

Bioinformatics and Genome Analyses course

September 18 - December 15, 2017

Institut Pasteur Tunis, Tunis - Tunisia.

Final Course Program

- [List of Useful links related to the course topics](#)
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Week 1: September 18 - 22

September 18: Welcome - Course and Participants Introductions

- [Public Introduction to the Bioinformatics and Genome Analyses course](#)
- [Introduction of the Bioinformatics and Genome Analyses course to participants](#)
- [Participants Self Introductions](#)

I. Unix/perl updates in the context of genome data analyses

September 19 - 21: Fredj Tekaia, Institut Pasteur Paris, France.

- [Introduction to Unix](#) (pptx), ([pdf](#))
- [Data and coding conventions for practical sessions](#) (BCGAIPT2017_DataNotation.pdf)
- [Practical sessions](#) (BCGAIPT2017_UnixPS.pdf)

September 22: Lab meeting

- Distribution of the USB flash drives each including more than 3000 bibliographic resources (mainly pdf papers and courses presentations).
- Sign in to receive TOCs from some scientific journals (including Sciences, Nature, Nature Genetics, Plos Biology, Plos Computational Biology, Plos Genetic, Bioinformatics, Nucleic Acid Research, PNAS, BioMed Central, BMC Genomics, BMC Biology, Human Molecular Genetics, Microbiology and Molecular Biology,...).
- Presentation of a list of suggested projects for Lab Meetings.
- [List of assigned projects](#)

Week 2: September 25 - 29

September 25 - 27: Fredj Tekaia, Institut Pasteur Paris, France.

- [Introduction to perl](#) (pptx), ([pdf](#))
- [Introduction to perl programming, the minimum to know for practice](#) (pptx), ([pdf](#))
- [Practical sessions](#) (BCGAIPT2017_PerlPS.pdf)

September 28:

- Updates in statistics (Functions, Matrices, Traditional models (Markov model, HMM, Monte-carlo,...) **Nabil Semmar, University Tunis El Manar, Tunis, Tunisia.**

September 29: Lab meeting

- First presentations of selected Projects (bibliography - plans)
- Presentations from TOCs:

-Schlebusch CM, Malmstrom H, Gunther T, et al. (2017).

Southern African ancient genomes estimate modern human divergence to 350,000 to 260,000 years ago. *Science*. 358(6363):652-655.

II. Updates in sequence analyses

Week 3: October 02 - 06

October 2 - October 5: Fredj Tekaia, Institut Pasteur Paris, France.

- [Introduction to Biology: Basic and Novel key concepts](#) (pptx), ([pdf](#)) **Fatma Guerfali, Institut Pasteur Tunis, Tunisia.**

- Note: October 02 is the starting day for Nobel price awards (<https://www.nobelprize.org>)

- [Introduction to Bioinformatics and Genomics](#) (pptx) ([pdf](#))

- [Sequence comparisons: Search for similarity](#) (pptx), ([pdf](#))

- [Practical sessions](#) (BCGAIPT2017_SeqCompPS.pdf)

- [BLAST: Introduction and Use](#) (pptx), ([pdf](#))

- [Practical sessions](#) (BCGAIPT2017_BLASTusePS.pdf)

- Science Webinar (**October 04**): [The rise of whole genome microbial sequencing: a new era for human microbiome analysis](#)

(Access the Webinar: [The webinar can be downloaded from this link](#))

October 06: Lab meeting

-Projects progress presentations

-CRISPR-Cas special presentation (definition, applications)

Presentations from TOCs of the week:

-Chari R, Church GM. (2017). Beyond editing to writing large genomes.

Nat Rev Genet. 18(12):749-760. doi: 10.1038/nrg.2017.59.

-Mensh B, Kording K (2017). Ten simple rules for structuring papers.

PLoS Comput Biol. 13(9): e1005619. <https://doi.org/10.1371/journal.pcbi.1005619>.

-McIntyre et al. (2017). Comprehensive benchmarking and ensemble approaches for metagenomics classifiers.

Genome Biology. 18:182. DOI 10.1186/s13059-017-1299-7.

Week 4: October 09 - 13

October 9 - October 12: Fredj Tekaia, Institut Pasteur Paris, France.

