

BM329 Workshop A: Microbial Identification

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Preface to the 2024-25 BM329 Block A workshop

Welcome to the BM329 (Biomedical Microbiology) Block A Microbial Identification workshop for 2024-25.

We would be very grateful to hear feedback about this material [by email](#) or through the [GitHub repository Issues page](#).

Overview

This workshop asks you to carry out common microbial identification analyses for a sequenced bacterial isolate to determine its likely identity. You will be using online bioinformatics services to do this.

Important Note

There is new material in this workshop that is not covered in lectures, and this material is examinable. Please take care to read the text in the expandable callout boxes, as well as that for the workshop, to be sure you have understood the topic and obtain full value from the exercise.

The workshop material will remain live online for the duration of BM329, and you can revisit it whenever you wish, for practice or revision.

You should be able to complete this workshop in under two hours.

Learning Objectives

By the end of this workshop, students will be able to:

- Obtain an identification for a bacterial isolate from its 16S sequence, using public bioinformatics 16S sequence-matching services
- Obtain an identification for a bacterial isolate from its assembled draft genome sequence, using a range of techniques, *via* public bioinformatics services

- Interpret sequence-based bacterial taxonomy assignments in the context of [LPSN](#) (the [List of Prokaryotic names with Standing in Nomenclature](#)), the arbiter of bacterial nomenclature
- Compare, and make an informed judgement between, alternative taxonomic assignments for the same isolate made using different computational approaches and databases.

Assessment

This workshop activity itself is not formally assessed although, as noted, all the material it contains is examinable. There is a formative assessment in the form of short answer questions [on MyPlace](#), which you should complete as part of the workshop.

1 Introduction

1.1 Say cheese!



Figure 1.1: Ballard Farmer's Market (Wikimedia Commons)

A few weeks ago you went to a food festival and farmer's market, and passed a cheese stall. You love cheese and the smell was making you hungry, so you tried a few samples, and bought the one you found tastiest. It was a delicious [blue cheese](#), made from [unpasteurised](#) cow's milk, and with natural [rennet](#).

You ate it on sourdough crackers, with some fig and plum chutney, and it was a savoury taste explosion. You thought to yourself what a great idea it was to go to the farmer's market. And it was even a local producer, so you kept the [food miles](#) down and supported the local community. You felt *great!*

1.2 A month later



Now it's about a month later. But you're not feeling great at all. You haven't felt great for a couple of days in fact, and you've got quite a list of signs and symptoms.

- you've had a fever for day or so
- you're sweating, even though it's cool
- you've got a nasty headache you can't shift, even with paracetamol
- you're not hungry and haven't felt like eating at all, since this started
- you're exhausted all the time
- all your joints ache, your muscles feel like you've wrestled an elephant seal, and don't get you started about your back

But you *were* out at the weekend, and caned it a bit. Maybe it's just a really bad hangover?

It's all very nonspecific. It's not '[flu season](#)' but even though there's no 'flu going round it feels like the worst 'flu of your life and worse than any hangover you've had so far. So you [called 111](#) and off you popped to the pharmacist like they said, who immediately suggested you go to your GP, who referred you without delay to Accident and Emergency with suspected bacteremia.

1.3 In the blood



Figure 1.2: A hospital room (Wikimedia Commons)

You're in a hospital room now, full of antibiotics and feeling terrible. Your bloods have been taken - so many bloods! - and you've been told that the phlebotomists have found an unexpected bacterium. They're trying to grow it up in agar right now. As you're a microbiologist you're naturally curious, and you ask if they've identified it yet.

It turns out they've been having difficulty finding a medium that the bacteria will grow on. They're trying blood and tryptose broth and, while that's meeting with some success, it's very, very slow-growing.

They've managed to get a preliminary identification from a small sample by [MALDI-TOF](#), (Barth et al. (2023)) which suggests that it's a *Brucella* strain of some sort.

Your heart sinks. You really, *really* do not want [brucellosis](#).

! Why you don't want brucellosis

Although uncommon in the UK, brucellosis is endemic in many developing countries (Laine et al. (2023)). The causative agents, *Brucella* spp. bacteria, grow less quickly in the

open environment than in their hosts, and are highly contagious intracellular pathogens readily spread between individuals and by infectious body fluids (Moreno et al. (2023)).

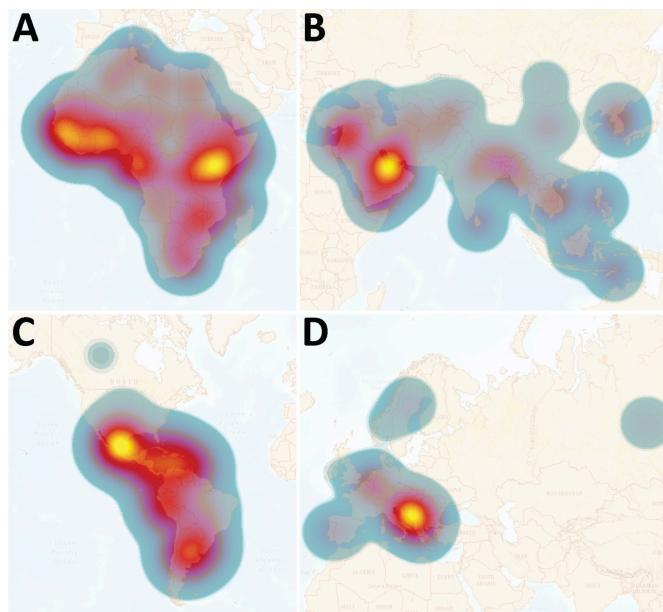


Figure 5. Heatmaps of regional annual incidence of human brucellosis estimated per 1 million population at risk. Each region has a different scale for incidence per 1 million population at risk. Heatmaps are intended to represent transnational zones that require priority control or surveillance initiative, not to represent the risk of individual countries. The heat scale shows high risk to low risk; yellow to blue. A) Africa: average risk is \approx 750 new cases per million; high is $>$ 3,000. B) Asia: average risk is \approx 500 new cases per million; high is $>$ 24,000. C) Americas: average risk is \approx 20 new cases per million; high is \geq 75. D) Europe: average risk is \approx 10 new cases per million; high \geq 100.

Figure 1.3: Figure 5 from (Laine et al. (2023)) illustrating estimated incidence of human brucellosis, worldwide.

In humans brucellosis is not often fatal, but it can be severely disabling. Brucellosis presents in both infectious and non-infectious forms and can be highly persistent, causing chronic debilitation and granulomas within organs. The most common presentations involve greatly enlarged liver and spleen, but other complications - including neurological - may be seen (Franco et al. (2007)). The presentation can be extremely variable, to the extent that “in endemic areas, everything can be due to brucellosis until proven different” (Bosilkovski, Keramat, and Arapović (2021)).

Blood and bone marrow culture remains the gold standard for diagnosis of brucellosis, but *Brucella* spp. grow slowly, and it's not unusual for a culture to take a week or more to reach a size suitable for diagnosis. ELISA is popular but less specific than many other diagnostic tests. Molecular methods such as PCR and MALDI-TOF have not been as widely validated (Franco et al. (2007)).

Treatment of brucellosis is unpleasant for the patient, and has hardly changed this century. Treatment requires simultaneous administration of multiple antibiotics for an extended period (e.g. 200mg doxycycline plus 900mg rifampicin, and perhaps a fluoroquinolone in support, for 6-8 weeks). Relapse rates are high (up to 25%) with oral delivery alone but lower with parenteral delivery (up to about 8%) (Franco et al. (2007), Bosilkovski, Keramat, and Arapović (2021)).

Hospital staff potentially exposed to the infectious agent undergo the same treatment as prophylaxis.

At the lab they've managed to sequence the bacterium that's in your blood, using an [Oxford Nanopore flongle](#) they had lying around. The assembled draft genome has come back, but the [NHS is chronically underfunded and the staff are massively overworked](#), so your consultant hasn't had time to learn how to classify bacteria from genome sequence data.

"I'll have a go, if you like," you say. Then the light starts to hurt and you have a nap.

