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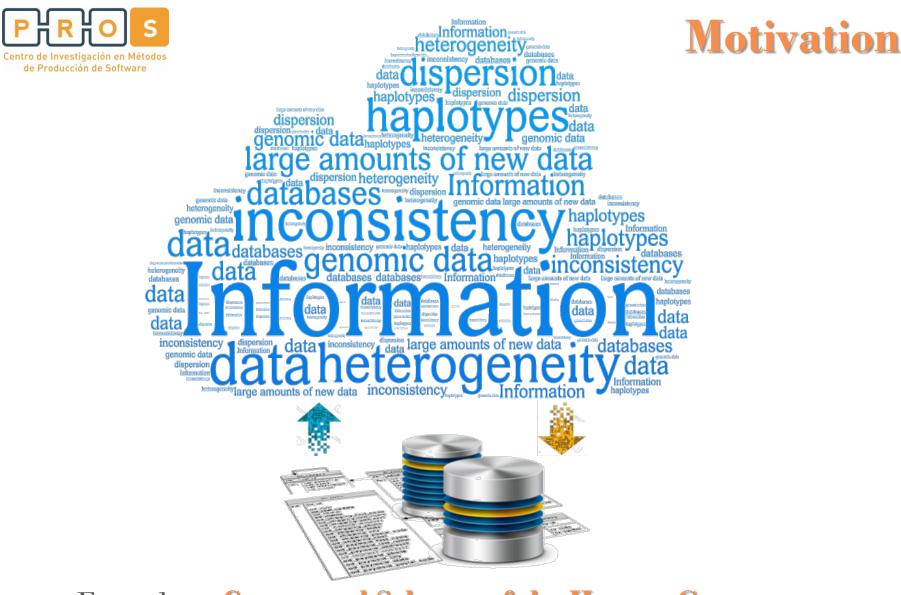
### Motivation

- ¿What does "haplotypes" mean?
- Research Methodology
- Conceptual Modeling and Alignment of Haplotypes
- Conclusions & Future Work









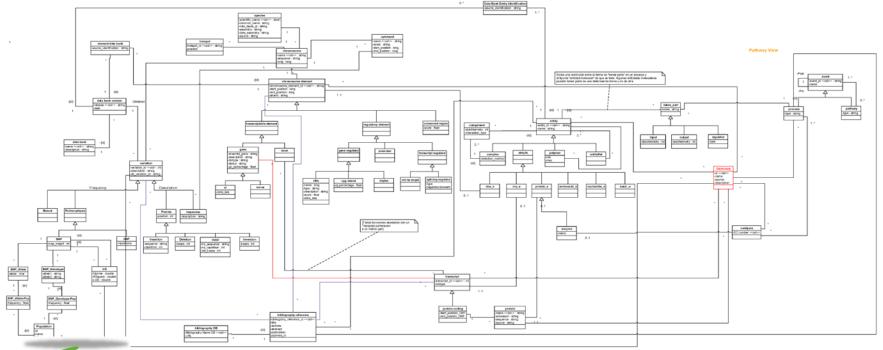
Extend our Conceptual Schema of the Human Genome (CSHG) to include the specification of Haplotypes.







#### Figure 1. Conceptual Schema of the Human Genome, version 3





### This model should be extended in two ways:

Integrating treatment of haplotypes.

The application of statistical models.





# What does "haplotypes" mean?

- From a Bioinformatics point of view, Haplotypes are a set of SNP's (single nucleotide polymorphism) that are inherited and found together on a chromosome.
- Currently, there is a significant set of genetic diseases where the influence of haplotypes has been well-stablished such as: breast cancer, alcohol sensitivity, and others.







