

MicrobeTrakr: A Web Service for Whole-genome Sequence-based Microbial Identification

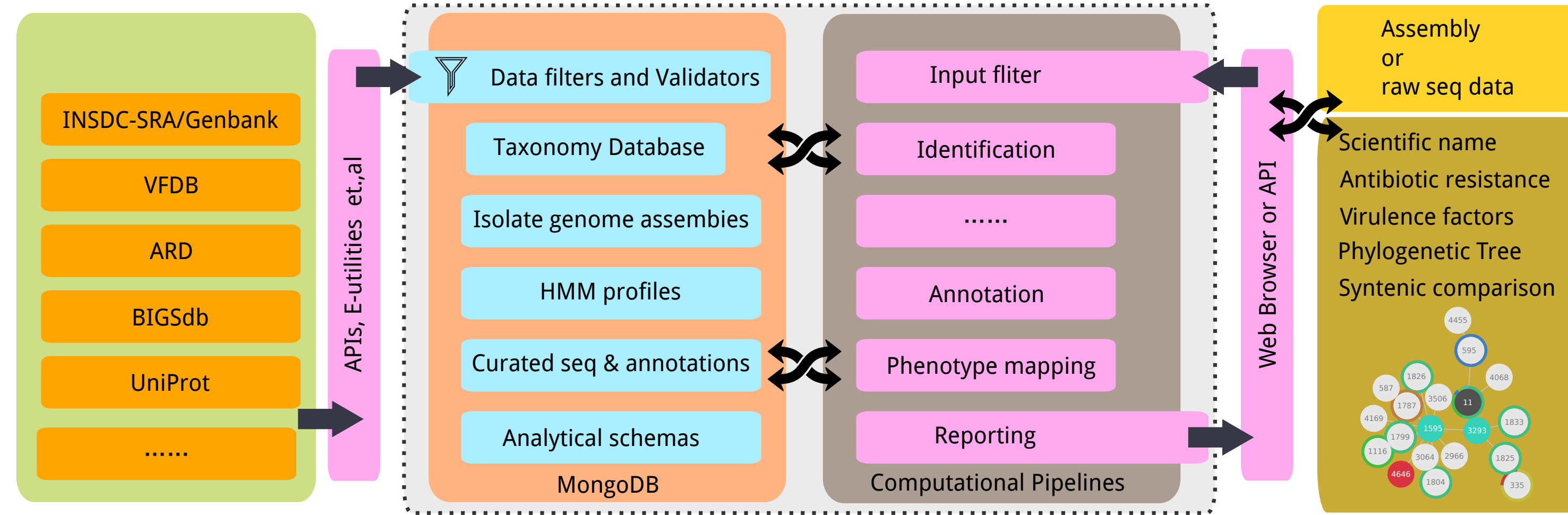
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Introduction:

MicrobeTrakr is a web service for WGS based microbial species identification and molecular epidemiology. MicrobeTrakr can perform smart data analysis, including species identification, subtyping, clinical and epidemiological related genes identification. Additional knowledge related to the query will be retrieved to help data interpretation. MicrobeTrakr takes assembled bacterial genome sequences as input(web browser) and can be accessed via API to upload raw data of HTS sequencer. MicrobeTrakr uses Needleman-Wunsch global alignment to identify house keeping genes in MLST schemes, ARGs and VFGs automatically. Further more MicrobeTrakr using well established algorithm to group STs and display relationship between the closed-related isolates of particular bacterial species. MicrobeTrakr generates the eBURST diagram and phylogeny tree to present evolution relationship of input isolate. Phenotypes of the query also predicted by mapping detected genotype to curated data.



Architecture:

MicrobeTrakr is a knowledge engine like service, it can generate sense-making results for user at all education levels. MicrobeTrakr uses the standard data exchange format and controlled-vocabularies defined by the INSDC, and can be invoked programmatically.

