The Good, the Bad and the Deadly
Characterisation of bacteria through DNA analysis

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The Good, the Bad and the Deadly:characterisation of bacteria through DNA analysis

Salvatore Cosentino

November, 2013
Preface

This Ph.D. thesis was prepared at the Center for Biological Sequence Analysis (CBS), Department of System Biology, Technical University of Denmark (DTU), under the supervision of Associate Professor Mette Voldby Larsen and Professor Ole Lund.

The results presented in the thesis demonstrate how bacterial Whole Genome Sequencing (WGS) can be used by clinical microbiologists to characterise known and novel bacteria causing infections in human.

The thesis consists of an introduction, followed by a collection of four research manuscripts produced during my Ph.D. study at CBS and at the Center for Genomic Epidemiology (CGE) during the period 2010-2013

Salvatore Cosentino
Lyngby, November 2013

[Signature]
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Summary

Sixty years have passed from the discovery of the DNA's double helix structure, and at the time it would have been impossible to imagine that today we could receive our own DNA with information about our ancestors, or potential diseases we could get, based on the analysis of the DNA sequences. High-throughput DNA sequencing started a revolution, which is still ongoing, in biology and medicine, bringing new ways of studying diseases that could not have been possible before. Millions of people die every year from bacterial infections, and given the trends toward globalization of travel and commerce, with urbanization and an aging population, infectious diseases are coming back as a possible global threat. At present thousands of completely sequenced bacteria are publicly available, with many hundreds of genomes completed every year, also due to the constantly decreasing costs for sequencing a bacterial isolate. Using this invaluable data, scientists are bringing a revolution in the way clinical microbiology is done and in the way infectious diseases are diagnosed and treated.

My PhD project focused on the use of Bacterial Whole Genome Sequence (WGS) data for the prediction of pathogenic features, and the identification of bacterial species and subtypes, as well as phenotypic traits like antibiotic resistance. The thesis starts with an introduction to the problems related to infectious diseases, as well as the history of DNA, DNA sequencing and its application in clinical microbiology are overviewed. The thesis continues with three chapters and concludes with a discussion on possible future applications of DNA sequence data in clinical and public health microbiology.

Chapter one introduces the challenges related to the use of WGS for the prediction of bacterial pathogenicity features. The manuscript included in this chapter describes a prediction method for bacterial pathogenicity, which was also the main topic of my PhD studies.

Chapter two introduces the possibility to identify bacterial species and subtypes through DNA sequence analysis and includes two manuscripts about this topic.

In chapter three the problem of antibiotic resistance is discussed and a manuscript describing a method for identifying antimicrobial resistant genes from bacterial WGS data is included.

The thesis terminates with a discussion on the possible future applications of sequencing technologies in clinical and public health microbiology.
Dansk resumé

Der er gået 60 år siden DNAs dobbelthelix struktur blev identificeret i en tid, hvor det var umuligt at forestille sig, at vi i dag kan få adgang til vores egen DNA, inklusiv information om vores forfædre og hvilke sygdomme vi er prædisponeret for, baseret på analyser af DNA sekvensen. High-throughput DNA sekventiering startede en fortørende revolution indenfor biologien og den medicinske verden. Denne revolution har medført nye måder at studere sygdomme på, som ikke ville have været mulige tidligere. Millioner af mennesker dør hvert år som følge af bakterielle infektioner, og givet den nuværende trend mod øget globalisering med rejser og samhandel, medregnet den øgede urbanisering og en aldrrende befolkning, er det sandsynligt at infektiøse sygdomme vil genopstå som en global trussel. Der er i dag tusindvis af fuldt sekventerede bakterier offentligt tilgængeligt, og hundreder af yderligere genomer færdiggøres hvert år – også p.g.a. den konstant faldende pris for sekventieringen af et bakterieisolat. Ved at anvende dette ucvurderlige data, muliggør forskere en revolution i forhold til den måde klinisk mikrobiologi udføres og den måde hvorpå infektiøse sygdomme diagnostikeres behandles.

Mit PhD projekt har hovedsageligt været fokuseret på anvendelsen af Hel Genom Sekvens (HGS) data til forudsigtelse af patogene træk og identifikation af bakterieart og -stamme, såvel som fænotypiske træk som antibiotika resistens. Afhandlingen indledes med en introduktion til de problemer, der er relateret til infektiøse sygdomme, såvel som historien bag DNA, DNA sekventiering og dens brug indenfor klinisk mikrobiologi. Afhandlingen fortætter med tre kapitler og slutter af med en diskussion om de mulige fremtidige anvendelser af DNA sekvensdata i forbindelse med klinisk medicin og indenfor folkesundhed.

Kapitel et introducerer de udfordringer, der er forbundet med brug af HGS data til forudsigtelse af bakterielle patogene træk. Manuscriptet inkluderet i dette kapitel beskriver en metode til forudsigtelse af bakteriel patogennitet, hvilket også har været fokuspunktet for mit PhD studie.

Kapitel to introducerer muligheden for at identificere bakterieart og stamme via DNA sekvensanalyser og inkluderer to artikler om dette emne.

I kapitel tre diskuteres problemet med antibiotika resistens og en metode til identifikation af antibiotika resistens gener fra bakteriel HGS data er inkluderet.

Afhandlingen afsluttes med en diskussion om de mulige fremtidige anvendelsesmuligheder for sekvensteknologi i forbindelse med klinisk mikrobiologi og indenfor folkesundhed.
Acknowledgements

It was a great pleasure to do my work as a PhD student at the Center for Biological Sequence Analysis (CBS), surrounded by exceptional people always ready for ready help to me in when I needed, to have stimulating discussions about scientific and non-scientific matters. I take here the chance to thank all CBSians. A big thank also goes to people at National Food Department and people at the Center for Genomic Epidemiology, from which my PhD studies were funded.

From here on I will try my best to thank the people that were close to me (not only at work) during these wonderful three years in Denmark:

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Thanks to my supervisor, Mette Voldby Larsen. If I do not remember any stressful time during my PhD is mainly thanks to her great supervision. All the suggestions she gave at the start of my PhD about the organisation and scheduling of all the tasks involved in a PhD student’s life proved to be perfect. I had learnt a lot from her and I am happy to be her first PhD student. Apart from being a great supervisor, she is one of the kindest people I have ever met.

Thanks to my co-supervisor Ole Lund, is not only a great scientist always ready to give very good suggestions when asked, but also a great group leader. I am not sure how he does, but if the immunological group at CBS is so nice and cheerful it is also thanks to him choosing the right people and leading the group. And of course a big thank you here goes to all members of the immunological bioinformatics group.

A big thank to John Damm Sørensen, who helped me a lot and without whom it would have been impossible to do my research, teaching me how to use CBS’s supercomputer facilities. He was always ready for a nice chat after tiresome working days, and he also was one of the first people from whom I have learnt about Danish culture and history.

Thanks to Kristoffer for helping me whenever I needed, giving me a wonderful office and desk and introducing me to the “let’s talk about it over a cup of coffee” philosophy.

Thanks to all the people working at the administration. Sometimes we do not realise it, but if we would have to deal with all the bureaucracy they deal with for us, we simply would not have time to do any research. A special thank to Lone, Karina and Dorthe for always being kind and helpful.
Thanks to Cecile and all the office helpers before her. Drinking a coffee (I did not do that much at CBS) or steaming your milk making a lot of noise is something that becomes normal at some point, but if the machine was not working, my day would have had a bad start. So, thanks to the office helpers for taking care of the small things that make CBS a comfortable place to work.

Thanks to Peter and Edita, my first office mates. Working in Peter’s office I understood how it is to work in what is, in my opinion, the most busy office at CBS.

Thanks to Greg, Txema and Li for being great office mates. Thanks to Txema for not getting too mad at me for systematically leaving something on his desk. By the way, you should try to smile, some people at CBS think you are very grumpy, and I know you are not...that grumpy. Thanks to Li for just being always so kind and for the nice time in and outside CBS.

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Thanks to Daniele and Stefania for being my friends for so long and for all the nice time spent during my PhD, before and I am sure after. I am sure Denmark would have been different without you “sbranjisati”.

Thanks to my neighbour and friend Karina, for making my life in Søborg less ordinary and for helping me in different situations, also some tragicomic ones.

Thanks to Yukako and Miki for helping me in designing the thesis cover.

And lastly, the biggest thank to my family and my nieces for always being close to me no matter how far I am living from them.
Papers included in the thesis


## Abbreviations

<table>
<thead>
<tr>
<th>Abbreviation</th>
<th>Description</th>
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<tbody>
<tr>
<td>AMR</td>
<td>antimicrobial resistance</td>
</tr>
<tr>
<td>bp</td>
<td>base pairs</td>
</tr>
<tr>
<td>CCD</td>
<td>charge-coupled device</td>
</tr>
<tr>
<td>CDC</td>
<td>Centers for Disease control and Prevention</td>
</tr>
<tr>
<td>CGE</td>
<td>Center for Genomic Epidemiology</td>
</tr>
<tr>
<td>DBG</td>
<td>De Bruijn graph</td>
</tr>
<tr>
<td>DNA</td>
<td>deoxyribonucleic acid</td>
</tr>
<tr>
<td>dNTP</td>
<td>deoxyribonucleic triphosphate</td>
</tr>
<tr>
<td>EBI</td>
<td>European Bioinformatics Institute</td>
</tr>
<tr>
<td>EMBL</td>
<td>European Molecular Biology Laboratory</td>
</tr>
<tr>
<td>FSG</td>
<td>First Generation Sequencing</td>
</tr>
<tr>
<td>HGT</td>
<td>Horizontal Gene Transfer</td>
</tr>
<tr>
<td>INSDC</td>
<td>International Nucleotide Sequence Database Collaboration</td>
</tr>
<tr>
<td>IT</td>
<td>information technology</td>
</tr>
<tr>
<td>MLST</td>
<td>Multi-locus Sequence Typing</td>
</tr>
<tr>
<td>MRSA</td>
<td>methicillin-resistant <em>Staphylococcus aureus</em></td>
</tr>
<tr>
<td>NGS</td>
<td>Next-Generation Sequencing</td>
</tr>
<tr>
<td>NIH</td>
<td>National Institute for Health</td>
</tr>
<tr>
<td>OLC</td>
<td>overlap layout consensus</td>
</tr>
<tr>
<td>PCR</td>
<td>polymerase chain reaction</td>
</tr>
<tr>
<td>PacBio</td>
<td>Pacific Bioscience</td>
</tr>
<tr>
<td>SNA</td>
<td>single-nucleotide addition</td>
</tr>
<tr>
<td>SMRT</td>
<td>single-molecule real time</td>
</tr>
<tr>
<td>USB</td>
<td>universal serial bus</td>
</tr>
<tr>
<td>WGS</td>
<td>Whole Genome Sequence</td>
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INTRODUCTION

Every year more than 7 millions deaths are the direct cause of bacterial infectious diseases. An estimated 0.2 million people die of pertussis and 1.3 millions of tuberculosis, while diarrhea, causing more than 2.5 million casualties, is one of the leading causes of death by infection worldwide [5].

To treat patients with bacterial infections that could not be cured using drugs selected based on the symptoms, is important to grow and isolate the bacteria responsible for the infection, identify its species, determine its pathogenic potential and assess its resistance to antimicrobial drugs.

Characterisation of bacteria are currently performed by clinical microbiologists using species-specific methodologies developed over decades, which are complicated and expensive in terms of both time and money. The characterisation of the bacterium under investigation can take from days (for fast growing species like *Escherichia coli*) to months for slow-growing bacteria like *Mycobacterium tuberculosis*. Time is very important in case of infections and it can make the difference in saving the patient’s life.

Apart from causing sickness and - in the extreme cases - the death of the infected person or animal, one of the main characteristics of infectious diseases is their ability to spread and cause bacterial infection outbreaks.

A disease outbreak is the occurrence of a given disease in excess of what would normally be expected in a determined community or geographical area. An outbreak can arise in a restricted geographical area and potentially extend to different cities or even countries causing a global epidemic. Outbreaks can last from days to months [38] and even years. Bacterial outbreaks usually involve novel bacterial strains that have acquired new genes or combinations of pathogenic features that make the diseases they are causing very difficult to treat, and aid the spread of the bacteria.

With the rapid advancement of genome technologies and with the consequent decreasing price of bacterial whole genome sequencing, new ways of characterizing bacteria and performing epidemiological surveillance has arisen. Modern high-throughput DNA sequencers can provide, with relatively low prices and reduced time, partially complete DNA sequences of disease-causing microbes that can be used by researchers to get insight on the mechanisms making the microbe under investigation pathogenic.

With additional improvements to high-throughput sequencing technologies and further simplification in sample preparation, DNA sequencing and related bioinformatics tools are likely to replace conventional culture-based and molecular typing methods to provide quicker and more reliable clinical diagnosis and data to be used for monitoring the epidemiology of infectious diseases [21].

Provided there is information sharing by all clinical and public health laboratories, these genomic tools could give life to a global system of linked
1. Introduction

databases of bacterial genomes that would ensure more efficient detection, prevention, and control of local, emerging, and other infectious disease outbreaks worldwide.

The 4 manuscripts accompanying this thesis and composing its main 3 chapters will focus on the following 3 tasks using bacterial WGS: identifying the species of a clinical isolate; testing its properties, such as resistance to antibiotics, virulence, and potentially novel features involved in pathogenicity; characterization of bacterial population though bioinformatics typing methods and their application in epidemiology surveillance.

1.1 From Watson and Crick’s double helix to usb-stick sized sequencers

The year 2013 marks the 60th anniversary of the discovery of the DNA double helix structure [72] by the biologists Francis Creek and James Watson in 1953 (Figure 1.1). From this discovery, which started the modern era of biology, 12 years passed before the first nucleic acid molecule was sequenced from Escherichia coli in 1965 [31], and 15 before the first experimental finding of a DNA sequence by Wu and Kaiser [75, 37]: It took 5 years for Wu and Kaiser to complete a 12 bases long DNA sequence from bacteriophage lambda [75], which also represents the first example of DNA sequencing in the history of science.

The technique that was crucial in the history of modern sequencing technologies was introduced in 1975 by Sanger under the name of the ‘plus and minus method’ [58, 61]. Sanger soon refined his technique by the introduction of the ‘dideoxy method’ [62], which is the foundation of the so called Sanger sequencing or First Generation Sequencing (FGS), and also the technique that has dominated the DNA sequencing scene during the last 30 years. The first nucleotide sequence obtained using the Sanger method was the genome of the phiX174 bacteriophage [59, 60]. Later, right after the genomes of Mycoplasma genitalium and Haemophilus influenzae were completed in 1995 [26, 27], scientists started considering the possibility of studying the pathogenesis of bacteria based on their genome sequences [28].

The most important milestone achieved using FGS was the sequencing of the human genome [39, 70]. This was a 13-years long project, which was completed in 2003 [18] and which gave start to the era of genomics that we are still living in at present. In this introduction we will not describe the Sanger sequencing method, and interested readers are directed to related articles [47, 33].

In this short overview on sequencing technologies we will describe how the main instruments available in market work and spend a few lines on the future development in high-throughput sequencing technologies.

Second-Generation or Next-Generation Sequencing (NGS) includes various technologies that rely on a combination of template preparation, sequencing and imaging, together with genome alignment and assembly meth-
1.1. From Watson and Crick’s double helix to usb-stick sized sequencers

Figure 1.1: (left) Watson and Crick and their model of the DNA double helix (1953). (top-right) X-ray diffraction of the DNA taken by Raymond Gosling in the lab of Rosalind Franklin in 1952. (bottom-right) Aluminium template, representing the base adenine (A), part of Crick and Watson’s model of DNA.

ods. NGS has changed the way of doing applied and clinical research, and its potential applications are only limited by the imagination of the users.

The primary advantage offered by NGS is the ability to produce gigantic amounts of short-reads per sequencer run, with constantly decreasing costs. One of the side effects of this sequencing revolution is the constant increase of the data to be stored, with the European Bioinformatics Institute (EBI) at present storing 2 petabytes (10^{15} bytes or 1000 Terabytes) of genomic data. This amount is more than doubling every year since the advent of NGS in 2008 (Figure 1.2) [46]. The volume of data produced by biologists is reaching quantities that were once the domain of high-energy physics and astronomy researchers. The second side effect, caused also by the short length of the reads combined with the huge amount of data produced per instrument run, is the increasing need for powerful computational infrastructures to process and analyze the generated experimental data.

NGS technologies are being applied in many fields of both basic and clinical research, for example in gene-expression studies, where these new technologies are slowly taking the place of microarrays, identifying transcripts without prior knowledge of a specific gene and providing information about sequence variation in identified genes [73]. Re-sequencing of human genomes is probably one of the most common applications of NGS, with projects like the “1000 Genomes Project” [7], started in 2008 and completed in 2012
The amount of genetic sequencing data stored at the European Bioinformatics Institute takes less than a year to double in size.

**Figure 1.2:** increase of the quantity of genomic data stored in EMBL-EBI servers before and after the NGS sequencers started being affordable for most researchers.

[10], in which a team of researchers from different countries sequenced the genomes of more than 1000 participants from different ethnic groups, creating a huge sequence dataset and a refined human genome map freely available to the scientific community and public. In this work we will focus on the use of high-throughput sequencing technologies for bacterial whole genome sequencing.

Sequencing platforms available in the market can be separated in template amplification platforms and single-molecule sequencers. Template amplification platforms depend on the creation of clonally amplified templates, and all of the NGS sequencers, including Roche 454, Illumina and Ion Torrent instruments belong to this class of sequencers. The general workflow for these sequencers involves the following 3 steps: 1) library (or template) preparation; 2) template amplification; 3) sequencing.

**Library preparation** starts with the extraction and purification of genomic DNA. For single-end shotgun sequencing [64, 8], a fragmentation step is needed, and depending on the application and platform, the length of the fragments can be from 150 to 800 base pairs (bp).
Template amplification platforms also support **mate-pair** and **paired-end** sequencing. In mate-pair sequencing DNA fragments of given lengths (e.g. 3 kbp, 8 kbp or 20 kbp) are joined together in circular molecules and fragmented again before adaptors are added to the fragments flanking the joins. In paired-end sequencing fragments are sequenced from both the 3’ and 5’ ends. From mate or paired-end reads is possible to obtain higher quality genome assembly than those attainable from single-end reads.

**Amplification.** In NGS platforms amplification is performed by immobilizing millions of spatially separated template fragments on to a solid surface, which can be a flow cell (Illumina platform), ion sphere particles (Ion Torrent) or solid beads (454 and SOLiD). In SOLiD, 454 and Ion Torrent platforms it is performed using emulsion PCR [22], while in Illumina platforms the amplification is performed using bridge amplification (Figure 1.3).

NGS platforms use different chemistries to do the sequencing and different approaches (usually imaging) to read the sequences.

Roche 454 platforms use single-nucleotide addition (SNA). In SNA, at each cycle, one of the four possible dNTP (deoxynucleotide triphosphate) is, in turn, flown across the template DNA fragment. If there is complementarity between the added dNTP and the nucleotide in the next available position in the template, the base is attached to the extending DNA strand and hydrogen ions and pyrophosphate are released. This technique is known as pyrosequencing [56, 44] because the pyrophosphate released when a nucleotide is added to the extending strand is converted into visible light, which is measured using high resolution charge-coupled device (CCD) camera sensors. The output is a binary file in the standard flowgram format (SFF), containing the measured light peaks, that can be converted to a FASTQ [17] file containing the raw-reads.

