EUROPEAN CENTRE FOR
DISEASE PREVENTION
AND CONTROL

Virtual Training 8

Leptospira bigsDB PASTEUR

2024-07-22

Intended Learning Objectives

Leptospira bigsDB PASTEUR basic use

1. How to search in bigsDB Leptospira PASTEUR
2. How to blast a given sequence in bigsDB Leptospira PASTEUR (lfb1)
3. How to retrieve informations from clustering based on cgMLST

Outline

This session consists of the following elements

1. Introduction to bigsDB Leptpospira PASTEUR web interface
2. Introduction to cgMLST Leptospira in bigsDB PASTEUR
3. Practice of lfb1 blast and search for similar isolates

Please download and install the
Slido app on all computers you use

Audience Q&A Session

ⓘ Start presenting to display the audience questions on this slide.

slido

Please download and install the
Slido app on all computers you use

Leptospira molecular analysis

ⓘ Start presenting to display the poll results on this slide.

bigsdDB Leptospira web interface

Where : https://bigsdb.pasteur.fr/leptospira/

What : BIGSdb is software designed to store and analyse sequence data for bacterial isolates.

How : it hosts collections of curated, open or private databases of bacterial isolates, genomes and genotypes based on multilocus sequence typing

© Images : Institut Pasteur & © Design : Institut Pasteur

This page provides access to genotypic data for *Leptospira* isolates based on core genome MLST (cgMLST). See references for more details.

The BIGSdb website Policy concerning the platform & data use agreement and the privacy notice of BIGSdb-Pasteur was updated on March 25, 2024. Please consult it before using the platform and the data.

The procedure for submitting data for curation were updated on Mai 03, 2024. Please consult them before making a new submission. If any questions, contact us.

Alleles & profiles database

The typing database contains nomenclature - allele definitions that provide an identifier for every unique allele sequence, and MLST profiles that index each unique combination of alleles with a sequence type (ST).

Isolates & genomes database

The isolate database consists of isolate records containing provenance and phenotype information linked to molecular typing information. These records may also include genome assemblies.

Data submission

We appreciate if you can recognize our efforts in the acknowledgments section of your publications:

> We thank the Institut Pasteur teams for the curation and maintenance of BIGSdb-Pasteur databases at https://bigsdb.pasteur.fr/.

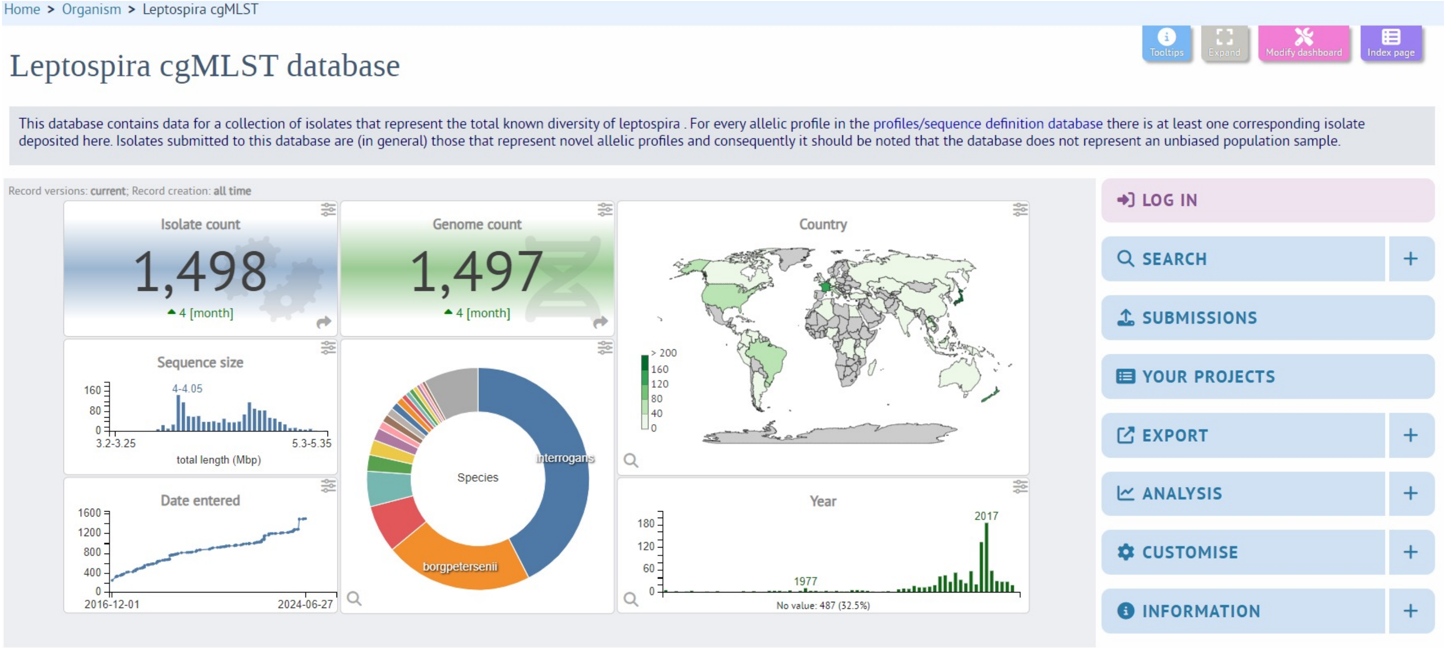
Curators access

Data Curation is performed on a voluntary basis and is based on a community effort.

Leptospira isolate database

To look for available isolates and metadata related to those curated sequence

- Possiblity to access to public isolates including related epidemiological data
- Possiblity to temporarily submit isolates in private environment (prior publication for example)



Home > Organism > Leptospira cgMLST

Leptospira cgMLST database

This database contains data for a collection of isolates that represent the total known diversity of leptospira . For every allelic profile in the profiles/sequence definition database there is at least one corresponding isolate deposited here. Isolates submitted to this database are (in general) those that represent novel allelic profiles and consequently it should be noted that the database does not represent an unbiased population sample.

Record versions: **current**; Record creation: **all time**

Isolate count: 1,498 (▲ 4 [month])

Genome count: 1,497 (▲ 4 [month])

Web interface bisgDB Leptospira and search tool

Search for isolate based on « species » and « serogroup » criterium

<u>Study case :</u>

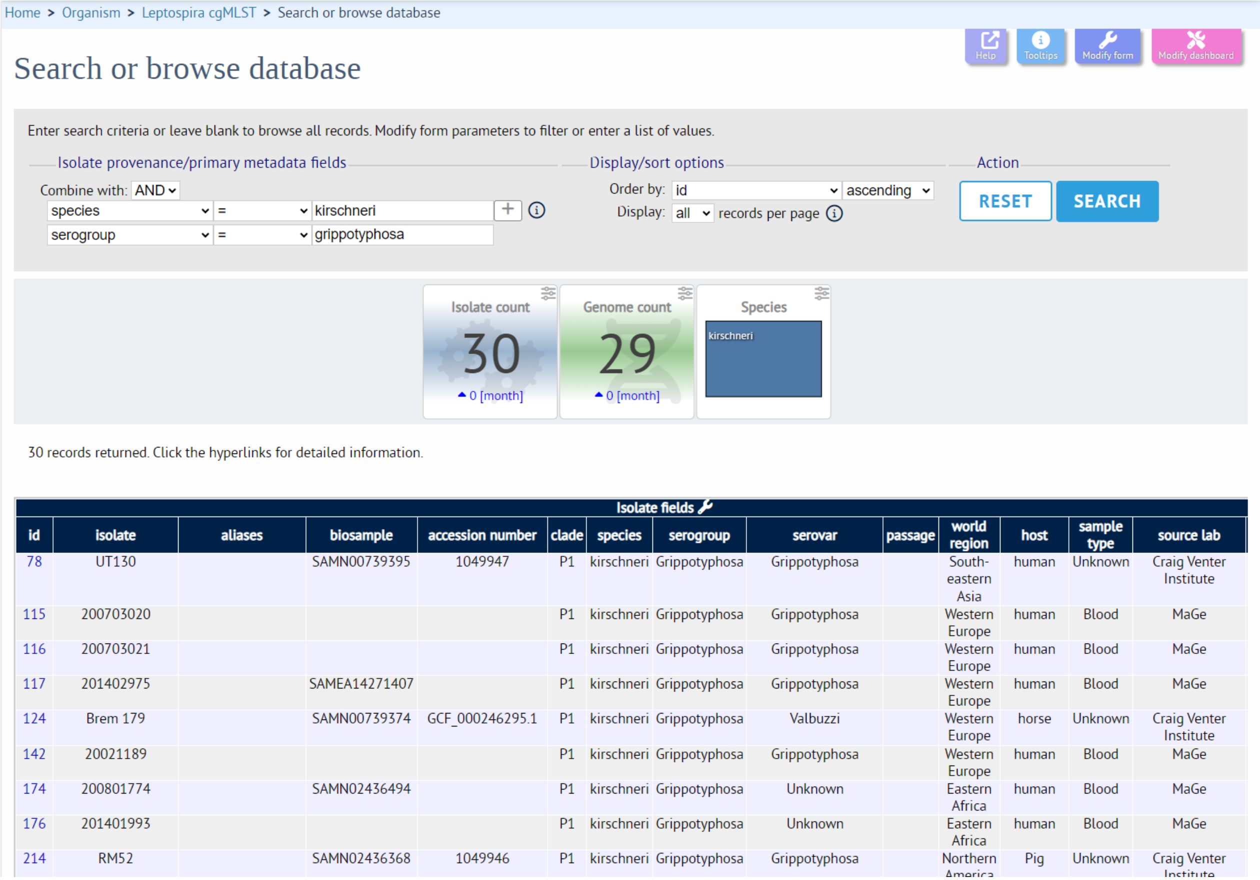
✓ species « kirschneri »
✓ serogroup « Grippotyphosa »

<u>Output :</u>

List of 29 genomes

<u>Type of metadata available :</u>

World region, host, sample type



Home > Organism > Leptospira cgMLST > Search or browse database

Search or browse database

Enter search criteria or leave blank to browse all records. Modify form parameters to filter or enter a list of values.

