

European Meningococcal Epidemiology in Real Time (EMERT II)

Keith Jolley



EMERT facilitates sharing of molecular typing information among reference laboratories



The screenshot shows the EMERT website interface. At the top left is the EMGM logo with the text 'The European Meningococcal and Haemophilus Disease Society'. A navigation bar contains links for 'EMERT Home', 'Database Home', 'Options', 'Search', 'Browse', 'ST query', 'Profile query', and 'Submit data'. The main heading reads 'Welcome to the European Meningococcal Epidemiology in Real Time (EMERT) isolate database'. Below this is a disclaimer box stating that data owners retain ownership and must be acknowledged. A note indicates that summary charts for clonal complex, serogroup, PorA, and finetype are available. The page is divided into three columns: 'Query isolates database' with links for search, browse, sequence type query, allelic profile query, list query, and query by cited publication; 'Database statistics' showing 19423 isolates, 1692 profiles, and a last update of 2016-10-27; and 'Profiles database' with a link to access the profiles database. A 'Database tools' section includes links for set options, description of fields, and concatenating sequences. The footer contains a 'Site Map' link and copyright information for 2008-2012, EMGM, with a note that the site is designed and maintained by Keith Jolley.

EMGM *The European Meningococcal and Haemophilus Disease Society*

[EMERT Home](#) [Database Home](#) [Options](#) [Search](#) [Browse](#) [ST query](#) [Profile query](#) [Submit data](#)

Welcome to the European Meningococcal Epidemiology in Real Time (EMERT) isolate database

The laboratory submitting data to EMERT remains the owner of these data. To use unpublished data for publication purposes (conference presentations, internet presentations, journal publications), users of the database must obtain permission from the owner. However, the website must be acknowledged in all publications.

Summary charts for clonal complex, serogroup, PorA and finetype are now available.

Query isolates database

- [Search database](#) - advanced queries.
- [Browse database](#) - peruse all records.
- [Sequence type query](#) - find isolates with similar allelic profiles to your query ST.
- [Allelic profile query](#) - find isolates with similar allelic profiles to your query profile.
- [List query](#) - find isolates by a field matching an entered list.
- [Query by cited publication](#)

Database tools

- [Set options](#)
- [Description of database fields](#)
- [Concatenate sequences](#)

Database statistics

- Number of isolates: 19423
- Number of profiles: 1692
- Last updated: 2016-10-27
- [Detailed statistics](#)

