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StORF-Reporter: Finding Genes between Genes

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ABSTRACT

Large regions of prokaryotic genomes are currently without any annotation, in part due to well-established limitations of annotation tools. We present StORF-Reporter, a tool that takes as input an annotated genome and returns missing CDS genes from unannotated regions. StORF-Reporter consists of two parts. The first part begins with the extraction of unannotated regions from an annotated genome. Next, Stop-ORFs (StORFs) are identified in these unannotated regions. StORFs are Open Reading Frames that are delimited by stop codons.

We show that this methodology recovers complete coding sequences (with/without similarity to known genes) which were missing from both canonical and novel genome annotations. StORF-Reporter recovered sequences that exhibited high levels of sequence identity to proteins in the Swiss-Prot database and the proteomes of the genome they were identified from (gene-duplicates). We inspected in detail the results from the genomes of six model organisms, the pangenome of Escherichia coli, and a further 6,223 annotated prokaryotic genomes of 179 genera from the Ensembl Bacteria database. StORF-Reporter was able to extend the core, soft-core and accessory gene-collections, and identify novel gene families and families which were extended into additional genera, not previously identified in the canonical annotations. Many of the gene families these sequences form are routinely misreported or completely omitted by state-of-the-art annotation methods.

StORF-Reporter has been specifically developed to be interoperable with the PROKKA genome annotation pipeline due to the systematic use of its output format in downstream studies.

INTRODUCTION

Prokaryotic genomes are often observed with high levels of genome density, with the compact nature of their genes, both coding and non-coding, resulting in little 'extraneous' DNA (1). Much of this extraneous DNA is often referred to as intergenic, islands of DNA between functional elements such as genes, promoters or other functionally and structurally important elements. In eukaryota studies, the relative proportion of a genome reported to be intergenic has been linked to the biological complexity of the organism (2). In contrast, prokaryotic genomes contain less intergenic DNA which has been functionally overlooked despite reports they contain putative coding and non-coding genes (complete and pseudogenised) However, due to the much reduced proportion of their genomes reported as intergenic, prokaryotic intergenic regions are often assumed not to be functionally important, even though studies have reported finding putative coding and non-coding genes (both complete and pseudogenised) in them (3, 4, 5). Therefore, in this work, the term 'intergenic DNA' will be relabeled as *unannotated region* (UR) to reflect our belief that these regions are likely to contain yet to be discovered CoDing Sequences (CDS).

There is a distinct paucity in the analysis of prokaryote URs and what they may contain (4, 6). Those studies which have investigated the conservation and selection of putative UR sites have shown that there is "consistent evidence of strong purifying selection on IGRs [URs]" (7). These regions should now be investigated to determine whether they contain genes missed by contemporary prediction methods. This work specifically investigates their potential to harbor yet-to-be discovered CDS genes.

Unfortunately, the methods employed to study these regions often rely heavily on sequence alignments of the entire UR sequence to known proteins deposited in databases. This practice is inefficient and more importantly inaccurate, as the part of the UR which may exhibit similarity to a known protein may be overshadowed by the surrounding DNA which has no similarity to known sequences previously identified. Furthermore, similarity searching to previously identified genes is unlikely to work if there is a systematic reason behind why such genes are routinely missed by contemporary

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genome annotation, and therefore they are unlikely to have representatives in such databases.

To elucidate these regions and overcome the limitations in genome annotation, many of which continue to be outlined in the literature (8), we have developed a novel methodology to supplement genome annotation. This approach, named 'StORF-Reporter', is performed in two stages. First we extract URs from an annotated genome (see Figure 1. Then we identify and filter StORFs (Open Reading Frames that are delimited by two stop codons) from these extracted URs.

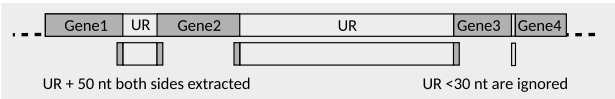

Figure 1. Visual representation of how Unannotated Regions (URs) are selected for extraction. URs that are less than 30 nt are not extracted. URs are extracted with an additional 50 nt on their 5' and 3' ends to allow for overlapping genes.

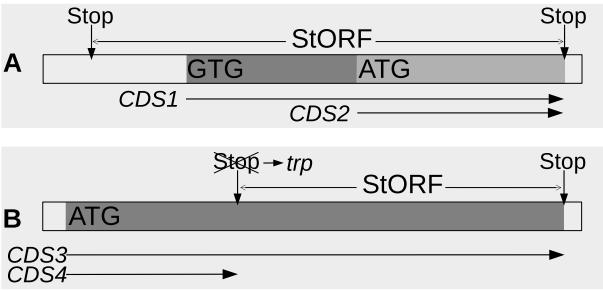

Figure 2. Visual representation of a StORF and how it can capture multiple potential start codons and stop codons in an unannotated region. Part **A** depicts a StORF capturing two possible start positions (GTG and ATG) for a CDS gene which could produce two distinct CDS sequences (*CDS1* and *CDS2*). Part **B** shows how a StORF can comprise of only a partial segment of a gene if that gene either recodes a canonical stop codon (Stop to trp) or has had an in-frame stop codon mutation resulting in one complete and one truncated transcript (*CDS3* and *CDS4*)

An example of a StORF, extracted from a previously annotated genome, can be seen in Figure 2, potentially capturing multiple possible start codons. Shifting the focus from locating the start codon to the stop codon simplifies the problem as it removes the need to identify genomic features such as the Shine–Dalgarno motif (9), promoter regions (10), ribosomal binding sites, and operons (11). This is due to out of frame stop codons having been observed as a widespread phenomenon among prokaryotes and theorised to carry functional significance of being selected in the course of genome evolution to act against unintended frameshift (12). Thus, the length of a StORF and whether it is overlapping other StORFs or existing genes, are likely to be useful factors in their discovery and verification.

Current prokaryotic annotation tools still struggle to determine the correct start codon, resulting in the detection of an incomplete gene or missing it entirely (8). The reporting of StORFs, therefore, can also remove the potential for an incorrect or alternative start codon selection to truncate the start of a protein product, as the entire coding potential of the CDS is encapsulated by the StORF. This is important as while the canonical 'ATG' codon is most-often used to initiate approximately 80% of prokaryotic CDS genes, many species and cross-species gene families have been shown to use very different start codon profiles (13, 14). Furthermore, there is growing evidence of the existence of "organisms that adjust their genetic code in response to changing environments", thus making traditional start codon identification ever more complex (15). Although stop codon usage in prokaryote CDS genes has also been linked to a number of genomic features such as GC content, there is still much we do not yet know and many theories concerning their selection are still being posited by researchers (16, 17). However, unlike start codons, the three canonical stop codons (TGA, TAG, TAA) are the terminus for almost all CDS genes across almost all species, meaning that identification can be based solely on their presence.

The existence of multiple, and often contrary, definitions of an ORF has been recently raised (18) with the merits of each definition discussed. Interestingly, while most prokaryotic annotation tools will annotate from start codon to stop codon, the Sequence Ontology (19) makes no reference to the start codon in its definition of ORF. It is described as "the in-frame interval between the stop codons of a reading frame which when read as sequential triplets, has the potential of encoding a sequential string of amino acids.". StORFs therefore use the same interpretation as the Sequence Ontology but for clarity and due to their specific use case, will continued to be named StORFs hereafter.

