

## **BIO 6260/3260 - Génomique microbienne**

Hiver 2015

mardi 13-16h

Instructor: Jesse Shapiro

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### DESCRIPTION

*Connaissances pratiques des outils génomiques, métagénomiques et bioinformatiques avec accent sur l'évolution et l'écologie microbienne. TP sur une compréhension des bases conceptuelles des analyses bioinformatiques sans expérience en programmation.*

### GOALS OF THE COURSE

The focus of this course will be on the *concepts* and *logic* of microbial genome analysis. The course will consist of in-depth discussion of recent and important papers in the field, and an independent research project, where you will get to analyze some of your own data, or write a grant proposal if you don't have data in hand.

The goal of this course is to provide both *breadth* and *depth* in the study of microbial genomes. The breadth will be achieved through lectures and discussion of the primary literature. The depth will be achieved through independent research projects: each student will choose a project that suits their interests or is related to their ongoing thesis research. This project can take the form of a research paper or grant proposal, and will be developed over the course of the semester.

### EXAMPLE LECTURE TOPICS

1. Introduction to genomics and sequencing technologies.
2. Natural history of microbial genomes.
3. Sequence alignment and assembly.
4. Sequence evolution: Motifs, substitution models & phylogenetics.
5. Signatures of natural selection in sequence data.
6. Transcriptomics & clustering analysis.
7. Metagenomics, 16S analysis and microbial ecology.

### EVALUATION

#### 45% self-directed project:

- 15% grant or research paper format (10-15 pages)
- 15% 'midterm' technical presentation ("project pitch"). Lab-meeting style, troubleshooting and explaining methods.
- 15% final presentation.

#### 25% 'journal club' presentation

- each student will present a critical analysis of 1 or 2 original research articles chosen from a list of suggestions (below), and lead a ~1 hour discussion with the class. Students may also suggest their own choice of paper, with the approval of the instructor.

#### 15% participation in class discussion

#### 15% short homework assignments

- 3 assignments worth 5% each

## EXAMPLE READING TOPICS

### **1. Origins of species and higher-order taxa**

Nelson-Sathi, S., Dagan, T., Landan, G., Janssen, A., Steel, M., McNerney, J. O., ... Martin, W. F. (2012). Acquisition of 1,000 eubacterial genes physiologically transformed a methanogen at the origin of Haloarchaea. *Proceedings of the National Academy of Sciences of the United States of America*, 109(50), 20537–42. doi:10.1073/pnas.1209119109

Nelson-Sathi, S., Sousa, F. L., Roettger, M., Lozada-Chávez, N., Thiergart, T., Janssen, A., ... Martin, W. F. (2014). Origins of major archaeal clades correspond to gene acquisitions from bacteria. *Nature*. doi:10.1038/nature13805

Retchless, A. C., & Lawrence, J. G. (2010). Phylogenetic incongruence arising from fragmented speciation in enteric bacteria. *Proceedings of the National Academy of Sciences of the United States of America*, 107(25), 11453–11458.

Fraser, C., Hanage, W. P., & Spratt, B. G. (2007). Recombination and the nature of bacterial speciation. *Science*, 315(5811), 476–480.

### **2. The ecology and evolution of horizontal gene transfer**

Smillie, C. S., Smith, M. B., Friedman, J., Cordero, O. X., David, L. A., & Alm, E. J. (2011). Ecology drives a global network of gene exchange connecting the human microbiome. *Nature*, 480(7376), 241–244. Retrieved from <http://dx.doi.org/10.1038/nature10571>

Cordero, O. X., Wildschutte, H., Kirkup, B., Proehl, S., Ngo, L., Hussain, F., ... Polz, M. F. (2012). Ecological Populations of Bacteria Act as Socially Cohesive Units of Antibiotic Production and Resistance. *Science*, 337(6099), 1228–1231. Retrieved from <http://www.sciencemag.org/cgi/doi/10.1126/science.1219385>

Pal, C., Papp, B., & Lercher, M. J. (2005). Adaptive evolution of bacterial metabolic networks by horizontal gene transfer. *Nature Genetics*, 37(12), 1372–1375

### **3. The genomics of ecological adaptation**

Coleman, M. L., & Chisholm, S. W. (2010). Ecosystem-specific selection pressures revealed through comparative population genomics. *Proceedings of the National Academy of Sciences of the United States of America*, 107(43), 18634–18639.