# **Research Methodology**

We introduce our research methodology using the –*Engineering Cycle*– proposed by Roel Wieringa, which includes the following steps:

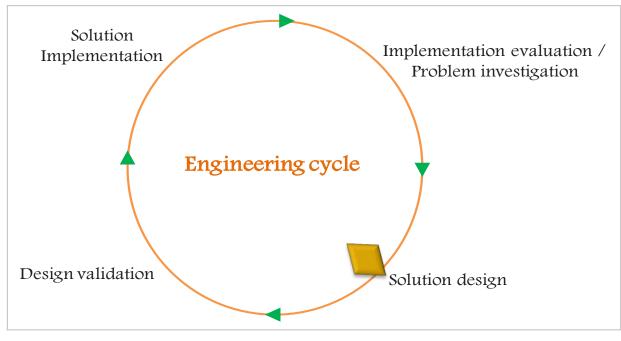
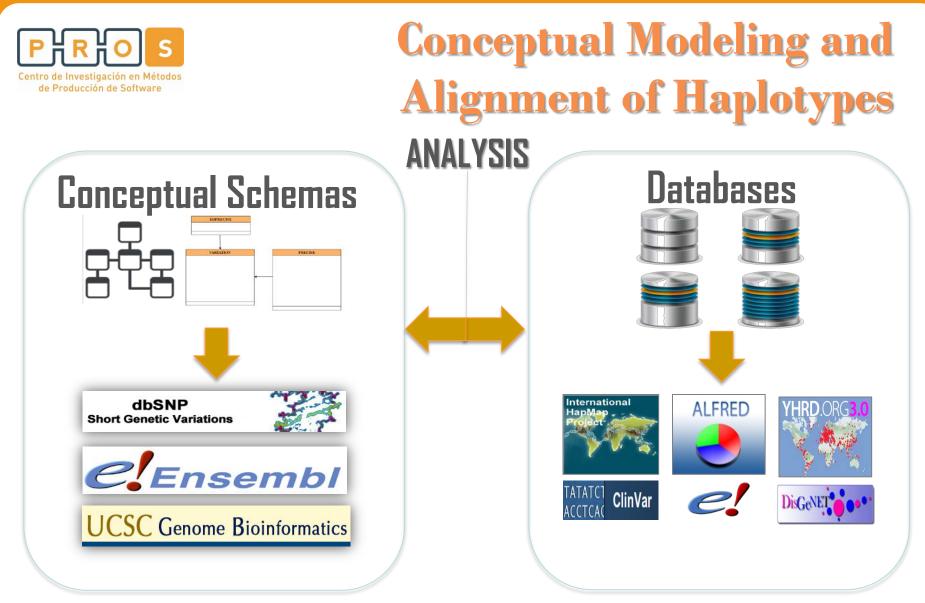


Figure 3. Engineering Cycle by Roel Wieringa





To evaluate this work, we have check if the concepts are suitable to support the information provided by popular haplotypes repositories: trying to represent a good conceptual alignment with validated databases from the community.





With this knowledge we can improve the generation of genetic diagnosis.



With the aim of providing conceptual models for improving diagnosis in medical contexts where *Genomic Information Systems (GeIS)* play a key role.

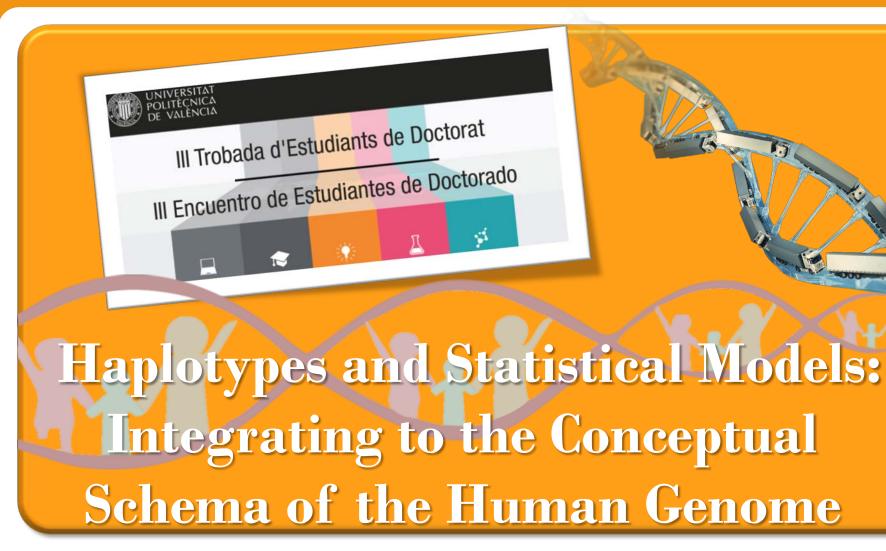




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