This work proposes the StORF-Reporter methodology specifically as an additional step to be performed on the output of contemporary prokaryotic genome annotation. The combination of these StORFs with the output from existing annotations (for example, from Ensembl, or from a tool such as Prodigal (20)) can be referred to an enhanced annotation and represent a refining of current annotations as opposed to the traditional mantra of reannotation. We investigate StORFs identified from three sets of genomes. Firstly, we look at six bacterial model organisms which exhibit many URs long enough to contain full length CDS genes that can expand the narrative of these well-studied genomes. While a number of StORF sequences recovered were found to be duplicates or at least shared a high level of sequence identity to genes already annotated elsewhere in the genome in the canonical genomic annotations from Ensembl (21), others exhibited high levels of sequence identity to proteins in the Swiss-Prot database (22).

We next investigate the presence of conserved StORFs across the *Escherichia coli (E. coli)* pangenome. As pangenomes consist of a species-wide collection of core genes that are present in most/all genomes and accessory genes that are only present in some genomes but are dynamically exchanged in response to exogenous pressures, missing annotations can have detrimental impacts on the utility of their study. Additionally, as shown in the literature, the types of genes most often missing from genome annotations are those that are transient or non-core accessory genes, which are less common or missing in genomic databases (8, 23). To investigate this further, StORFs were extracted from a large collection of *E. coli* genomes, and analysis of these StORFs showed that they formed and redefined a number of core, soft-core and accessory gene families. The resulting novel gene families and known families supplemented with additional strains identified through StORF sequences, has essentially rewritten the pangenome gene-collection of *E. coli*.

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Lastly, we apply the same methodology to 6,223 prokaryotic genomes from Ensembl Bacteria. We find highly conserved StORFs across different genera in both 'StORF-Only' gene families and as additional sequences, expanding the Ensembl annotated gene families. The high levels of sequence conservation observed between genera suggests that these StORF sequences are likely to be functional genes that must now be added to the canonical annotations.

MATERIALS AND METHODS

Datasets

The canonical annotation and sequence data for 44,048 genomes of 8,244 prokaryotic species, which included 43,347 bacterial genomes and 493 archaeal genomes, were acquired from the 46th release of Ensembl Bacteria (21). For each genome, two data files were downloaded; the complete DNA sequence (*∗_dna.toplevel.fa*) and the GFF (Generic Feature Format) file (*∗.gff3*) containing the position information for each gene (coding and non-coding). The genomic elements (including both coding and non-coding genes) presented in the Ensembl Bacteria GFF annotations were taken as reference annotations for this study. Fragmented genomes were removed by filtering out those with more than 5 contigs (not including plasmids). Next, genera which had less than 5 genomes were removed. This resulted in 6,223 genomes (see Supplementary Table 1). Out of this 6,223, the six model organisms; *Bacillus subtilis (B. subtilis)* BEST7003 strain, *Caulobacter crescentus (C. crescentus)* CB15 strain, *E. coli* K-12 ER3413 strain, *Mycoplasma genitalium (M. genitalium)* G37 strain, *Pseudomonas fluorescens (P. fluorescens)* UK4 strain, *Staphylococcus aureus (S. aureus)* 502A strain, shown in Table 1, were selected for this study. Additionally, *E. coli* was selected to undergo a pangenomic analysis of its Ensembl annotated genes and extracted StORFs. As many of the Ensembl Bacteria genomes were unlabeled at the species level, to make sure the correct genomes were extracted, only those labeled specifically as *'Escherichia_coli'* were extracted. This resulted in a group of 219 *E. coli* genomes from the original filtered group of 6,223 (see Supplementary Table 2 for further detail).

Model Organism	Genome Size (Mbp)	Genes **[Density]**
B. subtilis (BEST7003)	4.04	4,133 **[88.91%]**
C. crescentus (CB15)	4.02	3,875 **[90.60%]**
E. coli K-12 (ER3413)	4.56	4,257 **[86.28%]**
M. genitalium (G37)	0.58	559 **[92.03%]**
P. fluorescens (UK4)	6.06	5,266 **[84.75%]**
S. aureus (502A)	2.76	2,556 **[83.93%]**

Table 1. An overview of genome composition for the six model organisms used in the analysis of StORF-Reporter. This table shows the number of Ensembl-annotated genes (coding and non-coding). The gene density is presented in bold square brackets. These six organisms span a range of genome size (0.58 - 6.06 Mbp) and gene density (percentage covered with annotation, 83.93% - 92.03%).

StORF-Reporter

StORF-Reporter was developed as an additional supplementary step to be performed after a genome annotation has been undertaken. It consists of two distinct parts which can be used independently or together as they were in this study: UR_Extractor(.py) and StORF_Finder(.py). The processes of both are described in the following sections and the code is available at https://github.com/NickJD/StORF-Reporter. A third tool, StORF_Reporter(.py) is available to perform UR and StORF reporting of PROKKA (24) output and presents the user with a newly created PROKKA formatted GFF file for use in downstream tools which require the PROKKA format.

Unannotated Region – Extractor (UR-Extractor) To facilitate the extraction of URs from different prokaryotic genomes (and the various interpretations of the GFF format), UR_Extractor was developed. It allows user-defined genomic features (coding and non-coding genomic elements) to be used to identify the boundaries of genomic elements. Written in Python3 (25) and using the feature coordinates presented in an associated GFF3 file, regions of DNA without annotation were extracted from the provided DNA sequence file. GFF3 and FASTA files with the details of the sequence and loci for each UR were reported for further analysis (see Supplementary Section 2.1 for command line menu of UR_Extractor.py).

When recovering URs from a genome it is important to consider that StORFs may overlap with annotated genes (coding and non-coding) (26). Therefore, it was necessary to determine the extent to which the URs should be extended into the annotated regions. The 6,223 genomes from Ensembl Bacteria, including the six model organisms in Table 1 were studied to identify representative parameters for the extraction of URs across this large set of Ensembl Bacteria genomes. The median gene overlap observed for each of the six genomes was 3 nt and the 75th percentile was below 50 nt, as can be seen in the left half (A) of Figure 3. Furthermore, the median distance from a gene's canonical start codon to the nearest in-frame upstream stop codon (representing the untranslated region of a StORF) was 39 nt (see the right half (B) of Figure 3). The lengths of overlap between genes (both coding and non-coding) across the 6,223 prokaryotic genomes were investigated and as can be seen in Supplementary Figure 1, the gene overlap lengths observed for the 6 genomes are similar to the majority of the Ensembl annotated genomes. These findings further illustrate that these model bacterial genomes are relatively compact and demonstrate that StORFs most often contain very little extraneous upstream DNA. To account for the median gene and StORF features observed, URs were only extracted if they were at least 30 nt long but were extended by 50 nt at both ends (into annotated genes) by the UR Extractor tool (see Figure 1), totaling a minimum length of 130 nt. This extension of 50 nt at both the 5-prime and 3-prime ends, was to allow for the capture of the parts of StORFs which may overlap with existing gene annotations. This process took into account the untranslated region between the start of the StORF and putative start codon of the protein sequence it captured and was necessary as the direction of a potential StORF is not known in advance (see Figure 2 for an illustration of how a StORF captures upstream DNA).