1.4 Controversy

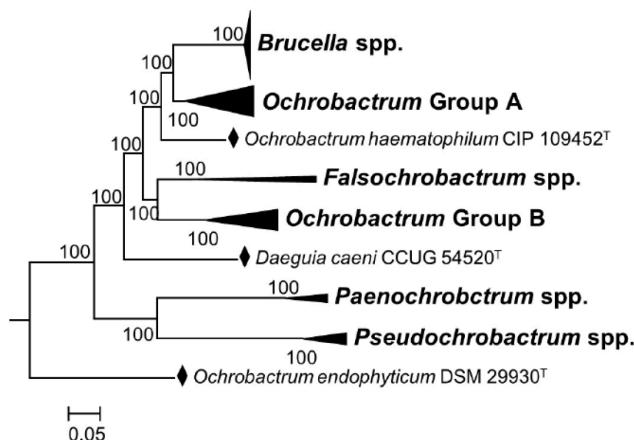


Figure 1. Phylogenetic relationships among genera of the family *Brucellaceae* based on whole sequence genome analysis (a black diamond denotes type strains). Node labels give percentage bootstrap support. *Rhizobium etli* (CFN42T) was used to root the phylogenetic tree (not shown). The tree was constructed using the maximum likelihood method, based on the general time-reversible model, as described by Ashford et al. [30] (adapted from Figure 4 of this reference).

Figure 1.4: Figure 1 from (Moreno et al. (2022)), showing the relationship between *Brucella* and *Ochrobactrum* species. *Brucella* is a group of bacteria nested within *Ochrobactrum*.

As an expert biomedical microbiologist, *you* know that there has recently been a lot of controversy around identification of *Brucella*, and that preliminary molecular and genomic identifications of *Brucella* spp. shouldn't necessarily be taken at face value.

You are aware that recent publications in microbial nomenclature renamed a whole genus of much less worrying bacteria, belonging to the *Ochrobactrum* genus, to *Brucella* (Hördt et al. (2020)), even though *Ochrobactrum* spp. are only opportunistic pathogens and not particularly

virulent (Hagiya et al. (2013)). Many microbiologists who work in clinical settings, or with *Brucella*, object to the renaming (Moreno et al. (2022), Moreno et al. (2023)). Even so, some commercial diagnostic equipment has updated its databases and now calls bacteria *Brucella* that used to be called as *Ochrobactrum*.

! The *Brucella/Ochrobactrum* controversy

In 2020, a manuscript was published applying a bioinformatics methodology to over 1,000 genomes of *Alphaproteobacteria* type strains. *Alphaproteobacteria* is the taxonomic Class that contains both *Brucella* and *Ochrobactrum* genera (Hördt et al. (2020)).

In phylogenetic trees, *Brucella* and *Ochrobactrum* are closely-related. *Ochrobactrum* form a group called a clade (they share a single common ancestor), but *Brucella* appears as a coherent subgroup with multiple *derived characters* within this clade.

The bioinformatics method applied in Hördt et al. (2020) reproduced this relationship, and a proposal was made that, because *Brucella* was nested within *Ochrobactrum*, the entire group of bacteria - including all *Ochrobactrum* - should be named *Brucella*. It was argued in this paper that, even though *Brucella* and *Ochrobactrum* are not as virulent as each other, they should be considered to belong to different “risk groups,” but also to be fundamentally similar organisms (Hördt et al. (2020)).

Clinical microbiologists and other scientists rejected this proposal, arguing that the names of bacteria do more than indicate where they lie in a phylogenetic tree. They argue that the long-standing use of brucellosis to refer to the serious disease caused only by *Brucella* ends up being confused - potentially dangerously - if relatively low-risk bacteria such as *Ochrobactrum* are renamed as *Brucella*. They also argue that “typology,” taking into consideration more than phylogenetic placement, is necessary for meaningful naming and subdivision of bacteria, and that bioinformatics methods alone are not sufficient to define bacterial taxa. They consider that *Brucella* and *Ochrobactrum* strains show quite different phenotypes, and should therefore remain known by different names (Moreno et al. (2022), Moreno et al. (2023)).

Table 1. Comparison between the *Brucella* and *Ochrobactrum* genus.

Divergent Properties	<i>Brucella</i>	<i>Ochrobactrum</i>	References
Genome Size	3.1–3.4 Mb	4.7–8.3 Mb	[20,21]
Pangenome	Closed	Open	[20,22,23,24,25,26,27]
Plasmid	No	Variable (up to 6)	[20,21,23,25,28,29]
Phylogeny	Monophyletic	Polyphyletic	[8,30]
Active Phages	No	>4	[29,31]
Lateral gene transfer	Absent	Present	[29]
Speciation type	Allopatric	Sympatric	[32,33,34]
Cell envelope permeability	Permeable to hydrophobic probes and resistant to destabilization by polycationic peptides	Impermeable to hydrophobic probes and sensitive to polycationic peptides	[35,36]
Metabolic redundancy	Low	High	[22,37]
Degradation of complex molecules	No	A large variety of such molecules	[38,39,40,41]
Removing toxic metals	No	Yes (some species/strains)	[42,43]
Capable to root nodulation	No	Yes (some species/strains)	[44,45]
Life style	Pathogen (class 3)	Saprophyte	[6,44,46]
Natural habitat	Intracellular	Soil and root plant surfaces	[24,35,44]
Transmission	Host-host interaction/animal products	Mostly iatrogenic	[47,48]
Virulence	Finely tuned	Fortuitus/opportunistic	[6,46,47]
Virulence mechanisms	Escape from the immune response/deviation of the intracellular trafficking	No true ones and virulence depending on host immune status	[35,46,49,50]
Infection dynamics	Long-lasting infection and low proinflammatory response	Acute proinflammatory/pyogenic; self-limiting in immunocompetent hosts	[46,47,51]
Animal disease	Very important	Seldom	[46,48,52,53,54]
Human health	Very important	Negligible	[22,46,47,48,52]
Diagnosis	Well-standardized serological methods	No serological tests are available or necessary	[52,55]
Treatment	WHO recommended long bi-therapy in uncomplicated cases	Based on antibiotic resistance/short monotherapy	[47,56,57]
Antibiotic resistance	Seldom and well-defined	High	[25,47,56,57,58,59,60,61]
Vaccine	Available (domestic ruminants) and critically important to control disease	Unnecessary	[62,63]
WHO/OIE/FAO regulations	Very important	Null	[57]

Figure 1.5: Table 1 from (Moreno et al. (2022))

Since the nomenclature change, there have been instances of bacteria formerly known as *Ochrobactrum* being identified as *Brucella* by commercial MALDI-TOF instruments in a clinical context, leading to avoidable prophylactic treatment of hospital staff (Moreno et al. (2023)).

Now that the name *Brucella* has been validly published in the literature for bacteria formerly known as *Ochrobactrum*, and is considered the “correct” name for the group, it is highly unlikely it would be withdrawn, under the the rules of the [International Code of Nomenclature of Prokaryotes](#) (ICNP, the Prokaryotic Code). The controversy continues.

You know that if you make a positive identification of this bacterium as something other than *Brucella*, you might avoid eight weeks of unpleasant multiple antibiotic treatment, and so can staff who were potentially exposed to *Brucella* through your sample. If this infection does turn out to be *Brucella* they would also need to undergo prophylactic treatment.

Your identification could save a lot of people - not least you! - quite a bit of unpleasantness.

1.5 Your challenge

Identify the infectious bacterium using bioinformatics methods

You will be provided with the assembled draft genome sequence of the organism that was isolated from your blood and sequenced on the flongle and, for convenience, some additional information (e.g. 16S sequence data) that may help with identification.

In the sections that follow, you will be guided through identification of the organism using a number of different bioinformatics approaches and online resources. Once you have conducted these analyses and identified your organism, you should complete the formative questions on MyPlace. These will ask you about your identification, and your reasons for making that identification.

Let's get started

Begin your analysis by clicking on the link to [Data](#) (here, or below)

2 Data

2.1 Your datasets

The hospital laboratory have provided you with the following data from the bacterium that was isolated from your blood:

- Draft genome sequence: [isolate_genome.fasta](#)
- 16S sequence from the draft genome: [isolate_16S.fasta](#)

💡 Downloading data files

You can download your data files using the links above. Clicking on the link may open the file in your browser. If this is the case, then you can use the `File -> Save As` menu option to save the file.

Alternatively, right-click (or `Ctrl`-click) on the link, and choose `Save file as...` (or similar) to save the file.

These data files are also available from the [BM329 MyPlace page](#).