Strain	Phenotype	PCR-Genotype	WGS-Genotype	WGS-ST	PCR-ST	#WGS-Plasmids
AUS 0002	VSE	nil	vanB	202	202	12
AUS 0006	VSE	nil	ND	17	17	11
AUS 0007	VSE	nil	ND	17	17	9
AUS 0010	VSE	nil	ND	32	32	9
AUS 0012	VRE	vanB	vanB	17	17	13
AUS 0015	VSE	nil	ND	17	17	7
AUS 0016	VRE	vanB	vanB	18	18	7
AUS 0018	VSE	nil	ND	252	252	14
AUS 0019	VSE	nil	ND	17	17	9
AUS 0021	VRE	vanB	vanB	17	17	9
AUS 0029	VSE	nil	ND	203	203	14
AUS 0030	VRE	vanB	vanB	252	252	7
AUS 0031	VRE	vanB	vanB	252	252	7
AUS 0038	VSE	nil	ND	252	252	8
AUS 0039	VSE	nil	ND	204	204	14
AUS 0040	VSE	nil	ND	203	203	9
AUS 0041	VSE	nil	ND	203	203	9
AUS 0045	VRE	vanB	vanB	203	203	11
AUS 0048	VRE	vanB	vanB	203	203	9
AUS 0050	VRE	vanB	vanB	252	252	13
AUS 0053	VSE	nil	vanB	203	203	13
AUS 0055	VRE	vanB	vanB	203	203	9
AUS 0057	VSE	nil	ND	252	252	9
AUS 0063	VSE	nil	ND	132	132	6
AUS 0064	VSE	nil	ND	252	252	4
AUS 0065	VSE	nil	ND	341	341	6
AUS 0069	VRE	vanB	vanB	414	414	7
AUS 0070	VRE	vanB	vanB	203	203	10
AUS 0071	VRE	vanB	vanB	252	252	10
AUS 0078	VSE	nil	ND	203	203	7
AUS 0080	VSE	nil	ND	17	17	6
AUS 0081	VRE	vanB	vanB	483	483	12
AUS 0084	VRE	vanB	vanB	17	17	13
AUS 0087	VRE	vanB	vanB	203	203	9
AUS 0090	VRE	vanB	vanB	203	203	7
AUS 0091	VRE	vanB	vanB	203	203	8
AUS 0092	VSE	nil	ND	55	55	3
AUS 0094	VSE	nil	ND	17	17	7
AUS 0098	VSE	nil	ND	17	17	7
AUS 0100	VSE	nil	ND	17	17	9
AUS 0101	VSE	nil	ND	22	22	8
RPH1	VRE	vanB	vanB	341	341	4
RPH2	VRE	vanB	vanB	203	203	8
RPH3	VRE	vanB	vanB	203	203	10

Results of WGS and PCR based genotyping

Evaluation:

Illumina reads of 44 *Enterococcus faecium* isolates were downloaded from the NCBI-SRA database(PRJNA205886)^[1] and processed by MicrobeTrakr pipeline. WGS-based MLST types of all 44 isolates confirmed the results from the PCR and conventional sequencing method^[1]. Truncated *vanB* operon were detected in 2 isolates(AUS0002 and AUS0053) using WGS method which PCR assays is *vanB* negative. Our preliminary evaluation suggest that WGS can give precise MLST results as conventional sequencing, and provide higher resolution for genotyping.

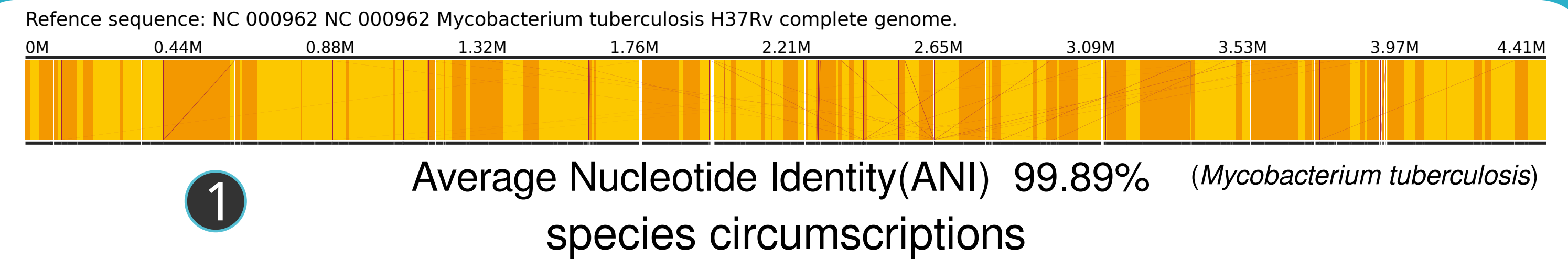
[1] Howden, Benjamin P., et al. "Genomic insights to control the emergence of vancomycin-resistant enterococci." MBio 4.4 (2013): e00412-13.