- [Bibliographic Resources for Bioinformatics and Genome Analyses](#) (pptx), ([pdf](#))

- [Multiple Sequence Alignment](#) (ptx), ([pdf](#))

- [Practical sessions](#) (BCGAIPT2017_msaPS.pdf)

- [Molecular Phylogeny Reconstruction in the Genome era](#) (pptx), ([pdf](#))

- [Practical sessions](#) (BCGAIPT2017_PhylAnalPS.pdf)

- [Molecular Evolution](#) (pptx), ([pdf](#))

- [Practical sessions](#) (BCGAIPT2017_MolEvolPS.pdf)

October 13: Lab meeting

-Projects progress presentations.

Presentations from TOCs of the week:

- Dannemann M, Kelso J. (2017). The Contribution of Neanderthals to Phenotypic Variation in Modern Humans. *Am J Hum Genet.* 101(4):578-589.
- Zahn LM (2017). A Fantastic Voyage in Genomics. *Science* 358 (6359), 56-57.

III. Genome analyses

Week 5: October 16 - 20

October 16 - October 19: Fredj Tekaia, Institut Pasteur Paris, France.

- [Genomes Sequencing: Main projects and Resources](#) (pptx), ([pdf](#))
- [Practical sessions](#) (BCGAIPT2017_ExplorGenomResoursPS.pdf)
- [Practical sessions](#) (BCGAIPT2017_CompleteGenomesPS.pdf)
- [Large-scale Genome Analyses](#) (pptx), ([pdf](#))
- [Practical sessions](#) (BCGAIPT2017_GenomCompPS.pdf)
- [Practical sessions](#) (BCGAIPT2017_ParalogsOrthologsPS.pdf)

October 20: Lab meeting

-Projects progress presentations.

Presentations from TOCs of the week:

- Shendure J, Balasubramanian S, Church GM, Gilbert W, Rogers J, Schloss JA, Waterston RH. (2017). DNA sequencing at 40: past, present and future. *Nature.* 550(7676):345-353.
- Nussinov R, Papin JA. (2017). How can Computation advance microbiome research? *PLoS Comput Biol.* 2017 Sep 21;13(9):e1005547. doi: 10.1371/journal.pcbi.1005547.
- Hager CL, Ghannoum MA. (2017). The mycobiome: Role in health and disease, and as a potential probiotic target in gastrointestinal disease. *Dig Liver Dis.* 49(11):1171-1176.
- Good BH, McDonald MJ, Barrick JE, Lenski RE, Desai MM. (2017). The dynamics of molecular evolution over 60,000 generations. *Nature.* 551(7678):45-50.
- Robin van der Lee, Laurens Wiel, Teunis J.P. van Dam and Martijn A. Huynen (2017). Genome-scale detection of positive selection in nine primates predicts human-virus evolutionary conflicts. *Nucleic Acids Res.* 45(18):10634-10648.

Week 6: October 23 - 27

October 23 - October 25: Fredj Tekaia, Institut Pasteur Paris, France.

- Practical sessions: Genome Analyses: mcl clustering of paralogs and of orthologs.
- [Introduction to Phylogenomics: Species Trees - Genome Trees](#) (pptx), ([pdf](#))

October 26: Fatma Guerfali, Institut Pasteur Tunis, Tunis, Tunisia.

- [Genome and Transcriptome Studies Using NGS Technologies: Past and Present](#) (Parts 1-2)

October 27: Lab meeting

-Projects progress presentations.

Presentations from TOCs of the week:

- Cohen Jon (2017). Base editors' open new way to fix mutations. *Science* 358 (6362), 432-433.
- Eggertsson HP, Jonsson H, Kristmundsdottir S, et al. (2017). GraphTyper enables population-scale genotyping using pangenome graphs. *Nat Genet.* 2017 Nov;49(11):1654-1660. doi: 10.1038/ng.3964.
- Koskella B, Hall LJ, Metcalf CJE. (2017). The microbiome beyond the horizon of ecological and evolutionary theory.

Nat Ecol Evol. 2017 Nov;1(11):1606-1615. doi: 10.1038/s41559-017-0340-2.

-Teh BT, Lim K, Yong CH, Ng CCY, et al. (2017). The draft genome of tropical fruit durian (*Durio zibethinus*). *Nat Genet.* 49(11):1633-1641. doi: 10.1038/ng.3972.

