Homework 1

Genetics and bioinformatics

Important dates:

- Submit report and presentation files before 5 November 2016, 24:00h
- The presentation will be on 8 November 2016

Marks:

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

Evaluation:

- For report, your work will be evaluated based on the accuracy and completeness of answers and report structure.
- For presentation, you will be evaluated based on the completeness of slides, your presentation, your understanding, and your answers to questions.

Instruction:

- Form a group of 2-3 persons and complete the homework in both parts (1&2).
- For presentation, you have to present within 15 minutes for each part and everybody in a group needs to present.
- A report and/or slides for presentation 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

Part 1: Genetic 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 study and create a presentation. Your presentation should cover objective, method, result (if available), literatures (if needed), your own discussion, and your own conclusion.

- van Dijk EL, Auger H, Jaszczyszyn Y, Thermes C. Ten years of next-generation sequencing technology. Trends Genet TIG. 2014 Sep;30(9):418–26.
- Tefferi A, Wieben ED, Dewald GW, Whiteman DAH, Bernard ME, Spelsberg TC. Primer on medical genomics part II: Background principles and methods in molecular genetics. Mayo Clin Proc. 2002 Aug;77(8):785–808.

Part 2: Population stratification and Genome-wide association study.

Select ONE of these papers to study and create a presentation. Your presentation should cover objective, method, result (if available), literatures (if needed), your own discussion, and your own conclusion.

- Peloso GM, Lunetta KL. Choice of population structure informative principal components for adjustment in a case-control study. BMC Genet. 2011;12:64.
- Gibson G. Rare and common variants: twenty arguments. Nat Rev Genet. 2012 Feb;13(2):135–45.