

2015 COURSE

- › [Home](#)
- › [Registration](#)
- › [Detailed Program](#)
- › [Presentations](#)
- › [Venue](#)
- › [Accommodation](#)
- › [2014 Course](#)

[Home](#)

Course Program

Submitted by oliveira on Tue, 01/27/2015 - 10:09

Course program (check for updates).

Don't forget to register for Rast - <http://rast.nmpdr.org>

Time	Fev 2 Monday	Fev 3 Tuesday	Fev 4 Wednesday	Fev 5 Thursday	Fev 6 Friday
9:00-10:30	9:00 - 9:15 Welcome Public data resources (Gabriel Fernandes)	General data production considerations, public tools and computational resources (Bent Petersen)	16S data production and analysis Qiime (Daniel Morais)	Shotgun sequencing data production and analysis Preprocessing, quality, error correction, assembly (Bent Petersen)	Transcriptome data analysis (Fabiano Sviatopolk-Mirsky Pais)
10:30-11:00	Interval	Interval	Interval	Interval	Interval
11:00-12:00	DNA sequencing technologies (Fabiano Sviatopolk-Mirsky Pais)	16S data production and analysis 16S structure and use as a taxonomic marker (Gabriel Fernandes)	16S data production and analysis BMP pipeline and UPARSE, 16S reconstruction from metagenomes (Victor Pyro - TC / Ulisses Rocha - TC)	Shotgun sequencing data production and analysis Gene prediction, functional characterization, taxonomic assignment for shotgun data (Gabriel Fernandes)	Bacteriophage genomes (Ramy Aziz / Martha Vives)
12:00-13:00	Lunch	Lunch	Lunch	Lunch	Lunch
13:00-14:30	Metagenomics sampling methods (Sara Cuadros)	16S data production and analysis 16S databases, RDP, GreenGenes, Silva, etc. (Gabriel Fernandes)	Shotgun sequencing data production and analysis Introduction to shotgun metagenomics (Bent Petersen)	RAST-TK and kBase (James Davis - TC)	Virus metagenomes (Ramy Aziz)
14:30-15:00	Interval	Interval	Interval	Interval	Interval
			Paper Discussions	Paper Discussions	Paper Discussions Bacterial genome assembly

15:00-17:00	Paper Discussions Single cell genomics (Guilherme Oliveira)	Paper Discussions Great metagenomes (Sara Cuadros)	Genomes and virus-bacteria coevolution (Martha Vives, Angela Holguin)	Not just another accounting paper (Ramy Aziz)	(Gabriel Fernandes) Beyond bottlenecks and pipelines: Final words of wisdom about metagenomics (Ramy Aziz)
-------------	---	--	--	--	--

TC - By teleconference

References

- General references

Nat Methods. 2011 Jun;8(6):469-77. Computational methods for transcriptome annotation and quantification using RNA-seq. Garber M, Grabherr MG, Guttman M, Trapnell C. [Link](#)

J Microbiol Methods. 2014 Dec;107:30-7. Data analysis for 16S microbial profiling from different benchtop sequencing platforms. Pylro VS, Roesch LF, Morais DK, Clark IM, Hirsch PR, Tótola MR. [Link](#)

FEMS Microbiol Rev. 2014 Sep;38(5):916-31. Bacteria-phage coevolution as a driver of ecological and evolutionary processes in microbial communities. Koskella B, Brockhurst MA. [Link](#)

Ann Rev Mar Sci. 2014;6:393-414. Antagonistic coevolution of marine planktonic viruses and their hosts. Martiny JB, Riemann L, Marston MF, Middelboe M. [Link](#)

- Paper Discussions

Single cell genomics

Annu Rev Chem Biomol Eng. 2014;5:455-77. A new toolbox for assessing single cells. Tsioris K, Torres AJ, Douce TB, Love JC. [Link](#)

Nat Rev Genet. 2014 Sep;15(9):577-84. Recent advances in genomic DNA sequencing of microbial species from single cells. Lasken RS, McLean JS. [Link](#)

Great metagenomes

Biol Theory. 2014;9(4):392-400. Methodology and Ontology in Microbiome Research. Huss J. [Link](#)

Genomes and virus-bacteria coevolution

Not just another accounting paper

Cell. 2014 Jul 17;158(2):422-33. Cheese rind communities provide tractable systems for in situ and in vitro studies of microbial diversity. Wolfe BE, Button JE, Santarelli M, Dutton RJ. [Link](#)

Science. 2013 Jul 19;341(6143):295-8. Predicting and manipulating cardiac drug inactivation by the human gut bacterium *Eggerthella lenta*. Haiser HJ, Gootenberg DB, Chatman K, Sirasani G, Balskus EP, Turnbaugh PJ. [Link](#)

PLoS One. 2008 Feb 27;3(2):e1584. Microbial ecology of four coral atolls in the Northern Line Islands. Dinsdale EA, Pantos O, Smriga S, Edwards RA, Angly F, Wegley L, Hatay M, Hall D, Brown E, Haynes M, Krause L, Sala E, Sandin SA, Thurber RV, Willis BL, Azam F, Knowlton N, Rohwer F. [Link](#)

Infect Immun. 2008 Sep; 76(9): 3835–3836. Descriptive Science Arturo Casadevall, and Ferric C. Fang [Link](#)

Bacterial genome assembly

Obs: [PDFs are also available here](#)

SPONSORS:



Ministério da Saúde

FIOCRUZ

Fundação Oswaldo Cruz