Week 7: October 30 - 31 - November 01 - 03

October 30 - 31: Fatma Guerfali, Institut Pasteur Tunis, Tunis, Tunisia.

- [Genome and Transcriptome Studies Using NGS Technologies: Past and Present](#) (Part 3)

November 01 - 02: Fatma Guerfali, Institut Pasteur Tunis, Tunis, Tunisia.

- [R & Rstudio Basics for NGS data analysis](#) (Part 4)

November 02: Amel Ghouila, Institut Pasteur Tunis, Tunis, Tunisia.

- [Martin Krzywinski CIRCOS Course](#)

November 03: Lab meeting

-Projects progress presentations.

Presentations from TOCs of the week:

-Donovan H. Parks, Christian Rinke, Maria Chuvochina, et al. (2017).

Recovery of nearly 8,000 metagenome-assembled genomes substantially expands the tree of life.

Nature Microbiology 2, 1533-1542.

-Andrzej Zielezinski, Susana Vinga, Jonas Almeida and Wojciech M. Karlowski. (2017).

Alignment-free sequence comparison: benefits, applications, and tools.

Genome Biology 18:186 DOI 10.1186/s13059-017-1319-7.

-Thompson LR, Sanders JG, McDonald D, et al. (2017). A communal catalogue reveals Earth's multiscale microbial diversity.

Nature. 551(7681):457-463.

-Kaiser J. (2017). Gut microbes shape response to cancer immunotherapy. *Science.* 358(6363):573. doi: 10.1126/science.358.6363.573.

-Nasmyth K. (2017). How are DNAs woven into chromosomes? *Science.* 358(6363):589-590. doi: 10.1126/science.aap8729.

Week 8: November 06 - 10

November 06 - November 09: Fredj Tekaia, Institut Pasteur Paris, France.

- Genome Analyses (mcl clustering of orthologs - meme analyses of clusters of orthologs):
- [Practical sessions](#) (BCGAIPT2017_ParalogsOrthologsPS.pdf)
- [Introduction to Whole Genome Alignments](#) (pptx), ([pdf](#))
- Practical sessions (continued) and Wrap up.

November 10: Lab meeting

-Projects progress presentations.

Presentations from TOCs of the week:

-Yamagishi J, Asada M, Hakimi H, Tanaka TQ, Sugimoto C, Kawazu SI. (2017).

Whole-genome assembly of *Babesia ovata* and comparative genomics between closely related pathogens.

BMC Genomics. 18(1):832. doi: 10.1186/s12864-017-4230-4.

-Zhang DF, Zhi XY, Zhang J, Paoli GC, Cui Y, Shi C, Shi X. (2017).

Preliminary comparative genomics revealed pathogenic potential and international spread of *Staphylococcus argenteus*.

BMC Genomics. 2017 Oct 23;18(1):808. doi: 10.1186/s12864-017-4149-9.

-Melinda A. Yang, Xing Gao, Christoph Theunert, et al. (2017).

40,000-Year-Old Individual from Asia Provides Insight into Early Population Structure in Eurasia. *Current Biology* 27, 3202-3208.

Week 9: November 13 - 16

November 13 - November 16: Gary Benson, Boston University, USA.

- [Next Generation Sequencing: Technologies, mapping and Analysis](#) (pptx)
- [Algorithms for Read Mapping](#) (pptx)
- [Tandem Repeat Variants in the Human genome](#) (pptx)
- Practical sessions: [notebook1](#), [notebook2](#), [notebook3](#), [notebook4](#).
- [Practical session introduction: search for tandem repeats using Tandem Repeat Finder \(trf\)](#) (pptx),(pdf)
- [Practical sessions](#) (BCGA2017_MotifSearchPS.pdf).

November 17: Lab meeting

-Projects progress Presentation.

