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### Simulating Human Origins and Evolution

The development of populations over time and, on longer time scales, the evolution of species are both influenced by a complex of interacting, underlying processes. Computer simulation provides a means of experimenting within an idealised framework to allow aspects of these processes and their interactions to be isolated, controlled and understood.

In this book, computer simulation is used to model migration, extinction, fossilisation, interbreeding, selection and non-hereditary effects in the context of human populations and the observed distribution of fossil and current hominoid species. The simulations described enable the visualisation and study of lineages, genetic diversity in populations, character diversity across species and the accuracy of reconstructions, allowing new insights into human evolution and the origins of humankind for graduate students and researchers in the fields of physical anthropology, human evolution and human genetics.

KEN WESSEN has Ph.D.s in both Theoretical Physics and Human Evolution and has worked as a post-doctoral researcher in Computer Visualisation. He currently works in quantitative finance, and is an Adjunct Lecturer in the School of Anatomy and Human Biology at the University of Western Australia.

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# Simulating Human Origins and Evolution

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*University of Western Australia*



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*Each change of many-coloured life he drew  
Exhausted worlds, and then imagined new.*

*Samuel Johnson 1709–84*

*For Cindy, Jessamine and Xanthe*

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## *Preface*

Recent times have seen a great deal of activity and progress in human origins research, from the advent of molecular methods in the 1960s to the many important fossil hominid discoveries of the past few years. Nevertheless, the debate over whether particular fossil species are direct human descendants or not, and whether the fossil record and molecular results support a recent African origin or multiregional continuity, continues to rage. There is clearly a substantial need for fundamental work studying the methods employed in the interpretation of these data. The primary aim of the research presented in this volume is to begin to address this need by means of direct computer modelling and simulation of the many underlying and interacting processes.

Specifically, this volume describes the development and application of two related, but distinct, simulations, each designed to model important aspects of evolution in general, and the origin and evolution of humans in particular, as well as to provide substantial analysis and a wide variety of visualisations of the results.

The first simulation, *Specialist*, models the evolution of species and subspecies over millions of years, by starting with a single ancestral species with a particular suite of morphological ‘characters’ and allowing it to evolve in discrete steps. The characters are either hereditary or non-hereditary, and at each step a small number of these characters may change, either owing to random mutation or as a result of a change in the nature of the home environment of each species. Random extinction, fossilisation, interbreeding of subspecies, migration between four continents, and selective advantage are included in the model.

The main focus is on using the resulting species data to construct a phylogeny and migration history, which is then compared against the known true phylogeny. Two techniques of reconstruction are employed. The first technique involves matching existing species and fossils to the most closely (morphologically) related earlier fossil, whereas the second involves a reconstruction based on differences between the characters of the existing species only.

The second simulation, *Genie*, models several generations of individuals in up to three independent populations, thus allowing study of the effects of different mating patterns, fertility, adult sex ratio, migrations of various types, limiting population size, selective advantage and the impact of external,

natural disasters on common ancestry and the mixing of lineages generally. Once a complete genealogy is generated, common ancestry, lineage mixing and migrations are determined and analysed for the purely paternal and maternal genealogies (corresponding to Y chromosome and mitochondrial DNA inheritance), as well as the *biological* genealogy, or pedigree, where lineages are traced back through both parents simultaneously. This analysis is carried out on both a small sample of individuals and the full population, and individuals in the population carry both sex-specific and autosomal genes that are subject to mutation and recombination in controlled ways.

The simulations presented are essentially simulations of evolutionary change, and as such may be applied across a very large range of problems. As is apparent from the title of this volume, I have chosen to focus on problems relating to human and hominoid evolution, but extensions to many other areas are relatively straightforward, especially for the species/subspecies simulation.

Both simulations can do either single runs, with various visualisations and interactions, or multiple runs, with more limited visualisation but with basic statistical analysis of the results and all the required information for more advanced analysis provided in a simple text report. In particular, the simulated demographic, genetic and genotype data from *Genie* may be easily exported into other programs to provide more detailed or custom analysis. This removes the need for *Genie* to try to cover the myriad of possible analyses.

The programs that implement the simulations may be freely downloaded by following the links from <http://school.anhb.uwa.edu.au/personalpages/kwessen>.

In the interests of quality control, some minor limitations have been placed on the downloadable versions of the software, but these limitations can be removed via a simple registration process that will also allow me to provide updates and maintain some degree of dialogue with users. It is my hope that making the software available will lead to much further and diverse development of the simulations in collaboration with other researchers.

In addition, many of the figures in this book are black and white, or otherwise adjusted, versions of colour visualisations produced by the simulations. For this reason, the majority of simulations presented in the text are available for download along with the software, enabling them to be viewed in colour, and also enabling the many interactions provided by the simulation program to be explored in the context of these particular simulations. In order to gain a full appreciation of the results presented in this book, readers are urged to download the associated software and familiarise themselves in a hands-on way with the models and visualisations employed.

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I take this opportunity to heartily thank Professor Charles Oxnard, without whose ongoing encouragement and highly infectious enthusiasm this project would never have begun, let alone finished. I also thank Professor Paul O'Higgins for his comments on an earlier version of this work; those comments were particularly instrumental towards providing the necessary impetus for me to undertake the publication of this work in book form. Professor Colin Groves also had several useful comments on an earlier manuscript, and various suggestions from Algis Kuliukas have led to valuable enhancements to the species simulation. Thanks are also due to Mat Abdy for his help in preparing this book's associated website.

And, of course, my most sincere and personal thanks go to my beautiful wife Cindy and lovely daughters Jessamine and Xanthe, each of whom will, I'm sure, very much share my relief at seeing this book complete!

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