Ion Torrent platforms also use the SNA method but, differently from the other NGS sequencers, they do not rely on imaging for reading the sequences and use instead a silicon chip to spot the positively charged hydrogen ions released every time a dNTP is added to the growing DNA strand [57].

Illumina platforms use an approach called cycling reversible termination developed by Solexa [12]. In each sequencing cycle, fluorescently labeled nucleotides are sprinkled across the flow cell. Nucleotides that are complementary to the next available position on the template strands, are incorporated in the growing DNA strands, and a laser is used to determine the incorporated nucleotide based on the fluorescent moiety. A new cycle starts after washing of the flow cell.

SOLiD platforms use the sequencing by ligation [69], in which fluorescent probes are iteratively hybridized and ligated to complementary nucleotides in the template strand at the 5’ end of the growing strand, before fluorescence imaging is used to detect the ligated probes.

**Single-molecule sequencers** have a more straightforward preparation of templates than NGS instruments, requiring less DNA and without the need of PCR. A single-molecule sequencer that available at present in the market
Figure 1.3: steps needed to run a sequencing experiment using the main high-throughput sequencing platforms available in the market. The schematic associates, to each platform, the sample preparation and template amplification procedures needed before sequencing. Illustration from [43], ©2012 Macmillan Publishers Limited
1.1. From Watson and Crick’s double helix to usb-stick sized sequencers

Figure 1.4: the MinION sequencer, announced by Oxford Nanopore Technologies, is the smalled instrument in the history of sequencing and can be used by simply plugging it to the USB port of a computer. ©2008-2013 Oxford Nanopore Technologies.

is the PacBio RS from Pacific Bioscience. The sequencing approach used by PacBio models is known as single molecule real time sequencing (SMRT) [24]. One of the striking characteristics of SMRT sequencers is the high length of the generated reads, with an average of 3000 bases while one of its limitations is in its rather high error rate, which it has recently been shown to be possible to reduce by post correcting the sequenced data [36].

Figure 1.3 shows the main high-throughput sequencing platforms available in the market today, and associates, to each platform, the sample preparation and template amplification procedures required before sequencing.

In February 2012, the sequencing community was shook by the demonstration, from a UK startup company called Oxford Nanopore Technologies, of a new revolutionary sequencing platform. Oxford Nanopore presented their two nanopore-based sequencers (the GridION and MinION), capable of delivering extremely long reads (they said there is not theoretical limitation on the maximum length) at very cheap costs (less than 1000$ for a human genome) and directly from blood samples. MinION (Figure 1.4) was the most admired also because of its USB memory-stick size [25]. The UK-based company recently started selling the sequencers to researches who would like to test the technology.

Nanopore DNA sequencing method involves passing single DNA strands through tiny (nano) pores. The pores (through which current is flowing), with a diameter of about 2 nanometers, will identify the bases by measuring the change in current flow caused by the bases passing through it. Recently
US National Institute for Health (NIH) has granted about $17 million to 8 research teams to conduct studies on the use of nanopore technology for DNA sequencing [2] which is another hint of the possibility for this revolutionary technologies to become a reality in the near future.

Together with the limitation related to the sequencing costs, nanopore sequencing, producing very long reads, could solve many of the problems related to de-novo assembly by directly generating almost complete genomes in a single instrument run. The solution to this problem will reduce also the costs related to expensive computer equipments required at present to assemble genomes from the output of sequencers currently in the market.

1.2 WGS data analysis and related applications

The fact that many sequencing instruments are available and competing in the market is an advantage for the final users, since the companies have to improve their technologies and reduce the prices if they want to keep their market shares. One of the downside is the fact that users will have to deal with different data formats, and giving the pace at which sequencing technologies are evolving, users are struggling to understand what are the best tools or pipelines to analyse their data, creating a scenario in which it is relatively easy and cheap to obtain WGS data, but everyday is getting increasingly complicated to analyse and interpret the data. High-end sequencers produce a quantity of data by each run for which storage and analysis would be too demanding for the average microbiology lab, whereas bench-top sequencers deliver quantities of data per run which better suits the IT equipment of the average microbiology research lab.

Once the run of the sequencer is completed, a preprocessing of the short reads, involving a quality filter and sequencing error correction, is performed before the assembly starts. Preprocessing aims at the removal of low-quality and erroneous reads from the data, with the final purpose of improving the quality of the subsequent assembly. Different technologies have different types of errors mainly derived by the sequencing chemistry they use, and correcting these errors is very important since de-novo assembly is particularly sensitive to these errors [53]. After the preprocessing of the data, algorithms are used to join the reads in a logical fashion to build the final sequences (contigs) that will compose the bacterial genome, in a process commonly called reads assembly. Depending on the kind of study a reference assembly or a de-novo assembly of the WGS data is performed.

Reference assembly basically consists in mapping the reads (through alignment algorithms) to the reference genome in order to identify genetic differences in the compared (usually highly related) genomes. Reference genomes are used, for example, to complete genomes of bacteria that have been partially assembled (draft genomes), or to study how different a given strain is in comparison to other strains of the same species. The latter is very important for epidemiological studies.
In a scenario in which the bacterium under study is unknown, we may want to perform a de-novo assembly of the WGS data, which consists in the reconstruction of the genome sequences without the help of any other information apart from the short reads. In de-novo assembly, reads alignment is done by comparing the reads with each other, or by overlapping k-mers (reads sub-sequences of k length). The final purpose of these alignments is the creation of contiguous sequences called contigs. Figure 1.5 depicts simple examples of both reference and de-novo assemblies. In an ideal situation the assembly will produce a single sequence containing, for example, the DNA composing the chromosome of the sequenced strain. Unluckily this is not so easy, in fact while short reads are good for reference assembly they are very difficult to assemble de-novo. Most de-novo assemblers are based on graph theory and represent overlaps (of either reads or k-mers) through vertices and edges in the graph that, after its completion, will be used to create the contigs. De-novo assemblers can be divided in Greedy, Overlap Layout Consensus (OLC) and De Bruijn Graph (DBG) type, depending on the approach they use to preform the assembly [51].

A typical difficulty for de-novo assembly algorithms is in finding a path in the overlap graph that passes through each vertex only one time (Hamil-
tonian path) or through each edge only once (Eulerian path). This problem is the reason why graph based assembly algorithms are very sensitive to sequencing errors [53]. Another limitation of these algorithms is related to the high amount of computer memory, and the powerful processors they need to be executed. This problem is both due to the nature of the mathematical problem these algorithms are trying to solve and to the high amount of short reads generated by NGS sequencers.

The OLC method is composed by the following 3 phases: 1) an overlap phase [52], in which all reads are aligned with each other to find overlaps, taking into account the minimum k-mer and overlap size, which will affect the quality of the final contigs; 2) a layout phase [51], in which a graph is built and iteratively updated, corrected and optimised; 3) a final consensus phase in which the final assembly is produced by means of multiple alignments. Among the assembly tools based on the OLC approach there are MIRA [16], ARACHNE [11], Celera Assembler (CABOG) [50], the PacBio-specific Allora and the commercial Newbler from Roche.

The DBG method [53] consists in building graphs in which each vertex represents a k-mer that will appear in the graph only one time. Reads are decomposed into k-mers that are then mapped to the graph, reducing the mathematical problem to the calculation of a Eulerian path [54] which can be solved in linear-time [67] even with millions of reads. Among the disadvantages of the DBG method there is the high amount of memory needed to execute the algorithm and the inability to calculate a priori the k-mer length to be used, which requires the algorithm to be run many times with different k-mer sizes in order to find the optimal settings. Most of the available genome assembly tools based on DBG are used to assembled reads from Illumina and SOLiD sequencers, and among these are ALLPATHS-LG [14, 29], SOAPdenovo [42], Velvet [77, 78], which is one of the most widely used, and Ray [13], which can assemble genomes by mixing 454 and illumina reads.

The Greedy approach iteratively aligns reads to identify the fragments with the largest overlap and merge them. This approach is used to assemble Sanger sequencing data, and among the tools based on it there are TIGR Assembler and PHRAP [55]. Some tools (SHASSAKE [71] and VCAKE [35]) use this approach to assemble short reads, but given their really high computational needs they never become popular among users.

Improving the quality and performances of genome assembly algorithms is one of the main challenges in computational biology. Given the importance of the topic and the high variety of available tools and pipelines communities, for testing, improving and evaluating genome assembly tools arose [23].

Even though genome assembly is one of the most important steps in WGS data analysis it is just the starting point for the characterisation of the bacteria under investigation. In fact after the genome assembly many other algorithms and tools will need to be applied for annotation, antibiotic resistant and pathogenic genes identification, typing, phylogenetic comparison and all other tests needed for the characterisation of the sequenced strain.
1.3 What is a Human Pathogen?

A pathogen is usually defined as a microorganism that causes, or can cause, a disease in a host. However, this definition is insufficient for describing what a pathogenic bacteria is, which takes us to an ongoing debate that dates back to 1880, when the German microbiologist Robert Koch defined a postulate to assess the pathogenicity of bacteria in human. Back then it was considered enough for a bacterium to have some virulence factors, for instance toxins, that could make a person sick, for it to be identified as human pathogenic. Koch’s postulate started becoming unreliable for the assessment of bacterial pathogenicity during the middle of last century when the first antimicrobial drugs were introduced and bacteria that were considered harmless at the time, like *Staphylococcus aureus* and *Clostridium difficile*, started causing serious infections.

The species just mentioned are usually classified today as *opportunistic pathogens*. The use of broad spectrum antibiotics is a major cause of opportunistic infections altering the population of commensal and pathogenic bacteria alike, while at the same time facilitating the proliferation of microbes resistant to the administrated drugs [20], which will grow uncontrolled and cause a new infection. Opportunistic infections also occur in people with compromised immune system due, for example, to hereditary genetic alterations. An example is the cystic fibrosis, in which the opportunistic pathogen *Pseudomonas aeruginosa*, normally found in healthy people, is the bacteria causing the infection.

Acquired antimicrobial resistance (AMR) is nowadays responsible for hundreds of thousands of infections worldwide [6]. Accordingly, it is considered one of the top health challenges facing the 21st century. AMR causes by multiple reasons among which: the misuse of antibiotics for treating human diseases [48, 1]; the use of high doses of antibiotics in livestock’s food [45]; the use of antibiotics in healthcare facilities [3]. Figure 1.6 shows the main reasons behind the development of antibiotic resistance and how it can spread to humans.

Another class of bacteria that are worth to mention are the *zoonotic pathogens*. These pathogens usually infect animals, but the infection can be transmitted to humans being in direct contact with the pathogen’s hosts, causing a zoonotic infection (or zoonosis). Zoonotic infections can also be caused by the consumption of contaminated food or water. In a systematic study it has been shown that out of more than 1400 bacteria infecting human, 66% were zoonotic [66]. Among the many zoonotic infections there are those caused by the methicillin-resistant *Staphylococcus aureus* (MRSA). The bacteria is usually found in livestock (cattle, pigs and poultry), from which can be transmitted to human through direct contact or through the consumption of contaminated meat, causing the zoonosis. Apart from being zoonotic MRSA is also one of the main causes of nosocomial infections, which are very difficult to treat also due to its antibiotic resistance. Recently MRSA infections are becoming a big threat in Denmark [1] and worldwide. The most
1. **Introduction**

**How Antibiotic Resistance Happens**

1. Lots of germs. A few are drug resistant.
2. Antibiotics kill bacteria causing the illness, as well as good bacteria protecting the body from infection.
3. The drug-resistant bacteria are now allowed to grow and take over.
4. Some bacteria give their drug-resistance to other bacteria, causing more problems.

**Examples of How Antibiotic Resistance Spreads**

- Animals get antibiotics and develop resistant bacteria in their guts.
- Drug-resistant bacteria can remain on meat from animals. When not handled or cooked properly, the bacteria can spread to humans.
- Fertilizer or water containing animal feces and drug-resistant bacteria is used on food crops.
- Drug-resistant bacteria in the animal feces can remain on crops and be eaten. These bacteria can remain in the human gut.
- George gets antibiotics and develops resistant bacteria in his gut.
- George stays at home and in the general community. Spreads resistant bacteria.
- George gets care at a hospital, nursing home or other inpatient care facility.
- Drug-resistant bacteria are now allowed to grow and take over.

Simply using antibiotics creates resistance. These drugs should only be used to treat infections.

**Figure 1.6:** Infographic showing how antibiotic resistance happens and how multi-drug resistant microbes can spread to humans. ©Centers for Disease Control and Prevention (CDC).
famous and deadly zoonosis was the Black Death, a bubonic plague outbreak, causes by *Yersinia pestis*, that killed more than 200 million people in Europe during the 14th century (Figure 1.7), and is still considered today the most devastating pandemic in human history.

From above, it is already clear how complicated it can be to classify a given bacterial strain as either pathogenic or commensal (Figure 1.8).

Although it is challenging is to predict the emergence of new pathogenic strains or simply separate pathogenic from opportunistic and commensal strains, there are nevertheless examples of models for the prediction or estimation of pathogenicity factors through the analysis of DNA sequences [9, 34, 19]. Apart from the difficulties deriving from the definition of pathogenic bacteria itself, one of the main difficulties in the creation of prediction models is related to the lack of well curated databases for microbes known to be human pathogenic. Luckily, projects like the 100k pathogen genome project [4], in which researchers are trying to sequence 100 thousand genomes of bacteria and viruses causing foodborne infections, will help in having better collections of strains that could be used for building reliable prediction models.

1.4 Web-based Tools for the Characterisation of Prokaryotes

With the constantly decreasing cost of sequencing and the continuous development of new tools for high-throughput sequencing data analysis, many
microbiology labs and healthcare institutions are gradually starting using DNA sequencing for the characterisation of the bacterial strains they are studying, and within a few years these labs are expected to use sequencing on a daily bases. Soon the limiting factor in genomic research will be not to obtain the sequenced data but to analyse it, which directly relates to the problem of training the lab’s staff [15].

The Center for Genomic Epidemiology (CGE) aims at the creation of web-based tools for the rapid analysis of sequence data, to be available for free to the global scientific and medical community. The web-tools target users that are scientists and clinicians with limited computer skills, whom would find it very difficult to use not user-friendly bioinformatics software.

Less than two years from the publication of the first CGE service (MLST) [40], the answer from scientific community has been more than positive, with the number of users and served jobs more than tripled in just one year (Figure 8), with users from more than 60 countries worldwide (Figure 9). At present (November 2013), the four published CGE web-tools [40, 76, 41, 19] are serving more than 1500 jobs per month, with MLST and ResFinder [76] being the most used tools. The users are mainly from developed countries.
Figure 1.9: jobs served by MLST [40], ResFinder [76] and snpTree [41] web-services from CGE in the period between August 2012 and August 2013.

(30% US, 15% UK), but 10% of the users are from developing countries like Philippines, Thailand, Indonesia and other countries in Africa and South America, for which using our tools for free can save important money for their research, considering the costs of the wet lab versions of both MLST and antimicrobial resistance assessment.

At present the CGE tools are able to de-novo assemble and analyse bacterial WGS data, and during the next 2 years a complete pipeline should allow users to have a fast and complete characterisation of the bacterial strains they are studying. The pipeline will be able to do taxonomy identification and typing on the input DNA sequences, as well as identification and prediction of phenotypic traits, e.g., antibiotic resistance and pathogenicity features (tools which are already available as single web-services). Together with the analysis needed to scientists and medics in order to understand what is the bacteria causing a given infection, the pipeline will implement tools [41] to be used for epidemiological studies, which would be very helpful to detect potential outbreaks.

Three [40, 76, 19] of the four articles included in this thesis result from the development of algorithms, and the related web-services, offered by CGE.
Figure 1.10: jobs served by country for MLST [40], ResFinder [76] and snpTree [41] web-services from CGE between August 2012 and August 2013. Users come from more than 60 countries, with developing countries like Philippines, Thailand, Indonesia and India accounting for about 10% of the total use of the CGE web-servers (Nov 2013).
BACTERIAL PATHOGENICITY PREDICTION USING
WHOLE GENOME SEQUENCE DATA

Although some of the most studied bacterial strains can cause serious diseases that could sometimes kill the infected person, not all bacteria are dangerous and many of them are innocuous or even beneficial to human. With almost 2600 publicly available complete genomes and more than 1900 submitted to International Nucleotide Sequence Database Collaboration (INSDC) (www.genomesonline.org, November 2013), many researchers are using this invaluable information to study the mechanism behind bacterial pathogenesis.

Nevertheless, as discussed above, one of the main difficulties in making prediction models for the emergence of pathogenic bacteria are related to the definition of human pathogen bacteria itself. Among the difficulties in building these prediction models there is the high similarity between pathogenic and commensal strains for species like Escherichia coli, also due to Horizontal Gene Transfer (HGT) [30, 65]. Opportunistic pathogens, which are bacteria that can be found in healthy people without causing any infection but can be deadly for people with compromised immune system, are another challenging problem related to the creation of bacterial pathogenicity prediction models.

In the manuscript proposed in this chapter [19] we started from the work proposed in [9], and we modify and extend the method to work with all kinds of bacteria. Each bacterial strain was tagged as human pathogenic if at least one case of human infection, or infections of other mammals caused by a given bacterium, was found in scientific literature. The bacterium would be tagged as non-pathogenic otherwise. Strains infecting fishes or plants with no evidence of zoonosis were also tagged as non-pathogenic.

With the results obtained in this manuscript we shown that it is possible to make prediction models for bacterial pathogenicity provided the availability of a relatively high amount of complete genomes for each species and at the same time a complete dataset containing a wide variety of species. The implemented method is available as a free to use web-service (http://cge.cbs.dtu.dk/services/PathogenFinder/) part of the services offered by the CGE project.
Manuscript I

PathogenFinder - Distinguishing Friend from Foe
Using Bacterial Whole Genome Sequence Data
PathogenFinder - Distinguishing Friend from Foe Using Bacterial Whole Genome Sequence Data

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Abstract
Although the majority of bacteria are harmless or even beneficial to their host, others are highly virulent and can cause serious diseases, and even death. Due to the constantly decreasing cost of high-throughput sequencing there are now many completely sequenced genomes available from both human pathogenic and innocuous strains. The data can be used to identify gene families that correlate with pathogenicity and to develop tools to predict the pathogenicity of newly sequenced strains, investigations that previously were mainly done by means of more expensive and time consuming experimental approaches. We describe PathogenFinder (http://cge.cbs.dtu.dk/services/PathogenFinder/), a web-server for the prediction of bacterial pathogenicity by analysing the input proteome, genome, or raw reads provided by the user. The method relies on groups of proteins, created without regard to their annotated function or known involvement in pathogenicity. The method has been built to work with all taxonomic groups of bacteria and using the entire training-set, achieved an accuracy of 88.6% on an independent test-set, by correctly classifying 398 out of 449 completely sequenced bacteria. The approach here proposed is not biased on sets of genes known to be associated with pathogenicity, thus the approach could aid the discovery of novel pathogenicity factors. Furthermore the pathogenicity prediction web-server could be used to isolate the potential pathogenic features of both known and unknown strains.