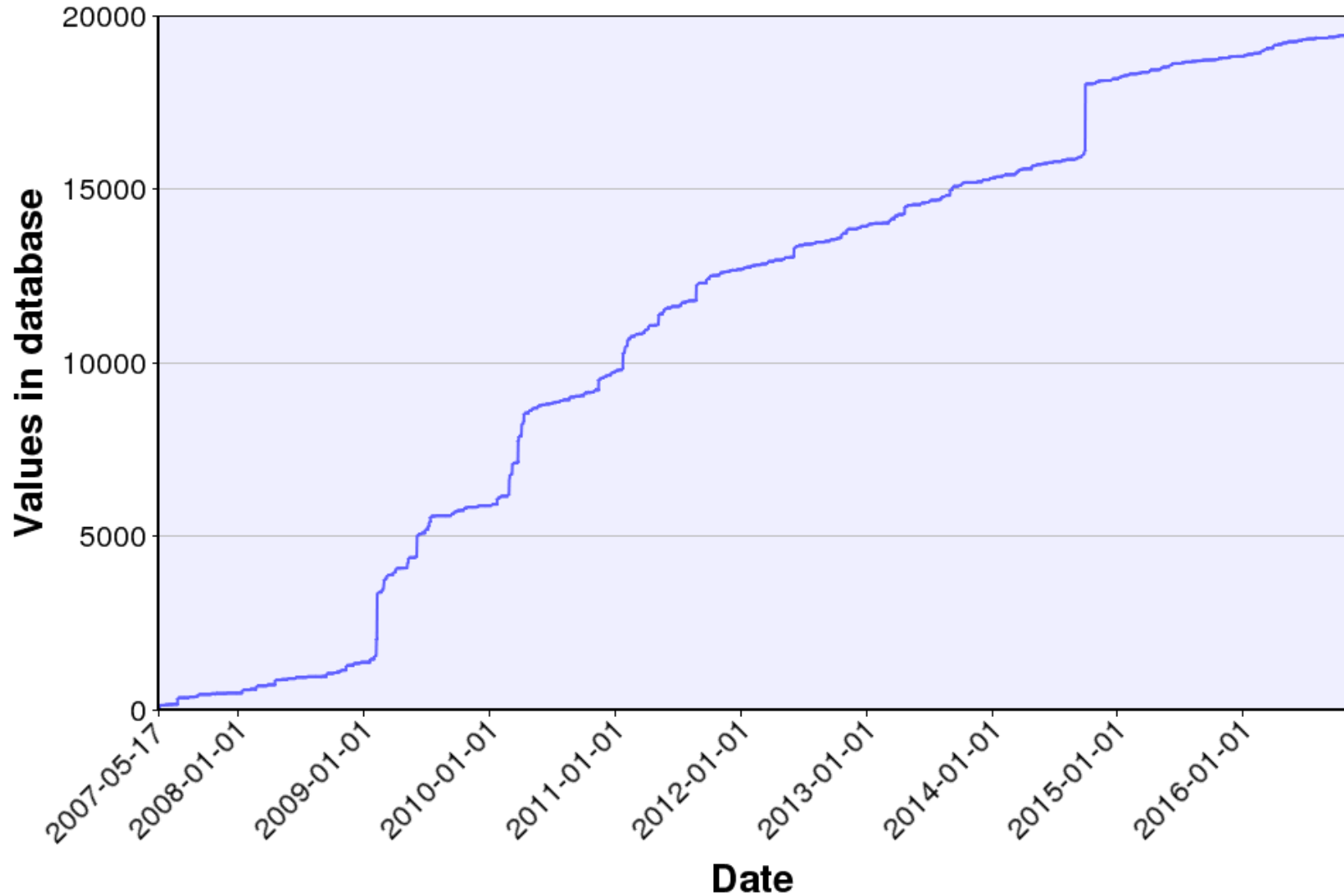
Profiles database

- [Access profiles database](#)