Isolate provenance/primary metadata fields

Combine with: AND
species = kirschneri
serogroup = grippotyphosa

Display/sort options

Order by: id ascending
Display: all records per page

Action

Isolate count 30 ▲0 [month]

Genome count 29 ▲0 [month]

Species

30 records returned. Click the hyperlinks for detailed information.

Isolate fields

id	isolate	aliases	biosample	accession number	clade	species	serogroup	serovar	passage	world region	host	sample type	source lab
78	UT130		SAMN00739395	1049947	P1	kirschneri	Grippotyphosa	Grippotyphosa		South-eastern Asia	human	Unknown	Craig Venter Institute
115	200703020				P1	kirschneri	Grippotyphosa	Grippotyphosa		Western Europe	human	Blood	MaGe
116	200703021				P1	kirschneri	Grippotyphosa	Grippotyphosa		Western Europe	human	Blood	MaGe
117	201402975		SAMEA14271407		P1	kirschneri	Grippotyphosa	Grippotyphosa		Western Europe	human	Blood	MaGe
124	Brem 179		SAMN00739374	GCF_000246295.1	P1	kirschneri	Grippotyphosa	Valbuzzi		Western Europe	horse	Unknown	Craig Venter Institute
142	20021189				P1	kirschneri	Grippotyphosa	Grippotyphosa		Western Europe	human	Blood	MaGe
174	200801774		SAMN02436494		P1	kirschneri	Grippotyphosa	Unknown		Eastern Africa	human	Blood	MaGe
176	201401993				P1	kirschneri	Grippotyphosa	Unknown		Eastern Africa	human	Blood	MaGe
214	RM52		SAMN02436368	1049946	P1	kirschneri	Grippotyphosa	Grippotyphosa		Northern America	Pig	Unknown	Craig Venter Institute

cgMLST Leptospira based on subselection

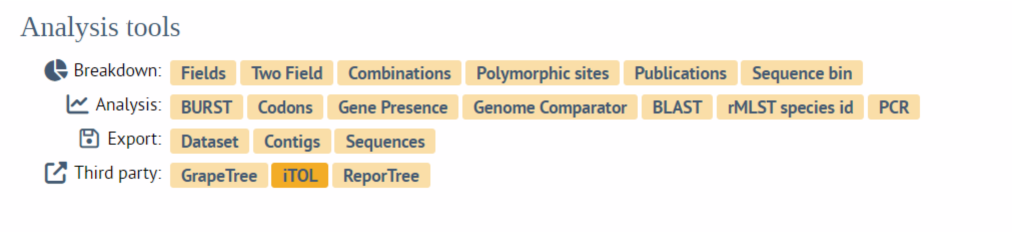
Several tool to analyse or download informations related to subselection of isolates

<u>Study case :</u>

tool « iTOL » to build cgMLST phylogeny
Subselection k29 kirschneri grippotyphosa isolates

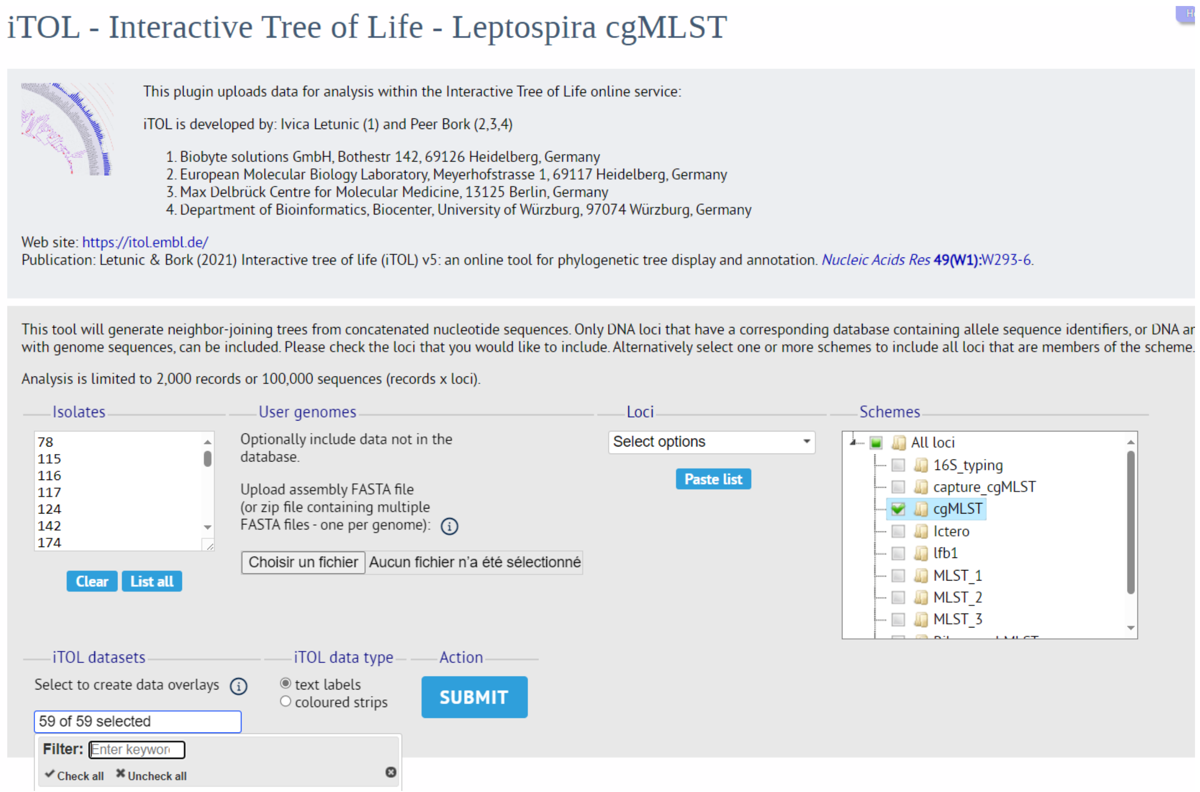
<u>Output</u>
Phylogeny annotated with metadata

Result to come in a few minutes



Analysis tools

Breakdown: Fields | Two Field | Combinations | Polymorphic sites | Publications | Sequence bin
Analysis: BURST | Codons | Gene Presence | Genome Comparator | BLAST | rMLST species id | PCR
Export: Dataset | Contigs | Sequences
Third party: GrapeTree | iTOL | ReporTree



iTOL - Interactive Tree of Life - Leptospira cgMLST

This plugin uploads data for analysis within the Interactive Tree of Life online service:

iTOL is developed by: Ivica Letunic (1) and Peer Bork (2,3,4)

1. Biobyte solutions GmbH, Bothestr 142, 69126 Heidelberg, Germany
2. European Molecular Biology Laboratory, Meyerhofstrasse 1, 69117 Heidelberg, Germany
3. Max Delbrück Centre for Molecular Medicine, 13125 Berlin, Germany
4. Department of Bioinformatics, Biocenter, University of Würzburg, 97074 Würzburg, Germany

Web site: https://itol.embl.de/
Publication: Letunic & Bork (2021) Interactive tree of life (iTOL) v5: an online tool for phylogenetic tree display and annotation. *Nucleic Acids Res* **49(W1)**:W293-6.

This tool will generate neighbor-joining trees from concatenated nucleotide sequences. Only DNA loci that have a corresponding database containing allele sequence identifiers, or DNA ar with genome sequences, can be included. Please check the loci that you would like to include. Alternatively select one or more schemes to include all loci that are members of the scheme.

Analysis is limited to 2,000 records or 100,000 sequences (records x loci).

Isolates
78
115
116
117
124
142
174
Clear | List all

User genomes
Optionally include data not in the database.

