

# Recap Exercise 5

# Center for Genomic Epidemiology

Welcome **metteb@cbs.dtu.dk**

- Map Overview
- Batch Uploader**
- Sample Manager
- Run Analysis
- Settings
- Log out

Home

Services

ets

## Overview of Services

### Workflows

[Bacterial Analysis Pipeline \(Batch Upload\)](#)

### Phenotyping

- [ResFinder](#)
- [PathogenFinder](#)
- [VirulenceFinder](#)
- [Restriction-ModificationFinder](#)

### Typing

- [MLST](#)
- [pMLST](#)
- [PlasmidFinder](#)
- [KmerFinder](#)
- [SpeciesFinder](#)
- [Reads2Type](#)
- [Tapir](#) (OBS! Only works for Firefox)
- [TaxonomyFinder](#)
- [SerotypeFinder](#)
- [spaTyper](#)
- [FimTyper](#)
- [PAst](#)



## Bacterial Analysis Pipeline - Batch Upload

The CGE Bacterial Analysis Pipeline executes a workflow of services with predefined parameters and stores the submitted data and result in the database at the user's disposal.

View the [version history](#) of this server.

**STEP 1:** [Download Metadata Template](#) [Template](#) ⓘ

**STEP 2:** Fill out template

**STEP 3:** [Upload Metadata File](#)

**STEP 4:** [Select Files](#) ⓘ

**STEP 5:** [Submit](#)

### Supported browsers

	Windows	Windows 10	Windows 7	Windows 8.1	OS X Yosemite	ubuntu
≥ V 8.0					✓	
V 10.0			✓	✓		
edge			✓	✓		
≥ V 36.0				✓	✓	✓
≥ V 41.0	✓	✓	✓	✓	✓	✓

### Progress Overview

Name	Size	Progress	Status
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[Remove all](#)

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## Sample Overview

[Download all data in an Excel spreadsheet?](#)

[Download the resistance data in a more detailed Excel spreadsheet format?](#)

Analyse selected samples

Delete selected samples

	<input type="checkbox"/>	Name	Date	Country	City	Origin	Action
+	<input type="checkbox"/>	Unknown3	2016-01-01	Denmark		unknown	<input type="button" value="Download"/> <input type="button" value="Analyse"/> <input type="button" value="Edit"/> <input type="button" value="Remove"/>
+	<input type="checkbox"/>	Unknown2	2016-01-01	Denmark		unknown	<input type="button" value="Download"/> <input type="button" value="Analyse"/> <input type="button" value="Edit"/> <input type="button" value="Remove"/>
+	<input type="checkbox"/>	Unknown1	2016-01-01	Denmark		unknown	<input type="button" value="Download"/> <input type="button" value="Analyse"/> <input type="button" value="Edit"/> <input type="button" value="Remove"/>

## Bacterial Analysis Summary Report

**Pipeline Version:** 1.1  
**Submission Date:** 2016-09-09  
**Sample Name:** Unknown3


### Contigs Analysis

Assembly File	No. of contigs	No. of bases	N50
unknown_3.fasta.gz	8	7483594	4918979

### Taxonomy

#### Predicted liniage:

cellular organisms; Bacteria; Firmicutes; Bacilli; Bacillales; Staphylococcaceae; Staphylococcus; Staphylococcus epidermidis; Staphylococcus epidermidis ATCC 12228

**Closest Match** *Staphylococcus epidermidis ATCC 12228*   
**Taxonomy ID** 176280

**MLST Scheme[ST]** **sepidermidis [ST-8]**  
**Plasmid[pMLST]**

### Resistance Genes

**Fosfomycin**

**Beta-lactam**

**Tetracycline**

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<input checked="" type="checkbox"/>	<input type="checkbox"/>	Unknown3	2016-01-01	Denmark		unknown	<input type="button" value="Download"/> <input type="button" value="Analyse"/> <input type="button" value="Edit"/> <input type="button" value="Remove"/>
<input checked="" type="checkbox"/>	<input type="checkbox"/>	Unknown2	2016-01-01	Denmark		unknown	<input type="button" value="Download"/> <input type="button" value="Analyse"/> <input type="button" value="Edit"/> <input type="button" value="Remove"/>
<input checked="" type="checkbox"/>	<input type="checkbox"/>	Unknown1	2016-01-01	Denmark		unknown	<input type="button" value="Download"/> <input type="button" value="Analyse"/> <input type="button" value="Edit"/> <input type="button" value="Remove"/>



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	<input type="checkbox"/>	Name	Date	Country	City	Origin	Action
-	<input type="checkbox"/>	<b>Unknown3</b>	2016-01-01	Denmark		unknown	<a href="#">Download</a> <a href="#">Analyse</a> <a href="#">Edit</a> <a href="#">Remove</a>

Service	Date	Status	Action
<a href="#">KmerFinder-2.1</a>	2016-09-09	Success	<a href="#">Remove</a>
<a href="#">ResFinder-2.1</a>	2016-09-09	Success	<a href="#">Remove</a>
<a href="#">ContigAnalyzer-1.0</a>	2016-09-09	Success	<a href="#">Remove</a>
<a href="#">MLST-1.6</a>	2016-09-09	Success	<a href="#">Remove</a>