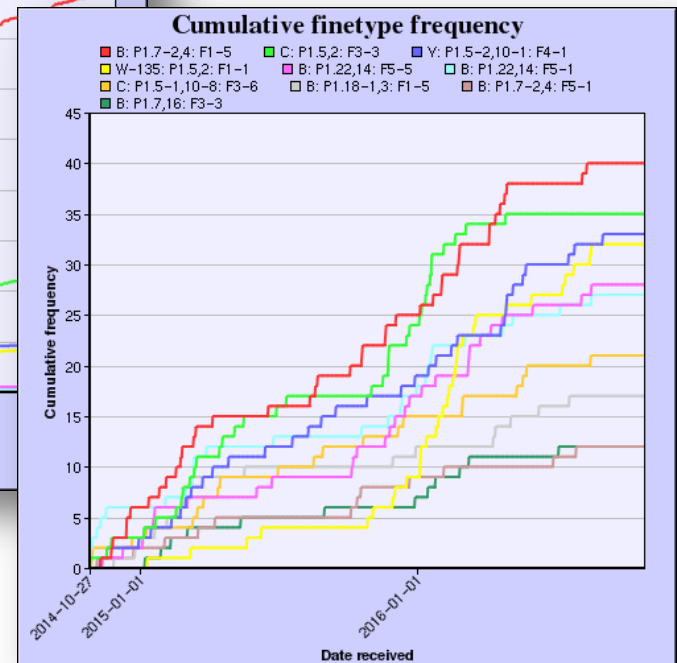
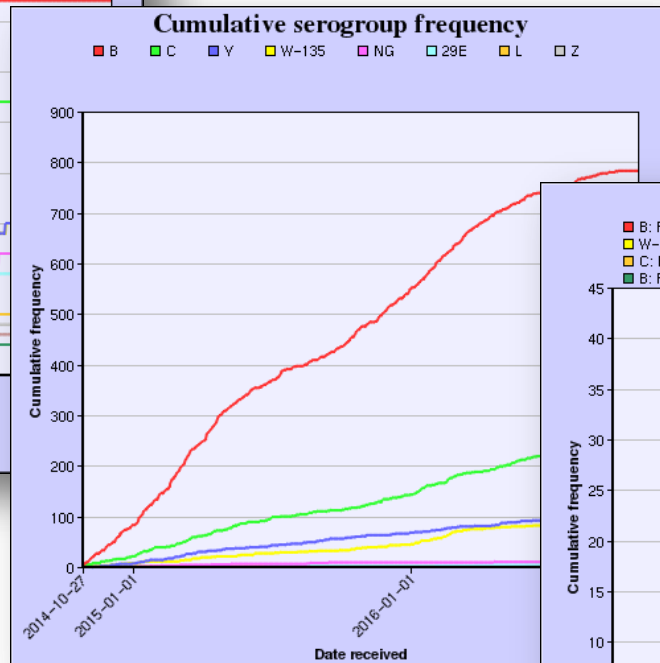
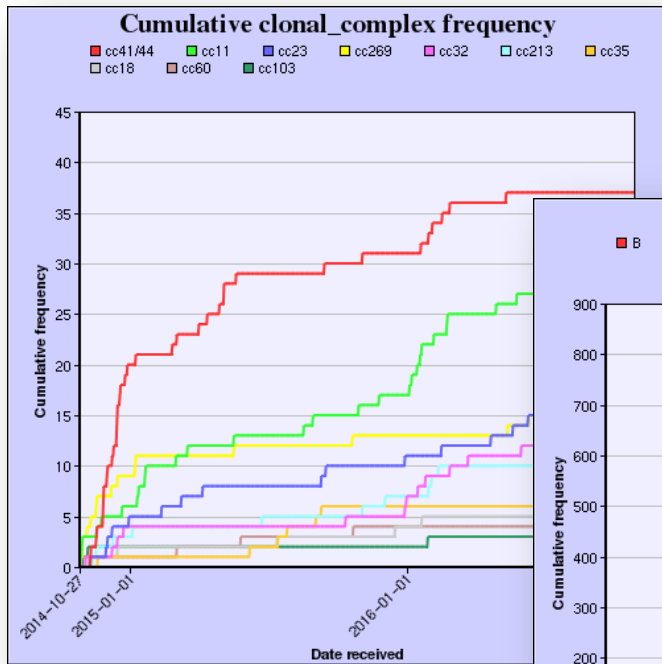
[Site Map](#)

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EMERT was established nearly 10 years ago