ℹ️ FASTA file format

The sequences you have been given are in [FASTA format](#). This is a very common standard format for representing biological sequences, and looks like this:

```
>R431BS_isolate_from_bloods 16S sequence obtained from full genome
CAACTTGAGAGTTGATCCTGGCTCAGAACGAACGCTGGCGCAGGCTAACACATGCAAGTCGAGCGCC
CCGCAAGGGGAGCGGCAGACGGGTGAGTAACGCGTGGGAATCTACCTTTGCTACGGAATAACTCAGGGA
AACTTGTGCTAATACCGTATGTGCCCTCGGGGAAAGATTATCGGCAAAGGATGAGCCCGCTTGGAT
TAGCTAGTTGGTGAGGTAAAGGCTCACCAAGGCGACGATCCATAGCTGGTCTGAGAGGATGATCAGCCAC
ACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGAATATTGGACAATGGCGCAAG
```

The general format is

```
>sequence_identifier sequence_description  
[symbols representing the biological sequence]  
>sequence_identifier sequence_description  
[symbols representing the biological sequence]  
[...]
```

Each new sequence in the file starts with a right angled bracket (>) to indicate a *header line*, which is immediately followed by a unique sequence identifier. This is typically, but not always, an accession number that uniquely identifies the sequence in a database.

If there are any space characters on the *header line*, all text after the space is taken to be a free-text description of the sequence itself.

The lines following the *header line* then contain the symbols (A, C, G, T for DNA, the protein alphabet for protein) that represent the biological sequence itself.

💡 Tip

FASTA files are a *plain text* format. You can open them in an editor like **notepad** (Windows), **emacs** (Linux) or **TextEdit** (macOS) to see their contents.

⚠️ Warning

Avoid opening FASTA files in Word or other word-processing software. This software can insert hidden characters which corrupt the data and make it unusable for analysis. If you save your sequence as a Word file it will be unreadable by bioinformatics programs.

2.2 Draft genome sequence

Your isolate's genome is not entirely complete, and is not in one single contiguous piece - therefore it is a *draft* genome. Instead, it is in 41 *contigs* (contiguous sequences) - distinct sections of the genome. The contigs are not in order which means that, on the real genome, the second contig may not follow the first (and so on), and the first contig may not be where the genome "starts".

The contigs are described in the [**isolate_genome.fasta**](#) file: one sequence per contig. Taken together, the total sequenced genome length is 5,116,355 bases, and the genome has a GC% content of 53.5%.

2.3 16S sequence

16S ribosomal RNA (16S rRNA) is an evolutionarily highly-optimised, essential component of bacterial SSU (small subunit) ribosomes. Because it is essential, and its function in protein synthesis is central to correct operation of the cell, its biological sequence is highly constrained ([it is unlikely that a change in the sequence will enhance or be neutral to function](#)). This has two main implications that make it useful for evolutionary analysis and microbial identification.

- The 16S sequence is similar enough to be recognisable in all prokaryotes
- The 16S sequence is usually most similar in organisms that share a recent common ancestor, and less similar in organisms that share a more distant common ancestor.

These properties enable the 16S rRNA sequence to be used to reconstruct evolutionary histories of prokaryotes, including the landmark paper that defined Archaea as a new domain of life (Woese, Kandler, and Wheelis (1990)). Several online reference databases with curated 16S sequence data are commonly used to enable bioinformatic identification of organisms.

Note

The properties noted above also make 16S rRNA useful for identifying which bacteria are present in complex communities: microbiome analyses (Johnson et al. (2019))).

The similarity of 16S sequences across all bacteria mean that a single set of primers (*universal primers*) can be used to amplify most 16S bacterial genes in a sample using PCR.

Sequencing the amplified 16S genes with [high-throughput sequencing](#) then allows the distinct identities of many bacteria in a sample to be determined simultaneously.

Disadvantages of 16S sequence data for identification and classification

16S sequence data has more recently fallen out of favour for bacterial classification and identification. This is in part due to the increased availability of high-throughput whole-genome sequencing; with this technology the whole genome can be obtained at the same time as the 16S gene sequence, and the extra information allows for more precise identification. But there are also inherent disadvantages of the approach.

- Whole-genome sequencing is practical, inexpensive, and provides more information, including the 16S sequence.
 - Amplifying a variable subregion of 16S provides about 300bp of information, sequencing the full 16S gene about 1500bp, and sequencing a genome between 1,500,000bp and 12,000,000bp (depending on organism)
- Some distinct species share identical 16S sequences (R. C. Edgar (2018a))

- Some organisms/species possess multiple distinct 16S sequences (R. C. Edgar (2018a))
- There is no universal level of similarity (percentage identity) between 16S sequences that always corresponds to a taxonomic division (R. C. Edgar (2018b))
- 16S databases contain many sequences that are incomplete, contain errors, or are annotated with the wrong taxonomic identity (R. Edgar (2018))

The 16S sequence for your isolate has been identified from the genome sequence and is described in the [isolate_16S.fasta](#) FASTA file.

 Begin your identification

You should begin the identification of your isolate by submitting the 16S sequence in [isolate_16S.fasta](#) to some of these public resources. click on the link to [16S](#) (here, or below), to get started.

3 16S

3.1 16S identification of your isolate

In this part of the workshop, you will use publicly available 16S sequence databases and resources to obtain an identification for your isolate.

! Important

Please ensure that you have downloaded the 16S sequence file for your isolate (`isolate_16S.fasta`) to a suitable location on your computer.

3.2 NCBI Blast

BLAST is a bioinformatics tool developed by [NCBI \(the National Center for Biotechnology Information\)](#) that takes as input a *query* sequence and searches for similar sequences in a reference database. BLAST ranks matches from most (first) to least similar. The tool can be downloaded and run on your own machine, or it can be used through the [NCBI-BLAST webservice](#).

- [NCBI-BLAST webservice](#)
- [NCBI-BLAST help pages](#)
- [How BLAST works](#)

NCBI are the repository of record for published biological sequence data, and provide several BLAST databases, including one that contains all publicly-available 16S sequence data. You will use the [NCBI-BLAST webservice](#), with your isolate's 16S sequence as the query, to search this database.



BLAST reports a number of useful measures for each match

- Percent coverage: what proportion (percentage) of the *query* is similar enough to the match to which it has been aligned
- Percentage identity: what proportion of the aligned region is identical in both the *query* and the reported match

- Expectation (E-value): the number of matches you would expect by chance from this database that are *at least as similar as this one*, if you used the *query* sequence to search in a database of the same size made up of completely random sequences

3.2.1 Analysing your data

1. Go to the [NCBI Blast webpage](#). You will see the landing page.

The screenshot shows the NCBI BLAST landing page. At the top, there's a banner with the NIH logo and the text "National Library of Medicine National Center for Biotechnology Information". To the right is a "Log in" button. Below the banner, the word "BLAST®" is displayed. On the left, there's a "NEWS" sidebar with the heading "Basic Local Alignment Search Tool". It describes BLAST as a tool for finding regions of similarity between biological sequences. A "Learn more" link is provided. On the right, a news box titled "BLAST+ 2.15.0 is here!" informs users about two new features included in the latest release. It includes the date "Tue, 28 Nov 2023" and a "More BLAST news..." link. Below the news box, there's a section titled "Web BLAST" featuring three buttons: "Nucleotide BLAST" (nucleotide > nucleotide), "blastx" (translated nucleotide > protein), and "tblastn" (protein > translated nucleotide). There's also a "Protein BLAST" button (protein > protein).

2. Select Nucleotide BLAST. This will take you to a new BLASTN search.

The screenshot shows the "BLAST® > blastn suite" search interface. At the top, it says "Standard Nucleotide BLAST". Below that, there's a "Enter Query Sequence" field where users can enter accession numbers or FASTA sequences. There are also fields for "Query subrange", "From", "To", and "Job Title". Underneath, there are options for "Or, upload file" (with a "Browse..." button) and "Align two or more sequences" (with a checkbox). At the bottom right, there are "Reset page" and "Bookmark" buttons.

3. Upload your `isolate_16S.fasta` file, or copy and paste the contents of the file into the box marked **Enter accession number(s), gi(s) or FASTA sequence(s)**.

