

## **Homework 1**

Genetics and bioinformatics

### **Important dates:**

- Submit report and presentation files before 4 November 2017, 24:00h
- The presentation will be on 7 November 2017

### **Marks:**

- Part 1 – 15 points
- Part 2 – 15 points

### **Evaluation:**

- For the reports, your work will be evaluated based on the accuracy and completeness of answers and the report structure when based on a paper (see doc “critical evaluation of a report / paper”).
- For the presentation, you will be evaluated based on the completeness of your slides, your presentation skills, your understanding of the matter, and your answers to questions (see the information given during the introductory class).

### **Instruction:**

- Form a group of 2-3 persons and complete the homework in both parts (1&2).
- For the presentation, you have to present within 15 minutes for each part and everybody in a group needs to present.
- A report and slides need to be submitted in electronic format via the website by the deadline. Please note that the submission system will be closed automatically.
- Compress all files into ONE zip file and submit to:

**[http://www.student.montefiore.ulg.ac.be/~GBIO009-1/GBIO0002\\_sys/index.php](http://www.student.montefiore.ulg.ac.be/~GBIO009-1/GBIO0002_sys/index.php)**

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**Part 1:** Genetics and DNA sequencing.

Select only ONE task from the list (A, B, or C).

**A:** Answer the following questions using a report format (introduction, discussion and conclusion sections).

- List the key features of the DNA structure.
- Explain which DNA feature(s) is (are) important for its genetic information encoding ability (think in terms of encoding the information but also decoding).
- Explain which feature(s) is (are) important for protecting the heredity information taking into account the context of the genome, cell structure and gene expression steps (DNA→mRNA →protein).

**B:** Answer the following questions using a report format (introduction, discussion and conclusion sections).

- Explain the Sanger DNA sequencing method. What are the main drawbacks of this method?
- Explain the cloning approach when sequencing large DNA fragments. What are the pro and cons of the method?
- Explain in details the bridge PCR technology?

**C:** Select ONE of these papers to compile a report and presentation. Your presentation should cover objective, method, result (if available), literatures (if needed), your own discussion, and your own conclusion.

- Van Dijk, Erwin L., et al. "Ten years of next-generation sequencing technology." *Trends in genetics* 30.9 (2014): 418-426.
- Tefferi, Ayalew, et al. "Primer on medical genomics part II: Background principles and methods in molecular genetics." *Mayo Clinic Proceedings*. Vol. 77. No. 8. Elsevier, 2002.

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**Part 2:** Genome-wide association studies - analytics.

Select only ONE of the following papers to compile a report and presentation. Your presentation should cover the objective, method, results (if available), literature references (if needed), your own discussion, and your own conclusions.

- Neale, Benjamin M., and Pak C. Sham. "The future of association studies: gene-based analysis and replication." *The American Journal of Human Genetics* 75.3 (2004): 353-362.
  - Cirulli, Elizabeth T. "The increasing importance of gene-based analyses." *PLoS genetics* 12.4 (2016): e1005852.
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