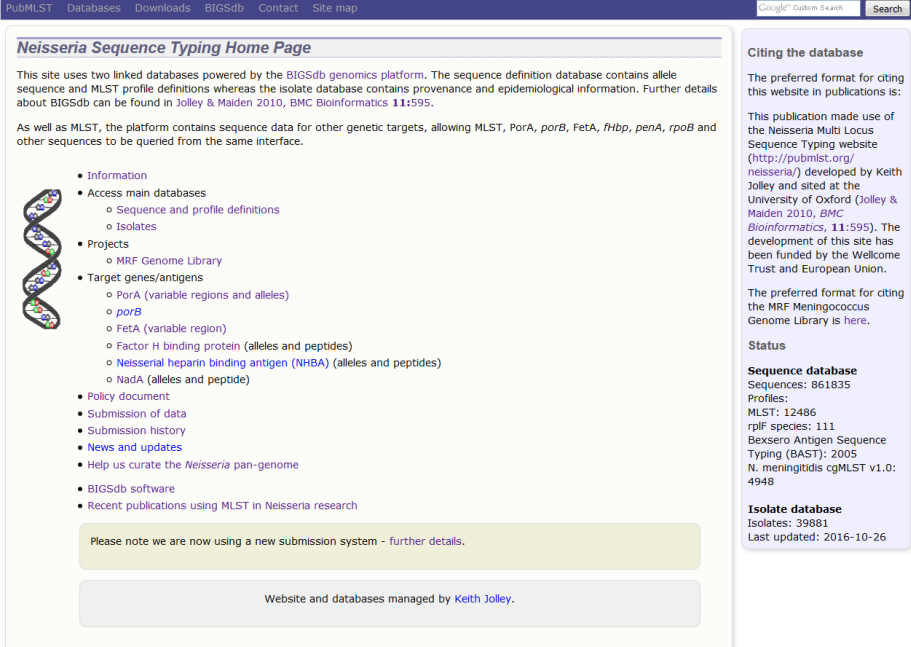


EMERT reports circulating clonal complex and fine-typing data to participating laboratories



Entering the genomic era

- EMERT-II will be incorporated in to the PubMLST *Neisseria* database
- Data can be optionally made public
- Submitters can edit
- Minimal or extensive data can be uploaded



The screenshot shows the 'Neisseria Sequence Typing Home Page' with a navigation menu (PubMLST, Databases, Downloads, BIGSdb, Contact, Site map) and a search bar. The main content area includes a title, a paragraph about the database's scope, and a list of links for information, databases, projects, target genes, and policy. A yellow box contains a note about a new submission system, and a grey box at the bottom states the site is managed by Keith Jolley.

Neisseria Sequence Typing Home Page

This site uses two linked databases powered by the BIGSdb genomics platform. The sequence definition database contains allele sequence and MLST profile definitions whereas the isolate database contains provenance and epidemiological information. Further details about BIGSdb can be found in Jolley & Maiden 2010, *BMC Bioinformatics* **11**:595.

As well as MLST, the platform contains sequence data for other genetic targets, allowing MLST, *PorA*, *porB*, *FetA*, *rHbp*, *penA*, *rpoB* and other sequences to be queried from the same interface.

- Information
- Access main databases
 - Sequence and profile definitions
 - Isolates
- Projects
 - MRF Genome Library
- Target genes/antigens
 - *PorA* (variable regions and alleles)
 - *porB*
 - *FetA* (variable region)
 - Factor H binding protein (alleles and peptides)
 - *Neisserial heparin binding antigen (NHBA)* (alleles and peptides)
 - *NadA* (alleles and peptide)
- Policy document
- Submission of data
- Submission history
- News and updates
- Help us curate the *Neisseria* pan-genome
- BIGSdb software
- Recent publications using MLST in *Neisseria* research

Please note we are now using a new submission system - further details.

Website and databases managed by Keith Jolley.

Citing the database

The preferred format for citing this website in publications is:

This publication made use of the *Neisseria* Multi Locus Sequence Typing website (<http://pubmlst.org/neisseria/>) developed by Keith Jolley and sited at the University of Oxford (Jolley & Maiden 2010, *BMC Bioinformatics*, **11**:595). The development of this site has been funded by the Wellcome Trust and European Union.

The preferred format for citing the MRF Meningococcus Genome Library is here.

Status

Sequence database
Sequences: 861835
Profiles:
MLST: 12486
rPlF species: 111
Bexsero Antigen Sequence Typing (BAST): 2005
N. meningitidis cgMLST v1.0: 4948

