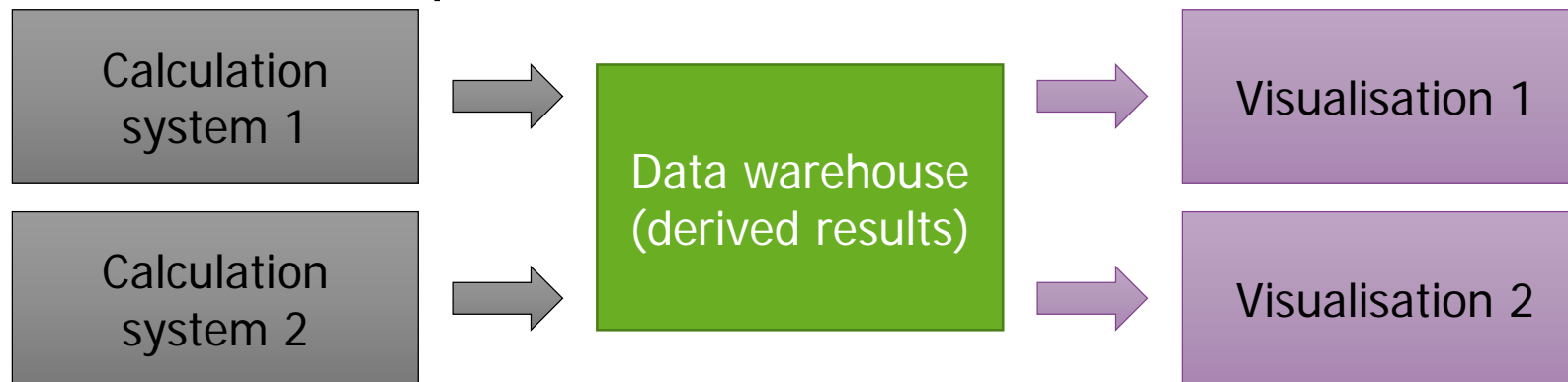


ECDC WGS system update

Erik Alm
2020-04-29

ECDC WGS system upgrade, design principles

- Re-use existing tools and resources for storage, calculation and visualisation
- Integrate data from several different calculation systems in the same Data Warehouse data model
- Encourage open data sharing while also fulfilling all data protection and access control requirements
- Focus on the user experience and service oriented architecture (data submission and data exploration)



WGS system update – features

A new user interface for data exploration – implements MicroReact

Improved feedback on uploaded data – QC, cluster matches, AMR and virulence genotyping