The screenshot shows the 'Standard Nucleotide BLAST' interface. At the top, there are tabs for blastn, blastp, blastx, tblastn, and tblastx. Below the tabs, a header says 'Enter Query Sequence'. A text input field contains the sequence: >R431BS_isolate_from_bloods 16S sequence obtained from full genome CAACCTTGAGAGTTGATCCTGGCTCAGAACGAAACGCTGGCGCAGGCTT AACACATGCAAGTCGAGGCC CCGCAAGGGAGCGGAGACGGGTGAGTAACCGCTGGGAATCTACCTT. To the right, there's a 'Query subrange' section with 'From' and 'To' fields. Below the sequence input, there are options to 'Browse...' for a file, set a 'Job Title' (R431BS_isolate_from_bloods 16S sequence obtained...), and a checkbox for 'Align two or more sequences'.

4. In the section headed **Choose Search Set**, select rRNA/ITS databases. This will autopopulate the database with **16S Ribosomal RNA sequences (Bacteria and Archaea)**, NCBI's complete database of 16S rRNA sequences.

Caution

NCBI do not manually curate (i.e. confirm sequence quality or correct identity) the data in their databases. Whole genome sequences are checked for completeness by looking at the collection of annotated proteins, and also by classification algorithms for taxonomic placement, but 16S sequences are not. Also, NCBI contains a large amount of historical data which may have been annotated using outdated or superseded taxonomies. The names of BLAST matches in 16S databases should be treated with some caution.

The screenshot shows the 'Choose Search Set' interface. Under 'Database', there are radio buttons for 'Standard databases (nr etc.)', 'rRNA/ITS databases' (which is selected), 'Genomic + transcript databases', and 'Betacoronavirus'. Below this, there's a link 'Try experimental taxonomic nt databases' with a 'Download' button. Under 'Organism' (Optional), a dropdown menu shows '16S ribosomal RNA sequences (Bacteria and Archaea)' with a 'Targeted Loci Project Information' link. There are also fields for entering an organism name and a checkbox for 'exclude'. Under 'Exclude' (Optional), there are checkboxes for 'Models (XM/XP)', 'Uncultured/environmental sample sequences', and 'Sequences from type material'. Under 'Limit to' (Optional), there's a text input field for an Entrez query. At the bottom, there's a 'Create custom database' link and a 'YouTube' icon.

5. Click on the **BLAST** button (towards the bottom of the page) and wait for the result to appear.

! Questions

1. What organism is the top hit to your query?
2. How similar is the top hit to your query (`Per. ident`/percentage identity column)?
What is the alignment coverage?
3. What are the remaining top five matches to your query?
4. How similar are the top five matches to your query sequence?
5. What conclusion would you draw about the identity of your isolate from this BLAST search?

3.3 SILVA

[SILVA](#) is a curated, quality-checked database of rRNA sequence data that has been run by the [Liebniz Institute DSMZ German Collection of Microorganisms and Cell Cultures](#) for about two decades. The SILVA site provides a number of online tools and services, including the [ACT](#) service that enables users to search the database with their own rRNA sequences to find the best matches and identify their organism.

- [SILVA rRNA database project](#)
- [SILVA Alignment, Classification, and Tree \(ACT\) webservice](#)
- [ACT online tutorial](#)

3.3.1 Analysing your data

1. Go to the [SILVA ACT](#) (Alignment, Classification, and Tree) service

ACT: Alignment, Classification and Tree Service

SINA 1.2.12

Input data

Paste your FASTA sequence here

or

upload an FASTA file

Basic alignment parameters

Tip: hovering over the options shows enhanced descriptions.

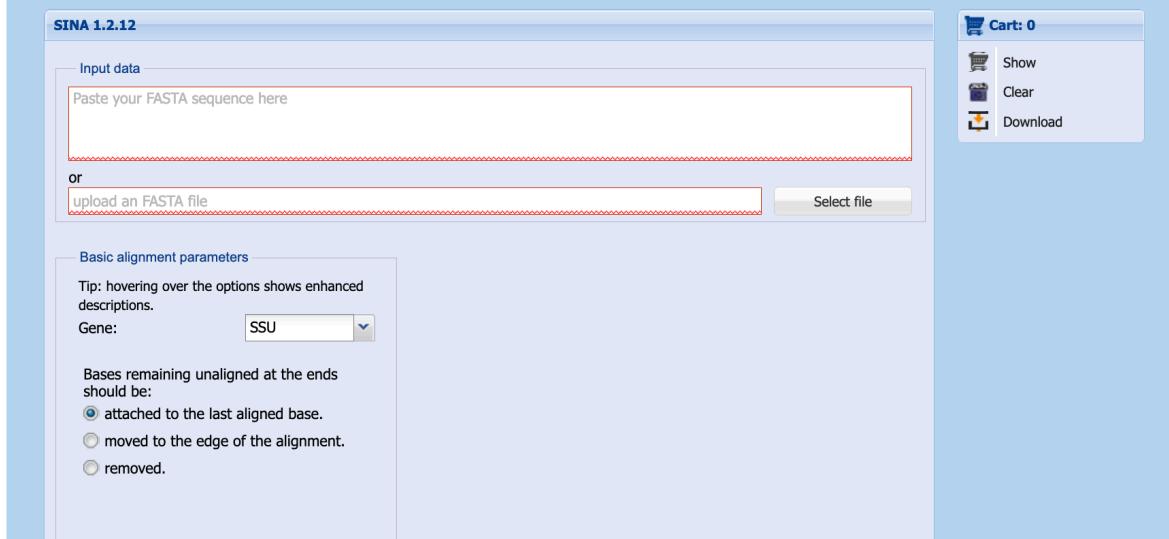
Gene:

Bases remaining unaligned at the ends should be:

attached to the last aligned base.
 moved to the edge of the alignment.
 removed.

Cart: 0

Show
Clear
Download



2. Upload your **isolate_16S.fasta** file, or copy and paste the contents of the file into the box marked **Input data**.
3. Check the box marked **Search and classify**, but leave all the other options as they are.

Search and classify

Min. identity with query sequence:

Number of neighbours per query sequence:

Compute tree

Workflow: Denovo with user sequences only

Program to use: FastTree

Model to use: GTR

Rate model for likelihoods: Gamma

Output settings

Format: FASTA FASTA w. meta-data ARB

Compression: none zip tgz

Reject sequences below identity (%):

Advanced alignment parameters

Advanced search and classification parameters

The Sequence Collection that is used for search and classification: Ref NR Ref

Select taxonomies used for classification: SILVA RDP GTDB LTP EMBL-EBI/ENA

search-kmer-candidates:

lca-quorum:

search-kmer-len:

search-kmer-mm:

search-no-fast:

search-kmer-norel:

Job Name:

4. Enter a name for your job in the field marked Job Name: (e.g. “BM432 Block A workshop” or “blood isolate”)

Job Name:

5. Click on the Run Tool button and wait for the result to appear.

Note

While the job is waiting it will appear in the Aligner Taskmanager as *Queued*, then *Starting*, then *Processing*. It may take a couple of minutes to produce a result.

Aligner Taskmanager								
#	Job Name	Creation Time	Job Type	Status	Quantity	Progress	Status Message	Elapsed Time Queue
1	BM329 block A works...	2024-01-16 12:43...	Align_AC	Queued	1		Waiting...	00:00:07 0

- When the job is complete, select your result in the Alignment Result Table, and click on **Display Classification**

Tip

You may need to adjust the widths of the headers in the result table to see the full classification

Alignment Result Table								
Jobid	#	Sequence Identifier	Full Name	Identity	Score	Cutoff Head	Cutoff Tail	E.coli Pos. Gene Bps Turn
12979...	1	R431BS_isolate_from_bloods	16S sequence obtained from f...	99.93	99	7	13	1 0 none

- Click on **Export to CSV** (lower left of Alignment Result Table) to download the classification result. You can view this file in Excel or in a plain text editor.

Questions

- What is the taxonomic identity of the **last common ancestor (LCA)** that SILVA assigns to your isolate (`lca_tax_slv` or `LCA tax`. `SILVA` column - this is the last column of data in the file)?
- How similar (`Identity` column) does SILVA say your isolate is to that last common ancestor sequence?

3.4 Summary

You have used two different databases, and two different techniques, to assign taxonomic identity to a 16S sequence. Are the results consistent with each other?

! Questions

1. Do the BLAST and SILVA analyses give the same taxonomic identity for your 16S sequence?
2. If the two results differ, how do they differ?
3. If the results differ, how important do you think is the difference between the results?
4. What is your current opinion about the identity of your isolate? Have you revised it since the BLAST search? How confident are you in the identification?