Isolate database
Isolates: 39881
Last updated: 2016-10-26

serogroup

finotyping

MLST

whole genome

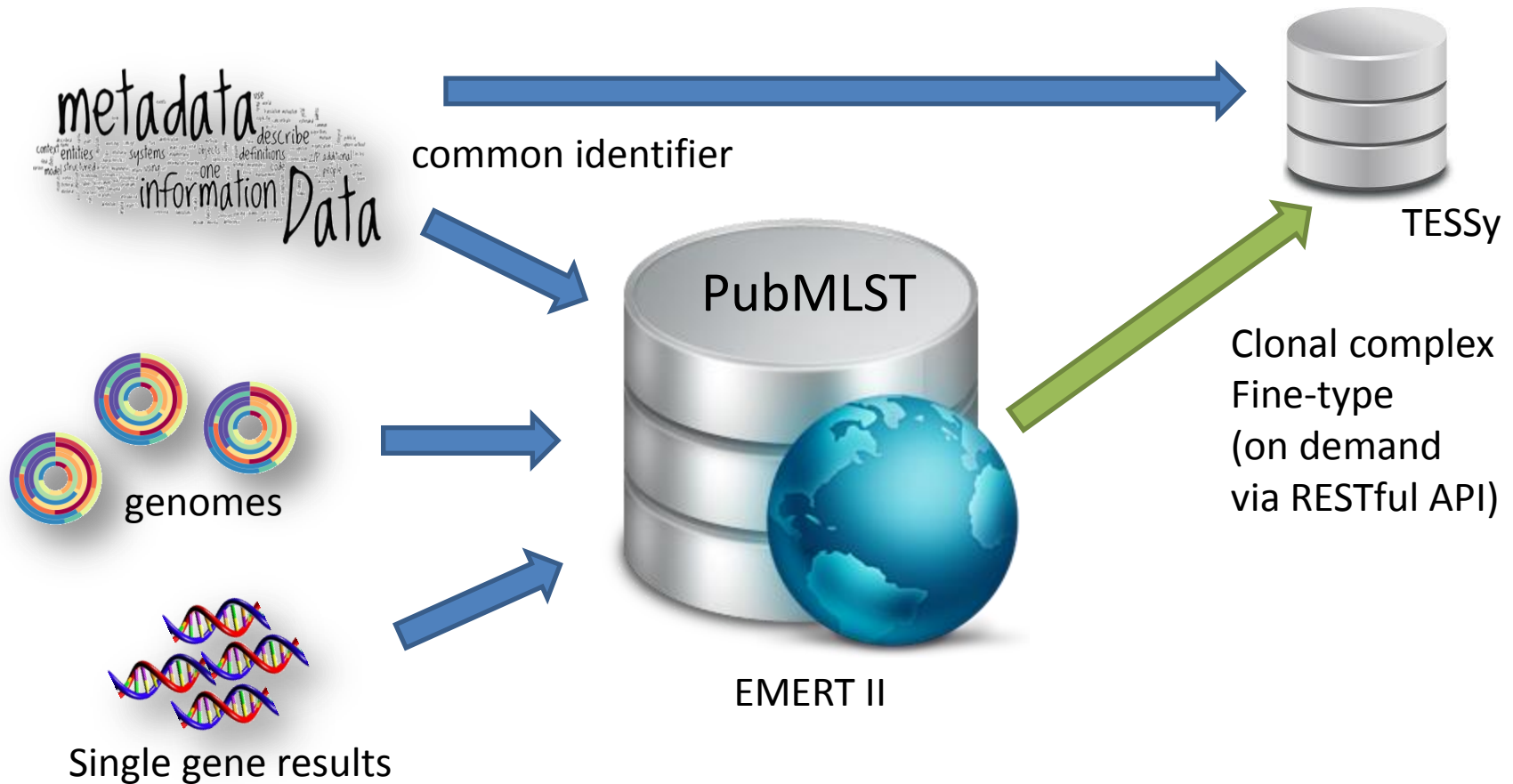
Use standard BIGSdb tools on EMERT data

Loci with sequence differences among isolates:

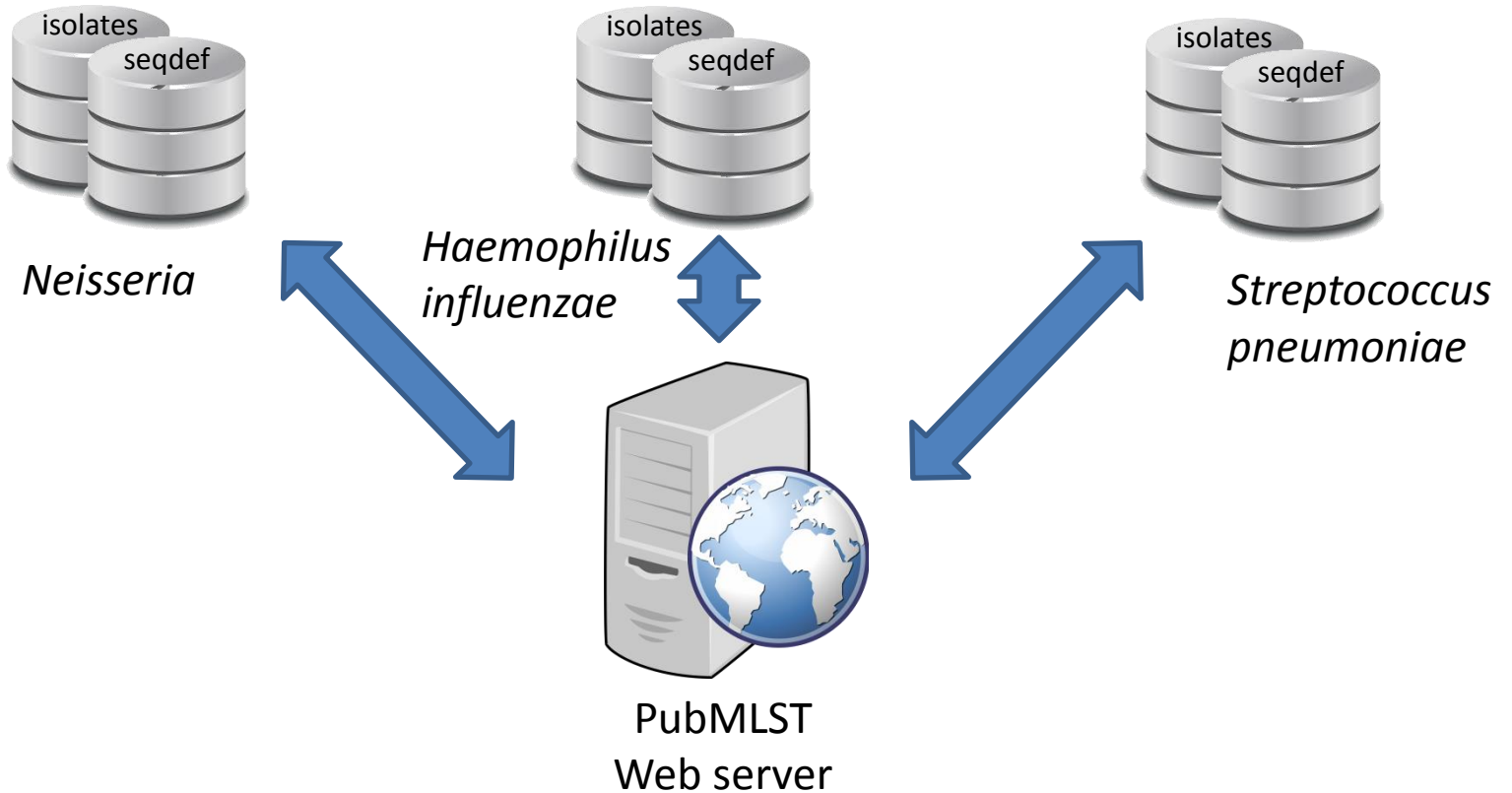
Variable loci: 987

Locus	Product	Sequence length	Genome position	Reference genome	644 (L93/4286)	662 (2837)	663 (2839)	664 (2838)	665 (2845)	666 (2843)	667 (2842)	669 (2846)	670 (2840)	671 (2844)	672 (2847)	698 (FAM18)
NMC0005	putative membrane protein	219	4476	1	2	3	3	3	3	3	3	4	3	5	3	1
NMC0006	putative glycerate dehydrogenase	954	4816	1	2	2	2	2	2	2	2	2	2	2	2	1
NMC0013	possible membrane protein	1266	15029	1	2	1	1	1	1	3	3	1	1	1	1	1
NMC0022	putative transposase	957	25628	1	2	2	2	2	1	1	1	1	2	2	2	1
NMC0024	putative inner membrane protein	285	27987	1	2	2	2	2	3	3	3	3	2	2	2	1
NMC0028	putative periplasmic protein	231	30882	1	1	1	1	1	2	1	1	1	1	1	1	1
NMC0034	putative inner membrane protein	2151	38697	1	2	3	4	4	1	1	1	1	3	3	3	1
NMC0044	putative inner membrane transport protein	2019	54031	1	1	1	1	1	1	2	2	1	1	1	1	1
NMC0049	conserved hypothetical protein (pseudogene)	1163	60012	1	2	2	1	1	1	2	2	1	2	2	2	1
NMC0050	conserved hypothetical protein	1383	61225	1	1	1	1	1	1	2	2	1	1	1	3	1
NMC0059	putative transcriptional accessory protein	2277	71060	1	2	2	3	3	1	4	4	1	2	2	2	1
NMC0060	putative DNA modification methylase (pseudogene)	1003	73367	1	2	2	2	2	1	1	1	1	2	2	2	1
NMC0061	putative modification methylase (pseudogene)	345	74362	1	2	2	2	2	1	1	1	1	2	2	2	1