## MLST-1.6 Server - Typing Results

Sequence Type: *ST-8*

Locus	% Identity	HSP Length	Allele Length	Gaps	Allele
<i>arcc</i>	100.00	465	465	0	<i>arcc_2</i>
<i>aroe</i>	100.00	420	420	0	<i>aroe_1</i>
<i>gtr</i>	100.00	438	438	0	<i>gtr_7</i>
<i>muts</i>	100.00	412	412	0	<i>muts_1</i>
<i>pyrr</i>	100.00	428	428	0	<i>pyrr_1</i>
<i>tpia</i>	100.00	424	424	0	<i>tpia_1</i>
<i>yqil</i>	100.00	416	416	0	<i>yqil_1</i>

[Results as text](#)[Hit in genome sequences](#)[MLST allele sequences](#)[extended output](#)

MLST Profile: *sepidermidis*

Organism: *Staphylococcus epidermidis*

# Results

Sample	Unknown_1	Unknown_2	Unknown_3
contigs	2	185	8
n50	4747819	168113	4918979
Species	Escherichia coli (100%)	Salmonella enterica (99.67%)	Staphylococcus epidermidis (100%)
MLST	ST-135	ST-19	ST-8
Resistance genes	aadA1, blaTEM-1B-like, catA1-like, dfrA1, mph(B), strA, strB, sul1, sul2, tet(A)	aadA2, aadA5, strA, strB, aph(3')-Ic, aph(4)-Ia, aac(3)-Iva, armA, mph(E), sul1, dfrA1, tet(G), msr(E), floR, blaCARB-2, blaTEM-1B	blaZ-like, fosA, tet(K)
Plasmids		IncX1, Col8282, ColRNAI	IncFIC(FII), IncFIB(AP001918), IncQ1

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Analyse selected samples

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## Bacterial Analysis Pipeline - Service Submission

Write the IDs of the samples here (comma separated!):

- Reassemble reads?
- Reanalyze contigs?
- Rerun Species Identification?
- Rerun Plasmid Identification?
- Rerun Multilocus Sequence Typing?
- Rerun Resistance Gene Identification?
- Rerun Virulence Gene Identification?
- Rerun Pathogen Prediction?

## Bacterial Analysis Pipeline - Service Submission

Write the IDs of the samples here (comma separated!):

- Reassemble reads?
- Reanalyze contigs?
- Rerun Species Identification?

Select the scoring method

winner takes it all

Select the database

bacteria organisms

- bacteria chromosomes
- bacteria organisms
- bacteria plasmids
- fungi**
- protists
- human viruses
- viruses
- vertebrate viruses
- antibiotic resistance database

- Rerun Virulence Gene Identification?
- Rerun Pathogen Prediction?

Submit

Clear fields

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-	<input type="checkbox"/>	Unknown3	2016-01-01	Denmark		unknown	<input type="button" value="Download"/> <input type="button" value="Analyse"/> <input type="button" value="Edit"/> <input type="button" value="Remove"/>
		<b>Service</b>	<b>Date</b>	<b>Status</b>	<b>Action</b>		
		<a href="#">KmerFinder-2.1</a>	2016-09-09	Success	<input type="button" value="Remove"/>		
		<a href="#">ResFinder-2.1</a>	2016-09-09	Success	<input type="button" value="Remove"/>		
		<a href="#">ContigAnalyzer-1.0</a>	2016-09-09	Success	<input type="button" value="Remove"/>		
		<a href="#">MLST-1.6</a>	2016-09-09	Success	<input type="button" value="Remove"/>		
		<a href="#">KmerFinder-2.1</a>	2016-09-16	Success	<input type="button" value="Remove"/>		
+	<input type="checkbox"/>	Unknown2	2016-01-01	Denmark		unknown	<input type="button" value="Download"/> <input type="button" value="Analyse"/> <input type="button" value="Edit"/> <input type="button" value="Remove"/>
+	<input type="checkbox"/>	Unknown1	2016-01-01	Denmark		unknown	<input type="button" value="Download"/> <input type="button" value="Analyse"/> <input type="button" value="Edit"/> <input type="button" value="Remove"/>

## KmerFinder-2.1 - Results

Sample: *Unknown3*

Database: *fungi*

Hit	Score	z-score	Query Coverage [%]	Template Coverage [%]	Depth
<a href="#">aspergillus_fumigatus</a> <a href="#">get sequence</a>	11173	204.3	66.70	17.34	0.17
<a href="#">rhizophagus_irregularis_daom_197198w</a> <a href="#">get sequence</a>	766	85899524.3	4.57	7660000000000.00	0.00



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Plasmids		IncX1, Col8282, ColRNAI	IncFIC(FII), IncFIB(AP001918), IncQ1
Special	MLST-64	Rotavirus A (100%)	Aspergillus (17.34%)