Upload assembly FASTA file (or zip file containing multiple FASTA files - one per genome): ⓘ
Choisir un fichier | Aucun fichier n'a été sélectionné

Loci
Select options
Paste list

Schemes
- All loci
  - ☐ 16S_typing
  - ☐ capture_cgMLST
  - ☑ cgMLST
  - ☐ Ictero
  - ☐ lfb1
  - ☐ MLST_1
  - ☐ MLST_2
  - ☐ MLST_3

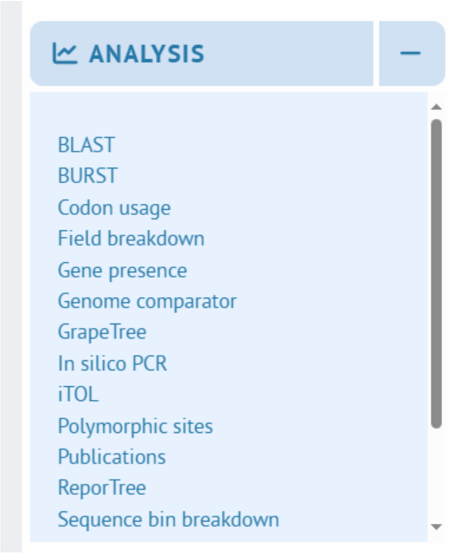
iTOL datasets
Select to create data overlays ⓘ
59 of 59 selected
Filter: Enter keywor
✓ Check all ✖ Uncheck all

iTOL data type
● text labels
○ coloured strips

Action
SUBMIT

BLAST tool to analyse lfb1 sequence

BLAST lfb1 sequence to find related sequence in database



<u>Study case :</u>

lfb1 sequence available in file
« GenEpiBioVirtualTraining8.txt »
Or displayed in chat

<u>Sequence</u>

« attcttcctcgcccttctagtattcggttttatttcgaccgcttacgcacagatcggtca
aatcaatccttcttccatcagcggtaaatacaaggtttctggaaccaacccgaacggtt
cctcttacggcggtagcgttacgatttctgaatctaacggagaataccttttacctgga
cagtcgccggtcaaactttcacaggaaccggaacccttgaaggtactactttgacagt
agattggggagaggttgaaccggtgatctatgaagtaaaaa »

Output BLAST lfb1 sequence

<u>Output :</u>
Table showing three sequence with 100% identity

Direct link to epidemiological data by click on isolate id

Job status viewer

Status

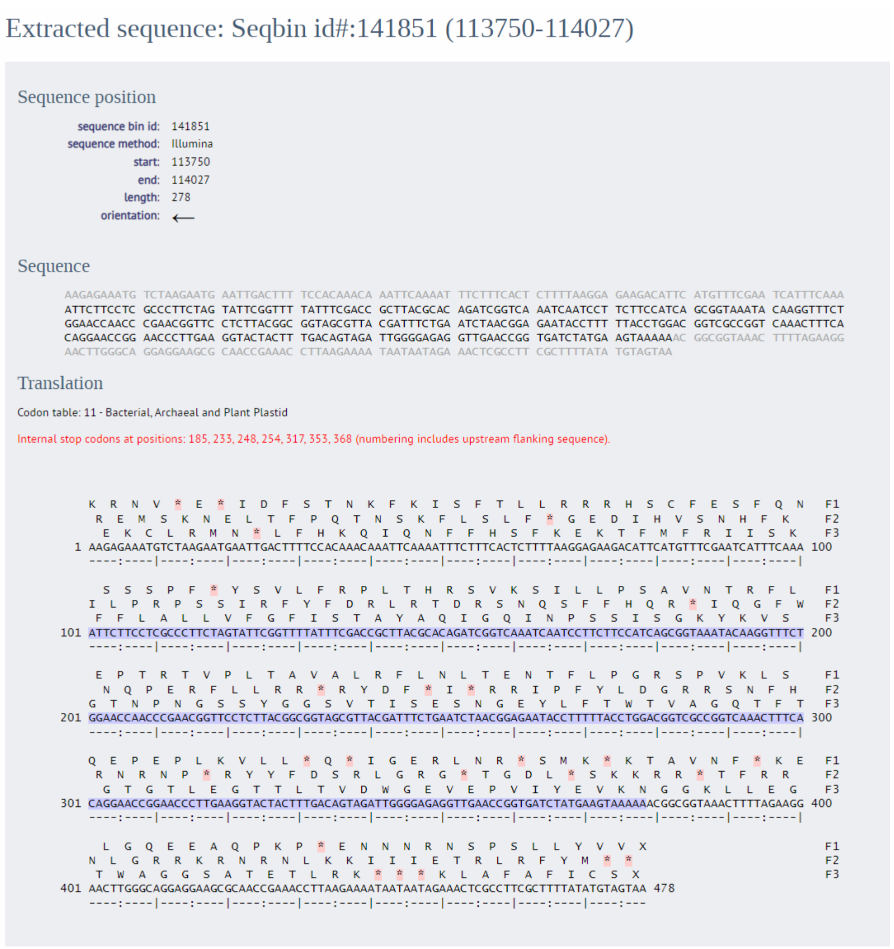
Job id: BIGSdb_3190924_4250059301_15065
Title: blast-lfb1-kirschneri-grippotyphosa
Submit time: 2024-07-11 17:26:58
Status: finished
Start time: 2024-07-11 17:27:02
Progress: 100%
Stop time: 2024-07-11 17:29:46
Total time: 2 minutes and 43 seconds

Output

Isolate id	Isolate	% identity	Alignment length	Mismatches	Gaps	Seqbin id	Start	End	Orientation	E-value	Bit score
78	UT130	99.281	278	2	0	22217	1931	2208 extract →	←	2.92e-140	493
115	200703020	99.640	278	1	0	30456	77465	77742 extract →	→	2.32e-141	498
116	200703021	99.640	278	1	0	30532	18788	19065 extract →	→	2.33e-141	498
117	201402975	99.640	278	1	0	30598	248097	248374 extract →	←	2.33e-141	498
124	Brem 179	99.640	278	1	0	31826	10255	10532 extract →	→	2.22e-141	498
142	20021189	99.640	278	1	0	37251	132174	132451 extract →	←	2.32e-141	498
174	200801774	99.640	278	1	0	44521	10269	10546 extract →	→	2.48e-141	498
176	201401993	99.640	278	1	0	44829	21782	22059 extract →	←	2.47e-141	498
214	RM52	99.640	278	1	0	48752	34353	34630 extract →	→	2.36e-141	498
305	Brem 127 Duyster	99.640	278	1	0	67447	4590	4867 extract →	←	2.29e-141	498
315	dessain	99.640	278	1	0	68584	10137	10414 extract →	→	2.17e-141	498
383	201600670	99.640	278	1	0	84571	19393	19670 extract →	→	2.46e-141	498
403	201700045	96.763	278	9	0	90417	41293	41570 extract →	←	1.68e-130	462
442	ratnapura1236	96.763	278	9	0	113117	44548	44825 extract →	←	1.68e-130	462
444	ratnapura1439	96.763	278	9	0	354527	71154	71431 extract →	→	1.68e-130	462
451	grippotyphosa1473	99.640	278	1	0	112446	33741	34018 extract →	←	2.31e-141	498
484	kirsch ratnapura1142	96.763	278	9	0	116521	14732	15009 extract →	←	1.70e-130	462
489	kirsch ratnapura1439	96.763	278	9	0	117699	44548	44825 extract →	←	1.69e-130	462
499	LEP1226	99.640	278	1	0	119642	15303	15580 extract →	←	2.32e-141	498
507	kirsch ratnapura1236	96.763	278	9	0	121926	6239	6516 extract →	→	1.69e-130	462
629	112/90	99.640	278	1	0	141851	113750	114027 extract →	←	2.31e-141	498
700	201900331;Moskva V	100.000	278	0	0	190637	4580	4857 extract →	←	5.52e-143	502
1030	202000079	99.281	278	2	0	235188	5397	5674 extract →	←	3.21e-140	493
1038	Ag07_2020	100.000	278	0	0	238872	4580	4857 extract →	←	5.54e-143	502
1094	200201189	99.640	278	1	0	254016	1214	1491 extract →	←	2.30e-141	498
1176	Wumalasena	96.763	278	9	0	276447	245675	245952 extract →	→	1.70e-130	462
1218	202103008	99.640	278	1	0	289398	4624	4901 extract →	←	2.31e-141	498
1618	Moskva	100.000	278	0	0	360801	121502	121779 extract →	→	5.48e-143	502
1624	200702274	99.640	278	1	0	363407	98183	98460 extract →	←	2.32e-141	498

Files

Id 700 : output BLAST lfb1 sequence



Extracted sequence: Seqbin id#:141851 (113750-114027)

Sequence position

sequence bin id: 141851
sequence method: Illumina
start: 113750
end: 114027
length: 278
orientation: ←

Sequence

```
AAGAGAAATG TCTAAGAATG AATTGACTTT TCCACAAACA AATTCAAAAT TTCTTTCACT CTTTTAAGGA GAAGACATTC ATGTTTCGAA TCATTTCAAA
ATTCTTCCTC GCCCTTCTAG TATTCGGTTT TATTTCGACC GCTTACGCAC AGATCGGTCA AATCAATCCT TCTTCCATCA GCGGTAAATA CAAGGTTTCT
GGAACCAACC CGAACGGTTC CTCTTACGGC GGTAGCGTTA CGATTTCTGA ATCTAACGGA GAATACCTTT TTACCTGGAC GGTCGCCGGT CAAACTTTCA
CAGGAACCGG AACCCTTGAA GGTACTACTT TGACAGTAGA TTGGGGAGAG GTTGAACCGG TGATCTATGA AGTAAAAAAC GGCGGTAAAC TTTTAGAAGG
AACTTGGGCA GGAGGAAGCG CAACCGAAAC CTTAAGAAAA TAATAATAGA AACTCGCCTT CGCTTTTATA TGTAGTAA
```

Translation

Codon table: 11 - Bacterial, Archaeal and Plant Plastid

Internal stop codons at positions: 185, 233, 248, 254, 317, 353, 368 (numbering includes upstream flanking sequence).