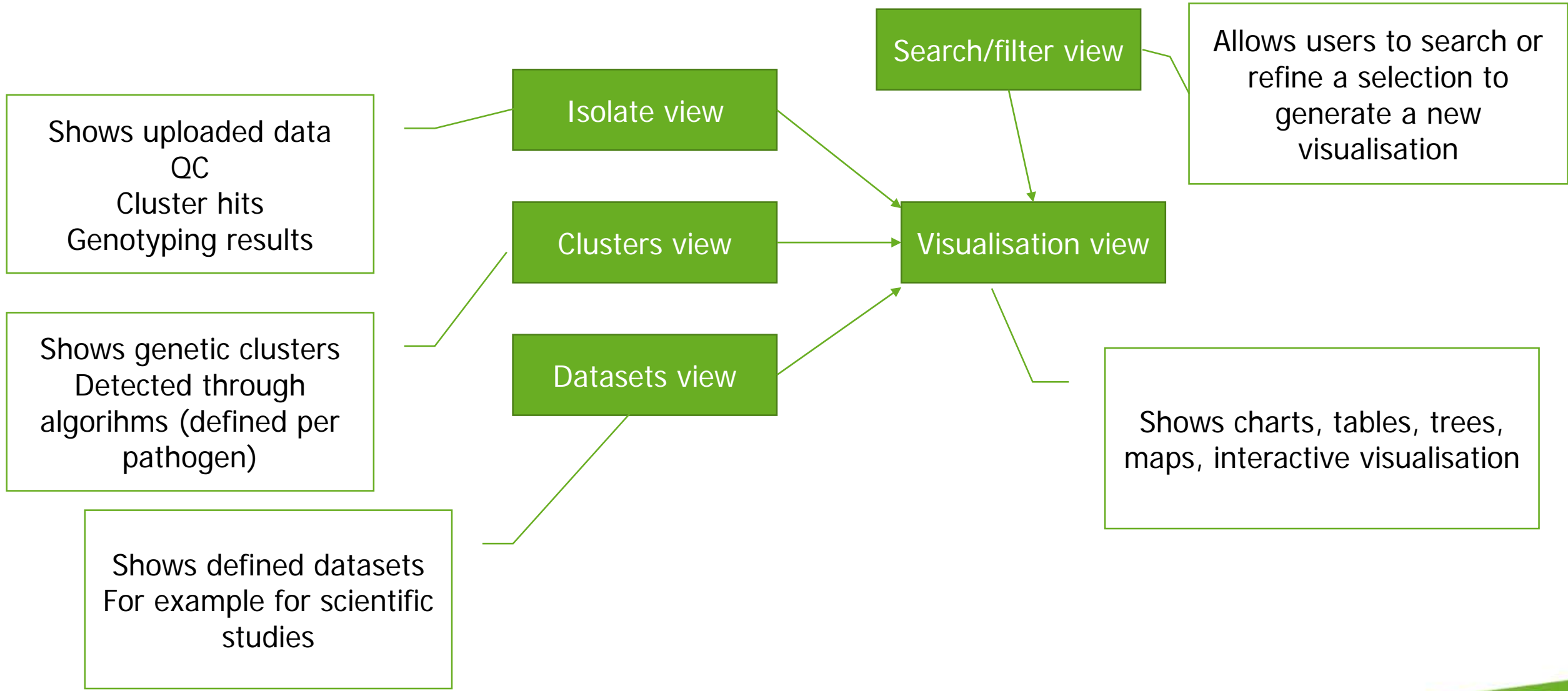
Improved data upload options

Data structured in an analysis-friendly format in a data warehouse

Restricted access to nominated users (nominated by the country)

Real-time exchange of allelic profiles with EFSA for cluster detection

WGS system update – user interface



WGS - Molecular Cluster Analysis Tool



[Molecular Clusters](#)
[Molecular Datasets](#)
[Visualisation](#)
[My Isolates Data](#)
[Help](#)

Hello, ECDCDMZ\test_fwd_ecdc1!

This table shows molecular clusters detected by ECDC by applying automated algorithms, see respective surveillance protocols for details. Only multi-country clusters & clusters in your country are shown. Included are also generated datasets of particular interest.

