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# Roles for technology in feeding an evolutionary feed-forward loop in the human lineage

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## Abstract

**Double Session: Philosophical Anthropology I & II (Honenberger, Michelini, Davis; Moss, Blad, Wasmuth)**

Repetitive sequences have long been ignored in genome comparative studies because they were thought to be without adaptive significance (e.g. The Chimpanzee Sequencing and Analysis Consortium, 2005). The passive accumulation of duplications, deletions and translocations that can happen in response to reductions in the stringency of natural selection, however, can increase the modularity of a genome (Lynch & Connery, 2003), and highly modular genomes have an enhanced potential for phenotypic adaptive flexibility. If accessible this potential can, in turn, help organisms circumvent selective constraints. Novel epigenetic and behavioral resourcefulness resulting from the creative deployment of increases in genomic modularity can, in principle, help sustain and buffer further increases (Varki, Geschwind & Eichler, 2008). Hypothetically speaking this situation can cause an evolutionary feed-forward loop in which organisms become more and more 'detached' from explicitly and linearly coded functional genetic information and rely instead on epigenetic ways of accessing 'implicit' functional information in the genome (Moss & Pavesich, 2011; Caporale, 2006). The evolutionary lineage towards human beings shows continual increases in genome modularity and repetitiveness that may indicate that such a loop has indeed come into existence. What roles may the unique technological history of humanity have played in the dynamics of human genome evolution, and in making the modular potential of the genome more accessible as a flexible resource for adaptive deployment in the context of the constructed niches of the *Homo* lineage?

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