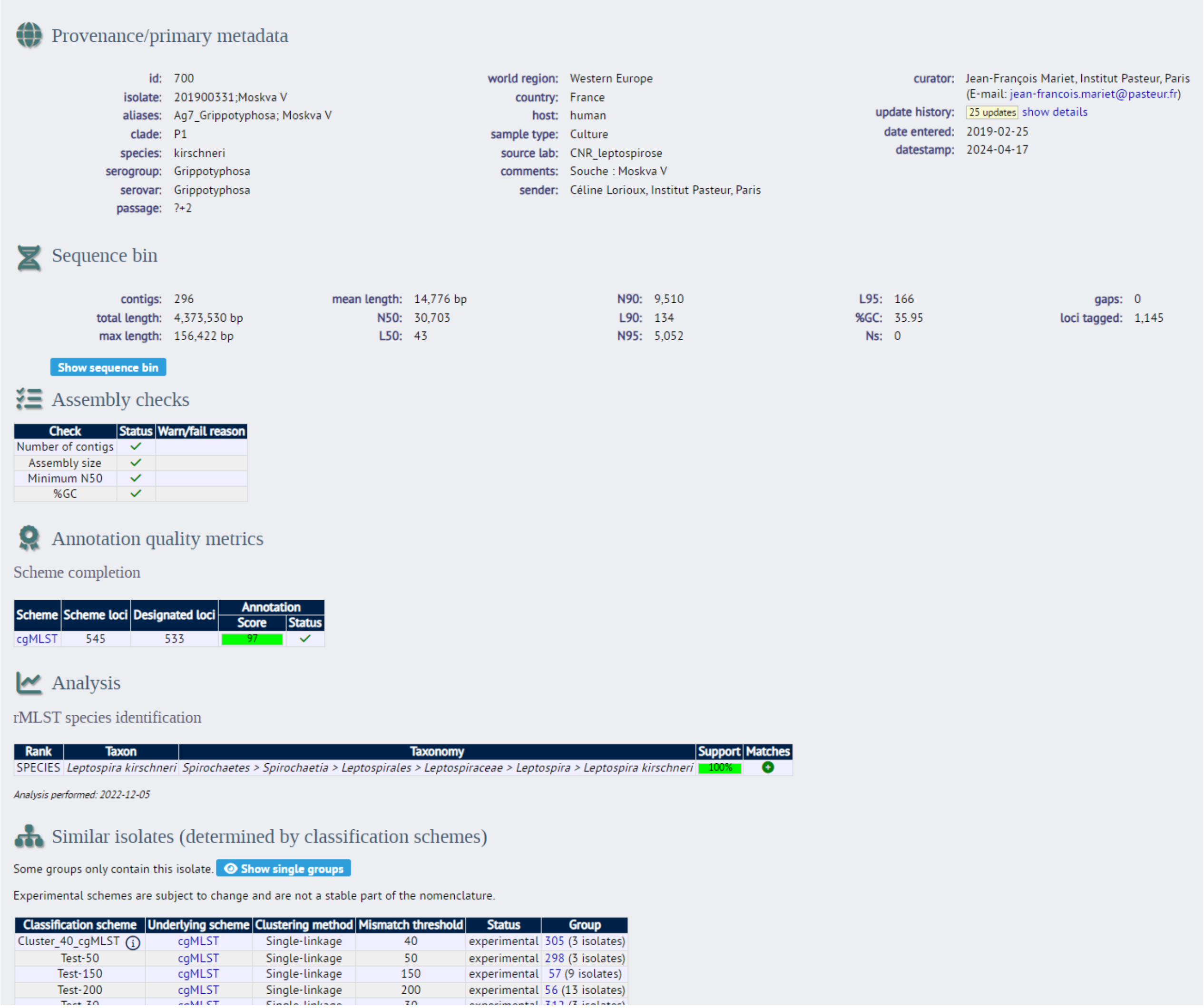
```
    K  R  N  V  *  E  *  I  D  F  S  T  N  K  F  K  I  S  F  T  L  L  R  R  R  H  S  C  F  E  S  F  Q  N    F1
     R  E  M  S  K  N  E  L  T  F  P  Q  T  N  S  K  F  L  S  L  F  *  G  E  D  I  H  V  S  N  H  F  K      F2
      E  K  C  L  R  M  N  *  L  F  H  K  Q  I  Q  N  F  F  H  S  F  K  E  K  T  F  M  F  R  I  I  S  K     F3
  1 AAGAGAAATGTCTAAGAATGAATTGACTTTTCCACAAACAAATTCAAAATTTCTTTCACTCTTTTAAGGAGAAGACATTCATGTTTCGAATCATTTCAAA 100
    ----:----|----:----|----:----|----:----|----:----|----:----|----:----|----:----|----:----|----:----|

      S  S  S  P  F  *  Y  S  V  L  F  R  P  L  T  H  R  S  V  K  S  I  L  L  P  S  A  V  N  T  R  F  L     F1
    I  L  P  R  P  S  S  I  R  F  Y  F  D  R  L  R  T  D  R  S  N  Q  S  F  F  H  Q  R  *  I  Q  G  F  W    F2
     F  F  L  A  L  L  V  F  G  F  I  S  T  A  Y  A  Q  I  G  Q  I  N  P  S  S  I  S  G  K  Y  K  V  S      F3
101 ATTCTTCCTCGCCCTTCTAGTATTCGGTTTTATTTCGACCGCTTACGCACAGATCGGTCAAATCAATCCTTCTTCCATCAGCGGTAAATACAAGGTTTCT 200
    ----:----|----:----|----:----|----:----|----:----|----:----|----:----|----:----|----:----|----:----|

     E  P  T  R  T  V  P  L  T  A  V  A  L  R  F  L  N  L  T  E  N  T  F  L  P  G  R  S  P  V  K  L  S      F1
      N  Q  P  E  R  F  L  L  R  R  *  R  Y  D  F  *  I  *  R  R  I  P  F  Y  L  D  G  R  R  S  N  F  H     F2
    G  T  N  P  N  G  S  S  Y  G  G  S  V  T  I  S  E  S  N  G  E  Y  L  F  T  W  T  V  A  G  Q  T  F  T    F3
201 GGAACCAACCCGAACGGTTCCTCTTACGGCGGTAGCGTTACGATTTCTGAATCTAACGGAGAATACCTTTTTACCTGGACGGTCGCCGGTCAAACTTTCA 300
    ----:----|----:----|----:----|----:----|----:----|----:----|----:----|----:----|----:----|----:----|

    Q  E  P  E  P  L  K  V  L  L  *  Q  *  I  G  E  R  L  N  R  *  S  M  K  *  K  T  A  V  N  F  *  K  E    F1
     R  N  R  N  P  *  R  Y  Y  F  D  S  R  L  G  R  G  *  T  G  D  L  *  S  K  K  R  R  *  T  F  R  R      F2
      G  T  G  T  L  E  G  T  T  L  T  V  D  W  G  E  V  E  P  V  I  Y  E  V  K  N  G  G  K  L  L  E  G     F3
301 CAGGAACCGGAACCCTTGAAGGTACTACTTTGACAGTAGATTGGGGAGAGGTTGAACCGGTGATCTATGAAGTAAAAAACGGCGGTAAACTTTTAGAAGG 400
    ----:----|----:----|----:----|----:----|----:----|----:----|----:----|----:----|----:----|----:----|

      L  G  Q  E  E  A  Q  P  K  P  *  E  N  N  N  R  N  S  P  S  L  L  Y  V  V  X                          F1
    N  L  G  R  R  K  R  N  R  N  L  K  K  I  I  I  E  T  R  L  R  F  Y  M  *  *                            F2
     T  W  A  G  G  S  A  T  E  T  L  R  K  *  *  *  K  L  A  F  A  F  I  C  S  X                           F3
401 AACTTGGGCAGGAGGAAGCGCAACCGAAACCTTAAGAAAATAATAATAGAAACTCGCCTTCGCTTTTATATGTAGTAA 478
    ----:----|----:----|----:----|----:----|----:----|----:----|----:----|----:---
```



Provenance/primary metadata

id: 700
isolate: 201900331;Moskva V
aliases: Ag7_Grippotyphosa; Moskva V
clade: P1
species: kirschneri
serogroup: Grippotyphosa
serovar: Grippotyphosa
passage: ?+2

world region: Western Europe
country: France
host: human
sample type: Culture
source lab: CNR_leptospirose
comments: Souche : Moskva V
sender: Céline Lorioux, Institut Pasteur, Paris

curator: Jean-François Mariet, Institut Pasteur, Paris (E-mail: jean-francois.mariet@pasteur.fr)
update history: 25 updates show details
date entered: 2019-02-25
datestamp: 2024-04-17

Sequence bin

contigs: 296
total length: 4,373,530 bp
max length: 156,422 bp
mean length: 14,776 bp
N50: 30,703
L50: 43
N90: 9,510
L90: 134
N95: 5,052
L95: 166
%GC: 35.95
Ns: 0
gaps: 0
loci tagged: 1,145

Assembly checks

Check	Status	Warn/fail reason
Number of contigs	✓	
Assembly size	✓	
Minimum N50	✓	
%GC	✓	

Annotation quality metrics

Scheme completion

Scheme	Scheme loci	Designated loci	Annotation	
			Score	Status
cgMLST	545	533	97	✓

Analysis

rMLST species identification

Rank	Taxon	Taxonomy	Support	Matches
SPECIES	*Leptospira kirschneri*	*Spirochaetes > Spirochaetia > Leptospirales > Leptospiraceae > Leptospira > Leptospira kirschneri*	100%	⊕

Analysis performed: 2022-12-05

Similar isolates (determined by classification schemes)

Some groups only contain this isolate.