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Introduction
Every year more than 15 millions deaths are the direct cause of infectious diseases, many of which are due to bacterial infections. Each year an estimated 1.3 million people die of tuberculosis and 0.2 millions of pertussis, while diarrhoea accounts for more than 2.5 millions deaths, and is one of the leading causes of death in worldwide [1]. But not all bacteria are dangerous and many of them are innocuous or even beneficial to human. The gut of a healthy adult human contains thousand of different microbial species, many of which are beneficial to their host, providing functions for nutrition and development, and regulating the immune response [2,3]. Nevertheless some bacterial species, like Escherichia coli, also include extremely deadly strains, causing for example diarrhoea, urinary tract infections, septicaemia etc. Thus identifying pathogenic strains and understanding the biological mechanisms that cause them to become pathogenic is highly important to perform timely interventions and design control strategies, including interventions such as restrictions on contaminated food products, isolation of patents, correct treatment and development of targeted vaccines.

Ever since the 1880s the pathogenicity of bacteria have been assessed using Koch’s postulates, for human pathogens using animal models. During the last 2 decades many discoveries have shown that Koch’s postulates are not enough to decide if a given bacteria is pathogenic or not. The existence of diseases caused by bacteria that cannot grow in pure culture medium [4,5], the discovery of polymicrobial diseases [6], the role of metagenonomic microbiota in chronic diseases [7], and last but not least, the discovery of Horizontal Gene Transfer (HGT) responsible for the swapping of genetic material between bacteria [8] (regardless the pathogenicity), are all cases in which the postulates have shortcomings. Already during his work with Vibrio cholerae Robert Koch himself discovered the shortcomings of animal models for correctly identifying human-specific pathogens. Thus, the use of animal models is not always reliable in defining if a given bacteria is human pathogenic. Moreover, assessing the pathogenicity by means of animal models or epidemiological studies is both time-consuming and expensive.

Among the molecular features that a bacterium needs to infect and survive inside its host [9] are exotoxins, endotoxins, two components systems [10], adherence factors, secretion systems (I to IV type) [11], through which bacteria can inject their toxins into its hosts cells [12]. Plasmids, secretion systems, and antibiotic resistance genes are commonly present in both commensal and pathogenic strains, while toxins are usually only present in pathogenic strains. There are many databases available containing genes encoding toxins and virulence factors along with other genes traditionally associated with pathogenicity [13,14].

One of the ways to classify a bacterium as human pathogenic using bioinformatics was (and still sometimes is) to look for some of these features in the genome of the isolate under investigation.
Unluckily this approach is not always reliable, partly because of HGT, which causes these features to be exchanged among pathogenic and innocuous strains of the same [13][16] or different species, an exchange which has been proved by the high amount of these features found in genomic islands [17]. Aside from the features directly associated to pathogenicity, there are also virulence “lifestyle” genes, important for the bacteria to survive inside the host and evade its immune system response [18][19], and genes that are, for example, needed to activate other genes, which are important in the processes of pathogenesis, even though they do not directly determine virulence. All the issues related to the prediction of bacterial pathogenicity based on phylogeny has caused researchers to look for different solutions.

The development of whole genome sequencing may open novel ways of predicting pathogenicity in bacterial species. In 1995 the genomes of Mycoplasma genitalium and Haemophilus influenzae [20,21] were completely sequenced, and scientists started considering the possibility of studying the pathogenesis of bacteria based on their genome sequences [22]. This was the start of a revolution that has been continuing during the last decade with the advent of Second-Generation or Next-Generation Sequencing (NGS), leading to a continuous decrease in sequencing costs and a fast development of sequencing technologies. At present, many different high-throughput sequencing systems are available [23–25] and the number of completely sequenced bacteria amount to almost 2,400 including more than 1,800 that have been submitted to the International Nucleotide Sequence Database Collaboration (INSDDC) (www.genomesonline.org, May 2013).

A few methods have been proposed which make use of Support Vector Machines (SVM), BLAST or other bioinformatics tools to search for pathogenic features [26,27] or predict bacterial pathogenicity [28] by searching in pre-computed databases of genes associated with pathogens. One shared aspect among these methods is the fact that they restrict their search to well known pathogenic bacteria. Moreover, our hypothesis-free approach gave us the chance to build, together with a phylogenetic-independent model using all the organisms we have, more specific models that have been continuing during the last decade with the advent of Second-Generation or Next-Generation Sequencing (NGS), leading to a continuous decrease in sequencing costs and a fast development of sequencing technologies. At present, many different high-throughput sequencing systems are available [23–25] and the number of completely sequenced bacteria amount to almost 2,400 including more than 1,800 that have been submitted to the International Nucleotide Sequence Database Collaboration (INSDDC) (www.genomesonline.org, May 2013).

As an alternative to the above mentioned prediction methods, we here developed a novel approach, building on a previous study [31]. In this study we selected groups of genes which are frequently found either in human pathogenic bacteria or in the innocuous ones, and show that this is more effective than using global similarity. Since we did not make any pre-assumption on the genes contained in our training-sets, we are able to identify new proteins associated to pathogenicity and also features shared among non-pathogenic bacteria. Moreover, our hypothesis-free approach gave us the chance to build, together with a phylogenetic-independent model using all the organisms we have, more specific models.

### Table 1. Training, test data and model parameters.

<table>
<thead>
<tr>
<th>Model Name</th>
<th>Training Set</th>
<th>Test Set</th>
<th>Model Parameters</th>
</tr>
</thead>
<tbody>
<tr>
<td>Pathogenic</td>
<td>Non-pathogenic</td>
<td>Total</td>
<td>Pathogenic</td>
</tr>
<tr>
<td>TM-Alphaproteobacteria</td>
<td>29</td>
<td>60</td>
<td>89</td>
</tr>
<tr>
<td>TM-Betaproteobacteria</td>
<td>26</td>
<td>26</td>
<td>52</td>
</tr>
<tr>
<td>TM-Epsiloproteobacteria</td>
<td>17</td>
<td>5</td>
<td>22</td>
</tr>
<tr>
<td>TM-Gammaproteobacteria</td>
<td>122</td>
<td>97</td>
<td>219</td>
</tr>
<tr>
<td>TM-Acinobacteria</td>
<td>27</td>
<td>44</td>
<td>71</td>
</tr>
<tr>
<td>TM-Bacteroidetes</td>
<td>7</td>
<td>12</td>
<td>19</td>
</tr>
<tr>
<td>TM-Firmicutes</td>
<td>98</td>
<td>87</td>
<td>185</td>
</tr>
<tr>
<td>TM-Tenericutes</td>
<td>6</td>
<td>8</td>
<td>14</td>
</tr>
<tr>
<td>COMPL</td>
<td>40</td>
<td>174</td>
<td>214</td>
</tr>
<tr>
<td>WDM</td>
<td>372</td>
<td>513</td>
<td>885</td>
</tr>
</tbody>
</table>

Training, test data and model parameters. The last 3 columns show the MinORG, LT and HT parameters used to create the pathogenicity families and build the model for each of the 10 models. \( \text{Zthr} \) is a threshold value, calculated for each model at the cross validation phase, which is used, given the final prediction score, to decide if the input organisms will be predicted as pathogenic or non-pathogenic. The parameters for each model are chosen after 5-fold cross-validation tests.

doi:10.1371/journal.pone.0077302.t002

### Table 2. MCC on cross validation and independent test-set.

<table>
<thead>
<tr>
<th>Organism subset</th>
<th>S-fold CV</th>
<th>TM or COMPL</th>
<th>WDM</th>
</tr>
</thead>
<tbody>
<tr>
<td>All Bacteria</td>
<td>0.847</td>
<td>0.736</td>
<td>0.758</td>
</tr>
<tr>
<td>G-proteobacteria</td>
<td>0.949</td>
<td>0.886</td>
<td>0.873</td>
</tr>
<tr>
<td>F-proteobacteria</td>
<td>0.923</td>
<td>0.855</td>
<td>0.79</td>
</tr>
<tr>
<td>X-proteobacteria</td>
<td>0.741</td>
<td>0.686</td>
<td>1.0</td>
</tr>
<tr>
<td>Y-proteobacteria</td>
<td>0.825</td>
<td>0.666</td>
<td>0.661</td>
</tr>
<tr>
<td>Actinobacteria</td>
<td>0.681</td>
<td>0.816</td>
<td>0.826</td>
</tr>
<tr>
<td>Bacteroidetes</td>
<td>0.889</td>
<td>0.535</td>
<td>0.383</td>
</tr>
<tr>
<td>Firmicutes</td>
<td>0.915</td>
<td>0.756</td>
<td>0.785</td>
</tr>
<tr>
<td>Tenericutes</td>
<td>0.866</td>
<td>–0.344</td>
<td>0.0</td>
</tr>
<tr>
<td>Remaining Organisms (^1)</td>
<td>0.940</td>
<td>0.793</td>
<td>0.877 (^2)</td>
</tr>
</tbody>
</table>

\(^1\)Organisms of phylum/class for which no TM model is available were tested using COMPL model. COMPL was trained on all organisms from classes or phyla for which only either pathogenic or non-pathogenic strains were available.

\(^2\)Overall MCC for all the TM models and the COMPL model.

doi:10.1371/journal.pone.0077302.t003
grouping organisms at different taxonomic ranks to improve the predictions in species like *E. coli*, in which the high amount of shared genes among pathogenic and commensal strains makes it particularly difficult to predict. In this study the original approach [31] was, furthermore, extended from γ-proteobacteria to all species and extended to not only give a prediction, but also identify which genes predicted to be most significantly associated with (or important for) pathogenicity or non-pathogenicity. Thus, the method will not only provide a prediction of pathogenicity, but may also be useful for identifying novel putative pathogenicity genes, supporting further functional genomic studies.

The predictor has been implemented as a free to use web-service, called *PathogenFinder*, to which users can upload raw reads, obtained from different NGS sequencing platforms, as well as assembled genomes, and obtain a fast estimation of the pathogenic potential of the bacteria they are studying, as well as the identification of potentially pathogenic genes. *PathogenFinder* could be helpful in situations of possible bacterial outbreaks, in which a fast analysis of the unknown strain is important to save lives, and follows the direction modern clinical microbiology [32] and global epidemiology [33] are taking driven by the revolution brought by high throughput DNA sequencing technologies.

**Results and Discussion**

**Overview on the Created Models**

In this work we developed a method for predicting the pathogenicity of novel bacteria. We did this by comparing the proteins of the strain under investigation to a protein family database (PFDB) composed of groups of proteins (protein families or PFs) that were either associated with pathogenic or non-pathogenic organisms. In the creation of the FFDB we used 885 complete bacterial genomes (Table S1), 372 of which were tagged as human pathogens and 513 as non-pathogens.

All the proteins encoded by the bacterial genomes were initially clustered, and significant clusters, in which the majority of the proteins originated from either pathogens or non-pathogens, were identified. The PFs were accordingly tagged as pathogenic or non-pathogenic and a weight (*Z*-score) was calculated for each of them (see Materials and Methods for further details). Eight models were built using bacteria belonging to the same phylum or class as the query organism. Both the set of matches used for the prediction and the raw matches from both the standard server output, that the proteins of the query organism are similar to, a prediction can be made.

**Table 3. Top 10 ranking pathogenic protein families and annotated functions of their proteins for TM-Gammmaproteobacteria model.**

<table>
<thead>
<tr>
<th>RANK</th>
<th>Z-score</th>
<th>P</th>
<th>N</th>
<th>Function</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>9.134</td>
<td>77</td>
<td>8</td>
<td>N-acetylmannosamine kinase (TCS)</td>
</tr>
<tr>
<td>2</td>
<td>8.500</td>
<td>49</td>
<td>0</td>
<td>Fimbrial proteins</td>
</tr>
<tr>
<td>3</td>
<td>8.170</td>
<td>62</td>
<td>6</td>
<td>Salic Acid Transporter</td>
</tr>
<tr>
<td>4</td>
<td>8.158</td>
<td>53</td>
<td>3</td>
<td>Transposition helper protein</td>
</tr>
<tr>
<td>5</td>
<td>8.023</td>
<td>62</td>
<td>7</td>
<td>Acetyltransferase, type III secretion proteins</td>
</tr>
<tr>
<td>6</td>
<td>8.023</td>
<td>62</td>
<td>7</td>
<td>Macrolide-specific efflux, membrane protein</td>
</tr>
<tr>
<td>7</td>
<td>8.023</td>
<td>62</td>
<td>7</td>
<td>Type II secretion proteins</td>
</tr>
<tr>
<td>8</td>
<td>7.922</td>
<td>69</td>
<td>10</td>
<td>Unknown function, possible membrane proteins</td>
</tr>
<tr>
<td>9</td>
<td>7.906</td>
<td>60</td>
<td>7</td>
<td>Unknown function</td>
</tr>
<tr>
<td>10</td>
<td>7.855</td>
<td>53</td>
<td>4</td>
<td>Cytochrome b$_{552}$</td>
</tr>
</tbody>
</table>

P and N columns contain the number of pathogenic and non-pathogenic organisms in the protein family respectively. doi:10.1371/journal.pone.0077302.t003

**Table 4. Top 10 ranking non-pathogenic protein families and annotated functions of their proteins for TM-Gammmaproteobacteria model.**

<table>
<thead>
<tr>
<th>RANK</th>
<th>Z-score</th>
<th>P</th>
<th>N</th>
<th>Function</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>−6.52</td>
<td>3</td>
<td>34</td>
<td>Protein-L-isoaaspartate</td>
</tr>
<tr>
<td>2</td>
<td>−6.44</td>
<td>2</td>
<td>31</td>
<td>Thl/PfpI domain protein</td>
</tr>
<tr>
<td>3</td>
<td>−6.43</td>
<td>6</td>
<td>40</td>
<td>Anthranilate synthase component I</td>
</tr>
<tr>
<td>4</td>
<td>−5.98</td>
<td>6</td>
<td>36</td>
<td>8-amino-7-oxononanoate synthase</td>
</tr>
<tr>
<td>5</td>
<td>−5.92</td>
<td>5</td>
<td>34</td>
<td>Unknown function, putative transcriptional regulator</td>
</tr>
<tr>
<td>6</td>
<td>−5.82</td>
<td>0</td>
<td>21</td>
<td>Adenosylmethionine decarboxylase</td>
</tr>
<tr>
<td>7</td>
<td>−5.81</td>
<td>8</td>
<td>39</td>
<td>Unknown function</td>
</tr>
<tr>
<td>8</td>
<td>−5.80</td>
<td>2</td>
<td>26</td>
<td>Unknown function, probable condensation protein</td>
</tr>
<tr>
<td>9</td>
<td>−5.68</td>
<td>0</td>
<td>20</td>
<td>Nitrite transporter</td>
</tr>
<tr>
<td>10</td>
<td>−5.62</td>
<td>1</td>
<td>22</td>
<td>Glucose-galactose transporter</td>
</tr>
</tbody>
</table>

P and N columns contain the number of pathogenic and non-pathogenic organisms in the protein family respectively. doi:10.1371/journal.pone.0077302.t004

**Results and Discussion**

**Overview on the Created Models**

In this work we developed a method for predicting the pathogenicity of novel bacteria. We did this by comparing the proteins of the strain under investigation to a protein family database (PFDB) composed of groups of proteins (protein families or PFs) that were either associated with pathogenic or non-pathogenic organisms. In the creation of the PFDB we used 885
and could hence be used for a more detailed analysis of the pathogenicity features of the organisms under investigation.

Performance on Five-Fold Cross Validation and Independent Test Data

The TM models were tested using only organisms belonging to the specific phylum/class, while in the case of the WDM model the whole independent data-set was used for the test.

Table 2 shows the performance of the ten models as obtained by 5-fold cross validation (CV) (column 2) and on independent test-sets of organisms from the same taxonomic group (column 3). As can be seen for the Tenericutes and Bacteroidetes phyla, the performances were very poor when compared to the MCC obtained in the CV tests. This is likely to be caused by the models being built using a small number of organisms (Table 1). For instance, the TM-Tenericutes model was trained on only 14 isolates. Furthermore, it was tested on a set of organisms from species that were not present in the training-set.

To compare the performance of the WDM model to those of the TM and COMPL models, we examined the MCC of the WDM on the same test-sets used for the other models (column 4 in Table 2).

For example, to examine the performance of the WDM in predicting the pathogenicity of Firmicutes bacteria, we tested it with the same organisms used to assess the accuracy of the TM-Firmicutes model.

The MCC obtained by the WDM (0.758) on all bacteria was higher than the overall accuracy of all the TM models and COMPL model combined (0.736). Nonetheless, the TM models performed better for bacteroidetes, α, β, and γ-proteobacteria, even though for the latter the difference from the WDM was not significant. The remaining TM models and the COMPL model had lower MCC than the WDM for the same organisms.

Performance on Draft Genomes and Escherichia coli

The models ability in predicting the pathogenicity of an isolate as based on a draft genome was tested using 259 sets of illumina raw reads from 6 different species. While in the case of Campylobacter jejuni, Klebsiella pneumoniae and Staphylococcus aureus (57 isolates in total) all the predictions were correct, the results were not satisfactory for Enterococci and E. coli. Of 50 Enterococcus

---

Table 5. Top 10 ranking pathogenic protein families and annotated functions of their proteins for the WDM model.

<table>
<thead>
<tr>
<th>RANK</th>
<th>Z-score</th>
<th>P</th>
<th>N</th>
<th>Function</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>10.18</td>
<td>38</td>
<td>0</td>
<td>Borrelia Plasmid partition proteins</td>
</tr>
<tr>
<td>2</td>
<td>9.49</td>
<td>33</td>
<td>0</td>
<td>TCS associated genes, unknown functions</td>
</tr>
<tr>
<td>3</td>
<td>9.19</td>
<td>31</td>
<td>0</td>
<td>Lipote-protein ligation, lipote metabolism</td>
</tr>
<tr>
<td>4</td>
<td>9.19</td>
<td>31</td>
<td>0</td>
<td>Unknown functions, flavin oxidoreductase</td>
</tr>
<tr>
<td>5</td>
<td>9.04</td>
<td>30</td>
<td>0</td>
<td>Exfoliative toxin A</td>
</tr>
<tr>
<td>6</td>
<td>8.89</td>
<td>29</td>
<td>0</td>
<td>Pili assembly proteins, Motility, Secretion</td>
</tr>
<tr>
<td>7</td>
<td>8.89</td>
<td>30</td>
<td>0</td>
<td>Unknown function, shikimate kinase</td>
</tr>
<tr>
<td>8</td>
<td>8.89</td>
<td>29</td>
<td>0</td>
<td>Pili assembly proteins, Motility, Secretion</td>
</tr>
<tr>
<td>9</td>
<td>8.74</td>
<td>28</td>
<td>0</td>
<td>Multiple antibiotic resistance (MarR) family</td>
</tr>
<tr>
<td>10</td>
<td>8.74</td>
<td>28</td>
<td>0</td>
<td>Mutarotase Yjht (sialic acid mutarotation), unknown functions</td>
</tr>
</tbody>
</table>

P and N columns contain the number of pathogenic and non-pathogenic organisms in the protein family respectively. doi:10.1371/journal.pone.0077302.t005

Table 6. Top 10 ranking non-pathogenic protein families and annotated functions of their proteins for the WDM model.

