COllaborative Management Platform for detection and Analyses
of (Re-) emerging and foodborne outbreaks in Europe

General Meeting
1-3 March 2017, WTC, Rotterdam, The Netherlands

Day 1, Wednesday, 1 March 2017

Time	Activity	Speakers	Location
09:00 – 09:20	Coffee and registration		Foyer
09:20 – 10:00	Welcome to General Meeting 2017 Report from Young COMPARE	Frank Aarestrup, DTU Marion Koopmans, EMC Miranda de Graaf, EMC	Diamond Room
10:00 – 10:45	WP3 & WP6 – Analytical workflows for frontline diagnostics & Underpinning research for frontline diagnostics	Overview: Surbhi Malhotra, UA Prediction of bacterial antimicrobial resistances from genomic data by a machine-learning approach: Sebastian Matamoros, UA LMM-UAntwerpen WGS pipeline: Basil Britto Xavier, UA	Diamond Room
10:45 – 11:15	Coffee break		
11:30 – 12:15	WP4 & WP7 – Analytical workflows for foodborne pathogen surveillance, outbreak detection, and epidemiological analysis & Underpinning research on foodborne outbreaks	Overview: Eva Møller Nielsen, SSI Virus detection: Julien Schaeffer, IFREMER Salmonella outbreak: Liljana Petrovska, APHA Source attribution: Nanna Munck, DTU	Diamond Room
12:15 – 13:15	Lunch		
13:15 – 14:00	WP5 & WP8 – Additional tools for detection of and response to (re-) emerging infections & Global phylogeography analysis of H5N8	Overview and H5N8: Thijs Kuiken, EMC NGS bioinformatics tools: Terry Jones, UCAM Overview of the global sewage metagenomic sequencing: Patrick Munk, DTU Sewage virome: Bas Oude Munnink, EMC	Diamond Room
14:00 – 15:00	WP9 – Data and information platform	Update on the COMPARE platform - what's available now and what's coming: Guy Cochrane, EMBL, Ole Lund, DTU, and Laszlo Oroszlany, WIGNER	Diamond Room
15:00 – 15:30	Coffee break		

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15:30 – 16:30	Breakout groups – Tutorials	Tutorial A: Installing COMPARE workflows for bioinformaticians and software engineers: Nima Pakseresht, EMBL Tutorial B: Reporting data into COMPARE for biologists and bioinformaticians: Marc Rossello, EMBL	Diamond Room/ Breakout room
16:30 – 17:30	WP Breakout Meetings	*WP 3/6, Breakout room* *WP 2, Diamond Room* *WP 9, Diamond Room* *WP 4/7, Diamond Room*	Diamond Room/ Breakout room
17:30 – 18:30	Poster Session with drinks		Foyer
19:00	COMPARE Dinner		WTC, 23rd floor

Day 2, Thursday, 2 March 2017

Time	Activity	Speakers	Location
08:30 – 09:30	WP14 - Cost effectiveness framework	Overview: Pieter van Baal, EUR Ebola case: Klas Kellerborg, EUR and My Phan, EMC	Diamond Room
09:30 – 10:00	Coffee break		
10:00 – 10:45	WP1 - Risk assessment and risk-based strategies for sample and data collection	Overview: Amie Adkin, APHA Potential of machine learning methods as a tool for predicting risk of illness applying next generation sequencing data: case of Listeria monocytogenes: Patrick Njage, DTU Harmonization of sampling and data collection strategies for investigation of infectious disease outbreaks: Reina Sikkema, EMC	Diamond Room
10:45 – 11:30	WP2 – Harmonised standards for sample processing and sequencing	WP overview, status, future plans: Martin Beer, FLI Standardization and LOPs: Claudia Wylezich, FLI Metagenomics - Virus PT "dry lab": Annika Brinkmann, RKI	Diamond Room
12:00 – 13:00	Lunch		
13:00 – 15:00	Cross-WP Session	Barriers or Risk Communication	Diamond Room/ Breakout room
15:00 – 15:30	Coffee break		
15:30 – 17:00	Cross-WP Session	WP9 tools and services under development, including search, retrieval, new reporting tools, file sharing, analysis workflows: various speakers from EMBL-EBI, EMC, DTU and WIGNER)	Diamond Room
15:30 – 17:00	Executive Board and EAP Meeting		Breakout room
	Dinner on your own		

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Day 3, Friday, 3 March 2017

Time	Activity	Speakers	Location
08:30 – 10:00	Cross-WP Session	Metagenomic Subgroup*	Diamond Room
10:00 – 10:30	Coffee break		
10:30 – 11:30	Cross-WP Session	NGS and MIC data reporting and access for the AMR working group: Nima Pakseresht, Marc Rosello and Clara Amid, EMBL	Diamond Room
10:30 – 11:30	Executive Board meeting		Breakout room
08:30 – 11:30	Small group meetings		
11:30 – 12:30	Wrap-up, next steps, and closing of meeting	Marion Koopmans, EMC & Frank Aarestrup, DTU	Diamond Room
12:30 – 14:00	Lunch for all		
14:00 – 15:00	Networking over coffee		

*Presentations in Metagenomic Subgroup

Ole Lund	DTU	Metagenomics urine fecal samples Metagenomics wounds, lungs and sepsis Bioinformatics methods
Claudia Wylezich	FLI	Graphical output of the RIEMS metagenomic pipeline Sample handling for metagenomic Eliminating bias in sequencing strategies Loss of data while sharing What you amplify is what you get:
Ariane Belka	FLI	Update on RIEMS metagenomic pipeline on the COMPARE datahub
Dennis Schmitz	RIVM	Results on clinical feces and serum
Sam Nooij	RIVM	Review of viral (meta)genomics pipelines.
Simone M Cacciò	ISS	Blastocystis in human metagenomics datasets Detection of multiple pathogens (and "commensal") in different matrices
Matthew Cotten	EMC	de novo assembly of viral genomes from mixed infections

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