1 The Information Continuum Hypothesis of Evolution

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7 Abstract

8 Life is information dancing through time, embedded in matter and shaped by natural selection. Few 9 biologists or philosophers concerned with evolution would object to this description. This apparent 10 accord could be taken to indicate universal agreement on the forces shaping evolution; but the devil 11 is in the details and disagreement is apparent if one looks behind the curtain. The decade strong 12 prevalent paradigm of the Modern Synthesis holds the position that evolution happens by random 13 changes and natural selection acting on genomic inheritance. But there is a new kid on the block; the 14 proponents of an Extended Evolutionary Synthesis argue that inheritance is more than genomes and 15 includes epigenetic information, niche constructs (ranging from the meerkats dens to humans 16 railroads) and culture among other factors – and that these factors are both inheritance and a force 17 shaping evolution. Here we introduce The Information Continuum Hypothesis of Evolution; a 18 conceptual framework that focus on the inherited information rather than the diverse representations 19 this inherited information may have (DNA, RNA, epigenetic markers, proteins, culture etc.). As a tool 20 we introduce the concept "hereditome" to describe the combined inherited representations of 21 information. We believe this framework may help bridge the apparent gap between the Modern 22 Synthesis and the Extended Evolutionary Synthesis.

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24 The Information Continuum Hypothesis of Evolution

25 Evolution of life is brought about by natural selection of traits encoded by gradually changing 26 hereditary information relayed through generations. For a generation of biologists trained under neo-27 Darwinian Modern Synthesis (MS) paradigm, our heuristic model of evolution asserts that the 28 hereditary information is found in the genome. The genome, in turn, is shaped by natural selection 29 among a collection of genomes brought about by random mutations, recombinations and 30 reorganizations. Furthermore, according to the MS, while the genome dictates what phenotypes an 31 organism can display, adaptive information is not transferred to the genome other than through 32 differential survival. Hence, to most biologists evolutionary adaptation takes place during the 33 transition of generations, and since the genome *is* the hereditary information interchanging the terms 34 would not matter much. But it is important to realize that the genome *is* not hereditary information. 35 Just as book is not a story, but a representation of language that may be interpreted as a story. Neither does the genome contain hereditary information – again, just as a book contains a representation of 36 37 a story and not the story itself. The genome contains a representation of hereditary information and 38 the information inferred depends on the living cells in which the representations are interpreted by 39 the cellular machinery¹.

The above may seem an unimportant distinction. But embrace for a second that a vital mitochondrial gene is non-sensical to the cytosolic ribosomal machinery only micrometers away; that the same genome produces as different cells as those found in brains and muscles; or the convincing fact that

- 43 when transferring the nucleus of one species to the enucleated egg of another, the resulting organism
- 44 is not representative of the species from which the nucleus originated². The living world is rife with
- 45 examples illustrating that genomes contain *representations* of information that may be read in very
- 46 different ways, just as religious texts are read in very different ways by highly educated scholars.

47 Genomes are not the only repository of inheritable information. Epigenetic methylation is inheritable and affects genome organization and gene expression³⁻⁶. Pathogen derived RNA molecules, with no 48 49 corresponding representation in the nuclear genome, can confer inheritable immunity towards the 50 pathogen⁷. Proteins can confer inheritable structural information affecting e.g. cellular organization 51 and metabolic activity of descendants^{8,9}. Epigenetic methylation patterns, lost during the post zygotic 52 demethylation, appear to be reinstated based on transcription factor binding patterns – an intriguing 53 example of information being relayed via alternating routes; methylation and protein binding ¹⁰. The 54 microbial flora of termites show colony to offspring inheritance and human maternal bacteria colonize 55 a fetus with lifelong effects on the child's health; both examples of inheritance not confined to the 56 germ cell¹¹⁻¹³. Culture – another example of a non-germline inheritance – is yet another source of 57 evolutionary important information affecting the fitness and evolution of those sharing it ^{14,15}. The 58 point should be very clear by now; hereditary information of evolutionary importance has diverse 59 representations and may travel along various, even alternating, routes. We suggest that the full gamut 60 of hereditary information representations should be referred to as the *hereditome*.

