

A New Population Genetics Algorithm with a Unique Origin of Humanity

Population genetics uses mathematical principles to describe how the genetic makeup of a population changes over time through mutations, natural selection, random genetic drift, recombination of chromosomes, and migration. It has been applied in order to infer that we share a common ancestry with apes, that our ancestors emigrated from Africa about 50 000 years ago, and that the Homo population was never smaller than a few thousand individuals. However, the theory is full of gaps and weaknesses. In this talk, Dr. Hössjer will describe a recently published algorithm based on the premise that humanity started from one single couple with created diversity. He will argue that it has great potential to fit real data better than the prevailing common ancestry algorithms, and briefly mention about ongoing work to implement the unique origin algorithm.

Ola Hössjer has been Professor of Mathematical Statistics at Stockholm University, Sweden, since 2002. He has done research in statistics and probability theory with applications in population genetics, epidemiology, and insurance mathematics. Hössjer is the author of 85 peer-reviewed papers, he has supervised 13 PhD students, and in 2009 he received the Gustafsson prize in Mathematics. He has also published several articles and book chapters on Christian apologetics and has written the forthcoming book *Becoming a Christian*. He is part of the elders board of a Pentecostal church in his hometown of Sollentuna, and he is the proud father of two daughters.

I. Human history models

A. Common descent with chimps

B. Unique origin of humans

II. Genetic data

A. DNA variation among humans

B. DNA variation between humans and chimps

C. DNA variation within chimps

III. Huge amount of data. We need statistics to summarize DNA variation.

A. Nucleotide diversity

- B. Allele frequency spectrum
 - C. Length of blocks with small variation
- IV. Use population genetics to fit human (chimp) history model to data. Mechanisms that explain genetic variation among humans (chimps):
- A. Mutations
 - B. Genetic drift
 - C. Selection
 - D. Recombination
 - E. Geographic variation (caused by colonization/migration)
 - F. CREATED DIVERSITY (only present in a unique origin model!)
- V. Simulation based approach to fit a human history model
- A. Propose a model for human history
 - B. Simulate DNA data many times from this model, using the six mechanisms of genetic change from IV.
 - C. Compare simulated data with observed data.
 - D. Choose model with a best fit between simulated and real data
- VI. Why testing a unique origin model?
- A. All models should be tested on equal grounds
 - 1. Only the common descent models have been tested with genetic data

2. Unique origin has not been tried, since created diversity is controversial from a secular perspective (methodological naturalism)

B. Unique origin model makes more sense scientifically

1. More consistent with observed block structure of DNA
2. Inbreeding depression less of a problem
3. Interbreeding with Neanderthals less of a problem

C. Unique origin model makes more sense theologically

1. Adam and Eve literal (Gen 1-3, 5, Luke 3, Rom 5, 1 Cor 15)
2. Fall of man a literal event
3. Mankind needs a Savior – Jesus Christ

Suggested Readings:

Ann Gauger, Ola Hössjer and Colin Reeves. (2017). Evidence for Human Uniqueness. Chapter 15 in *Theistic Evolution. A Scientific, Philosophical, and Theological Critique*. Eds. J.P. Moreland et al. (Wheaton, IL: Crossway, 2017)

Ola Hössjer, Ann Gauger and Colin Reeves. Genetic Modeling of Human History Part 1: Comparison of Common Descent and Unique Origin Approaches. *BIO-Complexity* 2016(3):1-15.

Ola Hössjer, Ann Gauger and Colin Reeves. Genetic modeling of human history Part 2: A Unique Origin Algorithm. *BIO-Complexity* 2016(4):1-36.

Ola Hössjer, Ann Gauger and Colin Reeves. (2017). An Alternative Population Genetics Model. Chapter 16 in *Theistic Evolution. A Scientific, Philosophical, and Theological Critique*. Eds. J.P. Moreland et al. (Wheaton, IL: Crossway, 2017)