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KITP Program Proposal
Population Genetics and Genomics

Organizers: L. Kruglyak (Princeton); L. Quintana-Murci, M. Vergassola (CNRS, Inst. Pasteur).

The program anticipates rapid development of the subject of Evolutionary and Population Genetics driven by Single Nucleotide Polymorphisms (SNP) mapping efforts and the opportunities opened by the advent of high-throughput techniques of genotyping, re-sequencing and phenotyping. Haplotype reconstruction, recombination hot-spot mapping, ancestry inference, and selective and demographic inference, all present computational and statistical challenges that could potentially benefit from the injection of methods from other fields and foster the development of novel ideas and approaches. Fruitful interactions will be facilitated by the peculiar status of the field in biology, traditionally featuring a stronger role of theory and models. Neutral dynamics provides for a general classical framework, of importance both for its rich statistical dynamics and for a benchmark to efficiently identify genomic loci affected by other mechanisms such as natural selection, demography and migrations. Experimental data currently produced require a detailed discrimination among these evolutionary scenarios and typically call for multiple-loci genomic methods and analysis of quantitative traits. Precious information is also extracted from comparative analyses and it is easily foreseen that their importance will further grow as the cost of sequencing methods steadily reduces. Infectious diseases exert strong selection pressures; genetic variants influencing human susceptibility to disease thus have an intimate relationship to selection that can be exploited for the identification of candidate disease loci. Data for human populations naturally couple the field to public-health issues. Association studies have already provided important clues on genomic loci involved in diseases and analysis of the diversity and differential response to drugs will be fundamental in developing individual-specific drug treatments.

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The scope of the program is to gather world experts in these different disciplines to present their state of the art and to foster interactions among them. A 2.5-3 month format seems the most appropriate to the scope of the project and the proposed time-slot is September-November 2008.

Key-words:

- Statistical mechanics and algorithms for population genomics
- What to do with Single Nucleotide Polymorphism and re-sequencing data?
- Databases (HapMap, Perlegen, etc.) inference and recombination hotspots
- Structural polymorphisms
- Signatures of natural selection on genomic scale.
- Comparative Genomics
- Demographic inference: Origins and migrations of populations
- The role of human genetic diversity in drug response and human diseases

List of possible participants:

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