Experimental schemes are subject to change and are not a stable part of the nomenclature.

Classification scheme	Underlying scheme	Clustering method	Mismatch threshold	Status	Group
Cluster_40_cgMLST ⓘ	cgMLST	Single-linkage	40	experimental	305 (3 isolates)
Test-50	cgMLST	Single-linkage	50	experimental	298 (3 isolates)
Test-150	cgMLST	Single-linkage	150	experimental	57 (9 isolates)
Test-200	cgMLST	Single-linkage	200	experimental	56 (13 isolates)
Test-30	cgMLST	Single-linkage	30	experimental	312 (3 isolates)

cgMLST Leptospira kirschneri output

Output
iTOL unrooted Phylogeny annotated with metadata, to reroot midpoint in advanced tree

Possiblity to chek metadata of interest to display close to the tree

Job status viewer

Status

Job id: BIGSdb_251876_2382014523_07518
Title: kirgri_cgMLST_itol
Submit time: 2024-07-12 13:29:54
Status: finished
Start time: 2024-07-12 13:30:01
Progress: 100%
Stop time: 2024-07-12 13:46:54
Total time: 16 minutes and 52 seconds

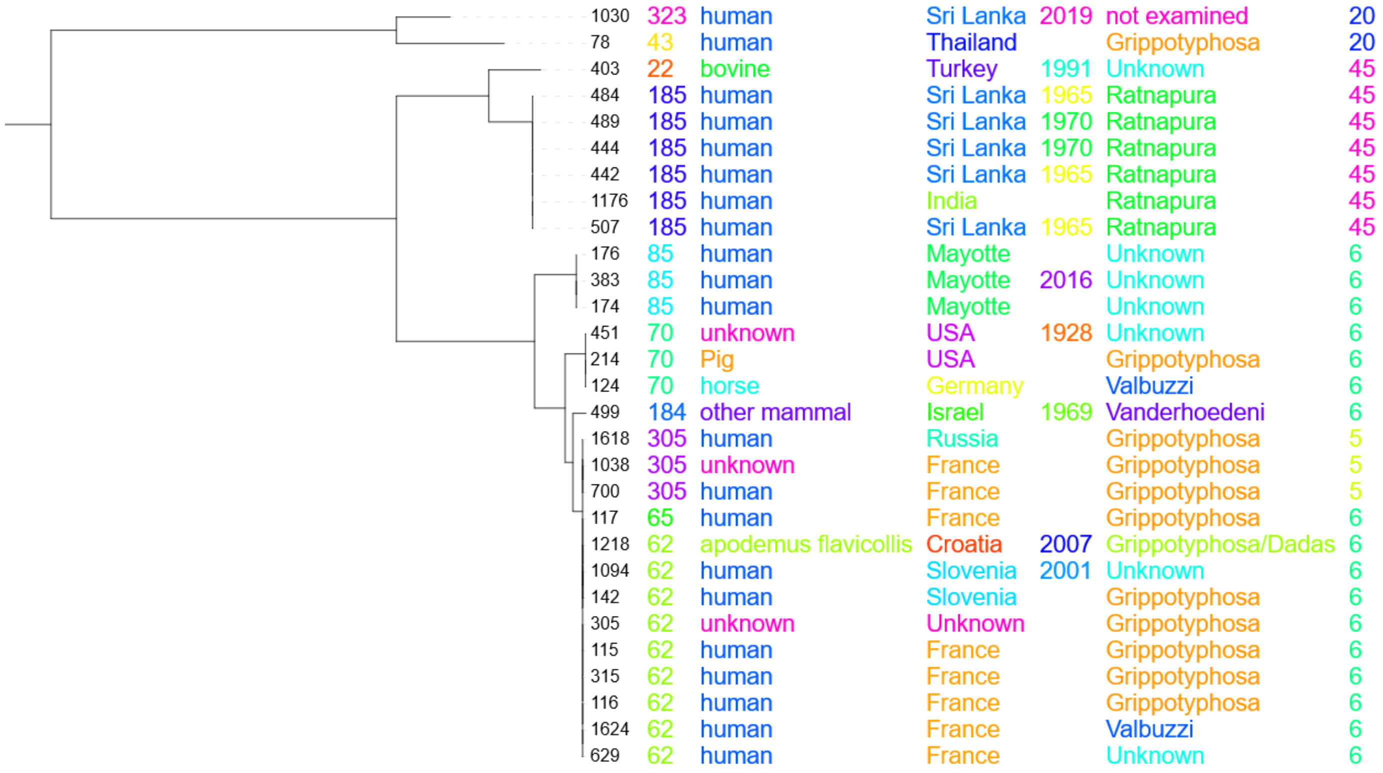
Output

The following ids had no sequences for all the selected loci: 485.

They have been removed from the analysis.

Files

- Concatenated FASTA (16.6 MB)
- NJ tree (Newick format)
- iTOL datasets (Zip format)
- Tar file containing all output files (only files <10MB included - download larger files separately)



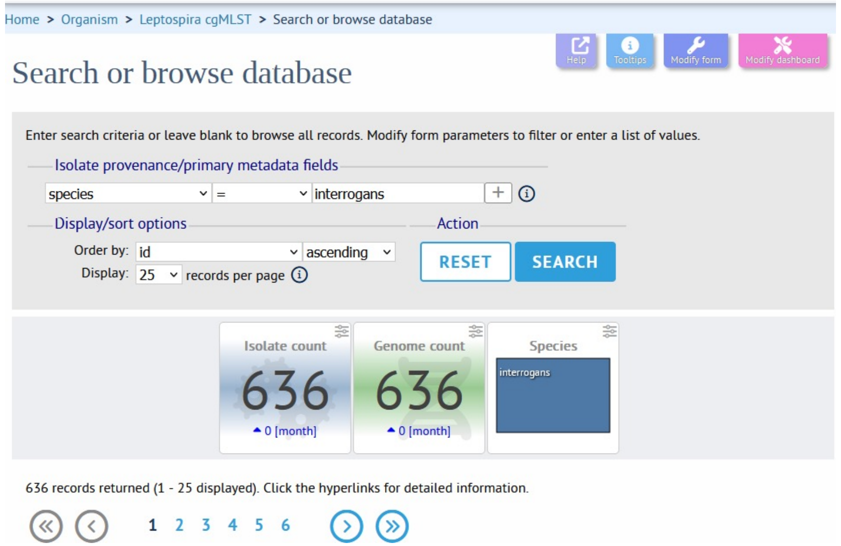
1030	323	human	Sri Lanka	2019	not examined	20
78	43	human	Thailand		Grippotyphosa	20
403	22	bovine	Turkey	1991	Unknown	45
484	185	human	Sri Lanka	1965	Ratnapura	45
489	185	human	Sri Lanka	1970	Ratnapura	45
444	185	human	Sri Lanka	1970	Ratnapura	45
442	185	human	Sri Lanka	1965	Ratnapura	45
1176	185	human	India		Ratnapura	45
507	185	human	Sri Lanka	1965	Ratnapura	45
176	85	human	Mayotte		Unknown	6
383	85	human	Mayotte	2016	Unknown	6
174	85	human	Mayotte		Unknown	6
451	70	unknown	USA	1928	Unknown	6
214	70	Pig	USA		Grippotyphosa	6
124	70	horse	Germany		Valbuzzi	6
499	184	other mammal	Israel	1969	Vanderhoedeni	6
1618	305	human	Russia		Grippotyphosa	5
1038	305	unknown	France		Grippotyphosa	5
700	305	human	France		Grippotyphosa	5
117	65	human	France		Grippotyphosa	6
1218	62	apodemus flavicollis	Croatia	2007	Grippotyphosa/Dadas	6
1094	62	human	Slovenia	2001	Unknown	6
142	62	human	Slovenia		Grippotyphosa	6
305	62	unknown	Unknown		Grippotyphosa	6
115	62	human	France		Grippotyphosa	6
315	62	human	France		Grippotyphosa	6
116	62	human	France		Grippotyphosa	6
1624	62	human	France		Valbuzzi	6
629	62	human	France		Unknown	6

bigsDB search for species Interrogans

Search for isolate based on « species »

<u>Study case :</u> species « interrogans »

<u>Output :</u> List of 636 genomes



Home > Organism > Leptospira cgMLST > Search or browse database

Search or browse database

Enter search criteria or leave blank to browse all records. Modify form parameters to filter or enter a list of values.