61 The different components of the hereditome have different properties. The genomic hereditome is 62 usually inherited from both parents and remarkably constant, while crucial variability is ensured by mutations, reconfigurations and recombinations. The mitochondrial hereditome, in contrast, is usually 63 64 maternally inherited and does not exhibit recombination, which renders it different evolutionary 65 properties¹⁶. While both the nuclear and mitochondrial genetic hereditomes are quite stable across generations, the epigenetic methylation hereditome is more dynamic with potential for rapid 66 67 modifications within both generations and cell types¹⁷. Where the epigenetic methylation hereditome 68 relay hereditable differences associated with the genome, the RNA hereditome and protein 69 hereditome may be equally dynamic, but are able to confer information not represented in the 70 genome^{7,8}. In addition, the RNA and protein hereditomes are inherited in a non-mendelian manner 71 just as is the maternally inherited bacterial flora^{7,8,13}. To some it may seem a bridge too far, but we will 72 argue that cultural inheritance has adaptive significance and therefore should also be considered a 73 component of the hereditome – a part with capacity for very rapid evolution affecting all members 74 sharing the same culture. The above examples are not exhaustive and additional hereditome 75 components, with yet different evolutionary characteristics, exist. And further hereditome 76 components are likely to remain to be identified.

77 Collectively, these hereditome components comprise information representations with a continuum 78 of evolutionary qualities; some hereditome components are stable while other are more dynamic; 79 some are readily modified by external cues while other are more static; some may cross species boundaries with relative ease whereas others do not^{3,8,18}. Sometimes hereditary information switches 80 81 between hereditome components on the journey through time, as illustrated by information 82 alternating between epigenetic methylation and protein binding representation¹⁰. At other times, 83 information more permanently move from one hereditome component to another, which is well 84 illustrated by the migration of mitochondrial genes to the nuclear genome¹⁹. Furthermore, one 85 hereditome compartment may leave imprints on other compartments, as may be illustrated by culturally defined killer whale ecotypes where the cultural hereditome leave imprints on both the 86 genomic and mitochondrial hereditomes through founding events and subsequent differentiation ¹⁴. 87 88 In symbioses the hereditomes of the symbionts are allowed variable degrees of entanglement 89 occasionally bestowing the involved symbionts with traits depending on their combined 90 hereditomes^{20,21}. In practical studies it is important to take into account that observed traits may be 91 concerted manifestations of information conveyed by different hereditome compartments. For 92 instance, the success of termites is best, if not only, understood by considering both information 93 embodied in the microbial and genetic hereditome components¹³.



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95 Figure 1. A conceptual representation of the Information Continuum Hypothesis of evolution. 96 Hereditary information is represented in the Hereditome components. The represented information 97 is expressed through interpretation and integration by the system the hereditome component is part 98 of. Natural selection acts on the manifested integrated expression and governs what information 99 remains represented in hereditome components. The hereditome components illustrated here are, 100 from left to right: DNA, mitochondrion, RNA, methylation (of DNA and histones), proteins, 101 microbiome, knowledge and culture. The list is not exhaustive and the localizations along the stability-102 instability axis is tentative.

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104 In summary, the central paradigm in the Information Continuum Hypothesis of Evolution (Figure 1) is 105 that life is propagating information and that the substrate for natural selection therefore is 106 information - not genes, RNA, proteins or other representations of information in and of themselves. 107 This information is embodied in the hereditome which comprise various components (genes, RNA, 108 proteins, microbiome etc.) with a continuum of evolutionary qualities. Since natural selection is the 109 result of the dissimilar ability of information to propagate itself, it tautologously follows that introduction of variation in the hereditome during propagation is indispensable for adaptation. So, in 110 111 contrast to the common notion that natural selection should promote hereditome replication fidelity 112 ²², evolution promotes mechanisms that strikes the degree of *infidelity* just right. Some parts of the

- 113 hereditome are able to undergo very rapid changes and evolution is therefore a continuous process -
- not a dotted line of events occurring at the transition of generations ^{6-8,23}. Finally, since natural
- selection operate on the information represented in the hereditome, it follows that the selection acts
- 116 at the level of information manifestation (selection may for instance occur at the level of a community 117 inherited symbiont bacterium, rather than at the level of the best)
- 117 inherited symbiont bacterium, rather than at the level of the host).