NMC0068	conserved hypothetical protein	1407	82013	1	2	2	3	3	1	1	1	1	2	2	2	1
NMC0071	putative lipoprotein	1017	84950	1	2	2	1	1	3	1	1	1	2	2	2	1
NMC0072	conserved hypothetical protein	198	85977	1	2	2	1	1	1	1	1	1	2	2	2	1
NMC0073	putative outer membrane transport protein	1401	86600	1	2	2	1	1	3	1	1	1	2	2	2	1
NMC0075	probable IS1016 transposase, partial CDS	330	90041	1	2	3	4	5	6	1	6	X	7	3	8	1
NMC0080	conserved hypothetical protein	237	91332	1	2	2	1	1	1	1	1	1	2	2	2	1
NMC0081	conserved hypothetical protein	228	91562	1	2	2	1	1	1	1	1	1	2	2	2	1
NMC0083A	conserved hypothetical protein	153	92356	1	2	2	1	1	1	1	1	1	2	2	2	1
NMC0084	putative inner membrane protein	138	92609	1	2	2	1	1	1	1	1	1	2	2	2	1
NMC0086	putative protein export protein	2088	94059	1	2	3	1	1	1	1	1	1	3	3	3	1
NMC0090	insertion element IS1016 transposase (pseudogene)	643	97831	1	X	2	3	3	1	4	1	X	5	2	6	1
NMC0092	putative inner membrane protein	552	98556	1	2	2	1	1	1	3	3	1	2	2	2	1
NMC0093	putative periplasmic peptidase (bacteriocin resistance)	660	99384	1	2	2	1	1	1	1	1	1	2	2	2	1
NMC0094	putative inner membrane protein	237	100024	1	2	2	1	1	1	1	1	1	2	2	2	1
NMC0095	hypothetical protein	676	100382	1	2	3	1	1	1	1	1	1	3	3	3	1
NMC0096	putative lipoprotein	159	101184	1	1	1	1	1	1	2	2	1	1	1	1	1
NMC0101	putative periplasmic protein (possibly peptidoglycan-binding)	1218	104601	1	2	1	1	1	1	1	1	3	1	1	1	1