It is inevitable that genomic repositories, including Ensembl Bacteria, are known to contain varying levels of assembly and annotation error due to a number of constraints (23, 27, 28). It can also be the case that genomes have missing annotations as

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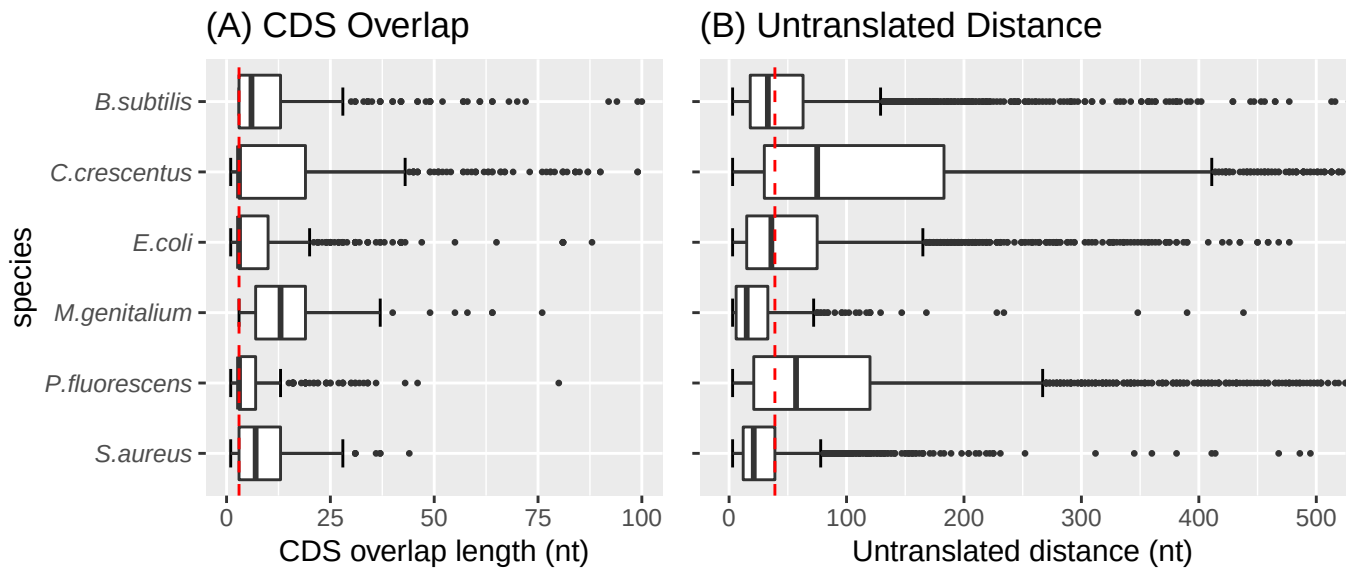

Figure 3. This double plot reports the analysis of the 6 model organisms which were used during the parameterisation of StORF-Reporter. Figure A reports the distributions of the Ensembl annotation gene overlap lengths for each model organism with a dotted red line representing the overall median (3 nt) with the x-axis truncated at 100 nt. Figure B reports the distance between an Ensembl gene's start codon and the first in-frame upstream stop codon for the model organisms with the x-axis truncated at 500 nt. The dotted red line represents the overall median (39 nt). These plots indicate that the extension of 50 nt from each end of the extracted intergenic regions is often enough to capture both the true overlap between an annotated gene and the putative gene identified by a StORF and the small amount of upstream non-coding DNA which the StORF will contain.

a result of human or software error, or limitations. Therefore, UR Extractor has a maximum UR length cutoff of 100 kb. A genome with a 100 kb UR either warrants further investigation for biological interest or is likely to contain annotation error.

Stop - Open Reading Frame – Finder (StORF-Finder) To identify StORFs, StORF-Finder starts by scanning the previously extracted URs (or alternatively any DNA sequence) for loci encapsulated by in-frame, user-definable stop codons (see Figure 2).

All three stop codons are frequently present in intergenic regions and also within genes but out-of-frame. This is hypothesised to prevent off-frame reading of gene sequences (29). To investigate whether StORF-Finder should preferentially select one stop codon over another, a comparison was performed on the abundance of the triplets with their usage as stop codons across the Ensembl Bacteria genomes. The results of this analysis (see Supplementary Figure 2) show that while there are differences between the three stop codons, they are not universal and it is likely not beneficial to make generalisations.

Additionally, as with start codons, stop codons are differentially preferred by groups of genes and gene-families both from within the same and across different species (30). For example, we can see in Supplementary Figure 2 that the codon TAA is often used more frequently than its distribution across the genomes suggests. Similarly, TGA is often used less frequently than its distribution across the genome would suggest in all 6 model organisms (with TGA never used as a stop codon in *M. genitalium* (31). For TAG, the usage is mostly in line with the overall distribution across the genomes. There is evidence of stop codon preference and even repurposing for amino acids in species such as *M. genitalium* and specific gene-types which utilise their T/UGA and T/UAG codons (32) for selenocysteine (33) and pyrrolysine (34). Nevertheless, these cases are rare and it can be assumed that for the majority of prokaryotic genomes, the three canonical stop codons can be treated equally.

While removing the need to identify the location of start codons, StORFs do have their own drawbacks. To be consistent with the universal genetic code in codon table 11, only ATG is translated to methionine in the StORF reporter output. This presents a problem when reporting StORFs since, alternative start codons (i.e. codons other than ATG which initiate translation) are incorrectly assigned the amino acid represented in the codon table 11 and not methionine as is observed in the protein (35). This is a difficult problem to overcome since we cannot predict alternative translation start codons in advance. To mitigate this, StORF-Finder reports both the DNA and amino acid sequences in its output.

As with traditional CDS prediction methods, without any form of filtering, StORF-Finder can report a very high number of overlapping and nested StORFs, even for short regions of DNA. Therefore, a filtering step was developed to reduce the number of StORFs reported. This is done by first ordering all StORFs by their length in descending order and then iteratively removing the nested or shorter StORFs in cases where two StORFs overlap beyond the defined length of 50 nt. This is done individually for each set of StORFs for each UR. This filtration method is applied to all StORFs equally and is intended to maximise the likelihood that recovered StORFs contain functional sequences. The remaining StORFs are reported in FASTA (DNA and/or amino acid form) and GFF format with both locus coordinates for their original position within the original genome sequence, and their position relative to the UR in which they were reported.

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Extracting StORFs from Prodigal and Ensembl annotations of the six Model Organisms

To investigate the ability of StORF-Reporter to add to and improve contemporary annotations, URs and StORFs were extracted from the 6 model organisms. This was done using the existing annotations provided by Ensembl Bacteria and for the annotations provided by running the Prodigal (20) genome annotation tool on all 6 organisms . The default parameters of UR_Extractor (-gene_ident "ID=gene") were used to identify the complete set of genomic elements (coding and non-coding) which were then used to extract URs from the Ensembl provided annotations. Prodigal was applied to the complete DNA sequences of the six model organisms and a novel CDS prediction was performed using the tool's default parameters. As Prodigal only predicted CDSs, UR_Extractor used the CDS coordinates to extract URs (-gene_ident "CDS").

Escherichia coli Pangenome Analysis

To investigate the impact that StORFs may have on the pangenome of a well-studied prokaryotic model organism, the Ensembl Bacteria protein sequences and StORFs extracted from *E. coli* strains were studied.