<table>
<thead>
<tr>
<th>RANK</th>
<th>Z-score</th>
<th>P</th>
<th>N</th>
<th>Function</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>−6.68</td>
<td>0</td>
<td>63</td>
<td>tRNA proteins</td>
</tr>
<tr>
<td>2</td>
<td>−6.62</td>
<td>0</td>
<td>62</td>
<td>ABC transporter related proteins (for δ and α-proteobacteria)</td>
</tr>
<tr>
<td>3</td>
<td>−5.18</td>
<td>0</td>
<td>54</td>
<td>Rubreythrin</td>
</tr>
<tr>
<td>4</td>
<td>−6.07</td>
<td>0</td>
<td>52</td>
<td>Rubreythrin</td>
</tr>
<tr>
<td>5</td>
<td>−6.01</td>
<td>0</td>
<td>51</td>
<td>Iron-sulfur binding domain proteins</td>
</tr>
<tr>
<td>6</td>
<td>−6.01</td>
<td>0</td>
<td>51</td>
<td>Hydroxymethylglutaryl-CoA synthase</td>
</tr>
<tr>
<td>7</td>
<td>−5.95</td>
<td>0</td>
<td>50</td>
<td>Unknown function</td>
</tr>
<tr>
<td>8</td>
<td>−5.89</td>
<td>0</td>
<td>49</td>
<td>Unknown function</td>
</tr>
<tr>
<td>9</td>
<td>−5.83</td>
<td>0</td>
<td>48</td>
<td>Unknown function</td>
</tr>
<tr>
<td>10</td>
<td>−5.70</td>
<td>0</td>
<td>46</td>
<td>Sulfite reductase subunit</td>
</tr>
</tbody>
</table>

P and N columns contain the number of pathogenic and non-pathogenic organisms in the protein family respectively. doi:10.1371/journal.pone.0077302.t006
faecalis and 49 Enterococcus faecium from healthy Danish pigs, all isolates were predicted as pathogenic. Our training-set only contained a single pathogenic E. faecalis and no E. faecium, which may explain these results.

The WDM as well as the TM-Gammaproteobacteria models predicted the 10 E. coli strains in the test-set as pathogenic, although 4 strains were annotated as non-pathogenic. A similar situation was observed for the 103 E. coli draft genomes. Accordingly, we decided to create a model only for the Enterobacteriaceae family, using the organisms in our training-set. The resulting model correctly predicted 1 of 4 non-pathogenic E. coli achieving an MCC of 0.41, but all draft genomes were still predicted as pathogenic. The model also showed improvements in predicting other Enterobacteriaceae, with an MCC of 0.675, while WDM and TM-Gammaproteobacteria had an MCC of 0.519 and 0.617, respectively.

To improve the predictions for E. coli further, we decided to create 2 special models. These models were called ecoli_boost and enterobac_boost, and they were trained on a set that was enriched with 14 extra non-pathogenic E. coli strains downloaded from the National Center for Biotechnology Information (NCBI) (Table S2). These two models had a noticeably improvement on both CG test-sets and on the 103 assembled E. coli isolates, on which MCC was 0.346 (Acc = 67%) and 0.360 (Acc = 68%) for enterobac_boost and ecoli_boost, respectively. The lists of organisms used to train the enterobac_boost and ecoli_boost models, together with more details on the results on E. coli can be seen in Table S2.

Comparison to other Prediction Methods

Presently, the literature describes two main approaches for predicting the human pathogenicity of bacteria based on whole genome sequencing data: the first, proposed by Andreotta et al. [31], is able to predict the pathogenicity of z-proteobacteria, and it was from this study we borrowed the concept of PFs; the second method, developed by Iraola et al. [28], uses SVM [35], and can predict the pathogenicity of all types of bacteria. In this method the authors selected 120 genes associated to pathogenicity from 600 complete genomes using SVM, and built a prediction model based on the selected genes.
### Distinguishing Friend from Foe Using Bacterial WGS

<table>
<thead>
<tr>
<th>Bacterial Phylum</th>
<th>Training Set</th>
<th>Test Set</th>
<th>Protein Families</th>
<th>Tot. Protein Families</th>
<th>PFDB Size (No.Seq./Mbytes)</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>TM-Alphaproteobacteria</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>non-pathogenic</td>
<td>67.4%</td>
<td>28.2%</td>
<td>84.2%</td>
<td>32961</td>
<td>179809/82.7</td>
</tr>
<tr>
<td>pathogenic</td>
<td>32.6%</td>
<td>11.9%</td>
<td>15%</td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>TM-Betaproteobacteria</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>non-pathogenic</td>
<td>50.0%</td>
<td>31.3%</td>
<td>44.3%</td>
<td>17090</td>
<td>76905/35.2</td>
</tr>
<tr>
<td>pathogenic</td>
<td>50.0%</td>
<td>43.3%</td>
<td>15.7%</td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>TM-Epsilonproteobacteria</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>non-pathogenic</td>
<td>22.7%</td>
<td>88.9%</td>
<td>54.2%</td>
<td>1494</td>
<td>13128/4.4</td>
</tr>
<tr>
<td>pathogenic</td>
<td>77.3%</td>
<td>85.8%</td>
<td>45.8%</td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>TM-Gammaphylococci</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>non-pathogenic</td>
<td>44.3%</td>
<td>49.1%</td>
<td>61.9%</td>
<td>40537</td>
<td>229030/100.6</td>
</tr>
<tr>
<td>pathogenic</td>
<td>55.7%</td>
<td>38.1%</td>
<td>38.1%</td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>TM-Actinobacteria</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>non-pathogenic</td>
<td>62.0%</td>
<td>40.0%</td>
<td>81.5%</td>
<td>19018</td>
<td>179809/29.6</td>
</tr>
<tr>
<td>pathogenic</td>
<td>38.0%</td>
<td>18.5%</td>
<td>18.5%</td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>TM-Bacteroidetes</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>non-pathogenic</td>
<td>63.2%</td>
<td>36.8%</td>
<td>61.9%</td>
<td>9620</td>
<td>33502/16.9</td>
</tr>
<tr>
<td>pathogenic</td>
<td>36.8%</td>
<td>38.1%</td>
<td>38.1%</td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>TM-Firmicutes</strong></td>
<td></td>
<td></td>
<td></td>
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<td></td>
</tr>
<tr>
<td>non-pathogenic</td>
<td>47.0%</td>
<td>29.1%</td>
<td>55.1%</td>
<td>16392</td>
<td>99754/41.7</td>
</tr>
<tr>
<td>pathogenic</td>
<td>53.0%</td>
<td>44.9%</td>
<td>44.9%</td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>TM-Tenericutes</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>non-pathogenic</td>
<td>57.1%</td>
<td>42.9%</td>
<td>57.6%</td>
<td>1536</td>
<td>3965/2.0</td>
</tr>
<tr>
<td>pathogenic</td>
<td>42.9%</td>
<td>42.5%</td>
<td>42.5%</td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>COMPL</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>non-pathogenic</td>
<td>81.3%</td>
<td>18.7%</td>
<td>91.1%</td>
<td>67150</td>
<td>31188/142.1</td>
</tr>
<tr>
<td>pathogenic</td>
<td>18.7%</td>
<td>8.9%</td>
<td>8.9%</td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>WDM</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>non-pathogenic</td>
<td>58.0%</td>
<td>34.5%</td>
<td>73.4%</td>
<td>192411</td>
<td>784316/346.5</td>
</tr>
<tr>
<td>pathogenic</td>
<td>42.0%</td>
<td>26.7%</td>
<td>26.7%</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

*Note: Tot. Protein Families, PFDB Size (No.Seq./Mbytes)*
To compare our method to the one proposed by Andreotta et al., we built a model using the same set of $\alpha$-proteobacteria organisms (155) and the same parameters (MinOrg, HT, LT) used by Andreotta et al. The key differences between our method and the one by Andreotta et al. are: 1) we used CD-HIT instead of BLAST in both the protein clustering and prediction phases; 2) we used Equation 3 to filter the significant matches of the query sequences, while Andreotta et al. filtered based on a BLAST e-value threshold; 3) We compute the final predictions using the Z-scores, while Andreotta et al. counted the number of pathogenic and non-pathogenic families matched. The obtained model was tested on the same independent set used by Andreotta et al. This set included 24 organisms (14 pathogenic), and our model was able to correctly classify 23 organisms (95.8%). This is equivalent to an MCC of 0.92, while Andreotta’s MCC was 0.837. The one organism that our method was not able to correctly classify, is *Salmonella enterica* Serovar Gallinarum str. 287/91 [Gen-Bank:30689], which is pathogenic for poultry, but not known to be for humans. The pathogenicity of this organism is restricted to chicken although it shares a high quantity of genomic features associated to pathogenicity with its human pathogenic ancestor *Salmonella Enteritidis* [36]. It is likely that these features mislead the prediction model, since also the method by Andreotta et al. wrongly classified this *S. enterica* strain.

To compare our method to the predictor proposed by Iraola et al., we used the test-set they used for their blind test evaluation. The test-set, originally composed of 233 organisms, contained 5 strains, which were excluded from the comparison, since they were also present in our training-set. Overall, for the comparison, we had a test-set composed of 228 organisms, 192 of which are tagged as human pathogens and the remaining 36 as non-pathogens.

PathogenFinder achieved an overall MCC of 0.67 for the taxonomy models and 0.65 for the WDM model. Both results are higher than the MCC of 0.6 obtained by the method proposed by Iraola et al. Table S3 contains a detailed description of the comparison, including the organisms used and the corresponding predictions from both methods.

**PFDB Analysis and Biological Interpretation**

For each created model, an analysis of its PFDB was performed and its PFs ranked based on their Z-scores. The scores above 0 are associated with pathogenic PFs, while those below 0 are associated with non-pathogenic PFs. No protein function analysis was done prior to the models creation, making the approach unbiased on the content of the organisms, regardless of their pathogenicity. In this paragraph we describe the analysis of the PFs of the TM-Gammaglobobacteria and WDM.

The analysis of the PFDB of TM-Gammaglobobacteria model showed that the high ranked pathogenic families (Table 3) contained proteins well known to be associated to pathogenicity. The family at rank 1 and 3 contained N-acetylmuramylasomine kinase, which is a key enzyme in sialic acid synthesis and sialic acid transport proteins. Sialic acid is important for virulence and is believed to help the microbes to disguise themselves as host cells in order to elude the host’s immune system response [37]. Fimbrial proteins (rank 2) are important for bacterial adherence [38]. At rank 10 we found cytotoxic Bact/280 proteins that help bacteria to survive and grow in conditions of poor oxygen [39]. Other high-ranked families contained proteins associated with secretion systems (II and III) and antibiotic resistance.

An interesting finding, which was also found in [31], was the presence of families containing proteins with unknown functions associated with pathogenicity. This finding suggests that those proteins with unknown function might have important roles in the bacterial pathogenesis and could form the basis for further functional studies improving our understanding of bacterial pathogenicity. Proteins with unknown functions were also identified as associated with non-pathogenic PFs (Table 4).

The analysis of the PFDB of the WDM enabled us to see if proteins involved (or not involved) in pathogenesis belong to organisms of different taxonomy, and at the same time gave us an insight on how proteins are conserved along the different phyla. Again, we found that the top ranked families associated to pathogenicity (Table 5) contained also proteins with unknown function.

The highest ranked PF contained proteins encoded by plasmids from different pathogenic *Bordetella* species (mainly *Burgoletfer*, which are involved in pathogenesis [40,41]. The family ranked 3 contained proteins associated with lipoate metabolism. The acquisition and use of lipoate by pathogens affect their virulence and the pathogenesis of the diseases they cause [42]. Among the toxins found were: exofilative toxin A (family-rank 5) in *Staphylococcus aureus* strains, causative of Staphylococcal scalded skin syndrome [43,44]; streptolysin (O and S), mainly found in *Streptococcus* pathogenic species [45]; hemolysin (I, II, III, z and $\beta$ types) found in PFs mainly composed of $\alpha$-proteobacteria [46,47] and firmicutes organisms [48]; shiga toxin, a common pathogenicity factor in many virulent *E. coli* strains [49]; dermonecrotic toxin (DNT), one of the main virulence factors in many *Bordetella* species [50] (pertussis in human), but at the same time present in plant pathogenic organisms like *Erwinia amylovora* [51] and *Erwinia pyrifoliae* [52]. The fact that we could find PFs containing DNT tagged as pathogens and others tagged as non-pathogenic (like the one containing DNT for *E. amylovora* and *E. pyrifoliae*) is an example of the ability of our clustering method to associate a given protein (a toxin in this case) to human pathogenicity as well as non-pathogenicity depending on the organism in which it is found.

Another example through which we could see the discriminatory power of our PFs, was in associating pathogenicity to the different secretion system types proteins (SST1–SST6). For SST3 we identified 294 protein families, 147 of which were tagged as pathogenic. The pathogenic PFs were composed of human pathogenic $\alpha$-proteobacteria strains, while the non pathogenic PFs contained plant pathogenic organisms from proteobacteria genera like *Xanthomonas*, *Agrobacter* and *Erwinia*, which use SST3 (and other secretion systems) to infect the hosts cells of plants [53,54]. The protein families with high rank associated with non-pathogenicity (Table 6) were usually composed of proteins present in bacteria living in hot springs, lake surfaces or deep in the sea, and the functions are associated to their ability to survive under those extreme environmental conditions. Among those proteins are Ruberythrin, found in anaerobic sulfate-reducing bacteria like *Geobacter* and *Desulfitobacter* [55]. When the PFs were not composed of proteins from environmental bacteria, they contained mainly probiotics or plant pathogens. It is important to note that...
since the WDM model was created with HT and LT parameters with values of 1.0 and 0 respectively, we only have PFs composed of proteins from either only pathogenic organisms or only non-pathogenic organisms.

Conclusions

There is an increasing need for fast identification of unknown bacteria with particular focus on the assessment of their potential pathogenicity. In this work we presented PathogenFinder, a web-server that by analysing the user-uploaded proteome can identify genomic features associated with both pathogenicity and non-pathogenicity. Given an input proteome the method quickly predicts its potential pathogenicity, making it a useful tool to be used together with other web-services developed for bacterial outbreak surveillance. Moreover, the possibility for the user to download the complete set of predicted pathogenicity features for the input organism makes PathogenFinder convenient for the analysis of pathogenic and harmless strains for microbiologists, epidemiologist and in general institutions studying bacterial pathogenesis.

One of the novel aspects in our approach is in the construction of the prediction models, which was carried out without any prior analysis of the proteins in our training-set, by just tagging our organisms as pathogenic or non-pathogenic and identifying protein families that were frequently found in pathogenic or non-pathogenic organisms.

It is important to notice that even though an isolate may have been obtained from a non-pathogenic environmental or animal or human related source it is not necessarily non-pathogenic. Such strain might in fact be highly pathogenic opportunistic pathogens. This naturally makes the creation of the optimal reference database difficult, but with increased number of isolates with well-defined meta data this is should still be doable.

We observed how PathogenFinder performs better than other pathogenicity prediction methods described in the literature, which usually rely on taxonomy and global sequence similarity with small sets of genes known to be associated with bacterial pathogenesis. We had less good results for species of the tenericutes phylum, and extra work need to be done to obtain statistically significant results for opportunistic strains (e.g. S. aureus) for which we could not tag any of our strains as non-pathogenic. The accuracy in predicting opportunistic bacteria could be improved by building specific models (e.g. at species level) as soon as new strains are available and there is a reasonable amount of both pathogenic and harmless strains. We have also shown how the prediction accuracy can be enhanced by increasing the number of organisms in the training-sets and/or making specific models at different taxonomic ranks, showing the example of E. coli, which is particularly difficult to predict because of the high similarity between commenal and pathogenic strains.

With the fast growing number of available bacterial complete genomes and with the increasing quality of the meta data we envision the possibility in the near future to build prediction models targeting only bacteria of a given genus or species, or even better, to build models to identify pathogenic features involved in specific diseases.

Materials and Methods

Training and Test Data

All available complete bacterial genomes (NCBI Genome Project, accessed on 10th Nov. 2010) were considered for the creation of the training-sets.

The pathogenicity information for the retrieved organisms were taken from NCBI genome project pages as described in Andreatta et al. [31], and for 885 of the 1,224 downloaded organisms, we were able to find pathogenicity information. The final complete training-set (Table S1) was composed of 513 organisms tagged as human non-pathogens and 372 tagged as human pathogens. For the human pathogenic organisms we checked for evidence in the literature. Opportunistic pathogens (e.g. from species like Staphylococcus aureus [56] or Pseudomonas aeruginosa [57]) were still tagged as pathogenic even though it has been shown that some of them can live inside the host without causing any disease, and their pathogenicity is sometimes related to the host’s health conditions.

From January 2012, NCBI removed pathogenicity information from its pages, redirecting the users to Genomes Online Database (GOLD) [58]. On 26th Feb. 2012 we queried GOLD for pathogenicity information about organisms that had been published after 5th Nov. 2010 (the date of the latest published bacteria in the training-set). We were able to extract pathogenicity information for 449 organisms, and subsequently retrieved the corresponding complete genomes and plasmids from NCBI based on the NCBI project ids.

The final test data (Table S1) was composed of 449 organisms, 294 of which were tagged as human non-pathogens and 155 as human pathogens.

Protein Clustering

The model creation consisted of the following 2 main steps:

I. Protein Clustering

II. PFDB Creation

The initial idea for clustering the proteins was to use BLAST [59], but due to the size of our dataset (almost 3 million proteins), it would not have been computationally feasible. Instead, we used CD-HIT [60], which made it possible to cluster all the proteins in approximately 24 days using 2 3 Ghz dual-core CPUs in parallel and a 8 Gb of RAM.

The output from the program were 3 files containing respectively: 1) a list of cluster ids followed by the FASTA headers corresponding complete genomes and plasmids from NCBI based on the NCBI project ids; 2) a FASTA file containing all the clusters representative sequences; 3) a FASTA file containing all the solitary sequences that could not be included in any cluster.

Protein Family Database (PFDB) Creation

Our prediction models are based on the concept of protein families as initially proposed in Adreatta et al. [31]. Protein families are groups of proteins with a certain degree of similarity. The PFs were created using a two-steps filtering of the clusters created using CD-HIT. To perform this filtering we used four parameters: MinORG, P_{ratio} HT and LT.

Let ORG be the number of organisms which have proteins in a given cluster i. We define MinORG as the minimum number of organisms that must have proteins in the i cluster for it to be considered significant. As such, MinORG is a lower threshold for the ORG value.

Equation 1. Ratio of human pathogenic organisms having proteins inside the cluster i on the total number of organisms having proteins in i. Newton’s Second Law

\[
P_{\text{ratio}}(i) = \frac{HP_i}{ORG_i}
\]
number of organisms in i (ORG), LT and HT are thresholds for the \( P_{\text{ratio}} \) that we used to define if a given significant cluster should be tagged as pathogenic or non-pathogenic according to equation 2.

**Equation 2.** Function used to define if a given significant cluster should be tagged as ‘pathogen family’ or ‘non-pathogen family’.

\[
f(i) = \begin{cases} 
-1 & \text{if } P_{\text{ratio}}(i) \leq LT \\
0 & \text{if } LT < P_{\text{ratio}}(i) < HT \\
1 & \text{if } P_{\text{ratio}}(i) \geq HT 
\end{cases}
\]  

Let \( f(\cdot) \) (Equation 2) be the function we use to decide if a given significant cluster should be tagged as pathogenic or non-pathogenic. If the number of sequences from pathogens and non-pathogens is too close in a given cluster (if \( P_{\text{ratio}} = 0.5 \) then \( f(i) = 0 \)), the cluster does not have any discriminative value for pathogenicity and is unusable.

