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The traditional view about our ancestors is that they lived in closed worlds where the interactions were limited to just a small number of relatives or lifelong close associates. However, given extent of genetic differentiation (using the Wright's F) in populations which are likely to have had population structures and characteristics similar to our ancestors, this idea seems to be incorrect. Under idealized assumptions in which only random migration and small group size are at work, the observed F 's values could be produced by small and isolated populations. However, this idealized situation is unlikely in the Pleistocene: there are five deviations of this idealized model: reproductive skew, population crashes, colonization processes, lineage-based group fission and non-random migration. In accordance with those deviations, the F 's observed values could not be produced by small isolated populations but by large and/or cosmopolitan ones.

The purpose of my work is to simulate a prehistoric population under the influence of each one of these deviations and of all of them in combination to show that our ancestors may have lived in large cosmopolitan groups and to estimate the effect on the F 's values of all the deviations working together and in various combinations.