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SÉMINAIRE

# Organization of genes along genome during evolution.

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The organization of genes along a genome is not random. There exists various proofs of specific rearrangements such that operon for procaryote organisms.In the goal to better understand how this organization can explain the correlation between chromosomic mutation in cancer, we studied the organization of co-functional genes on the human genome (pathways, protein complexes, RNAt, etc). Using statistics, we observed significant concentrations (or dispersions) for sets of co-functioning genes. We evaluated the organization of these sets of genes through three aspects: number of chromosomes involved, genomic distance, spatial intra-chromosomic distance. This organization seems to depend on the functional category (FunCat) of each set of genes. From this results, we start to work on the evolution of these concentrations and dispersions among various species.Moreover, in order to observe some (dis)similarities between genomes, it is necessary to define realistic models and measures. We have implemented models (based of graph theory and mathematic programming) to compute in particular common adjacencies between genomes. These models take into account increasingly biologic information despite the complexity of the studied problems.