

Genome analysis

BUSCO: assessing genome assembly and annotation completeness with single-copy orthologs

Felipe A. Simão[†], Robert M. Waterhouse[†], Panagiotis Ioannidis,
Evgenia V. Kriventseva and Evgeny M. Zdobnov*

Department of Genetic Medicine and Development, University of Geneva Medical School and Swiss Institute of Bioinformatics, rue Michel-Servet 1, 1211 Geneva, Switzerland

*To whom correspondence should be addressed.

[†]The authors wish it to be known that, in their opinion, the first two authors should be regarded as Joint First Authors.

Associate Editor: John Hancock

Received and revised on March 30, 2015; accepted on May 21, 2015

Abstract

Motivation: Genomics has revolutionized biological research, but quality assessment of the resulting assembled sequences is complicated and remains mostly limited to technical measures like N50.

Results: We propose a measure for quantitative assessment of genome assembly and annotation completeness based on evolutionarily informed expectations of gene content. We implemented the assessment procedure in open-source software, with sets of Benchmarking Universal Single-Copy Orthologs, named BUSCO.

Availability and implementation: Software implemented in Python and datasets available for download from <http://busco.ezlab.org>.

Contact: evgeny.zdobnov@unige.ch

Supplementary information: [Supplementary data](#) are available at *Bioinformatics* online.

1 Introduction

Genomics data acquisition continues to accelerate, however, the short lengths of sequencing reads make their assembly into full-length chromosomes extremely challenging. To gauge potential limitations and implement improvements it is thus important to assess the quality of the resulting data. Proposed measures (Clark *et al.*, 2013; Gurevich *et al.*, 2013; Hunt *et al.*, 2013; Simpson, 2014) reflect methodologies, e.g. per-base error rates, insert size distributions; or genome biases, e.g. *k*-mer distributions; or fragment (contig) length distributions, e.g. N50, which summarizes assembly contiguity in a single number: half the genome is assembled on contigs of length N50 or longer. However, such measures do not assess assembly completeness in terms of gene content: an important consideration that also affects data interpretation and helps to guide improved assembly and annotation strategies.

With the growing number of available sequenced genomes, knowledge of their gene content is consolidating and can be used to

develop an evolutionary measure of genome completeness. Here, we revisit the idea of using known genes to measure genome assembly and annotation completeness (Mende *et al.*, 2013; Parra *et al.*, 2009), by introducing a citable notation for well-defined measures, compiling the comprehensive datasets to support such assessments, and offering these as an off-the-shelf software.

As proposed previously (Waterhouse *et al.*, 2013), Benchmarking Universal Single-Copy Orthologs (BUSCO) are ideal for such quantifications of completeness, as the expectations for these genes to be found in a genome and to be found only in single-copy are evolutionarily sound. We used our OrthoDB database of orthologs (www.orthodb.org) to define BUSCO sets for six major phylogenetic clades. Sampling hundreds of genomes, orthologous groups with single-copy orthologs in >90% of species were selected. Importantly, this threshold accommodates the fact that even well-conserved genes can be lost in some lineages, as well as allowing for incomplete gene annotations and rare gene duplications. Subsequent

filtering, e.g. on sequence uniqueness and conservation levels [see [Supplementary Online Material \(SOM\)](#) for details], resulted in BUSCO sets representing 3023 genes for vertebrates, 2675 for arthropods, 843 for metazoans, 1438 for fungi and 429 for eukaryotes. We also adopted 40 universal marker genes proposed for the assessment of prokaryotic genomes ([Mende et al., 2013](#)). The clades spanning many phyla offer comprehensive coverage of the tree of life, while the more narrowly defined clades provide a much greater resolution with much larger BUSCO sets. These are applicable not only to the assessment of genome assemblies, but also to annotated gene sets, as well as assembled transcriptomes ([Fig. 1](#)). Additionally, as near-universal single-copy markers, the recovered genes are ideal for species phylogeny reconstructions.

We propose intuitive metrics to describe genome, gene set or transcriptome completeness in BUSCO notation - C:complete [D:duplicated], F:fragmented, M:missing, n:number of genes used ([Fig. 1](#)). The recovered genes are classified as ‘complete’ when their lengths are within two standard deviations of the BUSCO group mean length (i.e. within ~95% expectation, [Supplementary Fig. S1](#)). ‘Complete’ genes found with more than one copy are classified as ‘duplicated’. These should be rare, as BUSCOs are evolving under single-copy control ([Waterhouse et al., 2011](#)), and the recovery of many duplicates may therefore indicate erroneous assembly of haplotypes. Genes only partially recovered are classified as ‘fragmented’, and genes not recovered are classified as ‘missing’. Finally, the ‘number of genes used’ indicates the resolution and hence is informative of the confidence of these assessments.