Isolate provenance/primary metadata fields

species = interrogans

Display/sort options

Order by: id ascending

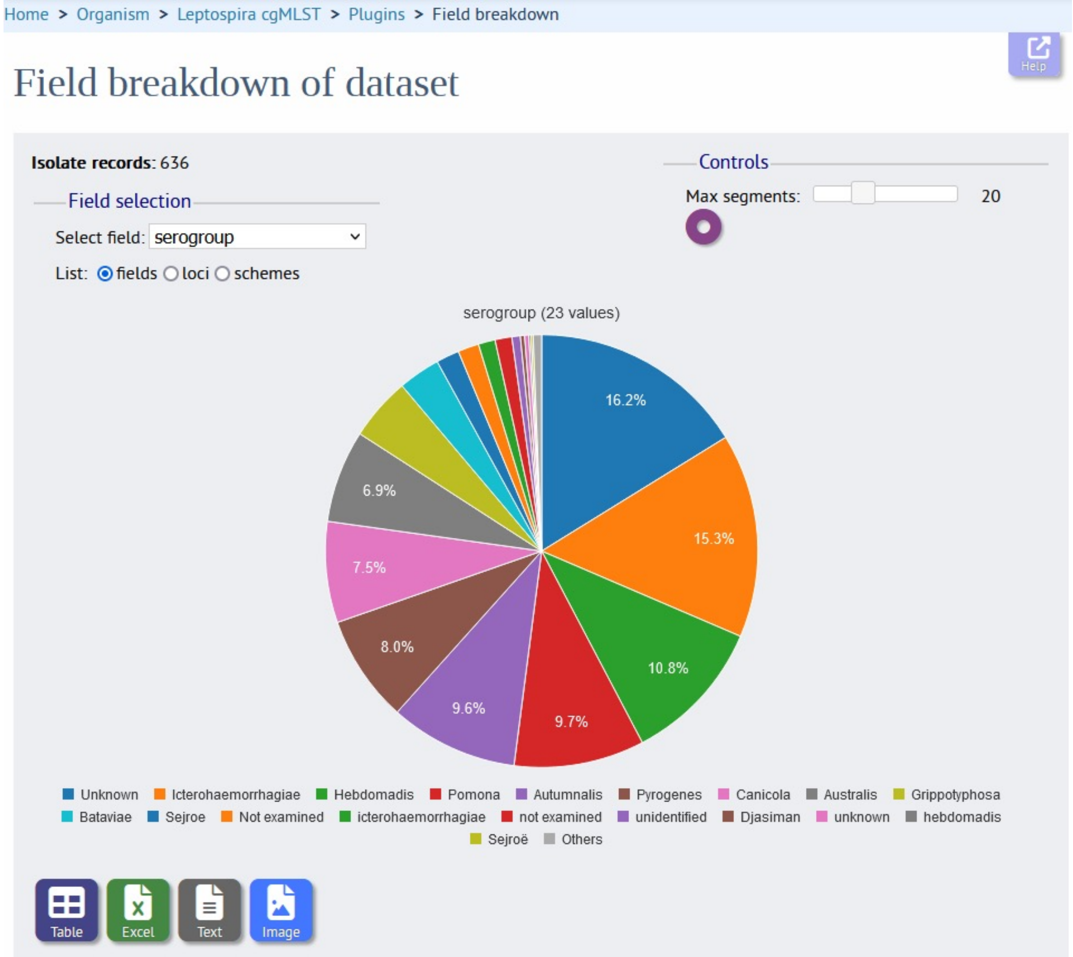
Display: 25 records per page

Isolate count 636 ▲0 [month]

Genome count 636 ▲0 [month]

Species: interrogans

636 records returned (1 - 25 displayed). Click the hyperlinks for detailed information.



Home > Organism > Leptospira cgMLST > Plugins > Field breakdown

Field breakdown of dataset

Isolate records: 636

Field selection

Select field: serogroup

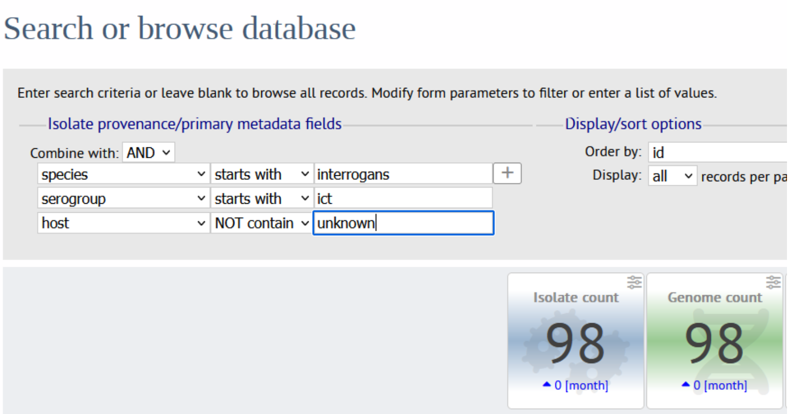
List: ● fields ○ loci ○ schemes

Controls

Max segments: 20

bigsDB search for species Interrogans

Then make a combined subselection
serogroup « Icterohaemorrhagiae »
+ select host NOT unknown



Search or browse database

Enter search criteria or leave blank to browse all records. Modify form parameters to filter or enter a list of values.

Isolate provenance/primary metadata fields

Combine with: AND

species | starts with | interrogans
serogroup | starts with | ict
host | NOT contain | unknown

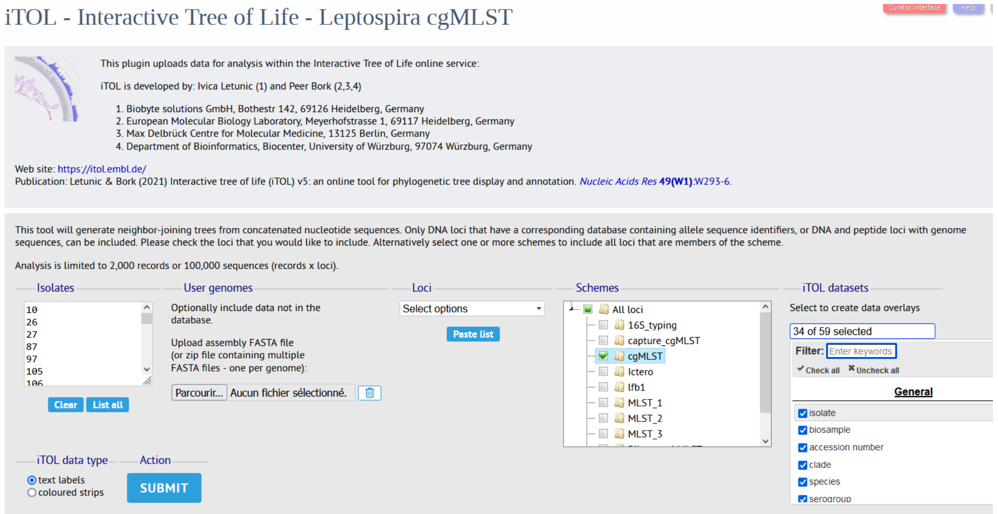
Display/sort options

Order by: id
Display: all records per pa

Isolate count 98
0 [month]

Genome count 98
0 [month]

Then ANALYSIS : iTOL schemes cgMLST datasets « General »



iTOL - Interactive Tree of Life - Leptospira cgMLST

This plugin uploads data for analysis within the Interactive Tree of Life online service:

iTOL is developed by: Ivica Letunic (1) and Peer Bork (2,3,4)

1. Biobyte solutions GmbH, Bothestr 142, 69126 Heidelberg, Germany
2. European Molecular Biology Laboratory, Meyerhofstrasse 1, 69117 Heidelberg, Germany
3. Max Delbrück Centre for Molecular Medicine, 13125 Berlin, Germany
4. Department of Bioinformatics, Biocenter, University of Würzburg, 97074 Würzburg, Germany

Web site: https://itol.embl.de/
Publication: Letunic & Bork (2021) Interactive tree of life (iTOL) v5: an online tool for phylogenetic tree display and annotation. *Nucleic Acids Res* **49(W1)**:W293-6.

This tool will generate neighbor-joining trees from concatenated nucleotide sequences. Only DNA loci that have a corresponding database containing allele sequence identifiers, or DNA and peptide loci with genome sequences, can be included. Please check the loci that you would like to include. Alternatively select one or more schemes to include all loci that are members of the scheme.

Analysis is limited to 2,000 records or 100,000 sequences (records x loci).