Listeria monocytogenes clusters

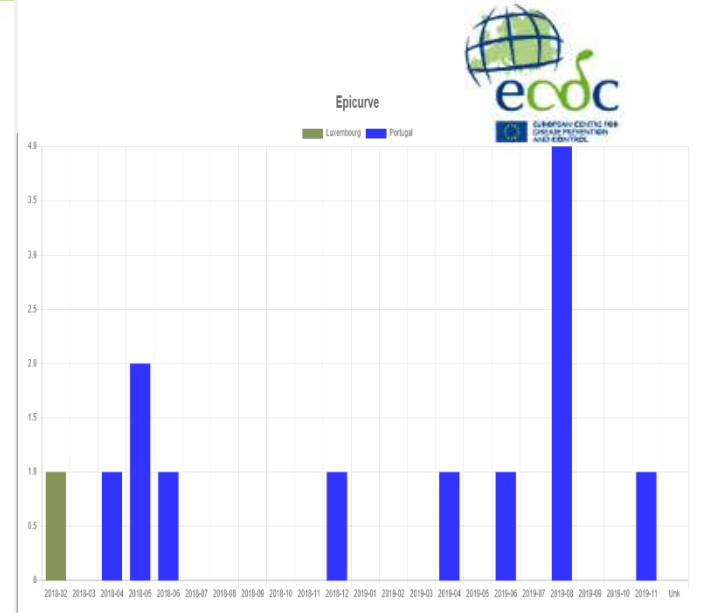
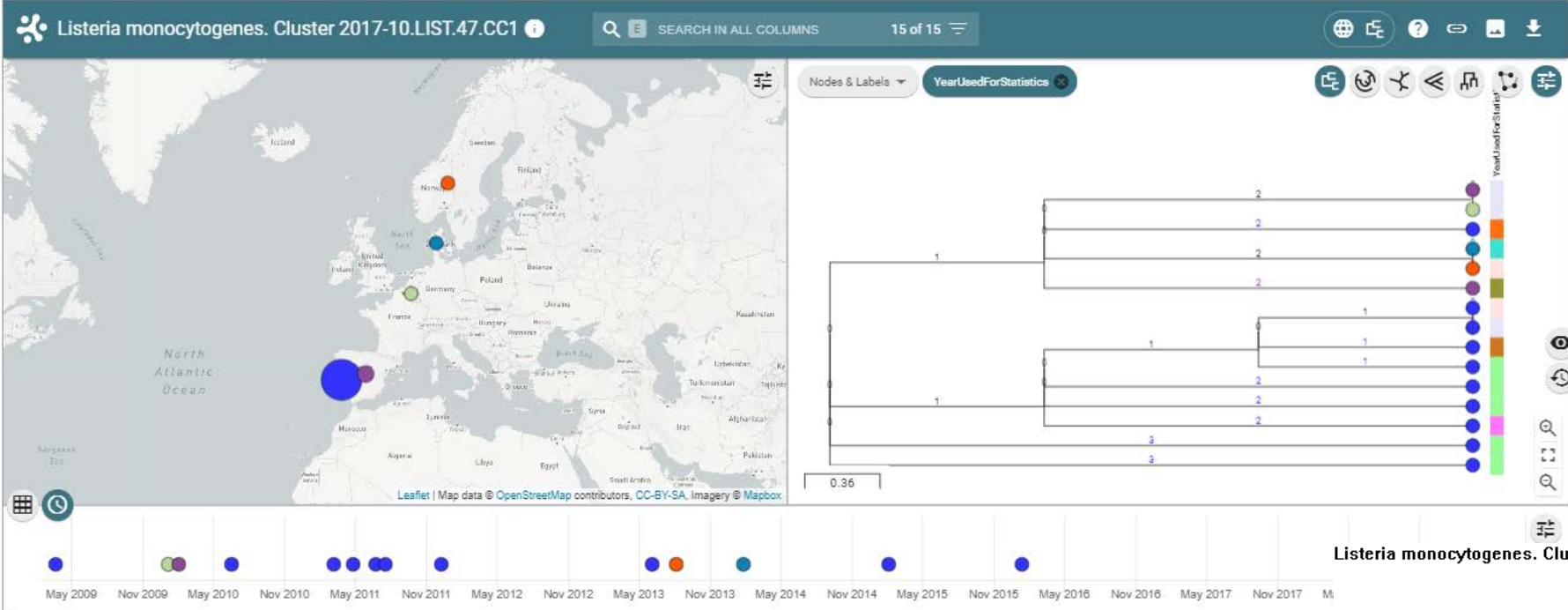
Column groups to hide




 Showing 1 to 10 of 542 rows rows per page

 ...