Given a protein cluster \( i \), it was considered a protein family if the following 3 conditions were satisfied:

I. \( \text{ORG}_i \geq \text{Min ORG} \)
II. \( f(i) \neq 0 \)
III. \( P_{\text{ratio}} \geq HT \) or \( P_{\text{ratio}} \leq LT \)

The significance of a protein family depends on its ORG value and its \( P_{\text{ratio}} \). A statistical measure called Z-score (\( Z \)) was used to take into account the above two values of a family and assess its significance. The estimation of the \( Z \) values was performed on the set \( C \) composed of all the clusters \( i \) satisfying condition I. Let \( \mu \) and \( \sigma \) be the average and standard deviation respectively of the \( P_{\text{ratio}} \) of the clusters in \( C \). \( Z \) is a measure representing by how many standard deviations \( \sigma \) the mean \( \mu \) of a sample (a cluster in our case) differs from the mean \( \mu \) of the population. Given a cluster \( i \) in \( C \), its mean corresponds to its \( P_{\text{ratio}} \), and we calculate the \( Z \) value for \( i \) as follows:

\[
Z_i = \frac{P_{\text{ratio}}(i) - \mu}{SE_i}
\]

Where \( SE \) is the standard error of the mean for \( i \), and it is:

\[
SE_i = \frac{\sigma}{\text{ORG}_i}
\]

To each protein family, a \( Z \) value was assigned, and these are used in the calculation of the final prediction score as well as a ranking value in the analysis of the protein families. Figure 1 shows the distributions of the \( P_{\text{ratio}} \) values and Z-scores for both significant clusters and protein families for the TM-Betaproteobacteria model, while Figure 2 shows for each of the models built the proportion of pathogenic and non-pathogenic families in the PFDB, together with the training-set and test-set for the 10 models built. All the sequences in the PFDB are used to perform the predictions.

**Models Optimisation**

The prediction models were verified by 5-fold cross validation. For each of the models, many trials and tests were performed before choosing the Min Org, LT and HT parameters for the final models. At each CV a parameter called \( Z_{\text{thr}} \), was further optimised. \( Z_{\text{thr}} \) is the threshold used to decide whether an input organism should be predicted as pathogenic or not, by comparing it to the summation of \( Z \) values obtained for the matching sequences in the input proteome. The parameters (MinOrg, LT, HT) of Table 1 of the models with the highest MCC in the CV tests were used to create the final models, and the corresponding \( Z_{\text{thr}} \) values will be used as thresholds for the predictions.

**Pathogenicity Prediction**

The prediction method takes as input a FASTA file containing the proteins of the organism for which we want to assess the potential pathogenicity. In case the input is a complete or draft genome, initial gene prediction is performed using PRODIGAL [61]. PRODIGAL outputs a set of proteins representing the predicted genes. This is then used as input to our method. Using CD-HIT-2D [60], the input file is compared to the PFDB, and the output will contain all the input sequences that matched sequences in the PFDB, and that are used to compute the final prediction.

The following 4 steps describe the process that leads to the prediction:

I. Compare the input proteins to the PFDB
II. Filter hits based on the identity threshold (Equation 3)
III. Calculate final score summing the \( Z \) values associated to the matched PFs
IV. Compare the final score to the model’s \( Z_{\text{thr}} \) threshold and give the final prediction.

From the comparison in step I, we obtain a list of clusters, the representatives of which are sequences belonging to the PFDB, while the non-representative sequences come from the input. Because it is possible that more than one of the input proteins fall inside the same cluster, the sequence with the highest identity percentage with the representative is chosen. 

**Equation 3.** Calculates the identity threshold to select significant matches that will be used in the final prediction. The calculation is based on statistics on the identity values obtained for all matching query sequences.

\[
idenThr(hits) = \begin{cases} 
\frac{\mu + \sigma + max}{2} & \text{if } \mu + \sigma \leq max \\
\text{otherwise} & 
\end{cases}
\]

The list of matches is then filtered based on an identity threshold that is dynamically computed at each prediction using the function idenThr (Equation 3). Let \( hits \) be a set containing all the percentage identity values for all our matches. Let \( \mu \) and \( \sigma \) be respectively the average and standard deviation of the percentage identity values in \( hits \). Let \( max \) be the maximum percentage identity obtained for the hits in PFDB. Remembering that, based on the settings of CD-HIT-2D, the minimum identity is 60%. Equation 3 calculates the identity threshold as the middle point between the maximum, and the average increased by one standard deviation, of the identities in \( hits \). Selecting all the matches with an identity higher than idenThr(hits), we will obtain a list of hits with a very high identity relatively to the distribution of identities of our hits.

The matches below that threshold will not be used in the final prediction. The process will sometimes greatly reduce the number of matches, but this is in favour of matches with higher identity, making the final prediction more reliable, if compared to the
results obtained using a fixed threshold, as we proved by using the paired student’s t-test (results not shown).

In the end we compute the summation of the Z-scores associated with the families matching the input sequences (III). If the sum of the Z-scores is above \( Z_{th} \) the input is considered pathogenic, otherwise it is considered non pathogenic (IV).

Supporting Information

Table S1  Training and Test organisms. xlsx file containing the list of organisms in the training and test-set and a table showing the phyla of the organisms in the training-set used to build the list of organisms in the training and test-set and a table containing a detailed description of the comparison of Pathogen-Finder and the method described in [28].

(XLSX)

Table S2  Extra Escherichia Coli Strains. xlsx file containing the training-sets used for building coli_boost and enterobac_boost models, including the list of extra E. coli strains and a summary of the results in the prediction of E. coli and enterobacteriaceae organisms.

(XLSX)

Table S3 Comparison with other methods. xlsx file containing a detailed description of the comparison of Pathogen-Finder and the method described in [28].

(XLSX)

Acknowledgments

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Author Contributions

Conceived and designed the experiments: SC OL. Performed the experiments: SC. Analyzed the data: SC MV. Contributed reagents/materials/analysis tools: MV. FMA. Wrote the paper: SC. Helped to review the manuscript: MV FMA OL.

References

Identification and classification is a basic requirement for anyone working with bacteria, whether commensals, pathogens, or bacteria used for industrial purposes. When the bacterium under investigation is a new or mutated strain that could potentially cause an outbreak, it is of crucial importance that the identification of the microbe causing the infection is rapid and precise.

Knowing what bacteria it is, usually means knowing what species the microbe belongs to. For the last 30 years, taxonomy identification of prokaryotes has mainly been done through the analysis of 16S rRNA gene sequences. The 16S-based method has, however, some limitations and other methods for taxonomic classification of prokaryotes using WGS data has been proposed.

In the first manuscript presented in this chapter we trained and benchmarked five methods for bacterial species identification on common datasets of complete and draft genomes, and raw-reads. One of the methods (SpeciesFinder) is based on the complete 16S rRNA gene, while the others use different bioinformatics approaches, like KmerFinder, which analyses the co-occurrence of k-mers in the input DNA sequences to identify the bacterial species. The results of the benchmark show how methods that only use core genes in the prediction have difficulties in identifying species, which have recently diverged. On the other hand, the method based on k-mers had overall the highest accuracy and robustness.

The second article included in this chapter [40] is about accurate strain identification (or typing). We developed a web-server that runs a bioinformatics method for bacterial strain typing based on multilocus sequence typing (MLST). The web-service uses a database of MLST schemes from www.pubmlst.org, to which it is weekly synchronised. Having a web-server like the MLST available for free reduces both the costs and time needed for scientists that want to perform strain identification.

The traditional MLST, performed in the lab, costs about 120$ per isolate, while strain-typing using pulsed-field gel electrophoresis (PFGE) costs approximately 150$ per isolate [63]. Considering that the WGS for a single bacterial isolate can be obtained for less than 100$ and the MLST web-service can be used free of charge, the advantages in terms of costs are clear, which might be particularly important for small microbiology labs in developing countries.

The MLST web-service is at present used by researchers from more than 40 countries worldwide, and serves more than 700 bacterial strain identifications every month.
Manuscript II

Multilocus Sequence Typing of Total-Genome-Sequenced Bacteria
Multilocus Sequence Typing of Total-Genome-Sequenced Bacteria

Mette V. Larsen, Salvatore Cosentino, Simon Rasmussen, Carsten Friis, Henrik Hasman, Rasmus Lykke Marvig, Lars Jelsbak, Thomas Sicheritz-Pontén, David W. Ussery, Frank M. Aarestrup and Ole Lund


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Multilocus Sequence Typing of Total-Genome-Sequenced Bacteria

Mette V. Larsen,* Salvatore Cosentino,* Simon Rasmussen,* Carsten Friis,² Henrik Hasman,² Rasmus Lykke Marvig,² Lars Jelsbak,² Thomas Sicheritz-Pontén,² David W. Ussery,² Frank M. Aarestrup,² and Ole Lund⁴

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Accurate strain identification is essential for anyone working with bacteria. For many species, multilocus sequence typing (MLST) is considered the “gold standard” of typing, but it is traditionally performed in an expensive and time-consuming manner. As the costs of whole-genome sequencing (WGS) continue to decline, it becomes increasingly available to scientists and routine diagnostic laboratories. Currently, the cost is below that of traditional MLST. The new challenges will be how to extract the relevant information from the large amount of data so as to allow for comparison over time and between laboratories. Ideally, this information should also allow for comparison to historical data. We developed a Web-based method for MLST of 66 bacterial species based on WGS data. As input, the method uses short sequence reads from four sequencing platforms or preassembled genomes. Updates from the MLST databases are downloaded monthly, and the best-matching MLST alleles of the specified MLST scheme are found using a BLAST-based ranking method. The sequence type is then determined by the combination of alleles identified. The method was tested on preassembled genomes from 336 isolates covering 56 MLST schemes, on short sequence reads from 387 isolates covering 10 schemes, and on a small test set of short sequence reads from 29 isolates for which the sequence type had been determined by traditional methods. The method presented here enables investigators to determine the sequence types of their isolates on the basis of WGS data. This method is publicly available at www.cbs.dtu.dk/services/MLST.

Correct, standardized classification is a basic need for anyone working with bacteria, whether pathogens, commensals, or bacteria used for industrial purposes. Especially in outbreak situations, it is of pivotal importance that the strains of infectious agents be rapidly and accurately identified. A recent example is the outbreak of hemolytic-uremic syndrome and bloody diarrhea caused by an Escherichia coli O104:H4 strain, which in the beginning of May 2011 started spreading in Germany and throughout Europe. Reliable classification, including determination of the multilocus sequence type (MLST), was needed to identify strains related to the outbreak (19, 23). Also, for a range of other species, MLST is used to classify isolates in an understandable and comparable global context (6, 12, 22, 31).

MLST was first developed for Neisseria meningitidis in 1998 to overcome the poor reproducibility between laboratories of older molecular typing schemes (18). The principle behind the MLST scheme is to identify internal nucleotide sequences of approximately 400 to 500 bp in multiple housekeeping genes. Unique sequences (alleles) are assigned a random integer number, and a unique combination of alleles at each locus, an “allelic profile,” specifies the sequence type (ST). Following the introduction of the Neisseria MLST scheme, MLST has been considered the “gold standard” of typing, and additional schemes that cover bacterial and fungal species have been developed. The MLST allele sequences and ST profile tables are stored in curated databases hosted at different sites around the world (1, 14, 15). The PubMLST site collects data from all databases and makes it easily accessible (multilocus sequence typing databases and software, December 2011 [http://pubmlst.org]).

Traditionally, MLST starts with a PCR amplification step using primers that are specific for the loci of the MLST scheme, followed by Sanger sequencing. The procedure is both costly and time-consuming. In this new era of high-throughput sequencing, it may be more rational to use whole-genome sequence (WGS) data for typing. The cost of DNA sequencing has steadily gone down roughly 10-fold every 5 years (25), and the development of next- and third-generation sequencing methods has provided equally great reductions in equipment investments, thus making the technology accessible to individual investigators and routine clinical and microbial laboratories. The challenge, however, is to extract the relevant information from the large amount of data generated by these techniques. To allow comparison with results obtained by other commonly used technologies and with historical data, it is also important to be able to relate the WGS data to typing schemes such as MLST.

We present here the publicly available MLST server (www.cbs.dtu.dk/services/MLST), which uses WGS data for identifying the STs of bacteria.

MATERIALS AND METHODS

MLST databases. MLST allele sequences and ST profile tables are stored in online databases hosted at five different sites around the world. The University of Oxford collects data from all databases and makes it easily accessible (http://pubmlst.org). In total, 66 bacterial MLST schemes are currently available. Most of them function at the species level, e.g., Escherichia coli and Staphylococcus aureus schemes, while a few function on the genus level, e.g., the Bifidobacterium and Neisseria schemes. Most schemes include 7 housekeeping genes, but schemes with as few as 5 and as many as 10 genes have also been developed. For four bacterial species, two different MLST schemes are available: Acinetobacter baumannii (2; Institut Pasteur,
Acinetobacter baumannii MLST database, December 2011 [http://www.pasteur.fr/recherche/genopole/PFB/mlst/Abaumannii.html]), Clostridium difficile (10, 17), E. coli (13, 32), and Pasteurella multocida (28; PubMLST, Pasteurella multocida multi-host MLST databases, December 2011 [http://pubmlst.org/pmultocida_multihost/]).

Data sets. (i) Assembled genomes. In August 2010, 1,212 completely sequenced and assembled bacterial genomes were collected from the NCBI Genome database (http://www.ncbi.nlm.nih.gov/sites/genome). For 336 of these genomes, MLST schemes have been developed and are available through the MLST databases (Table 1).

(ii) Sequence reads. Table 2 shows an overview of the species for which we had short sequence reads, along with the sequencing platforms available through the MLST databases (Table 1).

For 336 of these genomes, MLST schemes have been developed and are available through the MLST databases (Table 1).

implementation of MLST on completely sequenced bacteria. An automatic weekly download script was set up for all allele sequences and ST profiles from the MLST databases. Via a script written in Perl, the assembled bacterial genome was converted into a BLAST database. Using the specified MLST scheme, the genome was searched by BLAST for all MLST alleles for all genes. Statistically significant alignments between the query sequence (the MLST alleles) and sequences in the BLAST genome database are called high-scoring segment pairs (HSP) according to BLAST terminology. As the Expect threshold, we use the default value, which is 10.

The best-matching MLST allele is found by calculating the length score (LS) as $QL = HL + G$, where $QL$ is the length of the MLST allele, $HL$ is the length of the HSP, and $G$ is the number of gaps in the HSP. The allele with the lowest $LS$ and, secondly, with the highest percentage of identity (ID) is selected as the best-matching MLST allele. A perfectly matching MLST allele will have an LS of zero and 100% ID, meaning that all the nucleotides of the MLST allele match with the nucleotides in the genome across the entire length of the allele. Note that the BLAST HSP $E$ value or score cannot be used for selecting the correct allele, since a long allele with a percentage of ID below 100% can have a lower $E$ value (i.e., a higher score) than a shorter allele with 100% ID. Per definition, the shorter allele with 100% ID over the whole length is the correct allele.

RESULTS

MLST implementation. For MLST of completely sequenced bacterial genomes, short sequence reads are, in a first step, assembled to draft genomes as described in Materials and Methods. It is also possible to bypass the assembly step and to input a complete or partial preassembled genome. The minimum requirement for a partial genome is that it contain all the loci necessary for MLST. For a specific MLST scheme, the MLST alleles of each locus are alonged to the genome by using BLAST. The closest-matching MLST allele is selected, and the ST is determined based on the combination of MLST alleles.

Two different output formats are available. The short output format includes the identified ST and details about the concordance of each locus with the best-matching MLST allele in the database. Figure 1 shows an example of the short output format from the typing of a P. aeruginosa isolate. The extended output format additionally includes the nucleotide sequences of the MLST alleles identified (see Fig. S1 in the supplemental material). This format can be useful for drawing phylogenetic trees.

MLST of 336 assembled bacterial genomes. To evaluate our method, we used it for identification of the STs of 336 completely sequenced and preassembled bacterial genomes. These bacteria cover 56 MLST schemes. Table 1 shows the results with regard to the proportion of the MLST alleles in the tested genomes that were previously unseen and hence were not registered in the MLST
TABLE 1 MLST of preassembled, completely sequenced bacterial isolates

<table>
<thead>
<tr>
<th>MLST scheme</th>
<th>No. of loci in scheme</th>
<th>Avg no. of alleles per locus(^a)</th>
<th>No. of STs(^a)</th>
<th>No. of isolates(^b)</th>
<th>Proportion(^c) of:</th>
<th>New alleles</th>
<th>Unknown STs</th>
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\(^a\) Registered in the MLST database.  
\(^b\) Number of isolates with completely sequenced genomes tested for this scheme.  
\(^c\) Proportion of alleles found in the isolates, or proportion of STs found for the isolates, which were not already registered in the database.
Two MLST schemes exist for *E. coli; E. coli* scheme 1, which employs seven genes (*adk, fumC, gyrB, icd, mdh, purA, recA*) (32), and *E. coli* scheme 2, which employs eight genes (*dinB, icdA, pabB, polB, putP, trpA, trpB, uidA*) (13). When the 36 completely sequenced *E. coli* isolates were typed using the *E. coli* scheme 2, which contains 10 alleles (3.1%) were not in the database. This difference in the proportion of previously unseen alleles may reflect either the coverage of the MLST databases (that is, how large a fraction of the total number of alleles they contain) or the rates of evolution of the genes used by the two schemes. The database for *E. coli* scheme 1 contains on average 228 alleles per locus, while that for *E. coli* scheme 2 contains on average 143 alleles per locus. Accordingly, the higher number of previously unseen alleles found by using *E. coli* scheme 2 seems mostly to reflect the fact that this database is less complete than the database for scheme 1.

The three MLST schemes that resulted in the highest number of previously unseen MLST alleles were the *E. coli* schemes. The database for *E. coli* scheme 1 contains an average of 2,088 alleles per locus and as such is by far the largest database. Apparently, this does not mean that the database is in any way complete, since more than half of the alleles in the 10 *H. pylori* genomes tested are not in the database. This observation indicates that the genes selected for the *H. pylori* MLST scheme (33) are evolving faster than the genes that are generally used in the MLST schemes. This idea is in line with studies showing that in general, *H. pylori* has high rates of recombination and mutation (5, 7, 29).

Eight bacterial MLST schemes were not tested in this analysis, since we did not have access to complete genomes from these species. However, it is possible to use the MLST Web server with these species as well (*Brachyspira intermedia*, *Burkholderia cepacia* complex, *Campylobacter helveticus*, *Campylobacter insulae*ngiae, *Streptococcus oralis*, *Streptococcus equi* subsp. *zooepidemicus*, *Clostridium septicum*, and *Chlamydiales* spp.).