Presentations from TOCs of the week:

- Kupferschmidt K. (2017). Genomes rewrite cholera's global story. *Science* 358 (6364), 706-707.
- Weill et al., (2017). Genomic history of the seventh pandemic of cholera in Africa. *Science* 358, 785–789.
- Domman et al., (2017). Integrated view of *Vibrio cholerae* in the Americas. *Science* 358, 789-793.
- Booker et al. (2017). Detecting positive selection in the genome. *BMC Biology*. 15:98. DOI 10.1186/s12915-017-0434-y.
- Narzisi G, Mishra B. (2011). Comparing *De Novo* Genome Assembly: The Long and Short of It. *PLoS ONE* 6(4): e19175. doi:10.1371/journal.pone.0019175.
- Sergey Koren, Brian P. Walenz, Konstantin Berlin, et al. (2017). *Canu*: scalable and accurate long-read assembly via adaptive k-mer weighting and repeat separation. *Genome Research*. 27:722-736.

Week 10: November 20 - 24

November 20 - November 24: Daniel Lundin, Stockholm University, Sweden.

Metagenomics

- [Introduction to microbial ecology and omics](#) (pptx), (pdf)
- [Introduction to R and the tidyverse](#) (pptx), (pdf)
- [Handling amplicon sequences: where did the counts come from?](#) (pptx), (pdf)
- [Automation with make](#) (pptx), (pdf)
- [Introduction to ecological diversity measurements and ordination](#) (pptx), (pdf)
- [Shotgun methods for environmental genomics](#) (pptx), (pdf)
- [Working with vegan](#) (pptx), (pdf)
- [Microbial ecology](#) (pptx), (pdf)
- [Practical sessions](#)
- [Ecology/Microbiology - Handling amplicon data - Ecological diversity, ordination - Shotgun methods for environmental genomics](#) (original documents)

November 24: Lab meeting

-Projects progress Presentation

Presentations from TOCs of the week:

- Pennisi E. (2017). Survey of archaea in the body reveals other microbial guests. *Science* 358 (6366), 983.

Week 11: November 27 - 30

November 27 - November 29: Fredj Tekaia, Institut Pasteur Paris, France.

- Bacterial genome analyses (consider 5 Mycobacterial completely sequenced genomes (data will be distributed));
- Simple descriptions: GC%, aa composition, gene/protein sizes;
- Intra & inter proteome comparisons; Paralogs/orthologs inference and clustering using mcl.
- motif search in clusters of paralogs/orthologs using meme suite of programs.
- [Practical sessions](#) (BCGAIPT2017_ParalogsOrthologsMycoPS.pdf)

November 29: Christos Ouzounis, CERTH, Thessalonica, Greece.

- [Genomics & System Biology - Genome-aware methods and metaboloc networks](#) (pdf)

November 30: Lab meeting

Preparation of the final project version and training on final talks presentation.

Week 12: December 4 - December 8

- [Lectures on Bioinformatics and Genome studies: what did we learn and perspectives](#)

December 04

09:00 - 09:30 [Programme introduction](#)

09:30 - 10:30 [The rise of Genomes and Bioinformatics.](#) **Fredj Tekaia, Institut Pasteur Paris, France.**

10:30 - 11:00 Coffee-breaks

11:00 - 12:30 The rise of Genomes and Bioinformatics cont..

12:30 - 12:30 Lunch break

14:00 - 15:30 [Complexities of parasite genomes for high-throughput data interpretation: Leishmania as an example.](#) **Fatma Guerfali, Institut Pasteur Tunis, Tunis, Tunisia.**

15:30 - 16:00 Coffee-break

16:00 - 17:30 [Exploring Genome Data Using Correspondence Analysis.](#) **Fredj Tekaia, Institut Pasteur Paris, France.**

17:30 - 18:00 Questions/Comments

December 05

09:00 - 10:30 [SNV and SV calling.](#) **Guillaume Bourque, McGill, U. Montreal, Canada.**

10:30 - 11:00 Coffee-breaks

11:00 - 12:30 [NGS applications, data challenges and solutions.](#) **Guillaume Bourque, McGill, U. Montreal, Canada.**

12:30 - 12:30 Lunch break

14:00 - 15:30 [The evolution of the tuberculosis agent.](#) **Roland Brosch, Institut Pasteur Paris, France.**

15:30 - 16:00 Coffee-break

16:00 - 17:30 [Virulence determinants of Mycobacterium tuberculosis - special focus on ESX/type VII secretion systems.](#) **Roland Brosch, Institut Pasteur Paris, France.**

