and ecology of strains and species. However, it has become increasingly clear that bacterial core genes conserved between species play a major role in niche adaptation as well [2]–[7]. The McDonald-Kreitman (MK) test is a powerful test of selection [8]–[10] comparing patterns of non-synonymous and synonymous substitutions within a species to those separating this species from an outgroup species. In the first large-scale application of the MK test to prokaryotes, it was estimated that at least 50% of amino acid changes fixed in *Escherichia coli* and *Salmonella enterica* core genes were due to adaptation [9], demonstrating that prokaryote sequence evolution can in large part be shaped by natural selection.

The MK test is based on the premise that under neutral evolution, the ratio of synonymous and nonsynonymous substitutions within a species is the same as that between this species and an outgroup species. If a species has diverged due to positive selection (having changed its phenotype), an excess of nonsynonymous changes is expected between species relative to that within species. This is because adaptive mutations are fixed relatively rapidly and so contribute little to intra-specific polymorphisms but do contribute to between-species divergence. In contrast, when deleterious mutations segregate within a species because of inefficient purifying selection, nonsynonymous polymorphisms are overrepresented and adaptive divergence is underestimated. The standard summary statistic of the MK test is the Neutrality Index NI [11]:

$$NI = (P_N/D_N)/(P_S/D_S) \text{ or } (D_S * P_N)/(D_N * P_S) \quad (1)$$

Where P_N and P_S are non-synonymous and synonymous polymorphisms and D_N and D_S are non-synonymous and synonymous fixed differences between species. With $NI = 1$, there is no difference in the pattern between non-synonymous and synonymous substitutions and species diverge neutrally. With $NI < 1$, fixed differences between species are more often due to non-synonymous differences than expected and divergence is assumed to be selected for (positive selection). With $NI > 1$, fixed differences between species are less often due to non-synonymous divergence than expected. This is caused by selection against protein-changes (negative selection), with divergence primarily being driven by neutral fixation of synonymous substitutions (drift). Statistical deviation from $NI = 1$ can be assessed using a 2×2 contingency table and a Chi squared test. In some studies the inverse of the Neutrality Index [11], the Fixation Index, is used (e.g. [12]).

Because the MK test statistic NI is based on a ratio of two ratios, it cannot be calculated for genes where D_N or P_S is 0. This thus results in discarding many genes from datasets (e.g. [13]). To counteract this problem, Stoletski and Eyre-Walker [14] have proposed an alternative statistic, termed the Direction of Selection (DoS):

$$DoS = D_N/(D_N + D_S) - P_N/(P_N + P_S) \quad (2)$$

DoS can be calculated for all genes except those where both P_S and P_N and/or both D_N and D_S are zero. The significance of DoS can be assessed in the same way as NI.

It is useful to be able to quantify adaptive divergence for all orthologs shared between two taxa (the 'core genome'). Summing polymorphism and divergence for all

orthologs to calculate NI or averaging NI values for all individual orthologs however results in statistical bias [14]. To calculate an overall NI across genes Stoletzki and Eyre-Walker suggest using a variant of the Haenzsel-Mantel method for combining contingency tables. A novel weighted-average of the NI statistic for all shared genes, NITG (named after Tarone and Greenland) performs well regardless of heterogeneity of NI across genes and comes with a 95% Confidence Interval [14]:

$$NI_{TG} = \frac{\sum D_S P_N / (P_S + D_S)}{\sum P_S D_N / (P_S + D_S)} \quad (3)$$

In order to provide a user-friendly method to apply the MK test of selection to entire bacterial core genomes, we have developed a web service with a graphical user interface called ODoSE (Ortholog Direction of Selection Engine). The ODoSE pipeline enables researchers to select prokaryote genomes of interest from the NCBI database and/or upload their own genome data, after which the DoS statistic is calculated for every individual single-copy ortholog (SICO) and the NITG statistic is calculated for all SICOs combined, allowing for the genome-wide characterization of adaptive divergence.

Results

The ODoSE workflow is implemented in the Galaxy framework [15], which is supported by a large and active community, does not require programming experience or command line instructions and makes it easy to share results. Importantly, users have the possibility to customize the default workflow as they see fit. A brief overview of the pipeline is given below and in Figure 1. Log files are provided with each step in the analysis to summarize data and list any potential errors. A more extensive manual as well as two example runs are hosted on the ODoSE website www.odose.nl.

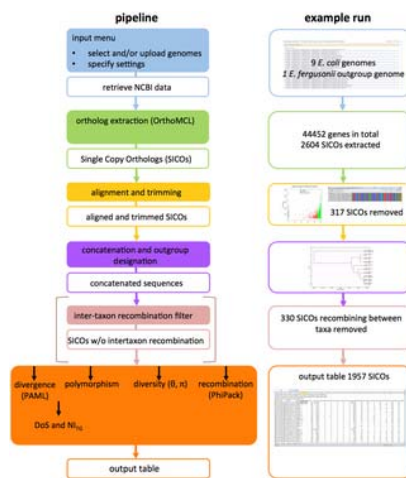


Figure 1. Schematic representation of the ODoSE workflow.

doi:10.1371/journal.pone.0062447.g001

Input

Genomes can be selected from all prokaryote genome projects deposited in NCBI RefSeq and the EMBL Nucleotide Sequence Database. All genomes are available through a daily updated mirror (mrs.cmbi.ru.nl) to guarantee access. User-generated genome data in the FASTA nucleotide coding region format (.fn) can be uploaded in combination with GenBank data or can be analysed independently. Both downloaded DNA sequences and translated protein sequences can be downloaded in a zip file for each selected genome.

