CBGP
Centre de Biologie pour la Gestion des Populations

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Salle de réunion

BIOINFORMATIC AND ANALYTICAL TOOLS FOR THE ANALYSIS OF WHOLE-GENOME SEQUENCE POLYMORPHISM DATA

par
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- Most of NGS datasets (diploid and pooled) are lacking of information about the linkage between variants (no phased data). Here we study a method that analyzes unphased data in order to detect incompatible genealogies, considering missing data and several populations.

- Furthermore, we have developed statistics and tests of neutrality for estimating the patterns of variability using NGS data containing large number of missing data. We have also developed new algorithms that allow an accurate estimation of the levels and patterns of variability in diploids but also in pooled data.

- Finally, we have designed bioinformatic tools that allow the user to use these algorithms and statistics in an efficient way.

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