**From short sequence reads to MLST.** MLST implementation was then tested on short sequence reads from 387 bacterial isolates covering 10 MLST schemes and four sequencing platforms. Table 2 shows the results. We have divided the genomic MLST loci that did not perfectly match an MLST allele in the databases into major and minor mismatches. The major mismatches occur when the MLST allele from the MLST database exceeds the length of the contig, meaning that the MLST locus is only partly contained in the contig. In Fig. S1 the supplemental material, the *aro* gene represents a major mismatch in a *P. aeruginosa* genome. The minor mismatches are all other types of mismatches and are equivalent to the “new alleles” of Table 1. In Fig. S1, the *acs* gene represents a minor mismatch.
MLST Results

Sequence Type: Unknown ST*

*Please note that one or more loci do not match perfectly to any previously registered MLST allele. We recommend verifying the results by traditional methods for MLST.

SETTINGS:
Organism: Pseudomonas aeruginosa
MLST Profile: paeruginosa

Genes in MLST Profile: 7

<table>
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<tr>
<th>Locus</th>
<th>Identity</th>
<th>HSP Length / Allele Length</th>
<th>Gaps</th>
<th>Allele</th>
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<td>acs</td>
<td>99.74%</td>
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<tr>
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<td>0</td>
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For 11 of the 15 sets of isolates sequenced by the Illumina technology for paired-end or single reads, and for all of the isolates sequenced on the Roche 454 GS platform, the frequency of alleles with minor mismatches was below 2%. For the remaining four sequenced on the Roche 454 GS platform, the frequency of alleles with minor mismatches was below 2%. For the remaining four sequenced on the Roche 454 GS platform, the frequency of alleles with major mismatches was below 2%. For the remaining four sequenced on the Roche 454 GS platform, the frequency of alleles with major mismatches was below 2%. For the remaining four sequenced on the Roche 454 GS platform, the frequency of alleles with major mismatches was below 2%

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FIG 1 MLST results for a P. aeruginosa isolate in the short output format. By use of the MLST Web server, a P. aeruginosa strain that had been sequenced on the Illumina platform generating single reads was typed. For the purpose of the example, we have chosen to show the results obtained by using short sequence reads that assemble into a draft genome with a low N_{50}. Shown are the name of the loci in the MLST scheme, the percentage of nucleotides that are identical in the best-matching MLST allele in the database and the corresponding sequence in the genome (% identity), the length of the alignment between the best-matching MLST allele in the database and the corresponding sequence in the genome (also called the high-scoring segment pair [HSP]), the length of the best-matching MLST allele in the database, the number of gaps in the HSP, and the name of the best-matching MLST allele. Note that for a perfectly matching allele, the percentage of identity will be 100%, the allele length will equal the HSP length, and the number of gaps will be zero. Green indicates a perfect match, while red indicates an imperfect match.

For 11 of the 15 sets of isolates sequenced by the Illumina technology for paired-end or single reads, and for all of the isolates sequenced on the Roche 454 GS platform, the frequency of alleles with minor mismatches was below 2%. For 11 of the 15 sets of isolates sequenced by the Illumina technology for paired-end or single reads, and for all of the isolates sequenced on the Roche 454 GS platform, the frequency of alleles with minor mismatches was below 2%

FIG 2 Distribution of log N_{50} values for 387 assembled draft genomes.

For 11 of the 15 sets of isolates sequenced by the Illumina technology for paired-end or single reads, and for all of the isolates sequenced on the Roche 454 GS platform, the frequency of alleles with minor mismatches was below 2%. For 11 of the 15 sets of isolates sequenced by the Illumina technology for paired-end or single reads, and for all of the isolates sequenced on the Roche 454 GS platform, the frequency of alleles with minor mismatches was below 2%

DISCUSSION

WGS of bacterial pathogens has become an option for more scientists than formerly and even for routine laboratories due to the convergence on the general quality of the assembled draft genomes. Furthermore, the variability can be very large, as evidenced by the two E. coli isolates that were sequenced on the Life Sciences Ion Torrent PGM platform. While the isolate sequenced by Life Technologies and the University of Münster had an N_{50} value of 28,537, the isolate sequenced by BGI was assembled into a draft genome with an N_{50} of 666. As a comment on this poor N_{50} value, it should be noted that only the FASTQ files from the sequencing, not the flowgram files, were available to us.

For the assembled P. aeruginosa genomes, 13.2% of the alleles contained major mismatches. However, more than 40% of the alleles with major mismatches were found in the assembled genomes of only five isolates. The average N_{50} of these five draft genomes was as low as 503 (95% CI, 175 to 831).

Figure 2 shows the distribution of the log N_{50} values for all assembled draft genomes. Fifteen draft genomes had a log N_{50} below 3.6 (N_{50} below 4,000). The remaining draft assemblies are contained within two peaks, roughly separating the draft genomes based on single reads from those based on paired-end reads.

For a small subset of the P. aeruginosa and S. aureus isolates, and for all K. pneumoniae isolates, the ST had been determined previously by traditional methods. For 10 of the E. coli isolates, the WGS data were obtained from publicly available sources. These isolates were all from the 2011 German E. coli O104:H4 outbreak, the causative agent of which has been found to belong to ST-678 (4, 19, 23). Table 3 shows that 25 of the 29 isolates with known STs were assigned the correct ST on the basis of our method for MLST. Three of the P. aeruginosa isolates were not assigned the correct ST. Instead, they all contained major mismatches and were assigned the ST “unknown” (N_{50} values, 371, 453, and 1,154). For the E. coli isolate sequenced by BGI using the Life Sciences Ion Torrent PGM, the MLST loci likewise contained major mismatches and the ST "unknown" was assigned.

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declining costs of sequencing and the increasing number of analytic methods available. WGS may be useful in trend studies, in diagnostics, and for surveillance. Depending on the technology, WGS can be performed in a couple of hours. By combining this speed with low costs and the right tools, real-time surveillance and quick detection of outbreaks will become possible. As both the costs of technology and the run times continue to decline, WGS will become increasingly available to routine diagnostic laboratories. The challenges will thus be not to produce the sequence data but to extract the relevant information so as to allow for comparisons over time and between laboratories. Ideally, this information should also allow for comparison to historical data.

We have developed, implemented, and evaluated an MLST predictor based on WGS data. The method is publicly available at www.cbs.dtu.dk/services/MLST. The user can upload either a pre-assembled complete or partial bacterial genome or short sequence reads from one of four sequencing platforms. Currently, 70 different MLST schemes for 66 species are available.

The MLST Web server was specifically designed for ease of use, for the benefit of investigators with limited bioinformatics experience. The first step is to upload the preassembled genome or short sequence reads. In the case of short sequence reads, the sequence platform also needs to be specified. After one selects the MLST scheme to be used, the job can be submitted.

Jolley and Maiden have developed a Web-accessible database system, BIGSdb, that can also use WGS for MLST (16). This system, however, works only on UNIX/Linux systems and requires the installation of a whole range of programs and databases. The MLST Web server presented here can be used by anyone with a computer and a reasonably fast Internet connection.

Although new typing methods are expected to emerge in the wake of complete genome sequencing, e.g., single nucleotide polymorphism (SNP) typing (9, 11) and pan genome family trees (27), these methods lack standardized implementation and general acceptance in the scientific community. We therefore believe that MLST will still be considered the “gold standard” for typing for some time. In addition, for many years, knowledge of the ST will be crucial for comparison to data from isolates that were characterized before complete genome data became easily available.

The MLST server will continue to be improved, e.g., by addition of an option for the automatic detection of species, and hence the selection of the MLST scheme to be used, based on 16S rRNA typing. Furthermore, it will become possible to obtain a phylogenetic tree as output, which will enable the user to see how the ST of the query isolate relates to other STs.

Additional features for analyzing WGS data are also under development. These include the identification of antimicrobial resistance and virulence genes, as in a study described recently (3). Furthermore, we are developing methods for species identification and phylogenetic analysis based on SNP and pan-genome analysis.

**ACKNOWLEDGMENTS**

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**REFERENCES**

21. Reference deleted.
Manuscript III

Benchmarking of Methods for Genomic Taxonomy
Bencharking of Methods for Genomic Taxonomy.

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1 Center for Biological Sequence Analysis, Department of Systems Biology, Technical University of Denmark, 2800 Kongens Lyngby, Denmark
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Abstract

One of the first questions that emerge when encountering a prokaryotic organism of interest is what it is that is which species it is. The 16S rRNA gene formed the basis of the first method for sequence-based taxonomy and has had a tremendous impact on the field of microbiology. Nevertheless, the method has been found to have a number of shortcomings.

In the current study we trained and benchmarked five methods for whole genome sequence based prokaryotic species identification on a common dataset of complete genomes; 1) SpeciesFinder, which is based on the complete 16S rRNA gene, 2) Reads2Type that searches for species-specific 50-mers in either the 16S rRNA gene, the GyrB gene (for the Enterobacteriaceae family) or the ITS gene (for the Mycobacterium genus), 3) The rMLST method that samples up to 53 ribosomal genes, 4) TaxonomyFinder, which is based on species-specific functional protein domain profiles, and finally 5) KmerFinder, which examines the number of co-occurring k-mers. The performances of the methods were subsequently evaluated on three datasets of short sequence reads or draft genomes from public databases. In total, the evaluation sets constituted more than 11,000 isolates covering 159 genera and 243 species. Our results indicate that methods that only sample chromosomal, core genes have difficulties in distinguishing closely related strains, which only recently diverged. The KmerFinder method had the overall highest accuracy and identified from 93%-97% of the isolates in the evaluations sets correctly to the species level.

Importance: The 16S rRNA locus has served as the backbone of prokaryotic taxonomy for more than 30 years, but has been recognized to be less than optimal for a number of species. The current advent of whole genome sequencing provides the opportunity to surpass 16S rRNA typing by including a larger fraction of the genome. Meanwhile, the ample amounts of WGS data in public databases enable us to perform educated proposals on how to optimally use this type of data.

INTRODUCTION

Rapid identification of isolated bacterial species is essential for surveillance for human and animal health and for choosing the optimal treatment and control measures. Since the be-

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gimming of microbiology more than a century ago, this has to a large extent been based on morphology and biochemical testing. However, for more than 30 years, 16S rRNA sequence data has served as the backbone for the classification of prokaryotes (1) and tremendous amounts of 16S rRNA sequences are available in public repositories (2; 3; 4). However, due to the conserved nature of the 16S rRNA gene, the resolution is often too low to adequately resolve different species and sometimes not even adequate for genus delineation (5; 6). Furthermore, many prokaryotic genomes contain several copies of the 16S rRNA gene with substantial inter-gene variation (7; 8). It is also considered problematic that this gene represents only a tiny fraction, roughly about 0.1% or less, of the coding part of a microbial genome (9).

Second- and third generation sequencing techniques have the potential to revolutionize the classification and characterization of prokaryotes. However, so far no consensus on how to utilize the vast amount of information in Whole Genome Sequence (WGS) data has emerged. Nevertheless, a number of different methods have been proposed. Roughly, they can be divided into those that require annotation of genes in the data and those that employ the nucleotide sequences directly.

One of the first attempts to employ WGS data for taxonomic purposes was carried out in 1999 (10). At the time, 13 completely sequenced genomes of unicellular organisms were available and distance-based phylogeny was constructed on the basis of presence and absence of suspected orthologous (direct common ancestry) gene pairs. Later it was recognized that methods that take into account gene content can be greatly influenced by Horizontal Gene Transfer (HGT) and alternative methods were developed that used homologous groups (gene family content) (11) or protein domains (12).

Functional protein domains also form the basis of a recent approach developed by our group (13). Here, the protein domains are combined into functional profiles of which some are species-specific and can thus be used for inferring taxonomy.

As an extension of 16S rRNA analysis, which focuses on a single locus, Super Multilocus Sequence Typing (SuperMLST) has been proposed (14). It relies on the selection of a set of genes that are highly conserved and hence can be used with any organism. In a publication from 2012, Jolley et al. suggested that 53 genes encoding ribosomal proteins are used for bacterial classification in an approach called ribosomal MLST (rMLST) (15). Not all 53 genes were found in all bacterial genomes, but due to the relatively high number of sampled loci, this is not considered as problematic. The rMLST method forms the basis of a proposed reclassification of Neisseria species (16) and has also been used for analyzing human Campylobacter isolates (17).

It is also possible to employ the sequence data directly without pre-annotation of genes. This can, for instance, be done by looking at k-mers (substrings of k nucleotides in DNA sequence data) that are sufficiently long to avoid co-occurrence in two random genomes. As an example, there are more than 4 billion different possible 16-mers, making their co-occurrence in two unrelated bacterial genomes unlikely. The number of co-occurring k-mers in two bacterial genomes can thus be considered a measure of evolutionary relatedness, and used to construct a phylogeny. Using this approach, all regions of the genome are considered, not only core genes. Furthermore, a gene segment will score highly despite the transposition of a gene segment within the genome, since only the flanking regions will be mismatched.

In the current study we have trained five different methods for species identification on a common dataset of complete prokaryotic genomes. 1) SpeciesFinder serves as the baseline, as it is based solely upon the 16S rRNA gene. 2) Reads2Type is a variant hereof, searching for species-specific 50-mers, predominantly within the 16S rRNA gene, with the help of non-species-specific 50-mers to quickly narrow down the search. 3) rMLST, which predicts species by examining 53 ribosomal genes. 4) TaxonomyFinder, which is based on species-specific functional protein domain profiles, and finally 5) KmerFinder, which predicts species
by examining the number of overlapping 16-mers.

The public available databases contain ample amounts of WGS data from prokaryotes, enabling us to conducting a large-scale benchmark study of the proposed methods. Hence, the process of reaching a consensus on how the WGS data should optimally be used for prokaryotic taxonomy is initiated.

MATERIALS & METHODS

Dataset

Training Data

In August 2011 a total of 1,647 complete genomes originating from Bacteria (1,535) and Archaea (112) were downloaded from the National Center for Biotechnology Information (NCBI, http://www.ncbi.nlm.nih.gov/genome ). For each genome, the annotated taxonomy according to GenBank was compared to the taxonomy according to Entrez, which was retrieved using the taxonomy module of BioPerl. Discrepancies were checked and corrected manually. For each genome, it was also examined if the annotated name was in accordance to the List of Prokaryotic names with Standing in Nomenclature ( http: //www.bacterio.cict.fr/allnames.html ). When possible, names that were not in accordance were corrected to valid ones. In this way, 1,426 genomes were assigned to 847 approved genus and species names. The remaining 221 genomes, which were either only assigned to a genus, e.g., Vibrio spp., or assigned to species with informal names, e.g., Synechococcus islandicus, were left in the training data under the assumption that they will influence the different methods for species identification equally. An overview of the training data is available in Supplementary Table 1.

Evaluation Data

Three datasets were generated for the purpose of evaluating the methods. The first consisted of assembled complete of draft genomes with assigned species, which were downloaded from NCBI in September 2012 and not already part of the training data. Only genomes assigned to species that were also present in the training data were included. The set is called NCBI drafts and consists of genomes from 695 isolates covering 81 genera and 149 species. The set includes three Archaea; two Methanobrevibacter smithii and one Sulfolobus solfataricus. An overview of the data can be seen in Supplementary Table 2.

Furthermore, In January 2012, 11,768 sets of Illumina raw reads were downloaded from the NCBI Sequence Reads Archive (SRA, http://www.ncbi.nlm.nih.gov/sra ) with assigned species (18). 10,517 of them had been sequenced by the Illumina Genome Analyzer II sequencer, while the remaining 1,251 had been sequenced by the Illumina HiSeq 2000 sequencer. Reads that could not be assembled to a draft genome were removed as were reads from species that were not present in the training. The final SRA reads dataset consists of 8,798 sets of paired-end reads and 1,609 sets of single reads, 10,407 sets in total.

The short reads of the SRA reads set were de novo assembled using velvet 1.1.04 (19). For of the draft assemblies the optimal k-mer length was estimated and used as described previously (20). The resulting set of draft genomes constitutes the SRA drafts evaluation set. To measure the qualities of the draft assemblies, the N50 values were calculated (21). The draft assemblies had an average N50 of 77,018, ranging from 101 to 779,945 (see Supplementary Figure 1), an average number of scaffolds of 697, and an average size of 3,301
kilobases. The SRA reads and SRA drafts sets both cover 167 different species from 120 genera with more than 5,000 strains from the Streptococcus, Staphylococcus and Salmonella genera. There are no species from Archeae. An overview of the SRA reads and SRA drafts sets is available in Supplementary Table 3.

Methods for species identification

SpeciesFinder

SpeciesFinder predicts the prokaryotic species based on the 16S rRNA gene. A 16S database was built from the genomes of the common training data using RNAmmer (22). The species predictions were performed differently depending on the input type. If the input was short reads, the prediction was done as follows:

I. The reads were mapped against the 16S database using the Burrows-Wheeler aligner (BWA) (23).
II. The BWA output was assembled using Trinity (24) to obtain the 16S rRNA sequences.
III. The BLAST algorithm (25) was used to search the output from Trinity against the 16S database.
IV. The best BLAST hit (see below) was chosen and the species associated with the best hit was given as the final prediction.

When the input sequence was a draft or complete genome, the prediction was performed as follows:

I. The 16S rRNA gene was predicted from the input sequences using RNAmmer.
II. Using the BLAST algorithm, the predicted sequence was aligned against the 16S database.
III. The best BLAST hit (see below) was chosen and the species associated with it given as the final prediction.

The best BLAST hit was chosen by ranking the output from the BLAST alignment by a combination of coverage, percent identity, bitscore, number of mismatches, and number of gaps. The highest ranked hit was chosen for the prediction.
SpeciesFinder is available at http://cge.cbs.dtu.dk/services/SpeciesFinder/.

rMLST

The rMLST method predicts bacterial species based on 53 ribosomal genes originally defined by Jolley et al. (15). The set of genes can either be used in an approach similar to Multilocus Sequence Typing (MLST), where each locus in the query genome is considered identical or non-identical to alleles of the corresponding locus in the reference database, and an allelic profile based on random numbers assigned to each of the alleles in the database is generated accordingly. Since the strains that we compare are more diverse than the ones compared in MLST, it is likely that many loci would have no identical matches in the database, making a simple cluster analysis based on allelic profiles problematic. To improve the resolution of the method, in our implementation of rMLST, the nucleotide sequence of each locus is aligned to the alleles in the reference database and a measure of the similarity of the locus and the
best matching allele is used subsequently, as described below.

Briefly, for each of the genomes in the training data, the 53 ribosomal genes were provided by Keith Jolley, Department of Zoology, University of Oxford, UK. In this way, for each genome, a gene collection of up to 53 ribosomal genes was assigned. To predict the species of a query genome, the query genome was first aligned to each gene collection using BLAT (26). Only hits with at least 95% identity and 95% coverage were considered as a potential match. If there were several potential matches, the best match was selected based on the best cumulative rank of coverage, percent identity, bitscore, number of mismatches, and number of gaps in the alignments. The final prediction was given as the organism with the highest number of best hits across all genes. Our implementation of rMLST performs predictions for draft or complete genomes, but not short reads.