Using HMMER 3 ([Eddy, 2011](#)) hidden Markov model (HMM) profiles from amino acid alignments, the core of the analysis workflow ([Fig. 1](#)) assesses whether BUSCO gene matches are orthologous or not (i.e. satisfy BUSCO group-specific bitscore cut-offs; detailed in [SOM](#)), and classifies positive matches as complete or fragmented. This core analysis is the same for assessing genomes, transcriptomes or gene sets. However, additional analyses are required to first annotate genes from transcriptomes and genomes. The simple longest open reading frame approach performs well for transcriptomes. For genomes, gene annotation is performed with Augustus ([Keller et al., 2011](#)), guided by amino acid BUSCO group block-profiles, on genomic loci detected with tBLASTn searches using BUSCO group consensus sequences (detailed in [SOM](#)). Although this gene prediction approach may have its limitations and biases, they are consistent across different species, making for fair comparisons. Conveniently, the thousands of confident BUSCO gene models provide an excellent gene predictor training set for use as part of genome annotation pipelines.

[Table 1](#) reports BUSCO notation assessments of five diverse species for both their genome assemblies and their annotated gene sets. Assessing 70 genomes, 163 gene sets, and 96 transcriptomes revealed substantial variability of completeness ([Supplementary Table S1](#)). Poor correlation with scaffold N50 ([Supplementary Fig. S2](#)) highlights how completeness provides important complementary

information for quality assessment. Nevertheless, the fact that some genome assemblies appear less complete than their corresponding gene sets (e.g. *H. sapiens* [Table 1](#)) reveals limitations of the BUSCO gene prediction step. On the other hand, a reversal of this trend (e.g. *A. nidulans* [Table 1](#)) suggests that the annotated gene set may be missing some BUSCO gene matches that are in fact present in the genome. Thus, it should be noted that while BUSCO assessments aim to robustly estimate completeness of the datasets, technical limitations (particularly gene prediction) may inflate proportions of ‘fragmented’ and ‘missing’ BUSCOs, especially for large genomes. More ‘missing’ BUSCOs may also be reported for species that are highly derived with respect to the assessment clade—even with high-quality genomes (e.g. *C. elegans* [Table 1](#))—reflecting the organism’s evolutionary history rather than an incomplete assembly.

Comparing genome to gene set completeness of 40 species using a 250-BUSCO eukaryotic subset reveals generally consistent assessments across highly divergent lineages from fungi to human ([Fig. 2](#)). Employing the 248 genes of the Core Eukaryotic Gene Mapping Approach (CEGMA) ([Parra et al., 2007](#)) in a like-for-like

Table 1. Assessment of fruitfly (*D. melo*), nematode worm (*C. eleg*), human (*H. sapi*), owl limpet (*L. giga*), and fungus (*A. nidu*) genome assemblies (upper row) and gene sets (lower row) in BUSCO notation (C:complete [D:duplicated], F:fragmented, M:missing, n: gene number)

Species	Size	BUSCO notation assessment results
<i>D. melo</i>	139 Mbp	C:98% [D:6.4%], F:0.6%, M:0.3%, n:2 675
	13 918 genes	C:99% [D:3.7%], F:0.2%, M:0.0%, n:2 675
<i>C. eleg</i>	100 Mbp	C:85% [D:6.9%], F:2.8%, M:11%, n:843
	20 447 genes	C:90% [D:11%], F:1.7%, M:7.5%, n:843
<i>H. sapi</i>	3 381 Mbp	C:89% [D:1.5%], F:6.0%, M:4.5%, n:3 023
	20 364 genes	C:99% [D:1.7%], F:0.0%, M:0.0%, n:3 023
<i>L. giga</i>	359 Mbp	C:89% [D:2.3%], F:4.3%, M:5.8%, n:843
	23 349 genes	C:90% [D:13%], F:7.8%, M:2.1%, n:843
<i>A. nidu</i>	30 Mbp	C:98% [D:1.8%], F:0.9%, M:0.2%, n:1 438
	10 534 genes	C:95% [D:7.3%], F:3.8%, M:0.9%, n:1 438

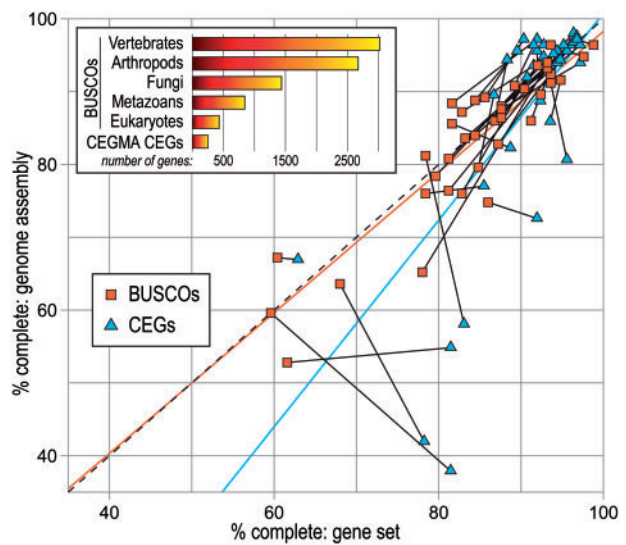


Fig. 2. BUSCOs (eukaryotic subset) and CEGMA CEGs recovered from 40 representative genome assemblies and their respective gene sets. Inset: number of genes in each BUSCO set and the CEGMA CEGs