💡 Continue your identification

Now you have a possible identification from 16S, you should continue the classification of your isolate by using Multi-Locus Sequence Typing (MLST) to try to gain a more precise taxonomic placement. Click on the link to [MLST](#) (here, or below), to get started.

4 Multi-Locus Sequence Typing (MLST)

4.1 MLST identification of your isolate

In this part of the workshop, you will use a public [Multi-Locus Sequence Typing \(MLST\)](#) database and resources to help identify your isolate.

! Important

Please ensure that you have downloaded the genome file for your isolate (`isolate_genome.fasta`) to a suitable location on your computer.

⚠ Multi-Locus Sequence Typing (MLST)

[Multi-Locus Sequence Typing \(MLST\)](#) is a widely-used method for bacterial identification. It is typically more precise and has more resolving power than 16S sequence analysis, but less precise than whole-genome sequence analysis (Maiden et al. (2013)).

MLST works by defining *marker sequences* for a taxon. These are typically well-conserved (“housekeeping”) genes which vary relatively little between organisms in the taxon, but enough to allow discrimination between them. The number of markers varies, but is usually somewhere around seven.

Each marker sequence has many *variants* (different sequences) within the taxon, and these are known as *alleles*. Each marker allele is given a unique number (starting at 1 and counting upwards) - its *allele number*. A single organism’s *sequence type (ST)* is determined by the list of allele numbers that it contains. Organisms with the same *sequence type* are considered to be part of the same group.

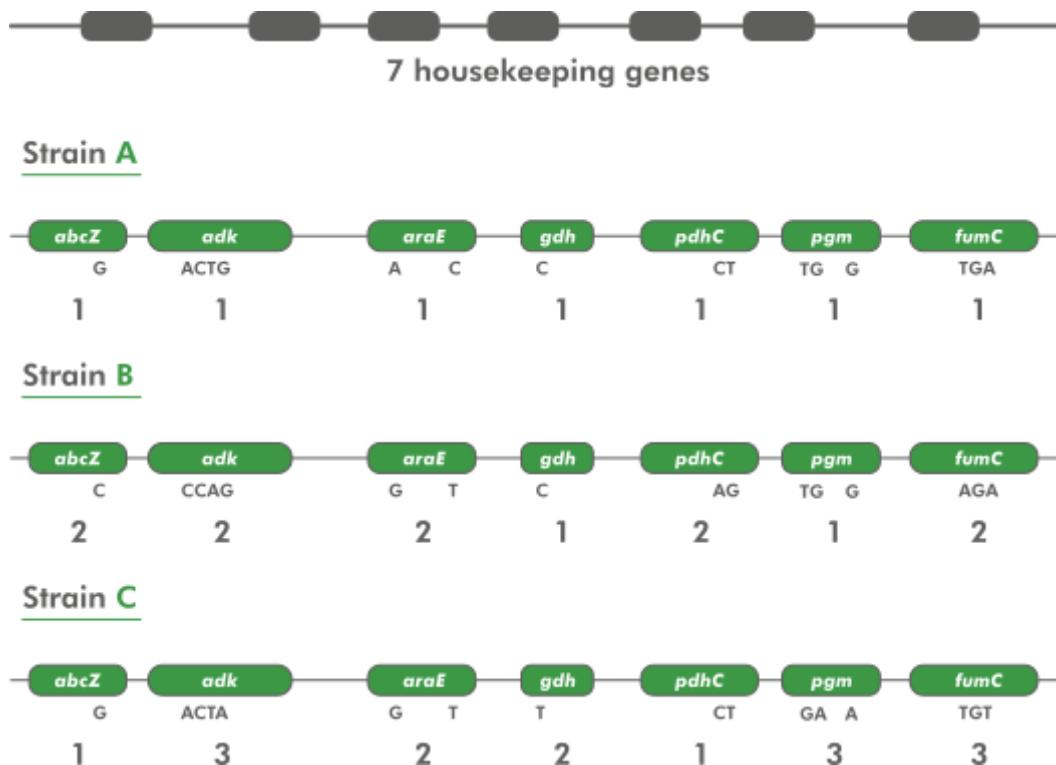


Figure 4.1: Schematic representation of MLST. In this typing scheme there are seven markers (“housekeeping genes”). One of these is the gene *adk*, which has a different sequence in each of the strains A, B, and C - so these have different allele numbers (1, 2, and 3). Another marker, *pdhC* has the same sequence (allele number) in strains A and C, but a different sequence (allele number) in strain B. The strains have allele numbers: 1,1,1,1,1,1,1 (A); 2,2,2,1,2,1,2 (B); 1,3,2,2,1,3,2 (C). These lists are different, so the strains have different sequence types.

4.2 pubMLST

- Go to the [pubMLST](#) website

PubMLST Public databases for molecular typing and microbial genome diversity [MY ACCOUNT](#)

HOME ORGANISMS SPECIES ID ABOUT US UPDATES

A collection of open-access, curated databases that integrate population sequence data with provenance and phenotype information for over 130 different microbial species and genera.

37,441,007 ALLELES 1,444,744 ISOLATES 1,164,147 GENOMES



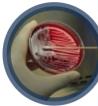
Organisms search [APPLY](#)



Organisms
Choose your organism from a list of over 130 species and genera-specific databases. Access molecular typing and isolate records.



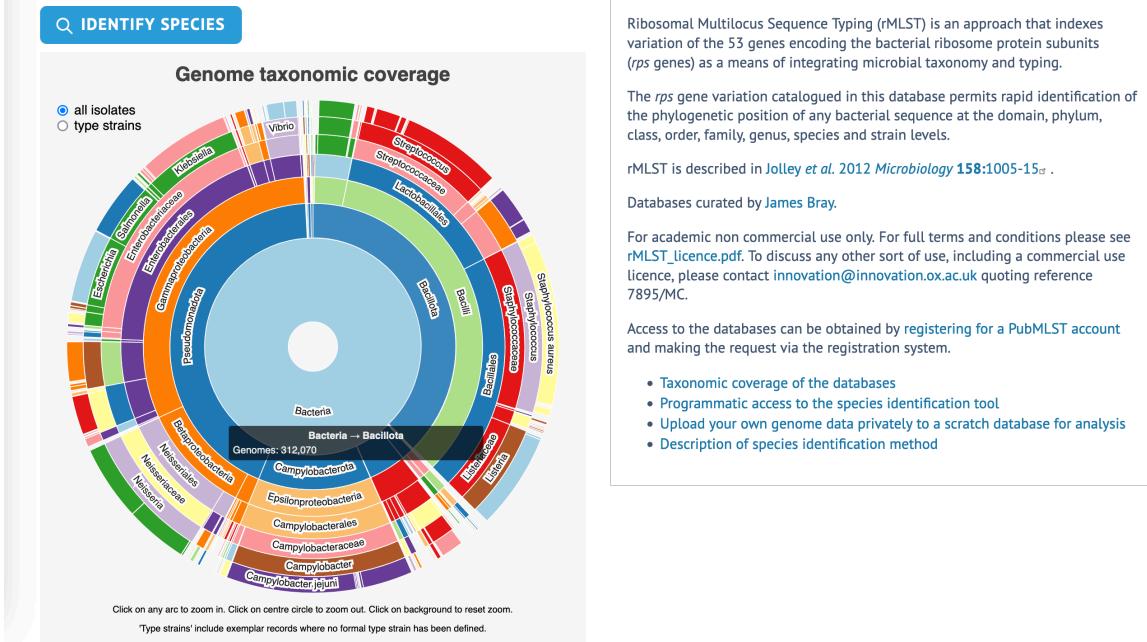
Species ID
Use ribosomal MLST to accurately identify bacterial species from a genome assembly.



Submit data
We welcome submissions to the databases we host. Submissions may consist of allele sequences, MLST profiles, or isolate records with or without genome assemblies.

- Click on **Species ID** to open the bacterial species identifier

Ribosomal MLST



- Click on Identify Species to start the identification process

Identify species

Please paste in your sequence to query against the database.

Enter query sequence (single or multiple contigs up to whole genome in size)

Alternatively upload FASTA file or enter Genbank accession

Select FASTA file:

Click to select or drag and drop..

Action

- Upload your `isolate_genome.fasta` file to the server either by clicking on Click to select or drag and drop and using the dialogue box to find your file, or by dragging the file onto the Select FASTA file field.