<input type="checkbox"/>	Cluster ID	Cluster info	Event ID	Cluster status	Number of isolates	Countries	Updated (7d)	First date	Last date	Last updated	Extended cluster
<input type="checkbox"/>	2019-03.LIST.02.CC1			OPEN	13	LU(1), PT(12)		2018-02-25	2019-11-07	2019-12-12	2019-03.LIST.02.CC1 +7AD
<input type="checkbox"/>	2017-06.LIST.70.CC1.Asci.0053.Apal.0040			OPEN	52	ES(51), NL(1)		2015-08-26	2019-10-09	2020-03-04	2017-06.LIST.70.CC1.Asci.0053.Apal.0040 +7AD
<input type="checkbox"/>	2019-11.LIST.08.CC1			OPEN	8	ES(7), PT(1)		2015-06-19	2019-10-05	2020-03-04	2019-11.LIST.08.CC1 +7AD
<input type="checkbox"/>	2019-02.LIST.04.CC7		UI540	OPEN	12	UK(9), DE(1), ES(2)		2018-07-01	2019-09-25	2020-01-18	2019-02.LIST.04.CC7 +7AD
<input type="checkbox"/>	2017-			OPEN	5	LU(2), NO(1), IT(1)		2017-07-15	2019-09-29	2019-10-09	2017-10.LIST.02.CC1



Listeria monocytogenes. Cluster 2017-10.LIST.47.CC1 (Generated 2020-04-28 10:17:23)

Isolates	38156	38487	40104	40857	41739	41935	41936	41937	41939	41940	41941	41946	41948	42095	42211
38156	0	6	6	4	6	3	4	3	4	1	1	1	3	4	6
38487	6	0	4	2	4	7	8	7	8	7	7	5	7	2	4
40104	6	4	0	2	4	7	8	6	8	7	7	5	7	2	0
40857	4	2	2	0	2	5	6	5	6	5	5	3	5	0	2
41739	6	4	4	2	0	7	8	7	8	7	7	5	7	2	4
41935	3	7	7	5	7	0	5	4	5	4	4	2	4	5	7
41936	4	8	8	6	8	5	0	5	4	5	5	3	5	6	8
41937	3	7	6	5	7	4	5	0	5	4	4	2	4	5	6
41939	4	8	8	6	8	5	4	5	0	5	5	3	5	6	8
41940	1	7	7	5	7	4	5	4	5	0	0	2	4	5	7
41941	1	7	7	5	7	4	5	4	5	0	0	2	4	5	7
41946	1	5	5	3	5	2	3	2	3	2	2	0	2	3	5
41948	3	7	7	5	7	4	5	4	5	4	4	2	0	5	7
42095	4	2	2	0	2	5	6	5	6	5	5	3	5	0	2
42211	6	4	0	2	4	7	8	6	8	7	7	5	7	2	0

ReportingCountry	DateUsedForStatistics	SampleOrigin	Cluster
ES	2010-02-02	HUMAN	2017-10.LIST.47.CC1
BE	2010-01-06	HUMAN	2017-10.LIST.47.CC1
PT	2016-01-13	HUMAN	2017-10.LIST.47.CC1
DK	2014-01-26	HUMAN	2017-10.LIST.47.CC1
NO	2013-08-06	HUMAN	2017-10.LIST.47.CC1
ES	2019-08-05	HUMAN	2017-10.LIST.47.CC1
PT	2013-06-05	HUMAN	2017-10.LIST.47.CC1
PT	2010-06-18	HUMAN	2017-10.LIST.47.CC1
PT	2015-02-04	HUMAN	2017-10.LIST.47.CC1
PT	2011-04-27	HUMAN	2017-10.LIST.47.CC1
PT	2011-07-19	HUMAN	2017-10.LIST.47.CC1
PT	2011-03-08	HUMAN	2017-10.LIST.47.CC1
PT	2009-03-22	HUMAN	2017-10.LIST.47.CC1
PT	2011-06-24	HUMAN	2017-10.LIST.47.CC1
PT	2011-12-10	HUMAN	2017-10.LIST.47.CC1

Planned specific features for FWD AMR

AMR genotyping using suitable software(s) and database(s)

Data warehouse where the AMR genotyping data are stored ready for analysis

Show AMR genotyping results in user interface

Two challenges:

- Choose the most suitable AMR genotyping software(s) and reference database(s)
- Create a data model that works for AMR genotyping data analysis

AMR genotyping software



The softwares and databases to be used routinely at ECDC is not yet decided

ResFinder has been used ad-hoc

Other suggestions of software and databases to look at?

Please type in the chat