Isolates
10
26
27
87
97
105
106

Clear | List all

User genomes
Optionally include data not in the database.
Upload assembly FASTA file (or zip file containing multiple FASTA files - one per genome):
Parcourir... Aucun fichier sélectionné.

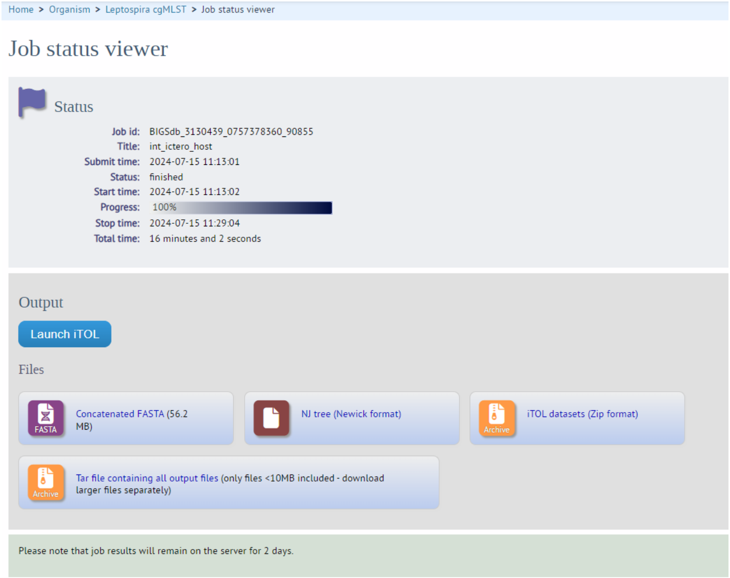
Loci
Select options
Paste list

Schemes
All loci
☐ 16S_typing
☐ capture_cgMLST
☑ cgMLST
☐ Ictero
☐ lfb1
☐ MLST_1
☐ MLST_2
☐ MLST_3

iTOL datasets
Select to create data overlays
34 of 59 selected
Filter: Enter keywords
✓ Check all ✗ Uncheck all
General
☑ isolate
☑ biosample
☑ accession number
☑ clade
☑ species
☑ serogroup

iTOL data type
● text labels
○ coloured strips

Action
SUBMIT



Home > Organism > Leptospira cgMLST > Job status viewer

Job status viewer

Status

Job id: BIGSdb_3130439_0757378360_90855
Title: int_ictero_host
Submit time: 2024-07-15 11:13:01
Status: finished
Start time: 2024-07-15 11:13:02
Progress: 100%
Stop time: 2024-07-15 11:29:04
Total time: 16 minutes and 2 seconds

Output

Launch iTOL

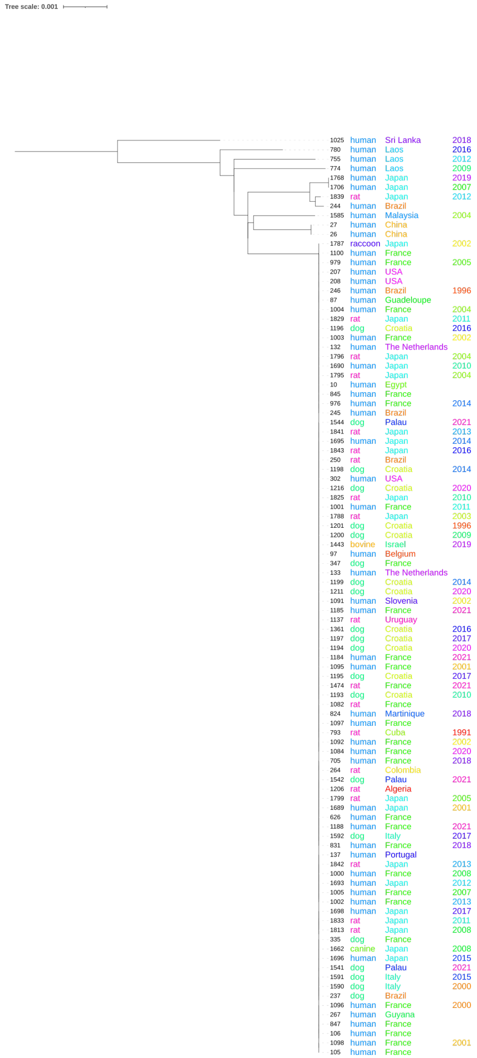
Files

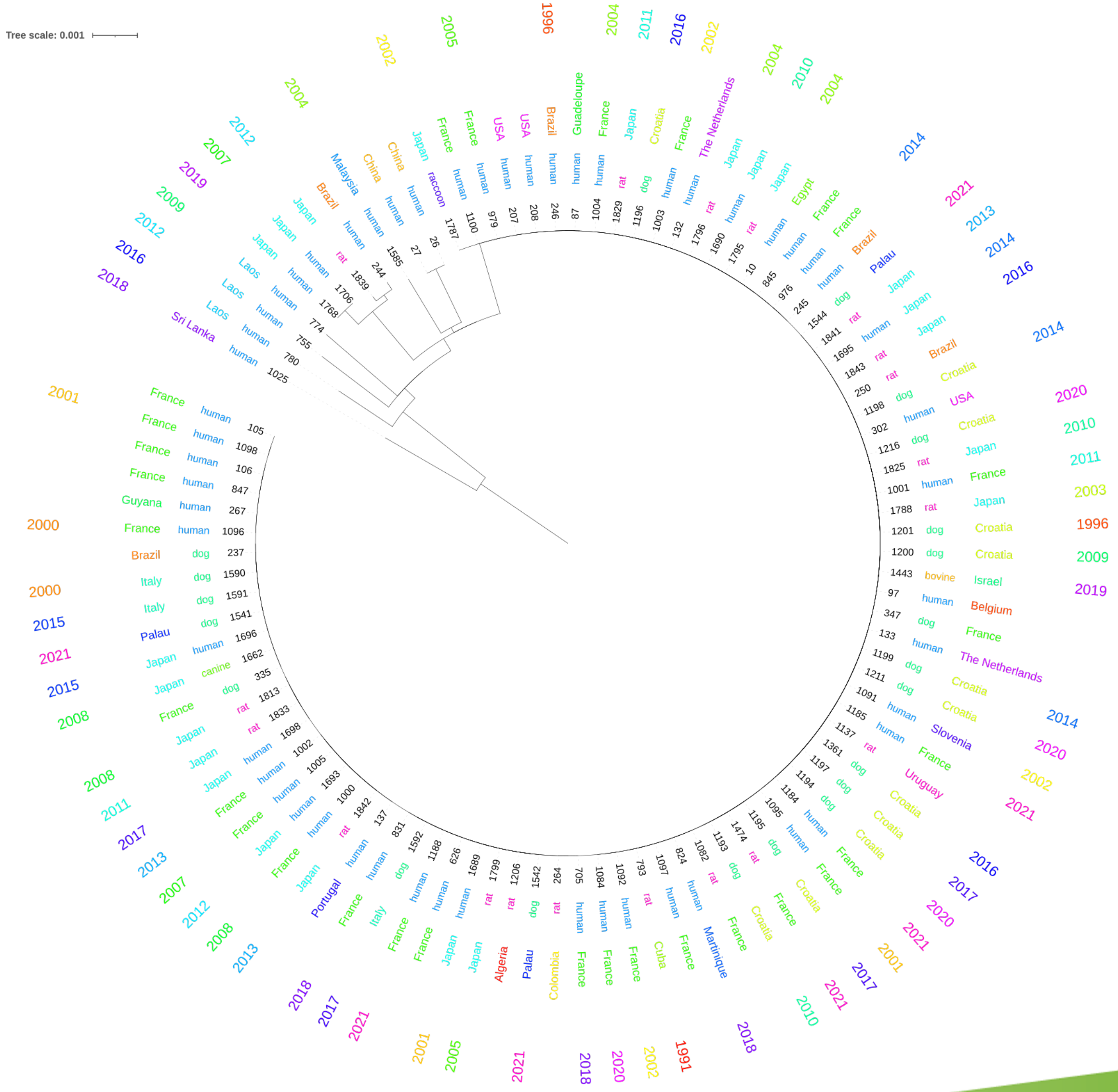
- Concatenated FASTA (56.2 MB)
- NJ tree (Newick format)
- iTOL datasets (Zip format)
- Tar file containing all output files (only files <10MB included - download larger files separately)

Please note that job results will remain on the server for 2 days.

