Homework 1

A tour in genetic epidemiology

Important dates:
- Presentation date: <u>10 April 2017</u>

Mark:
- 25 points

Instruction:
- Read Bessonov et al. (2015) paper and take Evans et al. (2013) as supporting document to address the following questions in your slides presentation.
- You can work in groups. One presentation per group is allowed (but everyone should present a part) and a score will be a group score.
- Presentation duration: 20min.
- Reference papers could be found from:

 http://www.montefiore.ulg.ac.be/~chaichoompu/CK/?Courses

Questions

1) What is the study design:
   a. Samples: unrelated individuals? Cohort? Case-control? Family? Would that make a difference for the subsequent analyses?
   b. Markers: which markers are used? How many?
2) How were dependencies (LD) between markers treated? This relates to "pruning". Why is this important?
3) How were markers coded in analytic models? Does this matter in terms of final epistasis results?
4) Which analytic framework / model was used? Regression? Parametric or non-parametric approach?
5) How was multiple testing dealt with?
6) What can be used as prior biological information? Is this information also relevant post analysis?
7) Which measures were taken to strengthen the findings?
   a. Does agreement between different analytic tools imply validity of findings?
   b. Replication?
   c. Validation?

Address all of the questions and work out in more details, using the aforementioned papers or information you can retrieve from:
http://www.montefiore.ulg.ac.be/~chaichoompu/CK/?Courses