TaxonomyFinder

The TaxonomyFinder method is based on taxonomy group-specific protein profiles (ref). It performs predictions for draft or complete genomes, but not for short reads. The common training data was used to create the taxonomy-specific profile database. Briefly, for each genome functional profiles were assigned based on three collections of Hidden Markov Models (HMMs) databases: PfamA (27), TIGRFAM (28), and Superfamily (29). Genes that did not match any entry in the HMM databases were clustered using CD-HIT (30). Further, genomes were grouped according to the taxonomy level, either phylum or species, and profiles that were specific to each taxonomic group were extracted. Profiles were considered specific to a taxonomic group, if they were conserved in most of the genomes within a phylum/species group and absent in all genomes outside of the group. The workflow of the TaxonomyFinder method is a four-step process, which includes:

I. Open-reading frame prediction using Prodigal (31).
II. Construction of unctional profiles from protein-coding sequences.
III. Assignment of unctional profiles.
IV. Functional profile comparison to the taxonomy-specific profile database. The number of architectures, matched to each of the taxonomy groups, is recorded, and the fraction of taxa-specific genes (score) is calculated. The best-matching taxonomy group is selected based on a consensus of the best score and highest number of matched architectures.

TaxonomyFinder is available at http://cge.cbs.dtu.dk/services/TaxonomyFinder/.

KmerFinder

The KmerFinder method predicts prokaryotic species based on the number of overlapping (co-occurring) k-mers, i.e. 16-mers between the query genome and genomes in a reference database. Initially, all genomes in the common training data were split into overlapping 16-mers with step-size one, meaning that if the first 16-mer is initiated at position N and ends at position N+15, the next 16-mer is initiated at position N+1 and ends at position N+16, and so on. To reduce the size of the final 16-mer database only 16-mers with the prefix ATGAC were kept. These 16-mers were stored in a hash table with links to the original genomes. When performing the prediction, the species of the query genome is predicted to be identical to the species of the genome in the training data with which
it has the highest number of 16-mers in common regardless of position. The input for KmerFinder can be draft or complete genomes as well as short reads. KmerFinder is available at http://www.cbs.dtu.dk/services/KmerFinder/.

Reads2Type

Reads2Type identified the prokaryotic species based on a database of 50-mer probes generated from chosen marker genes (Saputra D., Rasmussen S., Larsen M.V., Haddad N., Aarestrup F.M., Lund O., and Sicheritz-Pontén T., submitted for publication). The version of Reads2Type evaluated in this study requires short reads as input. For bacterial species not belonging to the Enterobacteriaceae family or the Mycobacterium genus, the 50-mer database relies on the 16S rRNA locus, while for Enterobacteriaceae, the gyrB locus is used, and for Mycobacterium the ITS locus. Briefly, the following steps were applied for building the 50-mer probe database:

I 16S rRNA sequences of the complete bacterial genomes of the common training set were predicted using RNommer (22).

II For species belonging to the Enterobacteriaceae family or the Mycobacterium genus, gyrB sequences and ITS sequences, respectively, were downloaded from NCBI.

III The above sequences were pooled and all possible 50-bp fragments were generated from that pool.

IV 16S rRNA probes unique for Enterobacteriaceae and Mycobacteria were removed from the pool of 50-mers.

V All 50-mer duplicates associated to the conserved regions of different strains but the same species were removed.

VI To further reduce the size of the final 50-mers database, 25 consecutive 50-mers previously fragmented from one 50 bp stretch of 16s rRNA belonging to the same list of organism were removed.

The resulting 50-mers probe database consists of a number of sequences found uniquely in one species, as well as other sequences shared between several species. Subsequently, each read was compressed into a suffix tree, which is a data structure for fast string matching. The compressed short reads were aligned to the 50-mer probe database using a "narrow-down approach" strategy, i.e., when a compressed read matched a probe belonging to a group of species, a much smaller probe database excluding other species was created on the fly, causing the read progress to be faster and the species to be identified much faster.

The Reads2Type method is available as a web server (http://cge.cbs.dtu.dk/services/Reads2Type/) and as a console. The web-based Reads2Type is unique in not requiring the short read file to be uploaded to the server. Instead, the 4.6 MB 50-mers probe database is automatically transferred into the client computers memory before initiating the species identification. All computations needed for the species identification is fully performed on the clients computer, minimizing the data transfer and avoiding the network bottleneck on the server.
Testing the speed

The speed of the methods was evaluated on non-published internal data from up to 450 strains covering eight species (Enterococcus faecalis, Enterococcus faecium, Eschericia coli, Escherichia fergusonii, Klebsiella pneumoniae, Salmonella enterica, Staphylococcus aureus, and Vibrio cholera) that had been sequenced by the Illumina sequencing method. Draft genomes were de novo assembled as described above for the SRA\textsubscript{drafts} set. The speed was tested on a Cluster with x86_64 architecture, 128 nodes, 4 tasks per node, 30 or 7G per node.

RESULTS

Performances on NCBI draft genomes

The SpeciesFinder, rMLST, TaxonomyFinder, and KmerFinder methods are able to perform species predictions on draft or completed prokaryotic genomes. Their performances were evaluated on the NCBI \textsubscript{drafts} set of 695 draft genomes covering 149 species. Supplementary File 1 lists all predictions, while Figure 1A summarizes the results. Overall, SpeciesFinder, which is based on the 16S rRNA gene, had the poorest performance, only correctly identifying 76% of the isolates down to species level. KmerFinder, which is based on co-occurring 16-mers, had the highest performance and correctly identified 93% of the isolates. For only three isolates (0.43%), KmerFinder did not even get the genus correct. These three isolates were two Escherichia coli predicted as Shigella sonnei and one Providencia alcalifaciens predicted as Yersinia pestis.

The NCBI \textsubscript{drafts} set contains three Archaeal isolates; two M. smithii and one S. solfataricus. SpeciesFinder, TaxonomyFinder, and KmerFinder predicted the species of all three isolates correctly, while rMLST, which was only intended for characterization of Bacteria (15) predicted the M. smithii correctly, but was unable to make a prediction for the S. solfataricus.

The overlap in predictions of the four methods was examined and illustrated in Figure 2A. All four methods correctly identified 428 out of 695 isolates (62%), and all methods misidentified the same six isolates. Table 1 lists these six isolates. Since all four methods agreed on these predictions, the isolates are likely to be wrongly annotated. Alternatively, the annotations of the isolates in the training data that the predictions were based on are incorrect.

As seen in Figure 2A, isolate predictions agreed upon by several methods are more accurate that predictions unique to a particular method. However, the KmerFinder method made unique predictions for 36 isolates of which 20 were in concordance with the annotation.

Predictions for the most common species in the dataset were examined more closely and illustrated in Figure 3 and in Supplementary Figure 2-5. In general, the wrong predictions by SpeciesFinder (that is, the ones that were in disagreement with the NCBI annotation) were typically scattered, often consisting of a few wrong predictions of each type. The rMLST method was, on the other hand, more consistent in its incorrect predictions. As an example, the rMLST method wrongly annotated all 14 Bacillus anthracis isolates as Bacillus thuringiensis, all 8 Brucella abortus as Brucella suis, and all 6 Burkholderia mallei as Burkholderia pseudomallei. In general, all four methods had difficulties identifying species within the Bacillus genus, such as isolates annotated as B. thuringiensis, but predicted to be Bacillus cereus or vice versa. Another mistake common to all methods was Streptococcus mitis being predicted as Streptococcus oralis or Streptococcus pneumoniae. Also, none of
Table 1: Isolates of the NCBI drafts set for which all four methods predict the species to be different from what it is annotated as.

<table>
<thead>
<tr>
<th>RefSeqID</th>
<th>Strain name</th>
<th>Annotated species</th>
<th>Predicted species</th>
</tr>
</thead>
<tbody>
<tr>
<td>NZ_ACLX00000000</td>
<td>AH621 uid55161</td>
<td>Bacillus cereus</td>
<td>Bacillus weihenstephanensis</td>
</tr>
<tr>
<td>NZ_ACMD00000000</td>
<td>BDRD ST196 uid55169</td>
<td>Bacillus cereus</td>
<td>Bacillus weihenstephanensis</td>
</tr>
<tr>
<td>NZ_ABDQ00000000</td>
<td>C Eklund uid54841</td>
<td>Clostridium botulinum</td>
<td>Clostridium novyi</td>
</tr>
<tr>
<td>NZ_ABXZ00000000</td>
<td>FTG uid55313</td>
<td>Francisella novicida</td>
<td>Francisella tularensis</td>
</tr>
<tr>
<td>NZ_AHIE00000000</td>
<td>DC283 uid86627</td>
<td>Pantoea stewartii</td>
<td>Pantoea ananatis</td>
</tr>
<tr>
<td>NZ_AEPO00000000</td>
<td>ATCC 49296 uid61461</td>
<td>Streptococcus sanguinis</td>
<td>Streptococcus oralis</td>
</tr>
</tbody>
</table>
the methods were able to correctly identify all annotated E. coli isolates, but identified at least some of them as Shigella spp. SpeciesFinder and TaxonomyFinder both had problems identifying the Borrelia burgorferi isolates, while SpeciesFinder and rMLST had problems distinguishing Yersinia pestis from Yersinia pseudotuberculosis. SpeciesFinder was the only method that had difficulties identifying Mycobacterium tuberculosis isolates, often predicting them to be Mycobacterium bovis.

Performances on SRA draft genomes

The SpeciesFinder, rMLST, TaxonomyFinder, and KmerFinder methods were next evaluated on the SRA drafts set of 10,407 draft genomes covering 167 species. The performances on the draft genomes, for which the methods were able to make a prediction, are depicted in Figure 1B, while the overlap in predictions is illustrated in Figure 2B. Again, SpeciesFinder had the lowest performance with only 84% correct predictions. The rMLST, TaxonomyFinder, and KmerFinder methods had almost equal performances of 94%, 95%, and 95%, respectively. There was, however, a difference in the percentage of draft genomes for which each of the methods failed to make any prediction. SpeciesFinder and KmerFinder were the most robust methods, failing to make predictions for only 0.2% and 0.4% of the draft genomes, respectively. TaxonomyFinder was not able to make a prediction for 1.8% of the draft genomes, and rMLST not for 3.5%. That rMLST was the least robust method was at least partly due to our implementation of the method, where only hits with at least 95% identity and
Figure 2: Overlap in predictions by the five methods for species identification. Numbers written in regular font indicate the number of isolates for which the predicted species corresponds to the annotated species. Numbers written in italics indicate the number of isolates for which the predicted and annotated species differ. A: The 16S, rMLST, KmerFinder and TaxonomyFinder methods evaluated on the NCBI drafts set. B: The 16S, rMLST, and KmerFinder methods evaluated on the SRA drafts set. C: The 16S, KmerFinder, and Reads2Type methods evaluated on the SRA reads set.

95% coverage were considered a potential match. On the other hand, the N50 values for the draft genomes that SpeciesFinder and KmerFinder could not make a prediction for, were approximately half the size of the corresponding values for rMLST and TaxonomyFinder (data not shown), meaning that the quality of the draft genomes had to be higher for rMLST and TaxonomyFinder to be able to make a prediction. This is in accordance with these methods relying on the presence of many complete genes in the draft genomes.

Predictions for the most common species in the dataset are shown in Figure 4 and in Supplementary Figure 6-9. As seen previously when evaluating on the NCBI drafts set, the rMLST method was more consistent in its predictions for a given species than the other methods. For instance, rMLST predicted all 15 Mycobacterium bovis isolates to be M. tuberculosis. As also seen when evaluating on the NCBI drafts set, it is evident that all methods had difficulties distinguishing E. coli from species within the Shigella genus. Furthermore, species within the Brucella genus were often wrongly identified. In particular, it was only TaxonomyFinder that was able to correctly identify most Brucella abortus isolates. Some of the common problems that were obvious when evaluating on the NCBI drafts set, were not obvious when evaluating on the SRA drafts set, since the problematic species were too scarcely represented here. For instance, there are only five species from the Bacillus genus and only one S. mitis in SRA drafts. The difference in species distribution between the NCBI drafts and SRA drafts set.
Figure 3: Predictions for the most common species of the NCBI drafts set. For each method, the results for a given species is only shown if the method made a prediction for five or more isolates annotated as this species (e.g., if there are five isolates annotated as species A in the dataset, but the method was not able to make a prediction for one of the isolates, the species is not shown), or two or more isolates are predicted as this species (e.g., there are no isolates annotated as species B in the dataset, but two isolates annotated as species C are predicted to be species B, then species B is shown).  

A: Predictions by SpeciesFinder.  
B: Predictions by rMLST.  
C: Predictions by TaxonomyFinder.  
D: Predictions by KmerFinder.
also explain why SpeciesFinder, TaxonomyFinder and rMLST all have increased performance on the SRA \textit{drafts} set: While more than half of the isolates in the SRA \textit{drafts} set belong to the Salmonella, Staphylococcus or Streptococcus genera, which none of the methods have particular problems identifying, these genera constitute less than 20\% of NCBI \textit{drafts}. Conversely, the NCBI \textit{drafts} set contains a high proportion of the problematic species \textit{E. coli} (8.8\%) and the genus \textit{Bacillus} (10\%). The corresponding proportions for SRA \textit{drafts} are 3.5\% \textit{E. coli} and 0.05\% isolates of the \textit{Bacillus} genus. Furthermore, the NCBI \textit{drafts} set is proportionally more diverse consisting of 149 species, while the almost 15 times larger SRA \textit{drafts} set consists of only 168 different species.

Performances on short reads from SRA

Only three of the methods were able to perform species predictions directly on short reads, without first assembling the reads. These methods were SpeciesFinder, KmerFinder, and Reads2Type. Their performances on the SRA \textit{reads} set of 10,407 sets of short reads representing 168 species are shown in Figure 1C.

Again, the SpeciesFinder method had the poorest performance with 86\% of the isolates being correctly predicted. Reads2Type performed a bit better (87\%), while KmerFinder achieved 97\% correct.

Figure 2C illustrates the overlap in predictions between the three methods, while predictions for the most common species are shown in Supplementary Figure 10. In general, the results correspond to those observed for the SRA\textit{drafts} set.

Speed

The speed of the methods was evaluated on a subset of draft genomes and short reads as described in the Material and Methods. Since the actual speed experienced by the user will depend on a number of factors, for instance, the network bandwidth capacity of the client computer and the number of jobs queued at the server, the relative speed of the different methods in comparison to each other is more relevant than the absolute speed.

<table>
<thead>
<tr>
<th>Method</th>
<th>Speed on draft genomes</th>
<th>Speed on short reads</th>
</tr>
</thead>
<tbody>
<tr>
<td>SpeciesFinder</td>
<td>00:13</td>
<td>3:14</td>
</tr>
<tr>
<td>Reads2Type</td>
<td>NA</td>
<td>1:20</td>
</tr>
<tr>
<td>rMLST</td>
<td>00:45</td>
<td>NA</td>
</tr>
<tr>
<td>TaxonomyFinder</td>
<td>11:33</td>
<td>NA</td>
</tr>
<tr>
<td>KmerFinder</td>
<td>00:09</td>
<td>03:10</td>
</tr>
</tbody>
</table>

**DISCUSSION**

In the present study we trained five different methods for prokaryotic species identification on a common dataset and evaluated their performances on three datasets of draft genomes
Figure 4: Predictions for the most common species in the SRA drafts dataset. For each method, the results for a given species is only shown if the method made a prediction for ten or more isolates annotated as this species, or two or more isolates are predicted as this species. A: Predictions by SpeciesFinder. B: Predictions by rMLST. C: Predictions by TaxonomyFinder. D: Predictions by KmerFinder.
or short sequence reads.

The SpeciesFinder method is based on the 16S rRNA gene, which has served as the backbone of prokaryotic systematics since 1977 (1). Accordingly, sequencing of the 16S rRNA gene is a well-established method for identification of prokaryotes and has in all likelihood been used for annotating some of the isolates in the training and evaluation sets. In the light of this potential advantage of the SpeciesFinder method over the other methods, it is noteworthy that it had the lowest performance on all evaluation sets. Previous studies have, however, also pointed to the many limitations of the 16S rRNA gene for taxonomic purposes. Examples, which are also observed in this study, include its inadequacy for the delineation of species within the Borrelia burgdorferi sensu lato complex and the Mycobacterium tuberculosis complex (32). Similarly, in silico studies of the applicability of the 16S rRNA gene for the identification of medically important bacteria led to the authors concluding that although the method is useful for identification to the genus level, it is only able to identify 62% of anaerobic bacteria (33) and less than 30% of aerobic bacteria (34) confidently to the species level.

The performance of SpeciesFinder was surpassed only marginally by Reads2Type. This is not surprising, since the two methods are conceptionally very similar: SpeciesFinder utilizes the entire 16S rRNA gene of approximately 1,540 nucleotides, while for most species, Reads2Type looks for species-specific 50-mers in the same gene. In terms of its future usability, Reads2Type has, however, one advantage over the other methods: Like most of the other methods it is available as a web-server, but uniquely it does not require the read data to be uploaded to the server. Instead, a small 50-mer database is transferred to the user’s computer and all computations performed there. As a result, bottleneck problems on the server are avoided and the data transfer is minimized, which may be particularly advantageous for users with limited Internet access.

While SpeciesFinder and Reads2Type only sample one locus, the rMLST method samples up to 53 loci – all ribosomal genes located to the chromosome of the bacteria. Evaluating on the dataset of SRA draft genomes, rMLST, TaxonomyFinder, and KmerFinder performed equally well. However, on the more diverse and difficult set of NCBI draft genomes, the rMLST method performed only marginally better than SpeciesFinder and significantly worse than TaxonomyFinder and KmerFinder. In particular, the rMLST method consistently made incorrect identifications of a number of closely related species, e.g., Y. pestis versus Y. pseudotuberculosis (35) and M. tuberculosis versus M. bovis (36). Also, rMLST consistently predicted the human pathogen B. anthracis to be B. thuringiensis. The latter is used extensively as a biological pesticide and is generally not considered harmful for humans. B. anthracis and B. thuringiensis are both members of the B. cereus group and genetically very similar, with most of the disease and host specificity being attributable to their content of plasmids (37; 38). It has even been suggested that all members of the B. cereus group should be considered to be B. cereus and only subsequently be differentiated by their plasmids (39). Hence, in concordance with rMLST sampling only chromosomal, core genes, it is not surprising that the method fails to distinguish these isolates. A similar example is given by the rMLST method identifying all E. coli isolates as Shigella sonnei. Although Shigella spp. isolates have been rewarded their own genus, its separation from Escherichia spp. is mainly historical (40; 41; 42). To be sure, some of the mistakes commonly made by rMLST as well as the other methods highlight taxonomic taxa that are intrinsically difficult to distinguish due to a sub-optimal initial classification: Although Shigella spp. has for several years been considered a sub-strain of E. coli, the practical implications of renaming it is considered insurmountable.

The TaxonomyFinder method was the second most accurate method on the set of NCBI draft genomes and performed in the top for the SRA drafts set. In contrary to the other methods it does not work directly on the nucleotide sequence of the isolates, but rather on
the proteome, utilizing functional protein domain profiles for the species prediction. It was
the slowest of the tested methods, but in return for the extra time, the user is rewarded with
an annotated genome.

The KmerFinder method performs its predictions on the basis of co-occurring k-mers,
regardless of their location in the chromosome. It had the overall highest accuracy, works
on complete or draft genomes as well as short reads, was found to be very robust as well as
fast. Furthermore, the KmerFinder method holds promise for future improvements, as the
implementation used for this study was very simple: Only the raw number of co-occurring
k-mers between the query and reference genome was considered, although a parallel analysis
indicates that the performance could be improved even further if more sophisticated measures
were used, also taking into account the total number of k-mers in the query and reference
genome.