Although gene loci information can be used to build a pangenome, many of the URs which potentially harbor the novel CDS genes that StORF-Reporter identifies are unlikely to be in the same location across all genomes. The fragmented state of the majority of genomes held in Ensembl Bacteria (as is the case for many repositories) further adds to the necessity to use alternative techniques to identify the pangenome. Amino acid sequence similarity is an established metric used to group gene families. It is used by the clustering tool CD-Hit, which does not require loci information (36). Amino acid sequences present in the *E. coli* genome were downloaded from Ensembl Bacteria *(.pep.all.fa)* and combined into one FASTA file and gene-clustering was then undertaken with CD-Hit (version 4.8.1) (36). Gene clustering was performed with the following parameters: aligned sequence identity threshold of 0.9 (90%), length difference cutoff of 0.6 (60%), and the '-g' option was set to the 'more accurate' option (see Supplementary Subsection 3 for more details). The consistent use of the 0.6 length difference cutoff between clustered sequences allowed for the instances where the StORF sequences contained additional upstream non-coding DNA which would have hindered the clustering of the matching coding regions. The strict sequence identity threshold of 0.9 ensured that the resulting clusters were very similar across the regions where they did align.

The output of CD-Hit consists of two datafiles, a '.clstr' (cluster) file containing the full sequence cluster metadata and a FASTA file containing the representative ID and sequence for each cluster. The CD-Hit cluster file, which consisted of the identified Ensembl gene clusters, was used as a baseline against which to compare the additional StORF predictions. The amino acid sequences represented by the *E. coli* StORFs recovered from the URs for the same set of 219 genomes were then combined with the previous CD-Hit output (FASTA) from the Ensembl proteins, which consisted of one representative sequence for each cluster (representatives are often the longer of the sequences in any one cluster). This combined FASTA file then underwent another round of CD-Hit clustering with the same parameters and produced the final *E. coli* pangenome datafiles (see Supplementary Subsection 4.2 for more details on the files created and used in this process).

The results of these clusters are complex and have been classified differently with respect to the origins of each sequence. As such they will be used throughout the rest of this paper and are referred to as follows:

- **Ensembl-Only**, which refers to the clusters with only Ensembl annotated protein sequences.
- **Ensembl-StORF**, which refers to the clusters which contain at least one Ensembl annotated protein sequence and one StORF amino acid sequence.
- **StORF-Only**, which refers to the clusters which solely contain StORF amino acid sequences.

To interpret the output from CD-Hit, a number of Python3 scripts were developed and are available on the StORF-Reporter GitHub repository https://github.com/NickJD/StORF-Reporter. The tool **CD-Hit_StORFReporter_Pangenome_Builder.py** was built to first identify the core-gene family groups for the 219 *E. coli* strains, and then identify whether any StORFs clustered with these representative gene cluster groups, but also whether there were any StORF-Only gene clusters spanning many *E. coli* strains. This allows for the recording of unique strains/genomes that make up each cluster and therefore the ability to calculate each cluster's pangenomic status (core, soft-core, accessory). Next, the .clstr file produced from the combined Ensembl representative sequences and StORF sequences was used to identify whether the Ensembl gene clusters had been added to by StORFs or whether there were any StORF-Only gene clusters. The StORF-Finder output sequence ID tag 'Stop-ORF' was used to distinguish between the Ensembl and StORF sequences.

It is difficult to predict what the result of clustering many thousands of protein sequences together could be. Through introducing hard-coded computation parameters into the natural world, it is inevitable that certain cases are unaccounted for. For example, multiple representatives from separate Ensembl gene clusters can be combined into a new single cluster with the addition of StORF sequences. To account for this, the Ensembl clusters which were combined when StORF sequences were added were first recorded separately in the Ensembl gene cluster results, and then additionally recorded in their new combined clusters with the additional StORFs (see results rows 1 and 2 respectively in Supplementary Table 3).

Extracting StORFs from 6,223 Ensembl genomes

An important aspect of gene family research concerns their diversity and spread across different genera. The StORF-Reporter methodology was applied to the multi-genera collection of 6,223 filtered Ensembl Bacteria genomes using the Ensembl annotations for the UR and StORF extraction. The diversity of assembly and annotation quality of these genomes presented a number of obstacles. As with the *E. coli* genomes, even after filtering, the genomes in this

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study were often in a fragmented state with a number of low quality regions containing large sections of ambiguous nucleotides. With this in mind, URs and StORFs were extracted individually for each of the 6,223 genomes using default parameters. The resulting StORF-Finder outputs were then combined into a single FASTA file with their original genus and species name appended to the start of each sequence header. For example, the full genome name of 'Enterobacter_cloacae_ecwsu1.asm23997v1' was appended to the start of the protein name 'AEW71445' to make 'Enterobacter_cloacae_ecwsu1.asm23997v1|AEW71445' The same CD-Hit parameters and workflow were undertaken as for the *E. coli* pangenomic study. A modification of the previously developed single species script (see Subsection) was built to handle multiple genera. This script records multiple levels of taxa information for each of the sequences such as genera, species and strain. However, as the analysis of the *E. coli* pangenome had already demonstrated StORF-Reporter's ability to capture gene sequences at the species level, only the genera specific to each sequence are reported in this study.

All scripts developed and used are available at https://github.com/NickJD/StORF-Reporter.

Validation of recovered StORFs

Different validation methods were required to determine what was being detected by the StORF sequences. For the StORFs identified from within the URs of the Prodigal annotations, an extension to the 'ORForise' platform (8) was developed, which originally was designed to compare annotations from different CDS prediction tools to a reference annotation. This extension, 'StORForise', was used to identify the Ensembl CDS genes missed by Prodigal that StORF-Reporter was able to recover. The default parameters of what classified a gene as 'detected' were taken from the ORForise package (a minimum of 75% coverage of an in-frame CDS prediction for a reference CDS gene). StORF-Reporter was only presented with the extracted URs according to the Prodigal CDS predictions. Mispredictions by Prodigal result in either elongation of an Ensembl CDS gene prediction, or prediction of a CDS where no Ensembl annotation existed. These would constrain the available regions that could be searched for by StORF-Reporter.

Therefore, as part of the ORForise platform, two additional scripts were developed to identify the Ensembl genes that Prodigal missed and specifically the number of missed Ensembl genes which were non-vitiated (not corrupted or contaminated) by the mispredictions of Prodigal (false positives, overlapping Ensembl genes by more than 50 nt).

The protein sequence aligner Diamond (37) (version v0.9.30.131) was used to align the recovered StORFs from the Prodigal and Ensembl annotations of the six model organisms to known proteins from both the same genomes and to the Swiss-Prot protein database (38) (release 2021_01, downloaded 05/03/2021). The sequence similarity alignments were performed with the Diamond blastp option with two separate parameter runs, one with a minimum bitscore of 60 and the second with the same bitscore but also a subject coverage cut-off of >=80%. This was done to report whether some StORFs were as a result of gene duplication or whether they had previously been identified in other studies. This was performed at the amino acid level as although the coding start sites are not identified by StORF-Finder, the coding frame is, and so the upstream region will include the start codon in the same frame (unless mutations are present). This indicates that StORFs can be directly translated into amino acid sequences, and then undergo similarity analysis to find homologous proteins already reported across other genomes and protein databases.

The full ORForise package along with StORForise and all other additional scripts are available at https://github.com/NickJD/ORForise and https://github.com/NickJD/StORF-Reporter.