Sheppard, S. K., Didelot, X., Meric, G., Torralbo, A., Jolley, K. A., Kelly, D. J., ... Falush, D. (2013). Genome-wide association study identifies vitamin B5 biosynthesis as a host specificity factor in *Campylobacter*. *Proceedings of the National Academy of Sciences*, 110(29), 11923–11927. Retrieved from <http://www.pnas.org/cgi/doi/10.1073/pnas.1305559110>

#### **4. Pathogenicity & Genomic Epidemiology**

Croucher, N. J., Harris, S. R., Fraser, C., Quail, M. A., Burton, J., van der Linden, M., ... Bentley, S. D. (2011). Rapid Pneumococcal Evolution in Response to Clinical Interventions. *Science*, *331*(6016), 430–434. Retrieved from <http://www.sciencemag.org/cgi/doi/10.1126/science.1198545>

Lieberman, T. D. T. D., Michel, J.-B. J. B., Aingaran, M. M., Potter-Bynoe, G. G., Roux, D. D., Davis, M. R. M. R., ... Kishony, R. R. (2011). Parallel bacterial evolution within multiple patients identifies candidate pathogenicity genes. *Nature Genetics*, *43*(12), 1275–1280. Retrieved from <http://www.nature.com/doi/10.1038/ng.997>

Lieberman, T. D., Flett, K. B., Yelin, I., Martin, T. R., McAdam, A. J., Priebe, G. P., & Kishony, R. (2013). Genetic variation of a bacterial pathogen within individuals with cystic fibrosis provides a record of selective pressures. *Nature Genetics*. Retrieved from <http://www.nature.com/doi/10.1038/ng.2848>

#### **5. Experimental evolution**

Barrick, J. E., Yu, D. S., Yoon, S. H., Jeong, H., Oh, T. K., Schneider, D., ... Kim, J. F. (2009). Genome evolution and adaptation in a long-term experiment with *Escherichia coli*. *Nature*, *461*(7268), 1243–1247.

Blount, Z. D., Barrick, J. E., Davidson, C. J., & Lenski, R. E. (2012). Genomic analysis of a key innovation in an experimental *Escherichia coli* population. *Nature*, *488*(7417), 513–518. Retrieved from <http://dx.doi.org/10.1038/nature11514>

Meyer, J. R., Dobias, D. T., Weitz, J. S., Barrick, J. E., Quick, R. T., & Lenski, R. E. (2012). Repeatability and Contingency in the Evolution of a Key Innovation in Phage Lambda. *Science*, *335*(6067), 428–432. Retrieved from <http://www.sciencemag.org/cgi/doi/10.1126/science.1214449>

#### **6. CRISPR and Phage-Bacteria interactions**

Weitz, J. S., Poisot, T., Meyer, J. R., Flores, C. O., Valverde, S., Sullivan, M. B., & Hochberg, M. E. (2013). Phage-bacteria infection networks. *Trends in Microbiology*, *21*(2), 82–91. doi:10.1016/j.tim.2012.11.003

Makarova, K. S., Grishin, N. V., Shabalina, S. a, Wolf, Y. I., & Koonin, E. V. (2006). A putative RNA-interference-based immune system in prokaryotes: computational analysis of the predicted enzymatic machinery, functional analogies with eukaryotic RNAi, and hypothetical mechanisms of action. *Biology Direct*, *1*, 7. doi:10.1186/1745-6150-1-7

Palmer, K. L., & Gilmore, M. S. (2010). Multidrug-Resistant Enterococci Lack CRISPR-cas. *mBio*, *1*(4), e00227–10–e00227–19. Retrieved from <http://mbio.asm.org/cgi/doi/10.1128/mBio.00227-10>

Seed, K., Yen, M., Shapiro, B., Hilaire, I., Charles, R., Teng, J., ... Camilli, A. (2014). Evolutionary consequences of intra-patient phage predation on microbial populations. *eLife*, *3*, e03497.

## **7. Structure and function of microbiomes**

Yatsunenko, T., Rey, F. E., Manary, M. J., Trehan, I., Dominguez-Bello, M. G., Contreras, M., ... Gordon, J. I. (2012). Human gut microbiome viewed across age and geography. *Nature*. Retrieved from <http://www.nature.com/doi/10.1038/nature11053>

Eren, a M., Borisy, G. G., Huse, S. M., & Mark Welch, J. L. (2014). Oligotyping analysis of the human oral microbiome. *Proceedings of the National Academy of Sciences of the United States of America*, *111*(28), E2875–84. doi:10.1073/pnas.1409644111

Forsberg, K. J., Reyes, A., Wang, B., Selleck, E. M., Sommer, M. O. A., & Dantas, G. (2012). The Shared Antibiotic Resistome of Soil Bacteria and Human Pathogens. *Science*, *337*(6098), 1107–1111. Retrieved from <http://www.sciencemag.org/cgi/doi/10.1126/science.1220761>

## **8. Single-cell genomics**

Kashtan, N., Roggensack, S. E., Rodrigue, S., Thompson, J. W., Biller, S. J., Coe, a., ... Chisholm, S. W. (2014). Single-Cell Genomics Reveals Hundreds of Coexisting Subpopulations in Wild Prochlorococcus. *Science*, *344*(6182), 416–420. doi:10.1126/science.1248575

Rinke, C., Schwientek, P., Sczyrba, A., Ivanova, N. N., Anderson, I. J., Cheng, J.-F., ... Woyke, T. (2013). Insights into the phylogeny and coding potential of microbial dark matter. *Nature*, 1–7. Retrieved from <http://www.nature.com/nature/journal/vaop/ncurrent/pdf/nature12352.pdf>

Stepanauskas, R. (2012). Single cell genomics: an individual look at microbes. *Current Opinion in Microbiology*, *15*(5), 613–620. Retrieved from <http://linkinghub.elsevier.com/retrieve/pii/S1369527412001166>