Extraction

A protein-level reciprocal BLAST to identify all orthologous sequences is performed by OrthoMCL [16]. Users can specify a minimal protein length for analysis (default is set to 30 amino acids) and the e-value for the reciprocal BLAST (default 10^{-5}). A table is produced listing the distribution of all genes in all selected genomes. A zip file containing all SICO DNA sequences is provided; the input menu also gives the option to download zip files containing multiple copy orthologs or orthologs that occur in a subset of genomes only.

Alignment and Trimming

Each extracted Single Copy Orthologous (SICO) gene is aligned using MUSCLE [17], back translated and trimmed to equal length. Orthologs that do not match user-defined alignment quality control parameters (% alignment overlap and indel length) are excluded. Zip files are provided containing aligned-, aligned and trimmed- and low quality SICOs. A scatterplot summarizes the alignment and trimming statistics.

Concatenation and Outgroup Designation

SICOs are concatenated for every selected genome and a UPGMA tree is constructed for these concatemers using dnadist and neighbour from the PHYLIP 3.69 package (<http://evolution.genetics.washington.edu/phylip.html>). The genome used as the outgroup in the MK analysis is automatically assigned on the basis of the first split in this tree. For some of the individual SICOs, inter-taxon recombination events will have changed the outgroup position, prohibiting MK test analyses. Therefore, the option is given to create UPGMA trees for each individual SICO to filter for congruency with the concatemer UPGMA tree in order to exclude such recombinants. Zip files containing concatemers, individual SICO alignments and SICOs listed per genome are provided. A PDF of the concatemer UPGMA tree is provided for visual reference.

Population Genetic Calculations

The codeml program in the PAML package [18], is used to calculate synonymous and non-synonymous divergence from the outgroup sequence. The site frequency spectrum and nucleotide diversity (π and θ) are tabulated using custom scripts. Custom scripts are used to calculate the DoS statistic for every individual SICO and the NITG statistic with associated confidence interval for the concatemer [14]. The package PHIPACK [19] is used to perform three tests of homologous recombination. A final output table summarizes all results. When the outgroup consists of multiple strains and the test can be performed for both taxa, a second output table is produced.

Discussion

A lack of software applications as well as statistical difficulties with the MK test have prevented it to be commonly used on a genome-wide scale [9], [20], [21]. The ODoSE pipeline offers an easy-to-use workflow to perform two new extensions of the MK test: to automatically quantify the impact of natural selection on every single gene shared by a taxonomic group of interest as well as all genes combined, allowing for systematic analysis of the evolutionary forces shaping core genome divergence. The use of the pipeline is not limited to the MK test but permits a wider range of population genomic analysis. For instance, the concatenated SICO sequences can be used to generate high-resolution phylogenetic trees, the distribution of all genes in all genomes is tabulated enabling pan genome analyses and zip files are provided with core and accessory genes (per genome and per gene) for downstream analyses. Finally, for more sophisticated analyses, the distribution of polymorphisms (the Site Frequency Spectrum) can be used as input for the program DFE-alpha, which uses a maximum-likelihood method to calculate the proportion of adaptive substitutions [22].

Acknowledgments

We thank the developers of software used in ODoSE for making their efforts publicly available, and Burkhard Linke for help with testing.

Author Contributions

Conceived and designed the experiments: MV MWJvP. Performed the experiments: MV TtB MWJvP. Analyzed the data: MV TtB MAvD MAH AEW MWJvP. Contributed reagents/materials/analysis tools: MV TtB MAvD MAH AEW MWJvP. Wrote the paper: MV MWJvP.