RESULTS

Unannotated regions of model organisms

UR-Extractor was first applied to both the canonical Ensembl annotations and the Prodigal predictions of the six model organisms. The results of this can be seen in Supplementary Tables 4 and 5. These show that the numbers of URs reported for each model organism were similar between the Ensembl and Prodigal annotations, except for *M. genitalium* which were 157 and 636 respectively. This was likely due to the inability of Prodigal to account for the re-purposing of the 'UGA/TGA' stop codon causing a number of reported ORF to be incorrectly truncated. The Ensembl annotations also included non-coding genes which were treated the same as coding genes by the UR-Extractor tool. As Prodigal does not predict non-coding genes, it is likely to report additional or longer URs than those recovered using the Ensembl annotations. This can explain some of the higher numbers and longer UR lengths in the Prodigal analysis. For example, while the longest UR length in *S. aureus* was 2,591 in the Ensembl annotation, this increased to 12,332 in the Prodigal annotation. However, this was not consistent across all model organisms. Interestingly, the longest UR in *P. fluorescens* decreased from 20,088 to 4,264 for Ensembl and Prodigal annotations respectively.

By studying the URs extracted with either the annotations of Prodigal or Ensembl, there were clearly a number that were long enough to contain complete CDS genes - these were studied further.

While some of the URs extracted from Prodigal's annotations are likely to contain a number of non-coding genes and other genomic elements reported in Ensembl annotations, StORFs are specifically designed to identify coding genes and these are the focus of this paper.

StORF-Reporter recovers Ensembl CDS genes missed by Prodigal

An analysis of the StORFs extracted from the URs of the six model organism genomes was undertaken using the annotations from Prodigal. StORF-Reporter was able to recover Ensembl-annotated genes that were missed by Prodigal, and also found many other potential genes that had sequence similarity to the Swiss-Prot database or proteins already annotated in the model organism genomes.

The ORForise platform reported that Prodigal was able to identify the vast majority of Ensembl genes from each of

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the model organisms, except for *M. genitalium* (8). For each of the model organisms, StORF-Reporter identified a high number of StORFs, as can be seen in Supplementary Table 6. However, StORF-Reporter is impeded by the mispredictions produced by Prodigal. For each model organism, Prodigal reported a number of CDSs which either had no equivalent in the Ensembl annotation, were elongated versions of Ensembl genes or were too inaccurate to be classified as 'detected', according to the ORForise platform. This meant that StORF-Reporter was only able to search for StORFs in the non-vitiated regions of the genome. For each model organism, between one and 26 non-vitiated missed Ensembl genes were recovered by using StORF-Reporter with the Prodigal annotations.

DIAMOND blastp was used to compare StORFs recovered from each model organism against the Swiss-Prot database and the proteomes derived from each respective model organism (see supplementary Table 7). Additionally, there were StORFs that had a high sequence similarity to proteins in Swiss-Prot that were not present in either the Prodigal or Ensembl annotations, and were investigated further.

StORF-Reporter finds complete CDS genes not present in Ensembl annotations

Model Organism	# URs/StORFs	Swiss-Prot **[Coverage >=80%]**	Intra-Genome **[Coverage >=80%]**
B. subtilis	2,711 / 2,322	26 **[20]**	8 **[2]**
C. crescentus	2,321 / 1,554	8 **[5]**	15 **[3]**
E. coli	2,743 / 2,798	148 **[107]**	57 **[13]**
M. genitalium	157 / 168	63 **[4]**	50 **[0]**
P. fluorescens	3,509 / 3,404	73 **[46]**	173**[42]**
S. aureus	2,556 / 2,503	23 **[4]**	17 **[3]**

Table 2. Table containing the number of StORFs found in the URs recovered from Ensembl annotations for six model organisms. The numbers of StORFs which had a high sequence similarity and >=80% subject coverage to a protein in Swiss-Prot and Ensembl proteome are listed.

StORF-Reporter found many StORFs representing potential genes in the URs from the curated Ensembl annotations for each of the six model organisms. A number of StORFs had high sequence similarity to known protein coding genes in the Swiss-Prot protein database. Each of these StORFs have the potential to contain not only undiscovered genes but also historic gene fragments or other functional units waiting to be characterised. There were also a number of StORFs long enough to be genes which did not have a high level of sequence similarity to Swiss-Prot.

The number of StORFs which attained a match to a protein sequence from the curated Swiss-Prot database are reported in Table 2. To study the possibility that StORFs may capture instances of gene-duplication, for each of the model organisms, the reported StORFs were aligned to protein sequence databases built from each of the Ensembl annotations. Between 8 and 173 StORFs were observed to contain a high quality alignment to putative duplicate CDS sequences from within the same genome. These StORFs are likely to represent genes that have undergone duplication and either subsequent loss of function mutation or have not been detected by the current genome annotation process. While we observed 50 intra-genome StORFs 'hits' in *M. genitalium*, it was the only model organism not to contain a StORF with an alignment of >=80% of an Ensembl sequence. This is likely due to the 'UGA/TGA' codon repurposing. These results are reported in Table 2.

Extending the *E. coli* pangenome

StORF-Reporter found StORFs that both extend the core gene set and create novel core gene clusters potentially extending our understanding of the *E. coli* pangenome.

219 *E. coli* genomes were extracted from the collection of 6,223 Ensembl Bacterial genomes. From the 1,042,068 Ensembl protein sequences annotated in these genomes, 34,737 gene-clusters were formed, of which 20,676 were non-singletons (ie clusters containing more than one sequence). A median number of 3,038 URs and 2,958 StORFs were identified from the 219 genomes for a total of 673,136 URs and 652,056 StORFs (see Supplementary Table 8 for more detail).

Representatives from each of the Ensembl-Only clusters (all 34,737 - including singletons) were combined with the 652,056 StORFs identified from the same 219 *E. coli* genomes (see Supplementary Table 8 for more detail) and the same CD-Hit clustering methodology was applied. This resulted in a total of 86,579 clusters, of which 31,676 were non-singletons. There were 51,929 StORF-Only clusters and 28,094 Ensembl-Only clusters. The remaining clusters contained both StORF and Ensembl sequences (Ensembl-StORF clusters).

Some of the clusters containing StORFs and Ensembl genes were formed from multiple Ensembl cluster representatives, thus combining multiple gene families which had previously been split apart. This was a result of StORF sequences effectively bridging the 'sequence similarity' gap between multiple Ensembl sequences (defined henceforth as StORF-Combined-Ensembl clusters).

Only 87 of the 6,643 Ensembl gene families that clustered with StORF sequences did not extend into additional *E. coli* genomes. Supplementary Figure 4 shows that the distribution of the unique *E. coli* genomes present in the Ensembl-Only, Ensembl-StORF and StORF-Only clusters all followed a similar U-shaped curve. Interestingly, the size of the clusters which were extended by the StORFs was often increased by an substantial amount. For example, the proportion of clusters with 10 or fewer unique genomes was reduced from just below 60% to 40% with the addition of the StORF sequences.

The 2,612 core-gene (found in $>=99\%$ genomes) gene families consisting of only Ensembl genes is a similar figure to that of the number of core genes found in other studies of *E. coli* strains (39). Taking the varying levels of genome assembly and annotation quality into consideration, a large number of gene clusters (with and without StORF sequences) were found to contain genes from more than 95% of the *E. coli* genomes (see Supplementary Table 3). Interestingly, some clusters which fell below this 95% level were extended into the 95% and 99% thresholds by the addition of their clustered StORF sequences. There were also StORF-Only clusters with sequences from more than 95% and 99% of the *E. coli* genomes.