- Alternatively, copy and paste the file contents - the *entire genome sequence* - into the **Enter query sequence** box.
- Click on the **Submit** button and wait for the results

! Questions

1. What is the predicted taxon of your isolate's genome? What level of confidence does the pubMLST tool assign to this prediction (**Support** column)?
2. How many marker genes in your isolate had an *exact* match in the database? Do you think this is a sufficient number for accurate taxonomic placement? Why do you think that?
3. How many different species in the database had an *exact* match to markers in your isolate's genome?
4. *Which* species in the database had an *exact* match to markers in your isolate's genome? What effect does this have on your confidence in your classification?
5. What is your current opinion about the identity of your isolate? Have you revised your opinion from 16S analysis due to the MLST analysis? How confident are you in your current identification?

💡 Continue your identification

Now you have further supporting information about the identity of your isolate, you should continue the classification of your isolate by using whole-genome comparison methods to try to pin down a more definitive taxonomic placement. Click on the link to [Whole-genome Comparison](#) (here, or below), to get started.

5 Whole-Genome Comparison

In this part of the workshop, you will use public resources for whole-genome identification and classification of prokaryotes to help identify your isolate.

! Important

Please ensure that you have downloaded the genome file for your isolate (`isolate_genome.fasta`) to a suitable location on your computer.

5.1 The Type (Strain) Genome Server (TYGS)

The [Type \(Strain\) Genome Server \(TYGS\)](#) is provided by the [Liebniz Institute DSMZ](#), the German collection of Microbes and Cell Cultures. It provides genome-based classification of organisms by comparison against a reference database of over 20,000 sequenced bacterial *type strains*. TYGS is tightly-coupled to the authoritative [LPSN \(List of Prokaryotic names with Standing in Nomenclature\) database](#), to ensure nomenclaturally-correct identification

⚠ Type Strains

A *type strain* is the representative of a taxon: the nomenclatural “type” on which the definition of a taxon (such as species) is based. Type strains must be deposited in at least two separate public culture collections, in different countries.

Not all taxa (in particular *Candidate phyla*) have type strains. It is a requirement for type strains that the organism is grown and cultured, as it cannot otherwise be placed in a culture collection. But it has been estimated that not only are the majority of bacteria and archaea so far uncultured, but they may even be unculturable in the laboratory (Hofer (2018)).

ℹ How TYGS Classification Works

TYGS takes a prokaryotic genome as input, and assigns a taxonomic identity after a series of pairwise genome comparisons.

First, the input genome is compared to the type strain database using an approach called MASH (Ondov et al. (2016)). The ten type strain genomes, and the ten most closely related type strains identified by 16S rDNA gene (extracted automatically from the input) similarity.

This set of 20 type strain genomes is then used to find the best 50 matching type strains. A phylogenetic tree is then constructed using the Genome BLAST Distance Phylogeny approach (GBDP, Henz et al. (2005)), and the resulting distances used to determine the 10 closest type strain genomes for each of the user genomes. The between-genome distances for this are calculated using digital DNA-DNA hybridisation (dDDH, Meier-Kolthoff et al. (2013)).

TYGS compiles classification output into a PDF file, and presents the resulting phylogeny on the TYGS website. All results tables and trees can be downloaded in shareable formats.

- Go to the [TYGS](#) server

Type (Strain) Genome Server

State-of-the-art genome-based taxonomy at your fingertips.
Published in Nat. Commun. (2019) and Nucleic Acids Research (2021).

[Submit your query](#) [Read TYGS paper](#) [Read TYGS/LPSN database paper](#)

Genome-based taxonomy

A truly genome-based classification and identification of your prokaryotic strains without overestimating phylogenetic confidence. Besides the phylogenomic approach, TYGS provides digital DNA:DNA hybridization values, differences in G+C content and more.

Large type strain database

In microbial taxonomy a **type strain** is the nomenclatural type of a species. Whether or not a novel strain belongs to a particular species is thus determined by comparison to type strains. The comprehensive TYGS database contains a comprehensive collection of currently 20196 microbial type-strain genomes.

Fast, reliable and easily interpretable analyses

The TYGS web service implements many established methods (GGDC, GBDP) from recent years and provides fast data analysis on an entirely new level.

- Click on **Submit your query** (top menu), or **Submit your job** (button) to reach the query page

Submit Your TYGS query

Tip #1: Did you know that you do not normally have to include type-strain genomes in your file or accession list (see FAQ)? ×

Queries in queue 16 Queries done 101220 Queries done last 24h 127 Type strains in database 20196

Specify up to 50 genomes (via FASTA/GenBank files or GenBank accession IDs) or see FAQ on larger uploads.

No files selected. ?

Add your GenBank accession numbers here.
 Quick guide:
 1) put all accessions of a specific genome in a single row,
 2) accessions should be either separated by spaces or hyphens (in case of accession ranges)
 Go to the FAQ for a detailed guide on how to specify accessions.

Restrict query to above data (genome files plus accessions)? ?

- Click on the **Browse...** button and navigate to your `isolate_genome.fasta` file to select it for classification.
- Enter your email address in the **Provide contact details** field

Provide contact details

Your correct contact e-mail for result receipt ... ?

- Click on **Submit query** and wait for the results

When will my results be available?

In approx. 103 minutes (estimation based on average case).
 Current usage of compute cluster: medium

How to proceed once the results are ready?

TYGS will send a notification e-mail once your job is done. Results **won't** be send as an e-mail attachment. Instead, these can be conveniently accessed via your unique result link (see above). For both privacy and data security reasons we will remove user data and results older than 14 days. Please let us know if you think that this retention period should be further increased.

⚠ Warning

This may take some time (maybe over an hour, depending on server load!), and may not be complete before the end of the workshop.

You can download TYGS example output (obtained 2025-01-29) from the links below

- [PDF output](#)
- [Whole-genome tree](#)

Please move on to the next section while you are waiting.

- When you get the result confirmation email, download and inspect the result PDF, and examine the whole-genome tree.

! Questions

- What is the predicted taxonomic classification of your isolate's genome?
- How similar is your isolate's genome to the closest match? (the d_4 result is the dDDH (digital DNA-DNA hybridisation) score)
- What are the most closely-related species and genera in the whole-genome tree? Is the distribution of genera consistent with what was previously known about *Ochrobactrum* and *Brucella* taxonomy?
- What is your current opinion about the identity of your isolate? How confident are you in the identification?

5.2 genomeRxiv

genomeRxiv is a recently-developed approach to bacterial classification that promises to identify and classify prokaryotic genomes quickly and accurately into categories called LINgroups (LIN: Life Identification Number). LINgroups are a taxonomy-independent, quantitative categorisation scheme that organises genome sequences by similarity in multidimensional “space”. These categorisations can then be used to relate alternative taxonomic assignments, and other annotations, to each other (Pritchard et al. (2022)).

How genomeRxiv works

genomeRxiv works in a similar way to [map grid references](#).

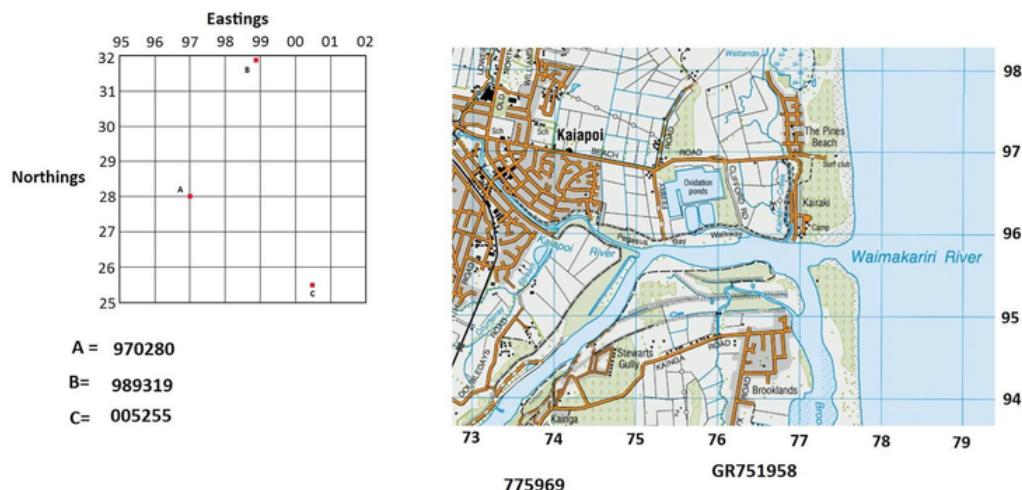


Figure 5.1: Example map grid references: point A has grid reference 970 (Easting) and 280 (Northing) as *x-y* co-ordinates, so the total reference is 970280. Similarly, point B is at 989319, and point C at 005255. All points in the map, however large or small, are uniquely assigned to a discrete location and, by subdividing the map into smaller and smaller squares (longer and longer numbers) an arbitrary level of precision can be reached

genomeRxiv compares input sequences to a reference database with a very fast bioinformatics algorithm (`sourmash`) to get a set of good matches, and then refines the match with a more precise but slower algorithm (`ANI`). genomeRxiv then assigns a LINgroup to the genome (Tian et al. (2021)). The LINgroup is a string of numbers, analogous to a map co-ordinate. The shorter the LINgroup, the lower the resolution of identification (Phylum, Family, etc.), and the longer the LINgroup, the finer the resolution (species, subspecies, strain, etc.).

