

Out of the mists of times: reconstructing ancestral genomes and their use in genomics

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Until today, most insights gained from analysing genomes were obtained by comparing modern genomes to each other. While this makes it possible to infer genomic similarities and difference, it would be, in principle, more logical to compare successive ancestral genomes up to their modern descendant, to better understand the changes that took place during evolution, in a chronological manner. However, the DNA of ancestral genomes dating back to the early vertebrates or early green plants do not remain today.

I will present AGORA, an algorithmic framework developed to reconstruct the organisation of ancestral genomes from their modern descendants. The method has been extensively validated using realistic simulations of genome rearrangements in vertebrate genomes. I will next describe how this information can be used to examine specific biological questions of interest. First, successive ancestral chromosomes provide a direct way of identifying branch-specific genomic rearrangements, including duplications and inversions. It thus become possible to identify the determinants of such rearrangement, and the answer to this question solves a long-standing issue in the field. Second, the reconstruction of ancestral coding sequences represents a new resource to observe the distribution of GC content along ancestral chromosomes, and helps answer important questions on the evolution of the compositional landscape of chromosomes. Ancestral genome reconstruction allow, like a telescope in astronomy, to look back in time and examine early founding events in the evolution of genomes and species. As the precision and coverage of the reconstructions improve, so will the discoveries that they enable.

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