The inherently limiting process of using hard-coded sequence similarity and length cutoffs to distinguish gene families has inevitably brought forward a number of interesting cases. One example can be seen in the combining of multiple Ensembl protein representative sequences, and

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thus clusters, into one new cluster by the addition of StORFs. The 71 amino acid representative protein AKD71933 of Ensembl cluster 4,714 (consisting of 59 sequences and spanning 24 strains, some of which have duplicates or paralogs within the same genome), was clustered with the 66 amino acid protein AHM40952 of Ensembl cluster 6,112 (consisting of 26 sequences from 26 strains) when the StORFs sequences were included in the CD-Hit clustering. Previously these proteins were distinct enough to be clustered separately. The two Ensembl representatives were clustered together in combined Cluster 4 with 335 StORFs from 99 strains. The StORFs in this cluster are longer than the Ensembl genes (around 100 aa), and so CD-Hit chose a StORF to be its representative sequence for the combined cluster. As can be seen in the Clustal Omega (40) multiple sequence alignment of the representative sequences of the above-mentioned clusters in Supplementary Figure 6, their sequence identity was high, $\geq 90\%$ (the minimum CD-Hit percentage identity for clustering) along the regions in which they aligned.

There were also examples of Ensembl gene clusters combined together with StORF sequences, which could completely change the dynamics of the Ensembl gene families. As seen in Supplementary Figure 7, the three Ensembl representative sequences, AHM40736, AIT36070 and AFS84250, are combined into a new cluster with a single StORF sequence (Cluster 17,575). As we can observe from their alignment, they are in fact very similar and are further examples of the limitations we impose on ourselves when attempting to categorise natural elements into computationally-friendly representations. There were 77 of these types of combined clusters which together had clustered 164 Ensembl representative sequences together. These clusters are presented separately in Supplementary Table 3. Interestingly, a number of these combined clusters contained more unique *E. coli* strains via the StORF sequences than via the Ensembl genes. Of the clusters that combined more than one previous Ensembl cluster, there were no cases of core ($>=99\%$) gene families but 1 example of soft-core ($>=95\%$ to $<99\%$) and 11 accessory gene families ($>=15\%$ to $<95\%$).

As can be seen in Supplementary Table 3, each of the three categories of the overall pangenome of *E. coli* have been extended by the addition of the StORF sequences. Among the most interesting results are the 178 gene-families which were extended to the core of the pangenome by the sequences identified by StORF-Reporter. These constitute gene families which are likely to have been left out of many studies... Additionally, there were clusters which contained both Ensembl and StORF sequences classified as core-gene families, on the basis of their StORF sequences alone. While they were grouped with additional Ensembl genes, the Ensembl genes did not contribute to the distribution of the cluster (9 were core, 15 were soft-core and 648 were accessory - see Table x). Most intriguingly, there were a large number of clusters which were made up entirely of StORF sequences (StORF-Only gene families) and spanned all three pangenome gene categories (239 were core, 216 were soft-core and 3,426 were accessory). These are novel gene families.. Lastly, there were 162 Ensembl clusters for which, although the sequences did cluster with StORF sequences, none of the StORFs were from additional genomes and as such were not counted in the above data.

StORFs identified within and across multiple genera

The previous analyses of URs and StORFs have been conducted on the same species. It could be assumed that even in the case of the *E. coli* pangenome, many of the StORFs which have been identified are remnants from a multitude of different genomic factors such as assembly error, genomic structural elements or additional processes we are yet to fully understand. In this study, all 21,503,164 Ensembl-annotated protein sequences were used from the 6,223 genomes from Ensembl Bacteria (see Supplementary Table 1 for details on genomes used). A median number of 2,305 and 1,981 URs and StORFs were identified for each of the 6,223 genomes for a total of 14,221,482 and 13,301,175 sequences respectively (see Supplementary Table 11 for more detail). By using CD-Hit, many clusters were identified with both Ensembl and StORF sequences from the same genera and genomes. While these are likely to represent important candidates for gene duplication studies, they were not the aim of this study. Additionally, Ensembl-Only, Ensembl-StORF and StORF-Only clusters, were identified spanning multiple genera across the 179 genera from Ensembl Bacteria. As would be expected, the distribution of genera in the Ensembl-Only clusters is wide and many clusters are reported with more than six different genera (see Supplementary Table 12). Furthermore, not only have Ensembl-Only clusters been added to and extended by StORFs (creating Ensembl-StORF clusters), but also substantial numbers of StORF-Only clusters have been found with StORFs from multiple genera.

StORFs have changed the diversity and spread of gene families by extending the canonical Ensembl gene clusters into additional genera which were not annotated in the Ensembl annotations. One example of this, is a singleton Ensembl-Only cluster (Cluster 1,845,585) which consisted of a 35 amino acid *E. coli* Ensembl gene (reported in GenBank as a hypothetical protein - *E. coli kte42* - gene ELF73632). This sequence, when combined with the StORF sequences from all 6,223 Ensembl genomes, was clustered into the 4th largest combined cluster (Ensembl-StORF combined 'Cluster 3'), with StORFs spanning multiple different genera. This cluster consisted of 1,162 StORF sequences from a total of 149 genomes and 5 genera (*Shigella, Escherichia, Pantoea, Klebsiella, Enterobacter*). The fact that the only organism to have this sequence annotated was *E. coli* may not be a coincidence, *E.coli* being the most-studied model organism.

As a final example, the small Ensembl Cluster 83,472, which consisted of 32 sequences between 63-70 amino acids long and spanning 4 genera (*Escherichia, Streptococcus, Yersinia* and *Shigella*) was extended significantly by 726 StORF sequences from 7 additional genera (*Pantoea, Klebsiella, Citrobacter, Enterobacter, Serratia, Salmonella* and *Bacillus*) as part of the Ensembl-StORF combined Cluster 14. The function of this protein is unclear. A BLAST search against the NCBI non-redundant protein database reported a number of different annotations which indicate that it could be either part of a transposase family, a plasmid stability protein or something else entirely.

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As with the *E. coli* pangenome study, the hard-coded cutoffs used for the CD-Hit gene family analysis produced a number of clusters which combined multiple Ensembl representative sequences which were previously clustered separately. Six Ensembl-StORF combined clusters were found to contain more than one Ensembl representative sequence and together combined 14 Ensembl-Only clusters. Additionally, many of the StORF sequences were found in genera which were not present in the original and separate Ensembl-Only clusters. An example of one such cluster, Ensembl-StORF cluster 124,470, combined three Ensembl-Only representatives together with seven StORF sequences. Supplementary Figure 8 shows the phylogenetic tree built with ClustalO and FastTree (41) and plotted with iTOL (42) (see Supplementary figure 9 for the multiple sequence alignment). This tree clearly reports the diversity and at the same time the similarity of the StORFs and Ensembl annotated sequences. Additionally, this multiple sequence alignment depicts how for some amino acid positions, StORF sequences can be more similar to one or more Ensembl gene as they are compared to each other. Therefore, it could be argued that as these StORF sequences bridge the gap between the three separate Ensembl gene families and as such have changed the dynamics of these inter-genera gene families. These type of clusters were included in the results of Supplementary Table 12, separately in row 'Ensembl-StORF-Combined'.