The first key difference between LINgroups and map co-ordinates is that LINgroups are not co-ordinates on a two-dimensional surface, but in many-dimensional space. The second is that a single number describes the location, rather than two numbers (the “Easting” and “Northing” of map co-ordinates). Finally, grid references represent a physical space (such as the surface of the Earth), and LINgroups represent “sequence space” - which is not physical (Mazloom et al. (2022)).

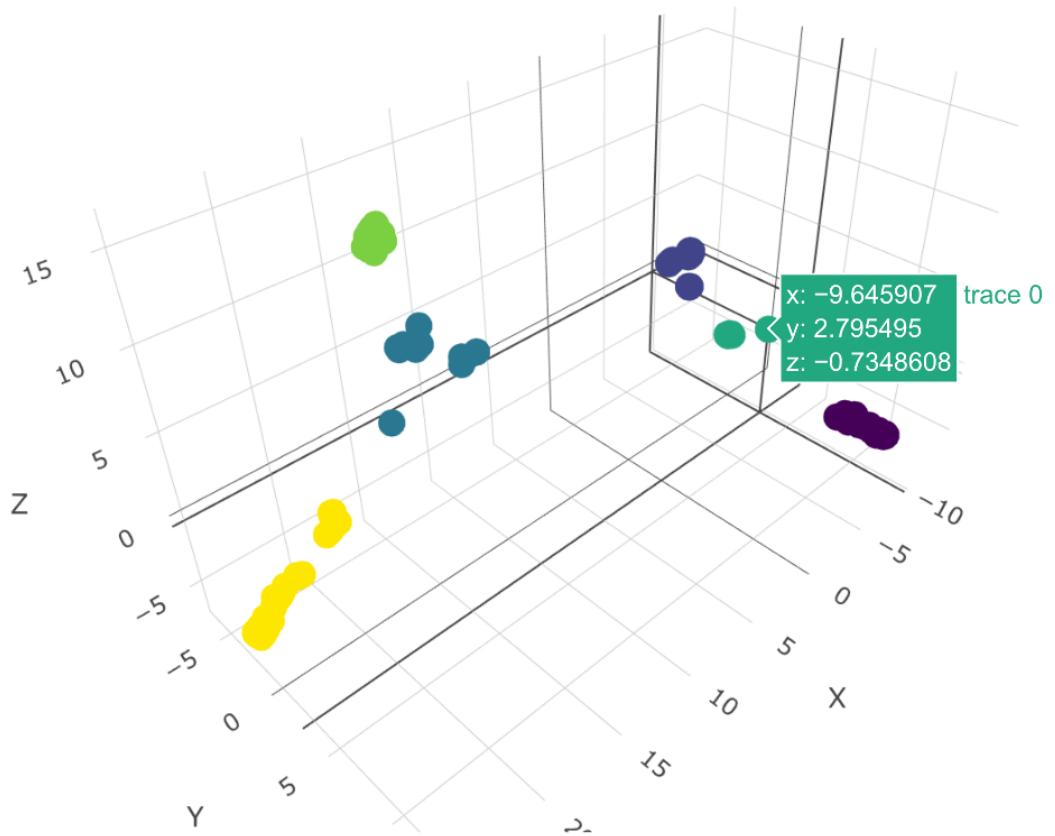


Figure 5.2: Example arbitrary projection of 380 *Ralstonia solanacearum* genomes into three dimensions, based on overall genome similarity. Each sphere is a single genome. The genomes can be clustered into groups of genomes that are more similar to each other than they are to other genomes in the dataset. These clusters are assigned different colours. Each genome, such as the one indicated, has a unique co-ordinate in this “sequence space.”

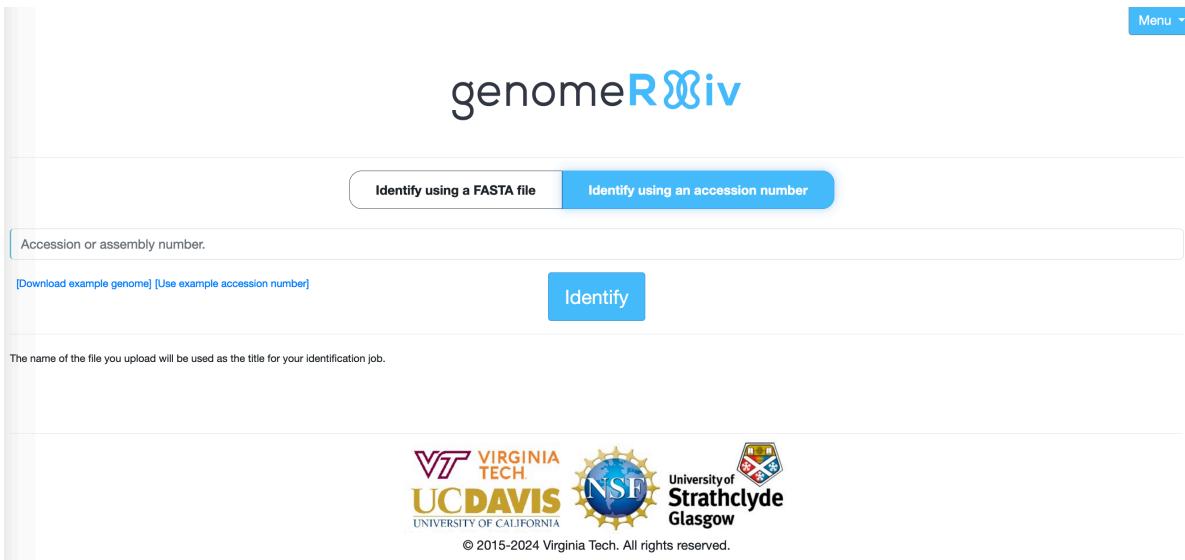
Taxa are then defined by the volumes in space circumscribed by genomes which are examples of each taxon. When a new unknown genome is added, a LINgroup is assigned and - if it lies within a volume of space contained only by members of a single taxon (e.g. *E. coli*), the genome is assigned that taxon.

The [genomeRxiv webservice](#) allows users to input their bacterial genomes and rapidly obtain, or predict, taxonomic assignments on the basis of genome sequence.

Warning

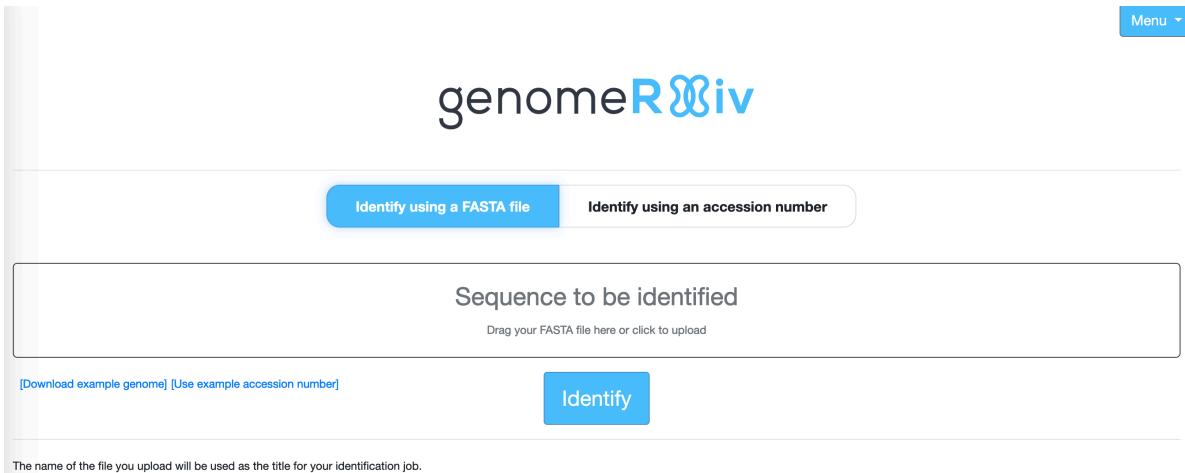
genomeRxiv remains under active development and is not yet fully-released, although it is public and usable.