17:30 - 18:00 Questions/Comments

December 06

09:00 - 10:30 [RNA-seq.](#) **Guillaume Bourque, McGill, U. Montreal, Canada.**

10:30 - 11:00 Coffee-breaks

11:00 - 12:30 [Understanding non-coding DNA and data sharing.](#) **Guillaume Bourque, McGill, U. Montreal, Canada.**

12:30 - 12:30 Lunch break

14:00 - 15:30 [Bacterial genomics: from sequencing one genome to thousands of genomes.](#) **Philippe Glaser, Institut Pasteur Paris, France.**
 15:30 - 16:00 Coffee-break
 16:00 - 17:30 [Studying bacterial communities by genomic methods: Gut microbiome dynamics and antimicrobial resistance ecology.](#) **Philippe Glaser, Institut Pasteur Paris, France.**
 17:30 - 18:00 Questions/Comments

December 07

09:00 - 10:30 [The Saga of giant viruses: historical, epistemological, and biological aspects.](#) **Jean-Michel Claverie, Universite Aix-Marseille, France.**
 10:30 - 11:00 Coffee-break
 11:00 - 12:30 [Qu'est-ce que la Science.](#) **Jean-Michel Claverie, Universite Aix-Marseille, France.**
 12:30 - 12:30 Lunch break

14:00 - 18:00 Selected presentations from participant's projects. (Participants)

14:00 - 14:30 Genome assembly methods. **Boutheina Ksibi**
 14:30 - 15:00 Gene prediction methods. **Hedia Tnani**
 15:00 - 15:30 Genome alignments: algorithmic aspects. **Bacem Saada**
 15:30 - 16:00 Coffee-break
 16:00 - 16:30 Human Gut Microbiome as a Diagnostic Marker of Diseases. **Ikram Ben Fraj**
 16:30 - 17:00 *M. Tuberculosis*: WGS bottlenecks in the characterization of the resistome. **Neira Dkhil**
 17:00 - 17:30 RNAseq data analyses strategies and applications in plant. **Amal Boukteb**
 17:30 - 18:00 Tardigrade genome. **Haifa Chahed**

December 08

09:00 - 10:30 [Introduction to Crystallography.](#) **Pedro Alzari, Institut Pasteur Paris, France**
 10:30 - 11:00 Coffee-break
 11:00 - 12:30 [The impact of structural genomics.](#) **Pedro Alzari, Institut Pasteur Paris, France**
 12:30 - 12:30 Lunch break

14:00 - 18:00 Selected presentations from participant's projects. (Participants)

14:00 - 14:30 Tree Of Life: methodological aspects. **Ghada Nouairia**
 14:30 - 15:00 Aptamers selection: new approach in diagnosis & Therapy. **Boutheina Marnissi**
 15:00 - 15:30 Red blood cell disorders. **Nawel Trabelsi**
 15:30 - 16:00 Coffee-break
 16:00 - 16:30 From DNA Barcoding to e-DNA meta-barcoding approach. **Mayssa Chattaoui**
 16:30 - 17:00 Evolutionary Dynamics in *Saccharomycetacea* phylum. **Salma Abbes**
 17:00 - 18:30 Course evaluation Questionnaire introduction and distribution. **Fredj Tekaia**

Week 13: December 11 - December 15

December 11

-Projects Presentations
 09:00 - 09:30 Metagenomics in sea environment. **Alif Chebbi**
 09:30 - 10:00 Genome editing. **Imen Mougou**
 10:00 - 10:30 Third Generation Sequencing. **Cherifa Ayari**
 10:30 - 11:00 Coffee-break

11:00 - 11:30 Methods for genomic structural variation analyses. **Hafedh Ben Zaabza**

11:30 - 12:00 NGS data analysis for colorectal cancer diagnosis. **Saifeddine Azouz**

12:30 - 12:30 Lunch break

14:00 - 18:00 -Scripts collection

-Unfinished work termination

December 12

-Unfinished work termination

-[Evaluation questionnaire results presentation](#)

-[Course evaluation: Oral presentations](#) (Large file)

December 13

-Save home directories

-Clean the computers from personal works

- [Course closure](#)

End of the course

December 14 - December 15

-Scientific and Financial reports final versions

[Courses home page](#)

Last Modified: May 09, 2018 EST

[Fredj Tekaia](#)