As seen in the types of clusters reported in Supplementary Table 12, StORF-Reporter was also able to identify a number of clusters containing only StORF sequences that spanned many different genera. The biggest of these, combined cluster 15,543, spans 22 genera and consists of 81 genomes and 92 sequences. At 380 amino acids long, the representative of this cluster had a 90% percent identity and 55% query coverage to the 'fatty-acid-CoA ligase fadD18' protein in GenBank. This large, widespread protein was mostly observed as a single gene in each genome but in 5 species it was found duplicated with between 2 and 6 copies in non-contiguous URs.

DISCUSSION

The unannotated regions of prokaryote genomes contain many potential genes

The high gene densities observed in canonical prokaryotic annotations have been "perceived as evidence of adaptive genome streamlining" (1), but are at odds with the observations that many prokaryote genomes contain large numbers of long URs constituting between 10-20% of their genomes (see Table 2 and Supplementary Tables 4 and 5). Despite all the advancements in computational biology, there are still clear problems in how genome annotation is undertaken. Previous findings (8) confirmed that while genome annotation methods in use today such as Prodigal (20) accurately detect the majority of CDS genes (in genomes which use the 'universal' codon table), large numbers of unannotated regions are still reported. As shown in this work, the six model organisms exhibited thousands of URs which were often overlooked and contain genes which are missed by state-of-the-art gene prediction methods and are also missing from the canonical Ensembl annotations.

We can only speculate as to whether these genes identified by StORF-Reporter are in fact expressed. Considering that experimental evidence of expression in the model organism *E. coli* is missing from large portions of their gene collections (43), it will undoubtedly require a large community effort. This work has clearly identified several novel CDS genes that are not in the current canonical genome annotations. It is difficult to know whether the proportion of the StORFs identified in this study are a result of the current ineffectiveness of genome annotation methods or in fact genes which are no longer expressed due to mutation, possibly of the upstream region (putative pseudogenes). However, clear evidence that we are finding read genes can be seen in the 'Intra-Genome' results in Table 2. StORF-Reporter identified the presence of duplicates of genes already present in the Ensembl annotations. While pseudogenes are often ignored, or worse, misnamed as 'junk DNA', even in human disease research (44), their presence is important and their absence from annotation is limiting to future studies. Therefore, the annotation of pseudogenes is worth considering in future studies, considering the vast numbers of StORFs with high levels of sequence similarity to Ensembl-annotated genes across many different genera, Swiss-Prot proteins and/or functional COG groups.

As many of these StORFs are part of previously reported gene families, they are possible examples of incomplete or inaccurate genome annotation. However, it could be argued that the most important findings of this work were in fact the StORF-Only clusters which did not have any similarity to any known genes. Many novel StORFs formed StORF-Only clusters which spanned more than 10 genera and as such are prime examples of the current level of omissions in genome annotation. As such, irrespective of whether they are CDS sequences or other more cryptic genomic elements, they are nonetheless target sequences that future developments in genome annotation and experimental work should investigate. Lastly, as coding and non-coding regions of prokaryote genomes are believed to evolve separately, reacting to intra- and inter-genomic pressures independently (45), SNP and mutation rate studies could be used as evidence to determine whether these are still functional genes.

The 'Stop - Open Reading Frame' is a valuable and transparent tool

As discussed, a StORF is defined the same as how the Sequence Ontology (19) defines an ORF - "The in-frame interval between the stop codons of a reading frame..". Therefore, while there seems to be little distinction, the canonical understanding of an ORF is that one begins with a start codon instead of a stop codon. This has been reflected in the numerous genome annotation tools (8). Nevertheless, unlike the use of 'ORF' in genome annotation, StORFs are transparent in their description and use. Furthermore, as StORFs are only reported from the URs already identified in previously annotation genomes, the need for complex and most-often opaque filtering algorithms is unnecessary.

While it could be thought that StORFs are exceedingly common in prokaryotic genomes, the 'more-than-could-be-expected-by-chance' presence of out of frame stop codons (both intergenic and genic) (12) means that there is a natural

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limitation on the StORFs that can be found. This provides a mechanism of early termination of translation in incorrect reading frames so that the metabolic cost and potential toxic bi-products associated with frameshift events can be reduced. This function of out-of-frame stop codons may have been selected for during the course of genome evolution to act against unintended frameshift expression. As such, the higher levels of stop codons observed in out-of-frame genic, intergenic and UR regions, lends further credence to the gene-length uninterrupted StORFs found in these regions.

Once StORFs are recovered, what remains?

The URs and StORFs identified by StORF-Reporter across the 179 genera from Ensembl Bacteria can be interpreted and used in a number of different ways. However, once StORFs have been recovered, the remaining regions of DNA in the collection of URs for any one genome are not without significance. For example, if we consider the interaction between bacteriophages and their hosts in isolation, it could be imagined that this continuous flow of genetic material, irrespective of whether it is coding or not, can be indicative of both the host and host-environment history (46). More recent studies have shown that it is not only phage-related and broken genetic material being passed, but also functional genes involved in host-related processes such as antibiotic resistance (47). The genesis of this genetic material and the mutations it accumulates can help decipher past and future organism interactions. Traditional methods of homology detection via similarity searching do not work well here, as many of these genomic elements have either never been characterised or are in too fragmented a state. However, the use of **UR-Extractor** makes it easier to study these cryptic regions, as the resulting regions after the extraction of StORFs could then be classified as the 'real unknown unknowns'. In addition to this, these remaining cryptic regions should be the target for future studies aiming to complete prokaryote genome annotations.

StORFs enhance existing annotations

The annotations provided by Ensembl Bacteria and Prodigal for the six model organisms can be taken to represent the current bar of prokaryotic genome annotation. However, to compare traditional genome annotation methods such as Prodigal to that of StORF-Reporter would be an unfair comparison as their intended purposes are at odds. Prodigal, as with many other annotation tools, is a complex, multifaceted tool that uses a number of advanced computing techniques and involves the building of its own model trained on each genome sequence with which it is presented. This is so that it can adjust its parameters according to features such as GC content that are specific to each genome sequence. Additionally, Prodigal predicts genes for the entire length of the target genome. StORF-Reporter on the other hand is a one-size-fits-all tool which not only specifically studies URs, but also has parameters that have been designed to detect the types of genes routinely missed by other tools (short, overlapping and genes which use alternative start codons). Therefore, as supported by our results that investigate StORF-Reporter's ability to identify genes not annotated by Prodigal or Ensembl, it is likely that one of the most beneficial ways to use StORF-Reporter is to generate additional (and likely missed) annotations for a genome (an enhanced annotation, as discussed in the introduction). With the StORF_Adder tool, which utilises part of the ORForise package (8), StORFs can be used to supplement existing genome annotations. The *E. coli* pangenome study presents the opportunity for this process to deliver improvement to contemporary annotations without sacrificing the hard work already undertaken. For example, while the *E. coli* genomes presented in the paper "A comprehensive and high-quality collection of Escherichia coli genomes and their genes" (48) have undergone extensive curation they still contain URs long enough to contain genes. Reannotating these genomes would undoubtedly lose much of the work and knowledge used by the authors in the process. Therefore, the ability to investigate only those regions of DNA without annotation and then combine the curated annotations with the additional StORF sequences is a clear advantage over just reannotation.