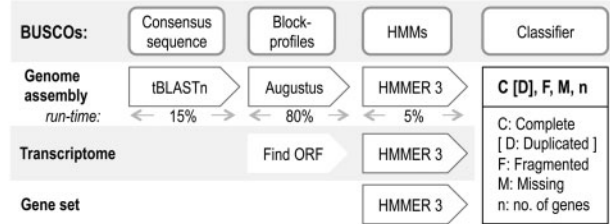


Fig. 1. BUSCO assessment workflow and relative run-times

comparison (i.e. implementing gene set assessments using CEGMA HMMs, see SOM for details) appears somewhat less consistent (Fig. 2, BUSCO linear regression is closer to the diagonal). Additionally, in comparable 250-BUSCO and 248-CEGMA assessments BUSCO run-times are substantially faster, $\sim 2\times$ for small genomes and $\sim 10\times$ for large genomes, but of course the higher resolutions achievable with the thousands of vertebrate, arthropod and fungal BUSCO sets do require longer run-times (Supplementary Table S2). Run-times are generally proportional to the size of the BUSCO set used and the sizes of the genomes being assessed, e.g. on 4 CPU cores with up to 8 GB memory: the 180 Mbp fruit fly genome ran for 3.2–7.6 h, while the 3381 Mbp human genome ran for 13–29 h with 843 metazoan and 2675 arthropod or 3023 vertebrate BUSCOs, respectively (Supplementary Table S2).

BUSCO quality assessments provide high-resolution quantifications citeable in the simple C[D],F,M,n notation for genomes, gene sets and transcriptomes. This facilitates informative comparisons, e.g. of newly sequenced draft genome assemblies to those of gold-standard models, or to quantify iterative improvements to assemblies or annotations. BUSCO assessments therefore offer intuitive metrics, based on evolutionarily informed expectations of gene content from hundreds of species, to gauge completeness of rapidly accumulating genomic data and satisfy an Iberian's quest for quality—'Busco calidad/qualidade'.

Acknowledgements

The authors thank colleagues and i5K members for user feedback. Some computations were performed at the Vital-IT (<http://www.vital-it.ch>) center for high-performance computing of the Swiss Institute of Bioinformatics.

Funding

This work benefitted from Swiss National Science Foundation grants 31003A_143936 and PDFMP3_137064 to E.M.Z. and Marie Curie International Outgoing Fellowship PIOF-GA-2011-303312 to R.M.W.

Conflicts of Interest: none declared.

References

- Clark, S.C. *et al.* (2013) ALE: a generic assembly likelihood evaluation framework for assessing the accuracy of genome and metagenome assemblies. *Bioinformatics*, **29**, 435–443.
- Eddy, S.R. (2011) Accelerated profile HMM searches. *PLoS Comput. Biol.*, **7**, e1002195.
- Gurevich, A. *et al.* (2013) QUAST: quality assessment tool for genome assemblies. *Bioinformatics*, **29**, 1072–1075.
- Hunt, M. *et al.* (2013) REAPR: a universal tool for genome assembly evaluation. *Genome Biol.*, **14**, R47.
- Keller, O. *et al.* (2011) A novel hybrid gene prediction method employing protein multiple sequence alignments. *Bioinformatics*, **27**, 757–763.
- Mende, D.R. *et al.* (2013) Accurate and universal delineation of prokaryotic species. *Nat. Methods*, **10**, 881–884.
- Parra, G. *et al.* (2007) CEGMA: a pipeline to accurately annotate core genes in eukaryotic genomes. *Bioinformatics*, **23**, 1061–1067.
- Parra, G. *et al.* (2009) Assessing the gene space in draft genomes. *Nucleic Acids Res.*, **37**, 289–297.
- Simpson, J.T. (2014) Exploring genome characteristics and sequence quality without a reference. *Bioinformatics*, **30**, 1228–1235.
- Waterhouse, R.M. *et al.* (2011) Correlating traits of gene retention, sequence divergence, duplicability and essentiality. *Genome Biol. Evol.*, **3**, 75–86.
- Waterhouse, R.M. *et al.* (2013) OrthoDB: a hierarchical catalog of animal, fungal and bacterial orthologs. *Nucleic Acids Res.*, **41**, D358–D365.