Recap Exercise 2

ResFinder

Known Mutations

parE
No mutations found in parE

parC
No known mutations found in parC

folP
No mutations found in folP

gyrA				
Mutation	**Nucleotide change**	**Amino acid change**	**Resistance**	**PMID**
gyrA p.S83A	TCG → GCG	S → A	Quinolones,Fluoroquinolones	15848289

pmrB
No known mutations found in pmrB

pmrA
No mutations found in pmrA

16S_rrsB
No known mutations found in 16S_rrsB

16S_rrsH
No known mutations found in 16S_rrsH

gyrB
No mutations found in gyrB

ampC
No known mutations found in ampC

16S_rrsC
No known mutations found in 16S_rrsC

23S
No known mutations found in 23S

GyrA and *GyrB* in *E. coli* are difficult cases as it is often a **combination** of mutations that leads to resistance

- According to ResFinder-3.0, the *E. coli* strain that caused the German outbreak has **one** point mutation in *gyrA* (S83A)
- Mutations at this position are usually related to resistance to quinolones/ flouroquinolones (ciprofloxacin, nalidixic acid)
- According to Grad et al, 2012, the *E. coli* strains are resistant to nalidixic acid, while susceptible to ciprofloxacin
- For ciprofloxacin, studies have shown that single mutations in *gyrA* only lead to modest increment in resistance - isolates would still be considered clinically susceptible. Only a second mutation in *gyrA* or a mutation in *parC* leads to a clinical level of resistance (PMID: 15942878)
- ResFinder-3.0 currently outputs resistance according to the environmental break point, not the clinical breakpoint

ResFinder

Unknown Mutations

parC		
Mutation	Nucleotide change	Amino acid change
parC p.E62K	GAA → AAA	E → K

gyrA
No unknown mutations found in gyrA

pmrB		
Mutation	Nucleotide change	Amino acid change
pmrB p.D283G	GAC → GGC	D → G
pmrB p.Y358N	TAC → AAC	Y → N

16S_rrsB	
Mutation	Nucleotide change
16S_rrsB r.80A>C	A → C
16S_rrsB r.89T>G	T → G
16S_rrsB r.93T>C	T → C
16S_rrsB r.250A>T	A → T
16S_rrsB r.253A>T	A → T
16S_rrsB r.273T>A	T → A
16S_rrsB r.474G>A	G → A

16S_rrsH	
Mutation	Nucleotide change
16S_rrsH r.80A>C	A → C
16S_rrsH r.89T>G	T → G
16S_rrsH r.90C>T	C → T
16S_rrsH r.93T>C	T → C
16S_rrsH r.250A>T	A → T
16S_rrsH r.253A>T	A → T
16S_rrsH r.273T>A	T → A
16S_rrsH r.1036A>G	A → G
16S_rrsH r.1120T>C	T → C

ampC		
Mutation	Nucleotide change	Amino acid change

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SerotypeFinder-1.1 Server - Results

H type						
Serotype gene	%Identity	Query/HSP length	Contig	Position in contig	Predicted serotype	Accession number
fliC	100.00	1050 / 1050	Supercontig_1.4	70365..71414	H4	AJ605764

O type						
Serotype gene	%Identity	Query/HSP length	Contig	Position in contig	Predicted serotype	Accession number
wzx	100.00	1278 / 1278	Supercontig_1.4	215774..217051	O104	KB021482
wzy	99.64	1113 / 1113	Supercontig_1.4	218280..219392	O104	AF361371

Predicted Serotype: O104:H4

extended output

Results as text | Results tab separated | Hit in genome sequences | Serotype gene sequences

Selected %ID threshold: *85.00 %*

Selected minimum length: *60 %*

Input Files: *escherichia_coli_c227-11.fsa*

CITATIONS

For publication of results, please cite:

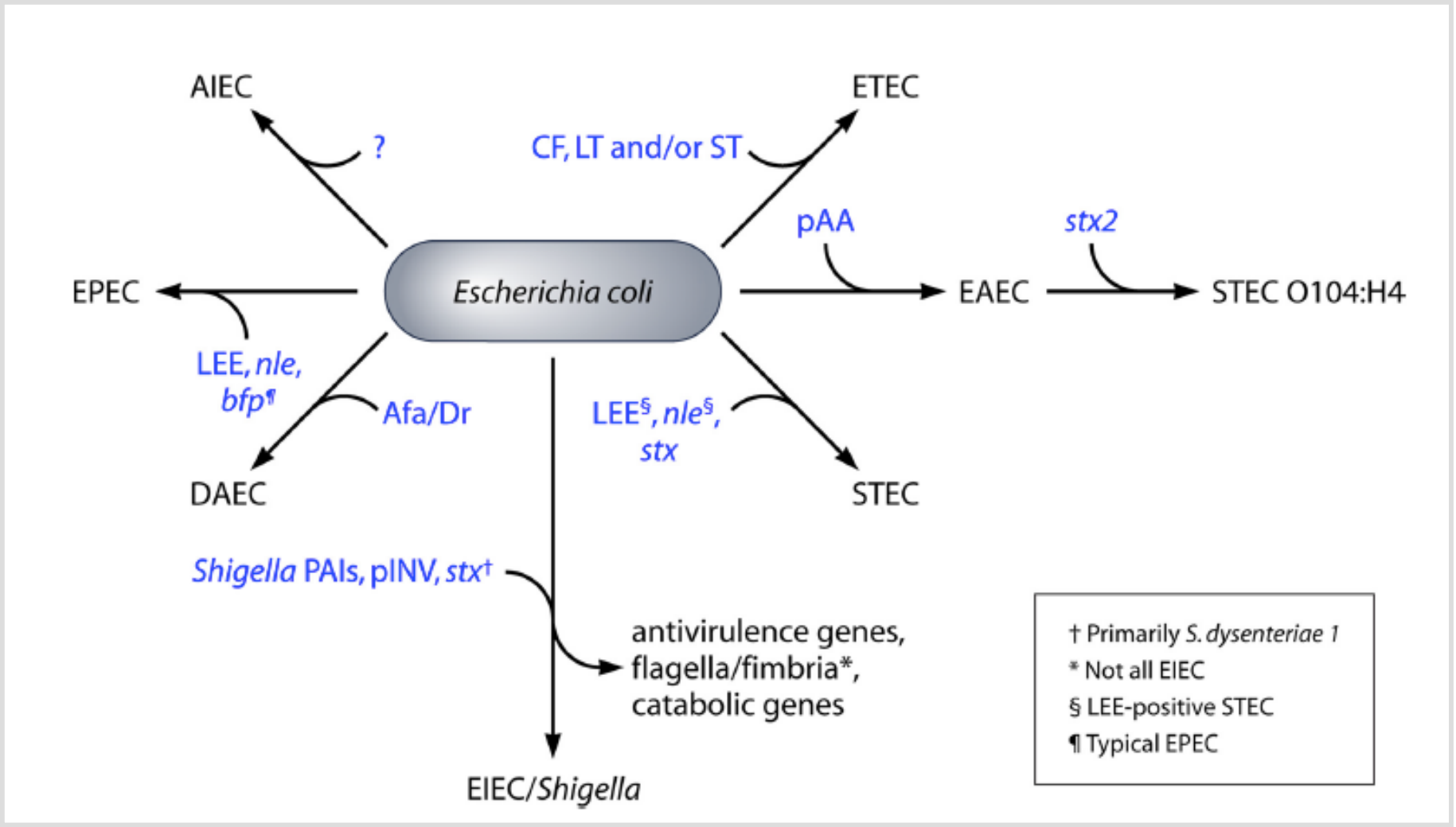
- Joensen, K. G., A. M. Tetzschner, A. Iguchi, F. M. Aarestrup, and F. Scheutz. 2015. Rapid and easy in silico serotyping of *Escherichia coli* using whole genome sequencing (WGS) data. J.Clin.Microbiol. 53(8):2410-2426. doi:JCM.00008-15 [pii];10.1128/JCM.00008-15 [doi]

  Link to the article

VirulenceFinder results

Gene	Associated pathotype	Present in isolate
iroN	UPEC	-
papG	UPEC	-
Stx1a	EHEC	-
Stx1b	EHEC	-
Stx2a	EHEC	+
Stx2b	EHEC	+
pic	EAEC	+
pet	EAEC	-
astA	EAEC	-
aggR	EAEC	+
sta1	ETEC	-
stb	ETEC	-
ltcA	ETEC	-

Pathogenic gene acquisition and loss for different pathotypes



PMID: 24092857

The positive control

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MyDbFinder-1.1 Server - Results