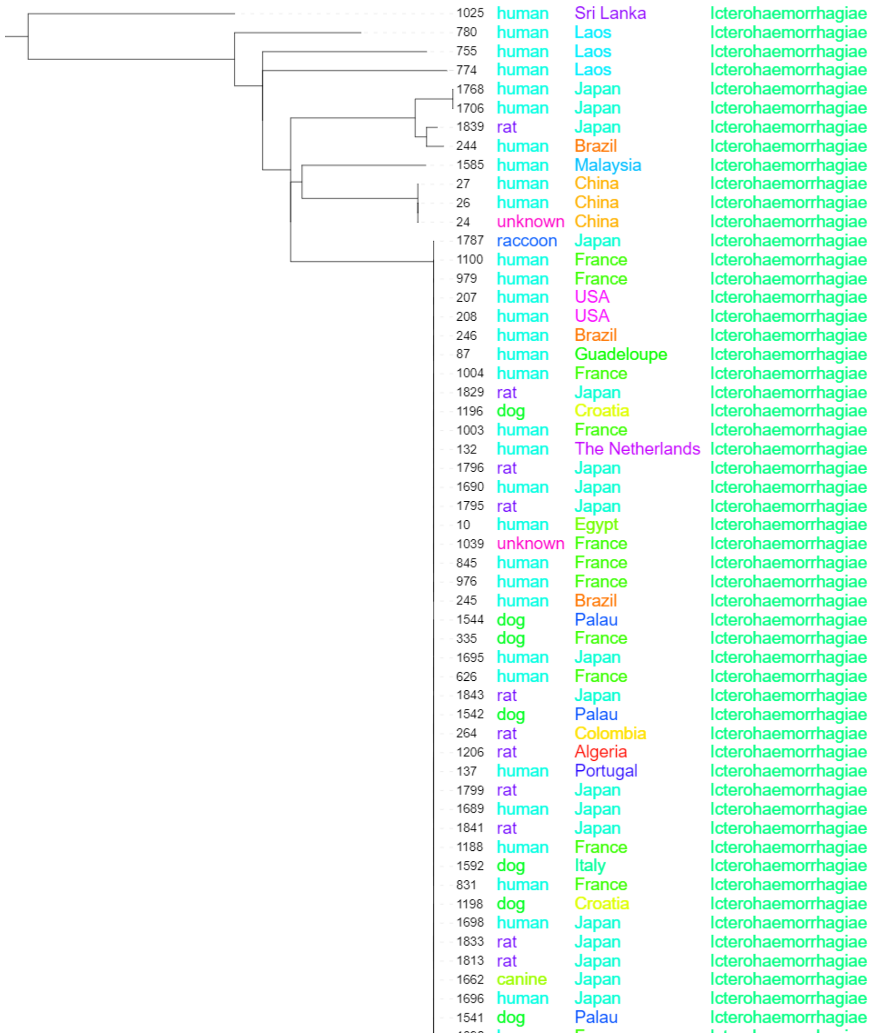
bigsDB search for species Interrogans

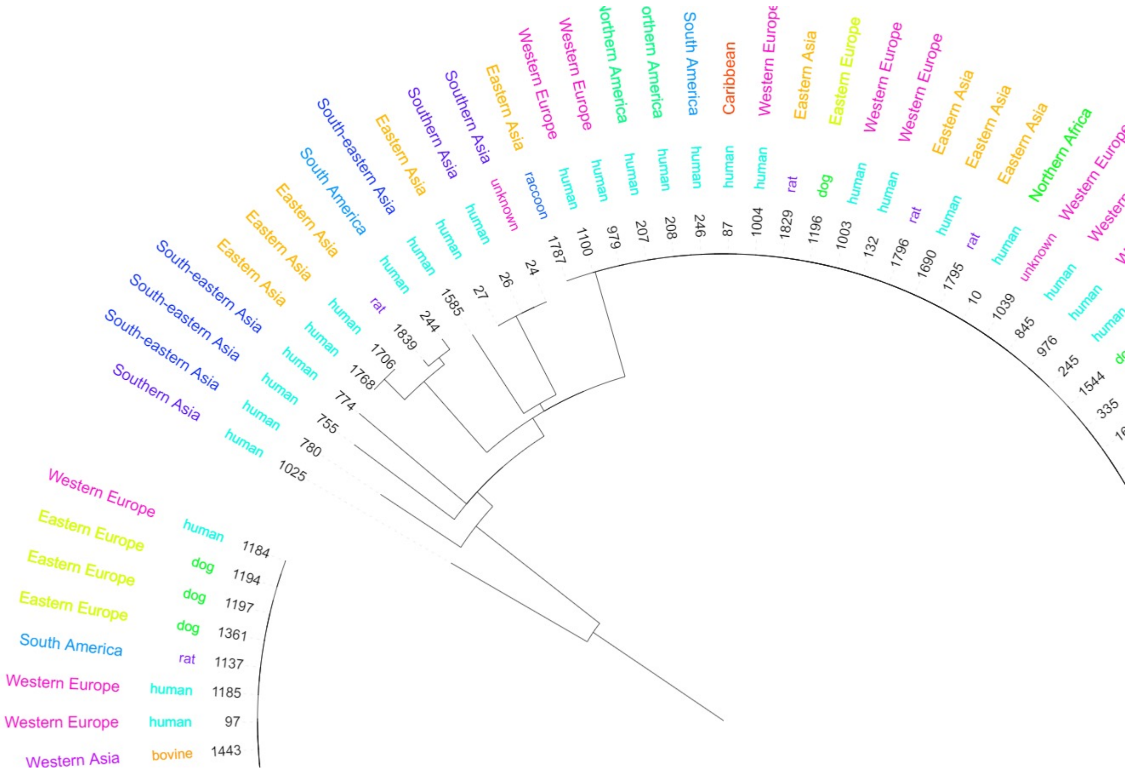
iTOL output





bigsDB search for species Interrogans





In summary

Discovery of power of bigsDB interface :

- Looking for existing isolates based on epidemiological data
- From known sequences how to retrieve closes isolates available

  example: lfb1 in subselection of Lesptospira kirschneri serogroup Grippotyphosa
- By combining epidemiological criteria search and sequence data build sequence relationship with public data

References

BIGSdb

Jolley, Keith & Maiden, Martin. (2010). BIGSdb: Scalable analysis of bacterial genome variation at the population level. BMC bioinformatics. 11. 595. 10.1186/1471-2105-11-595.

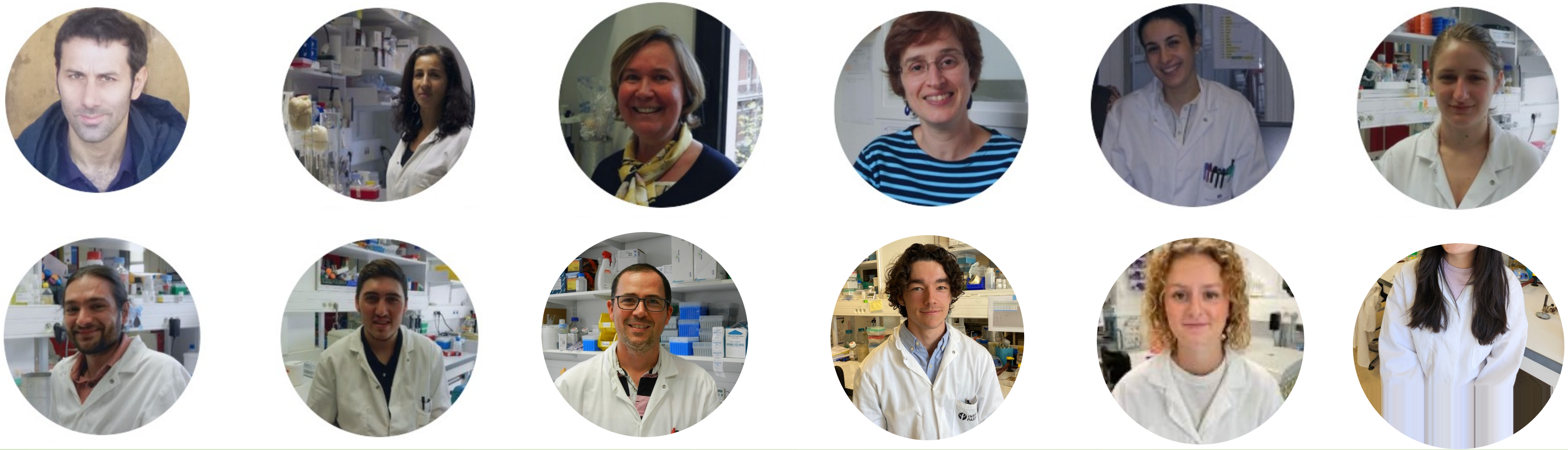
Jolley KA, Bray JE and Maiden MCJ. Open-access bacterial population genomics: BIGSdb software, the PubMLST.org website and their applications [version 1; peer review: 2 approved]. *Wellcome Open Res* 2018, 3:124 (https://doi.org/10.12688/wellcomeopenres.14826.1)

lfb1

Garcia-Lopez M, Lorioux C, Soares A, Trombert-Paolantoni S, Harran E, Ayral F, Picardeau M, Djelouadji Z, Bourhy P. Genetic diversity of Leptospira strains circulating in humans and dogs in France in 2019-2021 Front. Cell. Infect. Microbiol. Volume 13 – 2023 DOI : 10.3389/fcimb.2023.1236866

cgMLST

Guglielmini J, Bourhy P, Schiettekatte O, Zinini F, Brisse S, Picardeau M. Genus-wide *Leptospira* core genome multilocus sequence typing for strain taxonomy and global surveillance. *PLoS Negl Trop Dis.* **2019**; 13(4):e0007374. PMID 31026256



Biology of Spirochetes unit
National Reference Center for Leptospirosis
WHO Collaborating Center for Research and Reference on Leptospirosis

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