References

- van Passel MW, Marri PR, Ochman H (2008) The emergence and fate of horizontally acquired genes in *Escherichia coli*. *PLoS Comput Biol* 4: e1000059. doi: 10.1371/journal.pcbi.1000059.
CrossRef PubMed/NCBI Google Scholar
- Lefebure T, Stanhope MJ (2009) Pervasive, genome-wide positive selection leading to functional divergence in the bacterial genus *Campylobacter*. *Genome Res* 19: 1224–1232. doi: 10.1101/gr.089250.108.
CrossRef PubMed/NCBI Google Scholar
- Lefebure T, Bitar PD, Suzuki H, Stanhope MJ (2010) Evolutionary dynamics of complete *Campylobacter* pan-genomes and the bacterial species concept. *Genome Biol Evol* 2: 646–655. doi: 10.1093/gbe/evq048.
CrossRef PubMed/NCBI Google Scholar
- Soyer Y, Orsi RH, Rodriguez-Rivera LD, Sun Q, Wiedmann M (2009) Genome wide evolutionary analyses reveal serotype specific patterns of positive selection in selected *Salmonella* serotypes. *BMC Evol Biol* 9: 264. doi: 10.1186/1471-2148-9-264.
CrossRef PubMed/NCBI Google Scholar
- Xu Z, Chen H, Zhou R (2011) Genome-wide evidence for positive selection and recombination in *Actinobacillus pleuropneumoniae*. *BMC Evol Biol* 11: 203. doi: 10.1186/1471-2148-11-203.
CrossRef PubMed/NCBI Google Scholar
- Joseph B, Schwarz RF, Linke B, Blom J, Becker A, et al. (2011) Virulence evolution of the human pathogen *Neisseria meningitidis* by recombination in the core and accessory genome. *PLoS One* 6: e18441. doi: 10.1371/journal.pone.0018441.
CrossRef PubMed/NCBI Google Scholar
- Shapiro BJ, Alm E (2009) The slow-fast substitution ratio reveals changing patterns of natural selection in gamma-proteobacterial genomes. *ISME J* 3: 1180–1192. doi: 10.1038/ismej.2009.51.
CrossRef PubMed/NCBI Google Scholar
- Eyre-Walker A (2006) The genomic rate of adaptive evolution. *Trends Ecol Evol* 21: 569–575. doi: 10.1016/j.tree.2006.06.015.
CrossRef PubMed/NCBI Google Scholar
- Charlesworth J, Eyre-Walker A (2006) The rate of adaptive evolution in enteric bacteria. *Mol Biol Evol* 23: 1348–1356. doi: 10.1093/molbev/msk025.
CrossRef PubMed/NCBI Google Scholar
- McDonald JH, Kreitman M (1991) Adaptive protein evolution at the Adh locus in *Drosophila*. *Nature* 351: 652–654. doi: 10.1038/351652a0.
CrossRef PubMed/NCBI Google Scholar
- Rand DM, Kann LM (1996) Excess amino acid polymorphism in mitochondrial DNA: contrasts among genes from *Drosophila*, mice, and humans. *Mol Biol Evol* 13: 735–748. doi: 10.1093/oxfordjournals.molbev.a025634.
CrossRef PubMed/NCBI Google Scholar
- Presgraves DC (2005) Recombination enhances protein adaptation in *Drosophila melanogaster*. *Curr Biol* 15: 1651–1656. doi: 10.1016/j.cub.2005.07.065.
CrossRef PubMed/NCBI Google Scholar
- Hughes AL, Friedman R, Rivaille P, French JO (2008) Synonymous and nonsynonymous polymorphisms versus divergences in bacterial genomes. *Mol Biol Evol* 25: 2199–2209. doi: 10.1093/molbev/msn166.
CrossRef PubMed/NCBI Google Scholar
- Stoletzki N, Eyre-Walker A (2011) Estimation of the neutrality index. *Mol Biol Evol* 28: 63–70.
CrossRef PubMed/NCBI Google Scholar
- Giardine B, Riemer C, Hardison RC, Burhans R, Elnitski L, et al. (2005) Galaxy: a platform for interactive large-scale genome analysis. *Genome Res* 15: 1451–1455. doi: 10.1101/gr.4086505.
CrossRef PubMed/NCBI Google Scholar
- Li L, Stoekert CJ, Roos DS (2003) OrthoMCL: identification of ortholog groups for eukaryotic genomes. *Genome Res* 13: 2178–2189. doi: 10.1101/gr.1224503.
CrossRef PubMed/NCBI Google Scholar
- Edgar RC (2004) MUSCLE: multiple sequence alignment with high accuracy and high throughput. *Nucleic Acids Res* 32: 1792–1797. doi: 10.1093/nar/gkh340.
CrossRef PubMed/NCBI Google Scholar
- Yang Z (2007) PAML 4: phylogenetic analysis by maximum likelihood. *Mol Biol Evol* 24: 1586–1591. doi: 10.1093/molbev/msm088.
CrossRef PubMed/NCBI Google Scholar
- Bruen TC, Philippe H, Bryant D (2006) A simple and robust statistical test for detecting the presence of recombination. *Genetics* 172: 2665–2681. doi: 10.1534/genetics.105.048975.
CrossRef PubMed/NCBI Google Scholar
- Shapiro BJ, Alm EJ (2008) Comparing patterns of natural selection across species using selective signatures. *PLoS Genet* 4: e23. doi: 10.1371/journal.pgen.0040023.
CrossRef PubMed/NCBI Google Scholar
- Vos M (2011) A species concept for bacteria based on adaptive divergence. *Trends Microbiol* 19: 1–7. doi: 10.1016/j.tim.2010.10.003.

[CrossRef](#) [PubMed/NCBI](#) [Google Scholar](#)

22. Eyre-Walker A, Keightley PD (2009) Estimating the rate of adaptive molecular evolution in the presence of slightly deleterious mutations and population size change. *Mol Biol Evol* 26: 2097–2108. doi: 10.1093/molbev/msp119.

[CrossRef](#) [PubMed/NCBI](#) [Google Scholar](#)