Online Demo

Conclusions:

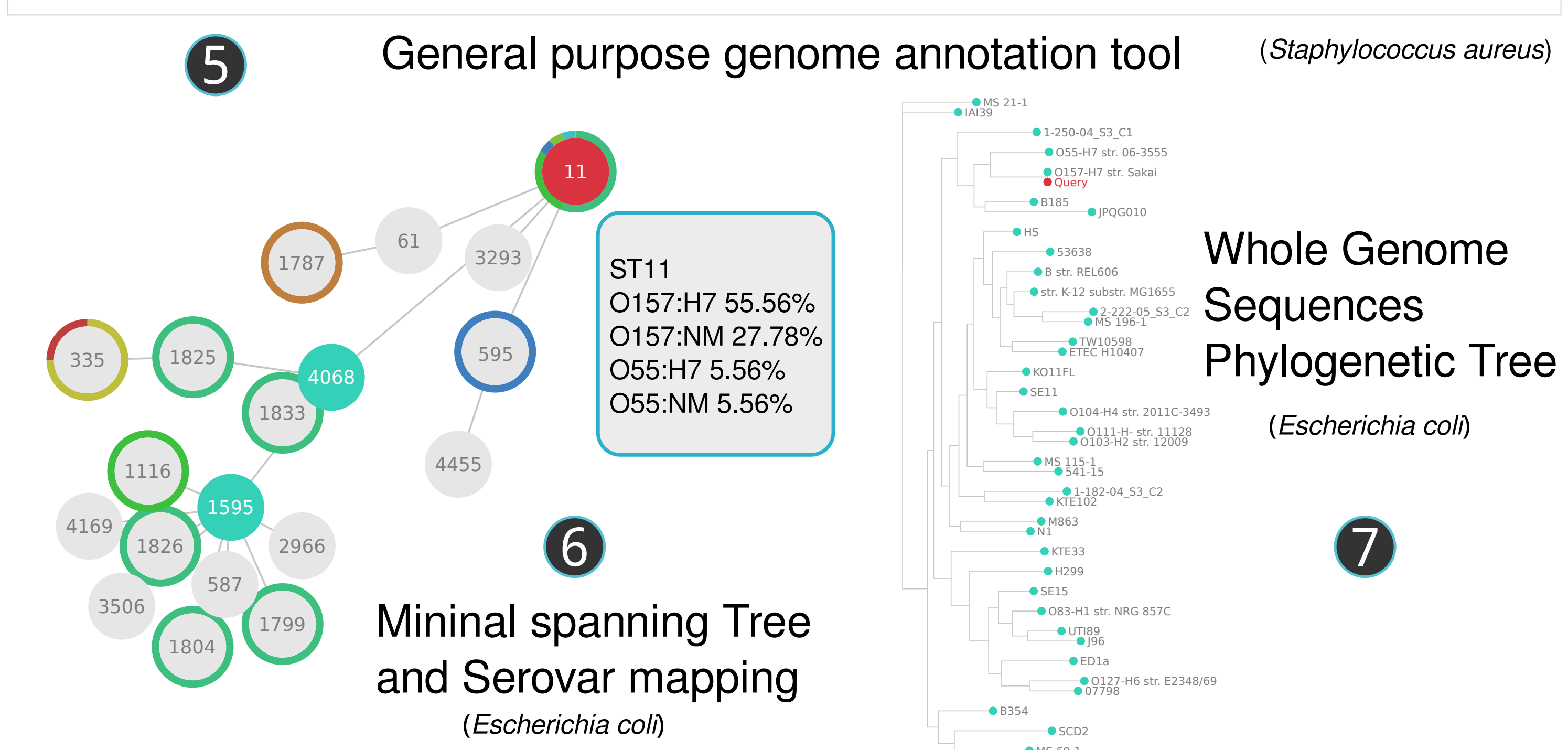
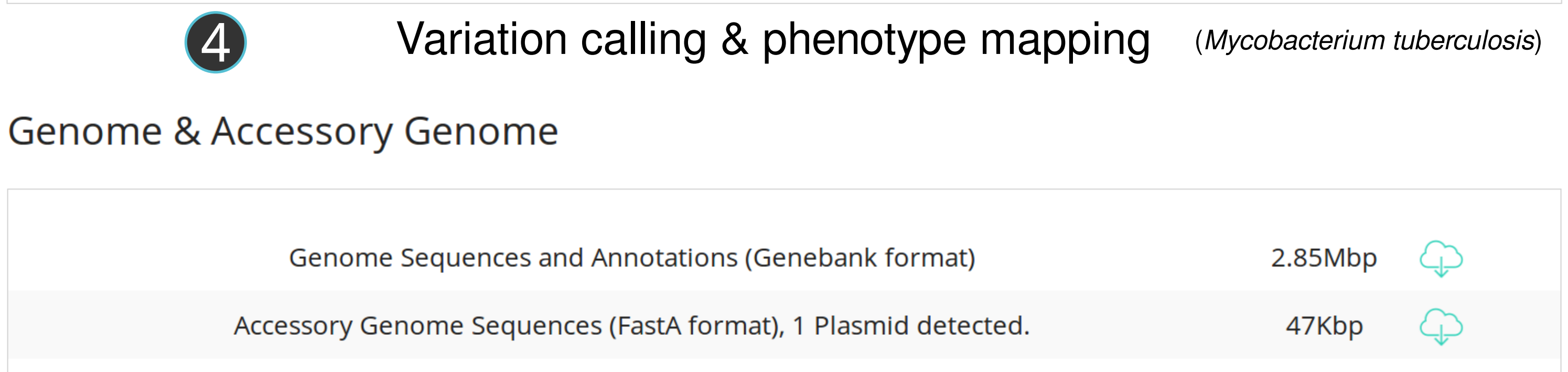
We believe that the WGS would change the diagnostic paradigm of microbiology and epidemiology in near future. However, standards for WGS and analysis is still under development. Easy use and automatically data analytic tools are also claimed. MicrobeTrakr is a comprehensive and ideal automatically data analytic tools for whole-genome sequencing based bacterial identification and subtyping. It can be used for epidemiological tracking and drug resistance prediction. MicrobeTrakr is freely available at <http://microbetrakr.org> and can be accessed programmatically.



ST No.	Lineage	Spoligotype Description	Octal
46	U (likely H)	[Spoligotype pattern]	777777770000000

class	factor	gene	gap	identity%	score	alignment
Cell surface components	Methyltransferase	mmaA4	0	100.0%	1583.0	[Icons]
Cell surface components	Mycolic acid trans-cyclopropane synthetase	cmaA2	0	100.0%	1614.0	[Icons]
Cell surface components	MymA operon	adhD	0	100.0%	1935.0	[Icons]
Cell surface components	MymA operon	chp	0	100.0%	2517.0	[Icons]

Protein	Resistance	Variant/Evidence	alignment
GYRA	Confers ciprofloxacin	94: D => G	[Icons]
KATG	INH	315: S => T 463: R => L	[Icons]
EMBB	EMB	497: Q => R	[Icons]



Features:

- MicrobeTrakr can take bacterial genome assembly in FASTA format sequence(s) to identify bacterial species, subtyping and further analysis.
- Use whole genome wide average nucleotide identity (ANI) to define species.
 - Smart subtyping using MLST or spoligotyping schema.
 - Context based virulence and antibiotic resistance related genes detection.
 - Accessory genome recognition and precise variation phenotypes mapping.
 - Whole genome-based phylogenetic tree reconstruction.