Genome annotation is a mature process and as such, there exist a number of domain-standard tools and pipelines. PROKKA (24) is a popular pipeline that many researchers use to annotate genomes. StORF-Reporter allows for the direct supplementation of PROKKA annotated genomes and retains the same output format. This allows downstream analysis tools such as Roary (49) and Coinfinder (50) to interpret these new annotations without further user involvement.

StORFs can extend pangenomes

It has been known for some time that a single genome is not enough to characterise the functional profile of a species as the speed and scope of prokaryotic differentiation continues to highlight the need for the study of pangenomics. The *E. coli* pangenome could be argued to be the most studied and characterised of any prokaryotic organism (51). One recent study estimated the pangenomic gene collection at more than 13,000 genes which has "tremendous implications in terms of the diversity and pathogenesis of the species *E. coli* and its ability to colonize and cause disease in the human host." (51). However, our pangenomic study of *E. coli* URs and StORFs have shed light on the potential for yet more diversity of not only accessory but also a much increased set of core-genes.

In the 6 model organism study, *E. coli* StORFs had the highest levels of sequence similarity to either Swiss-Prot or intra-genome proteins (see Table 2). Those results, and the high levels of StORFs found in Ensembl-StORF and StORF-Only clusters in the *E. coli* pangenome has highlighted the possible true number of coding and pseudogenised genes missing from the annotations of one of the most studied organisms. The importance of these potential gene families is yet to be fully explored. While numerous theories could be proposed from their presence and distribution, fundamentally, they are likely candidates for the study of how a species' pangenome can adapt to ever-changing environments (51). These StORFs, functional or pseudogenised genes or not, are additional genetic blueprints an organism continues to hold onto (or is in the process of losing), against the pressures for genome streamlining. Fundamentally, while the identification of these StORFs have provided additional genomic knowledge previously left in the dark corners of the URs of their genomes, to truly use the nascent information they may harbor, much expanded experimental work is needed.

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StORFs can extend intra- and inter-genera gene collections

The results of the StORFs reported in the six model organisms and across the *E. coli* pangenomes have shown wide levels of diversity and spread. However, it could be possible that many of these StORFs are artefacts of genome assembly and are species-specific structural elements and not primarily CDS genes. Therefore, the inter-genera analysis of the 6,223 genomes from Ensembl Bacteria was key to not only studying the presence of StORFs across further diverse species, but to also provide evidence to further validate them as putative CDS genes.

StORFs were found across many different genera at high sequence similarities ($>=95\%$) (see Supplementary Table 12). As with the *E. coli* pangenomic study, many StORFs from the same cluster were found in different locations across the various genomes, or in the case of duplication, in different regions and thus URs of the same genome. The presence of these StORFs, adds credence to the hypothesis that they are not structural elements or other genomic artefacts but instead functional (past or present) CDS genes.

StORFs which have clustered together, either with Ensembl genes or only with other StORFs, are often observed with different lengths. Because StORF-Reporter is species and start codon agnostic, we are able to observe the full spectrum of variation within a gene family. This provides yet further justification of the need for species-agnostic gene prediction methodologies which do not rely on established model organisms or databases. While these results may not fundamentally change the understanding of and structure of pangenomes or functional profiles of any one species, they could drastically change the landscape of the functional and phylogenetic interconnections between different genera.

Are some StORFs pseudogenised genes or genes that use an alternative genetic code?

The potential diversity of all possible protein sequences is vast (52). A typical protein length of about 300 amino acids can have more than 20^{300} different possible polypeptide chains, yet current protein databases only contain a tiny fraction of this, such as Swiss-Prot, which contains a little over 500,000 protein sequences. Many of these are duplicates or very similar to each other and many of these are not experimentally validated. Adding to this complexity are the vast numbers of pseudogenes, which were likely functional proteins in the recent past, identified through the extensive genome sequencing of the last few decades. While mutation rates have long been studied in prokaryotes (53, 54), there are still unresolved questions surrounding the speed at which pseudogenes are created and subsequently removed from the genome. Some studies have shown that pseudogenes are more likely to be a result of failed horizontal gene transfer (55). Additionally, while archaea and most non-pathogenic bacteria exhibit greater retention of ancient gene remnants, obligate pathogenic bacteria tend to have younger pools of pseudogenes (55). As such, the types of genes pseudogenised and the rate at which they are mutated are highly variable between species and are likely to be related to environmental specific cues.

However, current methods fail to address these questions, therefore, the true extent of possible pseudogenisation through mutation is likely to remain unclear for the foreseeable future. The StORF-Reporter methodology has the potential to capture of the true scale of gene-pseudogenisation. As a StORF reports potential ORFs regardless of the likelihood of them being functional and it captures a portion of the 5' untranslated region of a CDS gene, it can also catch pseudogene-creating mutations, such as start codon or ribosomal binding sites mutations. As reported by Goodhead *et al* (56), of the six different process causing a gene to be pseudogenised, a StORF has the potential to capture all of them (some in fragmentary form). However, the most easily identified is when pseudogenisation occurs because of a premature stop. While a single StORF could only report one fragment of a gene pseudogenised by a premature stop codon, the combination of multiple consecutive-StORFs has the potential to recover the entire sequence of the pseudogenised gene.

CONCLUSION

Genome annotation is a mature but continually developing field. With each new sequencing project, the proportion of uncharacterised sequences found can vary significantly depending on many different factors such as habitat (57). Often hundreds of novel genomes are discovered with little similarity to previously sequenced taxa (58), suggesting that there is much gene diversity yet to be discovered. Exacerbating this challenge, both historic and systematic biases and errors mean that some types of genes will almost always be missed in these studies, resulting in many tools reporting the same untranslated regions in genomes. This might lead researchers to feel a sense of false security when using standardised annotation tools, but as we have demonstrated, the StORF-Reporter methodology can enhance current annotations, reporting missed genes in these regions.

One major limiting factor shared across many genome annotation analysis studies is the use of a genomic database such as Ensembl Bacteria as a ground truth (under the assumption that they are a complete reference). In this study, we challenged that assumption of completeness through the use of StORF-Reporter to investigate the URs in over 6000 Ensembl genome annotations. In direct contradiction to the idea of genome annotation completeness, a high number of StORFs found across multiple genera were reported to be highly similar to known proteins. Furthermore, in the pangenomic study, over 200 StORF-Only gene families without similarity to Ensembl proteins, were found. These StORFs showcase how even highly-conserved gene families are still missing from canonical annotations. While both these groups of StORFs are therefore prime candidates to be added into their respective genome annotations, the majority of StORFs across all genomes were without similarity to known proteins in any database examined.

The processes which influence the emergence, distribution and subsequent loss of both novel and modified genes such as gene duplication, neofunctionalisation, 'genome streamlining' and purifying selection (59, 60, 61), suggests substantial pressure to 'lose' non-functional gene sequences. These factors make the resulting sequences which do persist (especially those found across multiple genera), regardless

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of similarity to known genes, more likely to be functionally important and/or active. Accessory genes, those most likely to be captured by StORFs (See Supplementary Table 3), are now thought to often carry out important and essential functions (1), often for adapting to environmental niches and changes (62). Therefore, not only has StORF-Reporter identified a priority of future work to be the better understanding of the relationship between these sequences, but also will itself be a part of their investigation.

Conflict of interest statement. None declared.

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