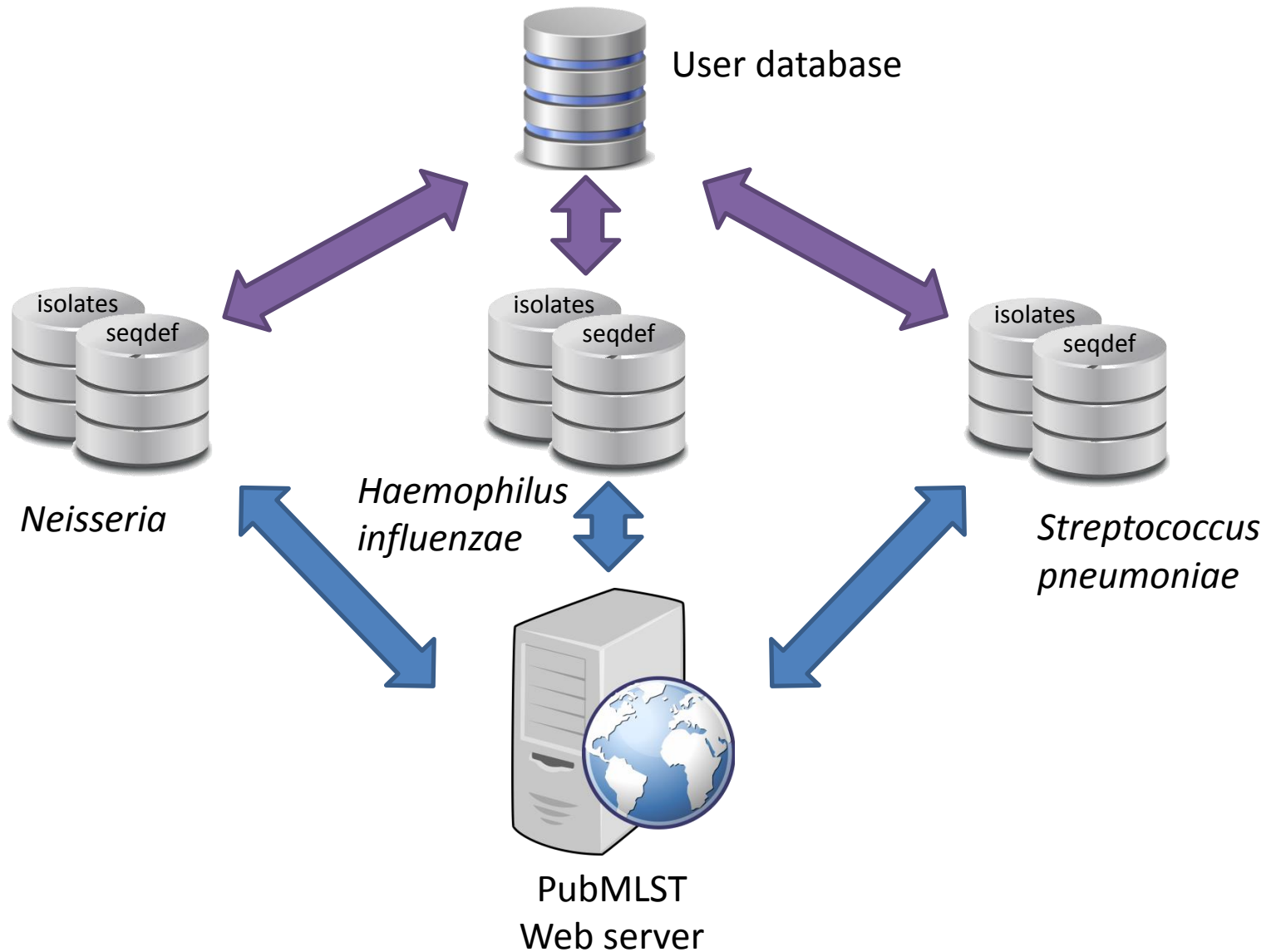
EMERT II will facilitate reporting of summary data to TESSy



Common user accounts across PubMLST



Common user accounts across PubMLST



Acknowledgements



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