- Go to the [genomeRxiv](#) server



The screenshot shows the genomeRxiv homepage. At the top right is a "Menu" button. The main title "genomeRxiv" is centered above two buttons: "Identify using a FASTA file" (white background) and "Identify using an accession number" (blue background). Below these buttons is a text input field with placeholder text "Accession or assembly number." Underneath the input field are links "[Download example genome]" and "[Use example accession number]". To the right of these links is a blue "Identify" button. A note below the input field states: "The name of the file you upload will be used as the title for your identification job." At the bottom of the page, there are logos for Virginia Tech, UC Davis, NSF, and University of Strathclyde Glasgow, followed by the copyright notice: "© 2015-2024 Virginia Tech. All rights reserved."

- Click on Identify using a FASTA file



The screenshot shows the "Identify using a FASTA file" page. At the top right is a "Menu" button. The main title "genomeRxiv" is centered above two buttons: "Identify using a FASTA file" (blue background) and "Identify using an accession number" (white background). Below these buttons is a large text input area with the placeholder "Sequence to be identified". Underneath the input area is the instruction "Drag your FASTA file here or click to upload". Below the input area are links "[Download example genome]" and "[Use example accession number]". To the right of these links is a blue "Identify" button. A note below the input area states: "The name of the file you upload will be used as the title for your identification job."

- Either click on the **Sequence to be identified** link to bring up a dialogue box through which you can upload the `isolate_genome.fasta` file, or drag the `isolate_genome.fasta` file onto the text.
- Click on **Identify** and wait for the results

Note

The genomeRxiv site may ask you to allow pop-ups. You should allow the pop-ups, as these contain the identification output you need.

Interpreting genomeRxiv results

genomeRxiv provides three classifications:

- **Tentative LIN:** this is the LIN specific to the submitted genome. It may or may not match an existing, previously-assigned LIN.
- **Closest Genome:** this is the LIN corresponding to the closest-matching genome in the genomeRxiv database. It is unlikely to match the LIN of the submitted genome exactly, even if it's a genome from the same species.
- **Member LINgroups:** this is the LINgroup that circumscribes a known taxon, as close to *and enclosing* the submitted genome, as possible. This is the likely identity of your isolate.

Questions

1. What is the predicted taxonomic classification of your isolate's genome? (Check the **Member LINgroups** result)
2. What is the taxonomic identity assigned to the most similar genome in the database?
3. How similar is your isolate's genome to the closest match? (Look at the **ANI to Target** value)
4. What is your current opinion about the identity of your isolate? Have you modified your classification? How confident are you in the identification?

Consider your final evaluation

You have now used a number of different online bioinformatics tools to obtain a possible taxonomic classification for the isolate in your blood sample. You should, by this point, have some idea of what you think the organism is, and how confident you are. Now it's time to take a look at the official prokaryotic nomenclature database, to get a little more context around the candidate taxonomic name. Click on the link to [LPSN](#) (here, or below), to keep going.

6 LPSN: the List of Prokaryotic names with Standing in Nomenclature

Although we have referred to authoritative sources there is, in fact, no official classification of prokaryotes (Tindall (1999)). Also, the terms *nomenclature*, *taxonomy*, and *phylogeny* are not interchangeable.

💡 Understanding the difference

- **phylogeny:** A *phylogeny* is the evolutionary history of a set of organisms, or a model (such as a phylogenetic tree) representing that history
- **taxonomy:** A *taxonomy* is a scheme for ordering objects into groups or classes, or the rules for doing so
- **nomenclature:** *Nomenclature* is the set of names assigned to groups in a taxonomy, or the set of rules for doing so

We do not know the “true” evolutionary histories of organisms, so the *phylogenies* we reconstruct as scientists are estimates - sometimes very precise estimates! - of evolutionary history.

The *phylogenies* we construct allow us to make decisions about how to organise organisms into a *taxonomy*: groups of organisms (taxa) that comprise species, genera, phyla, and so on.

The names we give to taxa are governed by the rules of *nomenclature*. Those names are regulated by the [International Code of Nomenclature of Prokaryotes \(ICNP\)](#). This document is produced by the [International Committee on Systematics of Prokaryotes \(ICSP\)](#), a group of about 35 scientists who compose the rules by which bacteria are named.

⚠ ICSP Do Not Have a Taxonomic Opinion

The ICSP do not decide which organisms go into any particular taxon (genus, species, etc.) - scientific opinion is ever-changing in this area. ICSP, through the ICNP, only decide what is a validly published name. The name of a taxon is validly published, and therefore *has standing in nomenclature*, only if certain criteria are met.

i The LPSN is the authoritative database of validly-published names for prokaryotes.

6.1 Investigating your classification at LPSN

- Go to the [LPSN](#) server
- Enter the species classification you think should be assigned to your organism in the **Search taxonomy** field, and hit **Return/Enter**. The result should appear immediately.

! Questions

1. What kind of taxonomic category does the name of your organism represent?
2. What does the name mean, and what does it imply about the organism?
3. Is the name you entered a validly published taxonomic name?
4. What is the parent taxon for this name?

- Click on the link by **Parent taxon**: (the value here is also the answer to question 4. above).

! Questions

1. What kind of taxonomic category does this name represent?
2. What does the name mean, and what does it imply about the bacteria?
3. Is the name you entered a validly published taxonomic name?
4. What is the **Taxonomic status** of this name?
5. Is this name the “correct name” for the organism?

⚠ What does “correct name” mean in a taxonomic context?

The precise meaning of “correct name” in this context is provided in a [glossary at LPSN](#). The key points in that text are:

- Any taxon may have only one *correct* name. This is usually the earliest validly published, legitimate name.
- The LPSN selects certain taxon names as *correct* names. If more than one option is available, then the LPSN’s choice reflects only *one* of the taxonomic opinions expressed in the literature.
- The *correct* name for an organism should be used in the literature.
- Other valid names are given *synonym* status.
- Other scientists may express distinct taxonomic opinions and are permitted to do

so, by using a *synonym*.

The term *correct* is therefore used in a technical sense, in a taxonomic context. The existence of a *correct* name for a taxon does not imply that other names (*synonyms*) are invalid or cannot be used.

- Read the **Notes** section on the LPSN page for *Ochrobactrum* (the genus).

! Questions

1. How do the notes on this page reflect the controversy over naming of *Ochrobactrum/Brucella* described in the [Introduction](#)?
2. Does the LPSN page affect your opinion about how you have classified your isolate?
3. Finally, what is the taxonomic name you think is most appropriate for your isolate?

7 Summary

In this workshop, you have:

1. gained experience using 16S and whole-genome sequence data to identify, bioinformatically, an unknown organism, using:
 - two 16S databases and associated search services to identify matching sequences from other organisms
 - the main reference MLST database (pubMLST) and its search tool to obtain a classification for your organism
 - two whole-genome classification approaches to obtain taxonomic classifications for your organism
2. considered and weighed the evidence from these approaches to draw an informed conclusion about the most likely taxonomic assignment, considering:
 - the relative information used by each method
 - the quality of the database(s) used in each approach
 - the bioinformatic approach taken
3. interpreted your classification according to the rules laid down in the ICNP (International Code of Nomenclature of Prokaryotes), a.k.a. the Prokaryotic Code, and at LPSN (the List of Prokaryotic names with Standing in Nomenclature).

Thank you

That's almost the end of the workshop. Thank you for participating. We hope you found it enjoyable and interesting, and that you now understand more about how bacterial classification works, in practice.

This year is the first presentation of this particular material, and we would be very grateful to hear feedback [by email](#) or through the [GitHub repository Issues page](#).

Completing the workshop

Please now proceed to the [BM329 MyPlace](#) page and complete the formative questions, to finish the workshop.

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