It has previously been noted that some of the isolates present in public databases, and
hence used in this study, are wrongly annotated (16; 43; 44). Based on the current study, it
is likely that at least the six isolates from the NCBI drafts set that all methods identified as
something different than the annotated species, are wrongly annotated. In agreement with
this, one of the isolates has indeed been re-annotated, since we initially downloaded the data.
Of the remaining five isolates, two B. cereus isolates were found to be most closely related
to the B. weihenstephanensis strain KBAB4 of the common training set. This strain is the
single representative of the species in the public database and not the type strain. Hence
there is no guarantee that the sequenced strain represents the named taxon (45). The same
is the case for the C. botulinum strain C Eklund, which is predicted to be a Clostridium
novyi based on its close resemblance to C. novyi strain NT of the training set. Clostridium
novyi strain NT is the only representative of this species in the database and not the type
strain.

While some taxonomists consider the goal of bacterial taxonomy to mirror the order of
nature and describe the evolutionary order back to the origin of life (5; 46), a more pragmatic
and applied view is likely to be advantageous for epidemiological purposes, where most out-
breaks last less than six months. The number of prokaryotic genomes in public databases is
currently sufficiently high to substitute theoretical views of which loci to sample for optimal
species identification by actual testing how different approaches perform. One locus (the
16S rRNA gene) was initially used for sequenced-based examination of relationships between
bacteria, and when the approach was found to have limitations, more loci were added in
MLST and MLSA (47; 48). The addition of still more loci has been suggested for improving
MLSA even further (32; 15). This study suggests that an optimal approach should not be
limited to a finite number of genes, but rather look at the entire genome.

CONCLUSION

The 16S rRNA gene has served prokaryotic taxonomy well for more than 30 years, but the
emergence of second- and third generation sequencing technologies enables the use of WGS
data with the potential of higher resolution and more phylogenetically accurate classifica-
tions. Methods that sample the entire genome, not just core genes located to the chromosome,
seems particularly well suited for taking up the baton.
ACKNOWLEDGEMENTS

This work was supported by the Center for Genomic Epidemiology at the Technical University of Denmark and funded by grant 09-067103/DSF from the Danish Council for Strategic Research.

We are grateful to John Damm Sørensen for excellent technical assistance. We are grateful to Keith Jolley, Department of Zoology, University of Oxford, UK for providing us with the rMLST genes for the genomes in the training data.
References


BACTERIAL ANTIBIOTIC RESISTANCE

Antibiotics are biochemical agents that inhibit the growth or kill bacteria. The possible existence of antimicrobial drugs was first proposed in 1877 by Louis Pasteur and Robert Koch. In 1895, Vincenzo Tiberio, physician of the University of Naples discovered that a mold (Penicillium) had an antibacterial action, which was followed in 1923 by the discovery of Penicillin, by Alexander Fleming. The first commercially available antibiotic (prontosil) was discovered by a team of researchers led by Gerhard Domagk in 1932 at the Bayer Laboratories in Germany. This event marked the start of the antibiotic era, with a period rich with discoveries of many synthetic and natural antimicrobial drugs with its peak around 70s and a dramatic decrease continuing in present days. When antimicrobial drugs were discovered many scientists and clinicians thought that all infections could be cured, but they did not consider the ability of bacteria to quickly evolve and become resistant to antimicrobial drugs.

Nowadays AMR is considered one of the biggest health challenges of 21th century, with the return of diseases like gonorrhoea (from Neisseria gonorrhoeae), pneumonia (from Klebsiella pneumoniae) and meningitis (from Neisseria meningitidis) becoming a threat again mainly because the bacteria causing it are becoming resistant to most of the antimicrobial drugs available in the market. Among the causes behind the increase of antimicrobial resistance [74] there is a misuse of antibiotics from people [48] (Figure 4.1), due also to the relatively easy access to these drugs and inaccurate prescriptions from medics, and also the, sometimes poorly controlled, use of antibiotics in agriculture and livestock’s food [45] (Figure 5). Studying bacterial antimicrobial resistance is very important in order to understand the mechanisms behind the resistance of AMR strains and find different treatments for the diseases caused by these bacteria. In the scenario of infections causes by novel or mutated strains, to quickly understand what antibiotic the bacteria is resistant to could help medics in choosing the proper drug to cure the infected patient, increasing the chances of saving the patient’s life and, at the same time, decreasing the possibility of potential outbreaks to spread. Assessing bacterial antibiotic resistance is still expensive and time consuming, and in the manuscript accompanying this chapter [76], we propose ResFinder, a free to use web-based tool (http://cge.cbs.dtu.dk/services/ResFinder/) for the fast identification of acquired antimicrobial resistant genes from WGS data.

ResFinder is at present the most used service among those offered by CGE, with about 1000 (and growing) jobs served every month with users from more than 60 countries. The web-service is proving to be very useful not only for researchers in developed countries with high-occurrence of AMR-related infections, but also for scientists and clinicians in developing countries,
Figure 4.1: the use of antibiotics for curing diseases in which bacteria are not involved is one of the causes of the increase of microbial resistance in bacteria [59, 60]

where the costs of traditional antibiotic resistance assessment are a limiting factor in this research.
Manuscript IV

Identification of acquired antimicrobial resistance genes
Identification of acquired antimicrobial resistance genes

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Objectives: Identification of antimicrobial resistance genes is important for understanding the underlying mechanisms and the epidemiology of antimicrobial resistance. As the costs of whole-genome sequencing (WGS) continue to decline, it becomes increasingly available in routine diagnostic laboratories and is anticipated to substitute traditional methods for resistance gene identification. Thus, the current challenge is to extract the relevant information from the large amount of generated data.

Methods: We developed a web-based method, ResFinder that uses BLAST for identification of acquired antimicrobial resistance genes in whole-genome data. As input, the method can use both pre-assembled, complete or partial genomes, and short sequence reads from different sequencing platforms. The method was evaluated on 1862 GenBank files containing 1411 different resistance genes, as well as on 23 de-novo-sequenced isolates.

Results: When testing the 1862 GenBank files, the method identified the resistance genes with an ID = 100% (100% identity) to the genes in ResFinder. Agreement between in silico predictions and phenotypic testing was found when the method was further tested on 23 isolates of five different bacterial species, with available phenotypes. Furthermore, ResFinder was evaluated on WGS chromosomes and plasmids of 30 isolates. Several of these isolates were annotated to have antimicrobial resistance, and in all cases, annotations were compatible with the ResFinder results.

Conclusions: A web server providing a convenient way of identifying acquired antimicrobial resistance genes in completely sequenced isolates was created. ResFinder can be accessed at www.genomicepidemiology.org. ResFinder will continuously be updated as new resistance genes are identified.

Keywords: antibiotic resistance, genotype, ResFinder, resistance gene identification

Introduction

The introduction of antimicrobial agents for treatment of infectious diseases is one of the most important achievements of the 20th century. However, soon after their introduction, isolates with acquired resistance emerged and this pattern has followed the introduction of each new antimicrobial agent.

A large number of different genes can be responsible for antimicrobial resistance. Identification of these genes is important to understand resistance epidemiology, for verification of non-susceptible phenotypes and for identification of resistant strains, when genes are weakly expressed in vitro. Detection of resistance genes has typically been performed using PCR1 or microarrays.2 However, in several cases, it is necessary to perform supplementary sequencing of the amplified PCR products.3 As a result, it is expensive and time-consuming to perform a complete identification of resistance genes present in a strain collection.

The cost of DNA sequencing has steadily gone down, by roughly 10-fold every five years. As a consequence, DNA sequencing is becoming increasingly accessible for routine use and was recently utilized for complete characterization of antimicrobial resistance and virulence gene content during the safety evaluation of 28 strains intended for use in human nutrition.4 The challenge is, however, to extract the relevant information from the large amount of data that is generated by these techniques.

The Center for Genomic Epidemiology (www.genomicepidemiology.org) aims at providing the bioinformatic and scientific foundation for processing and handling whole-genome sequencing (WGS) information in a standardized way useful for outbreak investigation, source tracking, diagnostics and epidemiological surveillance. The services are publically available through web servers specifically designed to be user-friendly—and also for investigators with limited bioinformatics experience.
We here present ResFinder, a web server that uses WGS data for identifying acquired antimicrobial resistance genes in bacteria.

Methods

Databases
Data on acquired resistance genes was collected from databases (http://faculty.washington.edu/marilyr/, http://arb.cbcb.umd.edu/ and http://www.ashey.org/Studies/) and published papers including reviews. All sequences were collected from the NCBI nucleotide database (http://www.ncbi.nlm.nih.gov/nucleotide) and used to build the ResFinder database. To our knowledge, we have created the largest collection of acquired antimicrobial resistance genes (see Table S1, available as Supplementary data at JAC Online).

Identifying resistance genes in completely sequenced bacteria
Draft assembly of short sequence reads was done as previously described. All genes from the ResFinder database were BLASTed against the assembled genome, and the best-matching genes were given as output. For a gene to be reported, it has to cover at least 2/5 of the length of the resistance gene in the database. The best-matching genes were identified as previously. It is possible to select a % identity (ID) threshold (the percentage of nucleotides that are identical between the best-matching resistance gene in the database and the corresponding sequence in the genome). The default ID is 100%.

Evaluation of method
Verification of the databases was made by testing ResFinder with the 1862 GenBank files from which the genes were collected, to verify that the method would find all genes with ID = 100%.

Short sequence reads from 23 isolates of five different species, Escherichia coli, Klebsiella pneumoniae, Salmonella enterica, Staphylococcus aureus and Vibrio cholerae, were also submitted to ResFinder. All 23 isolates had been sequenced on the Illumina platform using paired-end reads. A ResFinder threshold of ID = 98.00% was selected, as previous tests of ResFinder had shown that a threshold lower than this gives too much noise. Phenotypic antimicrobial susceptibility testing was determined as MIC determinations, which is possible to search for genes with specified similarity from 80% – 100% identity, and the best-matching genes are given as output. An example of the output format is shown and explained at www.cbs.dtu.dk/services/ResFinder/output.php.

Evaluation of method
In all cases, ResFinder identified the acquired resistance genes in the 1862 GenBank files from which the databases were created, with an ID = 100%.

Table 1 shows antimicrobial genes found by ResFinder, the predicted resistance profile and the phenotypic antimicrobial susceptibility test results for five bacterial isolates covering five different species. The exceptions were two S. aureus isolates that contained the mecA gene but were phenotypically susceptible to penicillins, and two S. aureus isolates, one resistant to spectinomycin and the other to tiamulin, neither of which was found to contain genes matching these phenotypes. The catB3 gene was found in all four K. pneumoniae isolates with an ID = 100%, but not in full length, consistent with all four testing phenotypically susceptible to chloramphenicol. One V. cholerae isolate contained part of floR and tested phenotypically susceptible to florfenicol.

Acquired antimicrobial resistance genes were found in 10 of the 30 strains from the NCBI genomes database (Table 2). For all except two isolates this coincided with the ResFinder results. K. pneumoniae KCTC 2242 was annotated to contain blafem, whereas ResFinder detected blafem. Nocardia farcinica IFM 10152 was annotated to contain a β-lactam gene as well as aph(2″), aph(3′) and aph(6), but ResFinder detected only the blafem-1 gene. These genes were further examined with BLAST (http://blast.ncbi.nlm.nih.gov/Blast.cgi), which demonstrated that the genes detected by ResFinder were correct.

Discussion
Since their original development by Alexander Fleming, phenotypic disc diffusion and MIC determinations have been the gold standard for antimicrobial susceptibility testing. These methods have the great advantage of determining the ‘true’ in vitro relationship between the antimicrobial agent and the strain tested, and will detect any new emerging resistance mechanisms.

Genotypic testing of suspected resistant isolates is often performed to verify phenotypic observations and for epidemiological purposes. The most widely used approach has been to perform PCR to detect the presence of selected genes. In many cases only a single or a few genes mediating resistance are tested, and such studies will often miss the simultaneous presence of multiple genes encoding the same resistance.

WGS has the great benefit that it potentially provides complete information, and thus new experiments do not have to be performed to search for the presence of novel genes—the analysis can simply be rerun. One major obstacle is the lack of available bioinformatics tools allowing simple and standardized analysis of the large amounts of data generated by WGS.

We have developed, implemented and evaluated ResFinder, a method to detect the presence of 1862 different resistance genes from 12 different antimicrobial classes in WGS data (www.genomicepidemiology.org). The current version only
covers horizontally acquired resistance genes and not resistance mediated by mutations, e.g. in housekeeping genes. ResFinder can also be used to ignore known acquired resistance genes in a search for new resistance genes.

ResFinder successfully identified all the genes from which the database was built, and correctly identified all genes present in 30 isolates of whole-genome data collected from the NCBI genomes database (http://www.ncbi.nlm.nih.gov/genome). Furthermore, phenotypic antimicrobial susceptibility tests of 23 isolates from five different species were compared with the results from ResFinder. With a few exceptions, complete agreement between predicted and observed phenotypes was found. All the *V. cholerae* isolates contained the catB9 gene, which has previously been shown to be phenotypically silent in its native position,\(^e\) consistent with all isolates testing phenotypically susceptible. The five *S. aureus* isolates examined in this study were from a collection of methicillin-resistant *S. aureus* (MRSA).\(^f\) Phenotypic detection of mecA-harbouring isolates can be difficult, indicating the superiority of WGS compared with phenotypic testing. Two of the *S. aureus* isolates, 9B and PR11_08, showed phenotypic resistance to spectinomycin and tiamulin, respectively, but without containing any matching resistance genes. Interestingly, we found two extended-spectrum β-lactamase (ESBL)-related genes (bla\(^\text{CTX-M-15}\) and bla\(^\text{SHV-28}\)) in

<table>
<thead>
<tr>
<th>Species</th>
<th>Isolate</th>
<th>ResFinder profile</th>
<th>Predicted phenotype</th>
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</tr>
</thead>
<tbody>
<tr>
<td><em>E. coli</em></td>
<td>Ødemsyge-186</td>
<td>tet(A)</td>
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<td>TET</td>
</tr>
<tr>
<td><em>K. pneumoniae</em></td>
<td>Kleb-6-1-264y</td>
<td>aac(3)-llb(^a), strA, strB, bla(^\text{TEM-1}), bla(^\text{CTX-M-15}), bla(^\text{OXA-30}), aac((6'))Ib-cr</td>
<td>GEN, STR</td>
<td>GEN, STR</td>
</tr>
<tr>
<td><em>S. enterica</em></td>
<td>Styph-0210H31581</td>
<td>aac((6'))-Iaa, aadA2, bla(^\text{OXA-2}), floR(^a), sul1(^b), tet(G)</td>
<td>SPT, STR, AMP</td>
<td>SPT, STR, AMP</td>
</tr>
<tr>
<td><em>S. aureus</em></td>
<td>2007-70-91-4</td>
<td>aac(3)-Ik(^a), mecA, blaZ, tet(K), tet(38)(^a), tet(M)(^a), dfrG, fusA(^a)</td>
<td>FOX, PEN</td>
<td>FOX, PEN</td>
</tr>
<tr>
<td><em>V. cholerae</em></td>
<td>Vchole-002</td>
<td>strA, strB, catB9, sul2, dfrA1, dfrA31</td>
<td>STR, CHL(^e), SMX</td>
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**Table 1.** ResFinder results for isolates of five different species compared with antimicrobial susceptibility data

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</tr>
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AMC, amoxicillin/clavulanate (2:1); AMP, ampicillin; CHL, chloramphenicol; CST, colistin; CTX, cefotaxime; FOX, cefoxitin; FFN, florfenicol; FLS, fusidic acid; GEN, gentamicin; PEN, penicillin; SMX, sulfamethoxazole; SPT, spectinomycin; STR, streptomycin; TET, tetracycline; TMP, trimethoprim; XNL, ceftiofur.

\(^a\)The gene is found with an ID<100%.
\(^b\)The found gene is shorter than the resistance gene.
\(^c\)Resistance to antimicrobials that were not included in the phenotypic antimicrobial susceptibility tests.
\(^d\)Phenotype not known.
\(^e\)Phenotypically silent in native position (19).
\(^f\)Antimicrobial drug associated with chromosomal mutations.
all four \textit{K. pneumonia} isolates. If we had used PCR to detect genes, we would probably not have found more than one, as it is common to cease looking for more genes after a matching gene is found. ResFinder can therefore potentially give more information than the existing method.

ResFinder is a further step in our development of bioinformatics tools for analyzing WGS data; the tools are specifically designed to be easy to use—and for investigators with limited bioinformatics experience. An online tool allowing identification of multilocus sequence types is already available. Additional tools under development include those for the identification of virulence genes and species, and identification and phylogenetic analysis based on single-nucleotide polymorphism and pan-genome analysis.

ResFinder will continuously be updated to include additional and novel emerging resistance genes as they are identified.

\section*{Acknowledgements}
We are grateful to Inge M. Hansen and John Damm Sørensen for excellent technical assistance.

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\section*{Transparency declarations}
None to declare.

\section*{Supplementary data}
Tables S1 and S2 are available as Supplementary data at \textit{JAC} Online (http://jac.oxfordjournals.org/).

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CONCLUSIONS AND FUTURE PERSPECTIVES

In this work we show how it is possible to use bacterial WGS to characterise bacterial strains and predict pathogenicity features of potentially pathogenic strains. The web-servers developed at CGE, and discussed in this thesis, are a good example of useful tools with web-interfaces simple enough to be used by people with low computer skills and at the same time, with an high need to use bioinformatics tools for their research and work.

The steps in the near future will be the creation of databases of bacterial strains, integrated in a system in which a user can see all the tests (e.g., MLST, antibiotic resistance etc.) he has done on strains of a given bacterial species that he is working on. Such a system will allow, for example, to quickly compare a set of strains of the same species, or strains involved in the same disease, to do epidemiological studies on a given bacteria or get insight of the mechanisms behind a given infectious disease.

The next step following the research described in this thesis will be the extension of the analysis to vira and metagenomic sample. Even though there are different sets of tools for the fast analysis and characterisation of bacterial WGS data, little has been done to develop tools for a fast and comprehensive analysis of clinical metagenomic samples. A few pipelines have been developed for the phylogenetic and functional analysis of metagenomes [32, 49, 68], but there is at present no pipeline focusing on the identification of genes and groups of microbes that might be responsible for the disease.

Metagenomic data obtained from, e.g., human urine or fecal samples contain a mix of microbes and moreover frequently contain only parts of each genome, thus making the analysis much more challenging than single-culture analysis. Metagenomic analyses have, however, two advantages of pivotal importance. Firstly, single-culture analysis is more time consuming, and secondly, some disease-causing bacteria cannot be grown in culture outside their natural environment.

The analysis of metagenomic data can give us a “picture” of the groups of microbes in the host, which is wider than the information we obtain using WGS data from single bacteria. If we consider for example antibiotic resistance, analyzing metagenomic samples we can find all the antimicrobial resistant genes that are the in host and possibly associate those to specific bacteria. This could be very useful to understand, for example, how a given patient would react to a given drug before the treatment has started. This kind of assessments are done at present when a patient is admitted to a hospital in order to reduce the risk for the patient to acquire nosocomial infections due to multi-drug resistant bacteria during treatment with antimicrobial drugs. The pipeline would help to speed up this kind of assessments and, given the steadily decreasing costs for sequencing, reduce also the costs.
for the healthcare related to both nosocomial infections and patients screening before treatment with antibiotics.
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