# Minisymposium in Metagenomics

Wednesday 22 June

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| 8:15-8:55 | **Registration** |
| 9:00-9:10 | Welcome by P. Junier |
| 9:10-9:40 | "An introduction to metagenomics"<br>**Patrick Chain**<br>Los Alamos National Laboratory/Genome Science JGI, USA. |
| 9:40-9:50 | Question and comments |
| 9:50-10:20 | "16S rDNA-based metagenomic analysis of bacterial communities"<br>**Vladimir Lazarevic**<br>Genomic Research Laboratory, University of Geneva, Switzerland. |
| 10:20-10:30 | Question and comments |
| 10:30-10:50 | Coffee break |
| 10:50-11:20 | "Metagenomic studies using a whole-genome sequencing approach"<br>**Vladimir Sentchilo**<br>Environmental Microbiology Laboratory, University of Lausanne, Switzerland. |
| 11:20-11:30 | Question and comments |
| 11:30-11:40 | "Microbial flora in the lungs"<br>**Markus Hilty**<br>Institute for Infectious Disease, University of Bern, Switzerland. |
| 11:40-11:45 | Question and comments |
| 11:45-11:55 | "Ultra deep sequencing of deep sea foraminiferal diversity challenges the unknowable"<br>**Frank Lejzerowicz**<br>Department of Zoology and Animal Biology, University of Geneva, Switzerland. |
| 11:55-12:00 | Question and comments |
| 12:15-13:40 | Lunch break |
| 13:40-14:10 | "Genomics and post-genomics of Xanthomonas"<br>**Frank-Joerg Vorhoelter**<br>CeBiTec, University of Bielefeld, Germany. |
| 14:10-14:20 | Question and comments |
| 14:20-14:50 | "The MetaSAMS system for the analysis of metagenome datasets"<br>**Sebastian Jaenicke**<br>CeBiTec, University of Bielefeld, Germany. |
| 14:50-15:00 | Question and comments |
| 15:00-15:30 | Coffee break |
| 15:30-16:00 | "Exploring microbial diversity of the Chilean Altiplano using metagenomics"<br>**Cristina Dorador**<br>Department of Fisheries, University of Antofagasta, Chile. |
| 16:00-16:10 | Question and comments |
| 16:10-16:40 | "The importance of metagenomics on biogeochemical studies: the case of Ammonia-oxidizing archaea in oxygen minimum zones"<br>**Veronica Molina**<br>Department of Marine Biology, University Andres Bello, Chile. |
| 16:40-16:50 | Question and comments |
| 16:50-17:00 | General discussion |

# Minisymposium in Metagenomics

Thursday 23 June

9:00-9:10 Welcome by P. Junier
9:10-9:40 "Sequencing technologie: 454 and SOLiD"
**Christof Wunderlin**
Microsynth, Switzerland.
9:40-9:50 Question and comments
9:50-10:20 "illumina sequencing technology: from the early days in 1996 in Switzerland to the new era of Quantum Biology"
**Laurent Farinelli**
Fasteris, Switzerland.
10:20-10:30 Question and comments
10:30-10:50 Coffee break
10:50-11:20 "Next Generation Sequencing"
**Georg Gradl**
Eurofins MWG Operon, Germany.
11:20-11:30 Question and comments
11:30-11:40 "Is metagenomics universal: the case of spore-forming bacteria"
**Thomas Junier**
Laboratory of Microbiology, University of Neuchâtel, Switzerland.
11:40-11:45 Question and comments
11:45-11:55 "A metagenomic characterization of salmonid egg microbial communities in their natural spawning grounds"
**Laetitia Wilkins**
Department of Ecology and Evolution, University of Lausanne, Switzerland.
11:55-12:00 Question and comments
12:15-13:40 Lunch break
13:40-14:10 "How metagenomics is challenging decades of old methods"
**Patrick Chain**
Los Alamos National Laboratory/Genome Science JGI, USA.
14:10-14:20 Question and comments
14:20-14:50 "The metagenome of waste-water"
**Vladimir Sentchilo**
Environmental Microbiology Laboratory, University of Lausanne, Switzerland.
14:50-15:00 Question and comments
15:00-15:30 Coffee break
15:30-16:00 "Can we predict the activity levels of specific functions within a microbial community from its metatranscriptome?"
**David Russell Johnson**
Department of Environmental Microbiology, Swiss Federal Institute of Aquatic Science and Technology (Eawag), Switzerland.
16:00-16:10 Question and comments
16:10-16:40 "The human metagenome"
**Vladimir Lazarevic**
Genomic Research Laboratory, University of Geneva, Switzerland.
16:40-16:50 Question and comments
16:50-17:00 General discussion

# Minisymposium in Metagenomics

Friday 24 June

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| 9:00-9:10 | Welcome by P. Junier |
| 9:10-10:10 | "Workshop I – IMG metagenomic tools"<br>**Patrick Chain**<br>Los Alamos National Laboratory/Genome Science JGI, USA. |
| 9:10-10:10 | "Workshop II – MetaSAMS"<br>**Sebastian Jaenicke**<br>CeBiTec, University of Bielefeld, Germany. |
| 10:10-10:40 | Coffee break |
| 10:40-11:40 | "Workshop I – IMG metagenomic tools"<br>**Patrick Chain**<br>Los Alamos National Laboratory/Genome Science JGI, USA. |
| 10:40-11:40 | "Workshop II – MetaSAMS"<br>**Sebastian Jaenicke**<br>CeBiTec, University of Bielefeld, Germany. |
| 11:40-11:50 | "Metagenomics/transcriptomics for functional diversity of reductive dehalogenases?"<br>**Aamani Rupakula**<br>Laboratory of Environmental Biotechnology, EPFL, Switzerland. |
| 11:50-11:55 | Question and comments |
| 11:55-12:05 | "Characterization of The Diversity and Metabolic Potential of Microorganisms in Opalinus Clay at The Mont Terri Underground Rock Laboratory"<br>**Alexandre Bagnoud**<br>Environmental Microbiology Laboratory, EPFL, Switzerland. |
| 12:05-12:10 | Question and comments |
| 12:15-13:40 | Lunch break |
| 13:40-14:50 | "Workshop III- Introduction in CAMERA and MGRAST"<br>**Vladimir Sentchilo**<br>Environmental Microbiology Laboratory, University of Lausanne, Switzerland. |
| 13:40-14:50 | "Workshop III- Introduction in XXX"<br>**Veronica Molina/Cristina Dorador**<br>University Andres Bello/University of Antofagasta, Chile. |
| 14:50-15:20 | Coffee break |
| 15:20-16:30 | "Workshop III- Introduction in CAMERA and MGRAST"<br>**Vladimir Sentchilo**<br>Environmental Microbiology Laboratory, University of Lausanne, Switzerland. |
| 15:20-16:30 | "Workshop III- Introduction in XXX"<br>**Veronica Molina/Cristina Dorador**<br>University Andres Bello/University of Antofagasta, Chile. |
| 16:30-17:00 | Final discussion |