User database				
Fasta header	**%Identity**	**Query/HSP length**	**Contig**	**Position in contig**
PapG	98.32	1011 / 1011	CFT073_NC_004431	3429593..3430603
PapG	98.52	1011 / 1011	CFT073_NC_004431	4940831..4941841
dsbD	98.17	1698 / 1698	CFT073_NC_004431	4972379..4974076

extended output

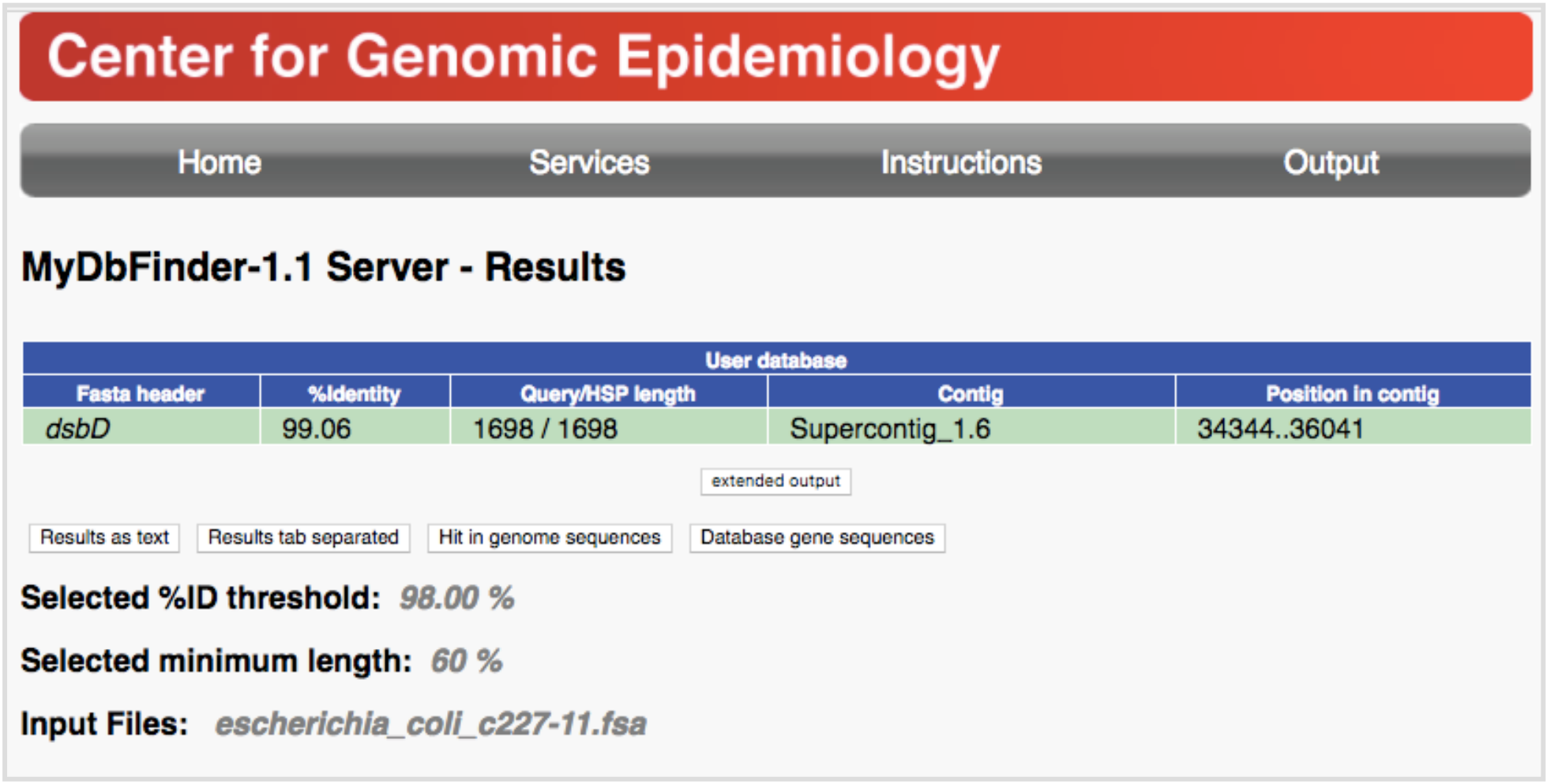
Results as text | Results tab separated | Hit in genome sequences | Database gene sequences

Selected %ID threshold: *98.00 %*

Selected minimum length: *60 %*

Input Files: *EC4.fsa*

escherichia_coli_c227-11.fsa



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MyDbFinder-1.1 Server - Results

User database				
Fasta header	%Identity	Query/HSP length	Contig	Position in contig
dsbD	99.06	1698 / 1698	Supercontig_1.6	34344..36041

extended output

Results as text | Results tab separated | Hit in genome sequences | Database gene sequences

Selected %ID threshold: *98.00 %*

Selected minimum length: *60 %*

Input Files: *escherichia_coli_c227-11.fsa*