118 The Modern Synthesis model of evolution has been, and remains, a formidable tool. The challenge is that "when all you have is a hammer (MS), then all you see is a nail (genome)". This may righteously 119 120 be argued to be caricature²⁴ - but this caricature describes our common heuristic model of evolution 121 too well to be ignored. We know there is more to heredity and evolution than genomes - and 122 understanding how the qualitative and temporal attributes of the hereditome components affects adaptive capacity is crucially important in an age of rapid environmental changes^{25,26}. As argued by 123 the proponents of the Extended Evolutionary Synthesis; our understanding of evolution will benefit 124 from expanding our selection of tools beyond the versatile hammer^{27,28}. It is our hope that the 125

- 126 Information Continuum Hypothesis may be such a tool.
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128 References:

- Noble, D. Central Dogma or Central Debate? *Physiology (Bethesda)* 33, 246-249,
 doi:10.1152/physiol.00017.2018 (2018).
 Sun, Y. H., Chen, S. P., Wang, Y. P., Hu, W. & Zhu, Z. Y. Cytoplasmic impact on cross-genus
 cloned fish derived from transgenic common carp (Cyprinus carpio) nuclei and goldfish
 (Carassius auratus) enucleated eggs. *Biol Reprod* 72, 510-515,
- 134 doi:10.1095/biolreprod.104.031302 (2005).
- 1353Perez, M. F. & Lehner, B. Intergenerational and transgenerational epigenetic inheritance in136animals. Nat Cell Biol 21, 143-151, doi:10.1038/s41556-018-0242-9 (2019).
- Gaydos, L. J., Wang, W. & Strome, S. Gene repression. H3K27me and PRC2 transmit a
 memory of repression across generations and during development. *Science* 345, 1515-1518,
 doi:10.1126/science.1255023 (2014).
- Jimenez-Useche, I. *et al.* DNA Methylation Regulated Nucleosome Dynamics. *Sci Rep-Uk* 3, doi:ARTN 212110.1038/srep02121 (2013).
- 142 6 Jeremias, G. *et al.* Transgenerational Inheritance of DNA Hypomethylation in Daphnia magna
 143 in Response to Salinity Stress. *Environ Sci Technol* 52, 10114-10123,
 144 doi:10.1021/acs.est.8b03225 (2018).
- Rechavi, O., Minevich, G. & Hobert, O. Transgenerational Inheritance of an Acquired Small
 RNA-Based Antiviral Response in C. elegans. *Cell* 147, 1248-1256,
 doi:10.1016/j.cell.2011.10.042 (2011).
- 1488Jarosz, D. F., Lancaster, A. K., Brown, J. C. S. & Lindquist, S. An evolutionarily conserved149prion-like element converts wild fungi from metabolic specialists to generalists. *Cell* **158**,1501072-1082, doi:10.1016/j.cell.2014.07.024 (2014).
- Holmes, D. L., Lancaster, A. K., Lindquist, S. & Halfmann, R. Heritable remodeling of yeast
 multicellularity by an environmentally responsive prion. *Cell* **153**, 153-165,
 doi:10.1016/j.cell.2013.02.026 (2013).
- 154 10 Kremsky, I. & Corces, V. G. Protection from DNA re-methylation by transcription factors in 155 primordial germ cells and pre-implantation embryos can explain trans-generational 156 epigenetic inheritance. *Genome Biol* **21**, 118, doi:10.1186/s13059-020-02036-w (2020).
- 157 11 Walker, W. A. The importance of appropriate initial bacterial colonization of the intestine in newborn, child, and adult health. *Pediatr Res* 82, 387-395, doi:10.1038/pr.2017.111 (2017).

- 159 12 Duranti, S. et al. Maternal inheritance of bifidobacterial communities and bifidophages in 160 infants through vertical transmission. Microbiome 5, doi:ARTN 6610.1186/s40168-017-0282-161 6 (2017). 162 13 Bourguignon, T. et al. Rampant Host Switching Shaped the Termite Gut Microbiome. Current 163 *Biology* **28**, 649-+, doi:10.1016/j.cub.2018.01.035 (2018). 164 14 Foote, A. D. et al. Genome-culture coevolution promotes rapid divergence of killer whale 165 ecotypes. Nat Commun 7, doi:ARTN 1169310.1038/ncomms11693 (2016). 166 15 Whiten, A. Culture extends the scope of evolutionary biology in the great apes. Proc Natl 167 Acad Sci U S A 114, 7790-7797, doi:10.1073/pnas.1620733114 (2017). 168 16 Allio, R., Donega, S., Galtier, N. & Nabholz, B. Large Variation in the Ratio of Mitochondrial to 169 Nuclear Mutation Rate across Animals: Implications for Genetic Diversity and the Use of 170 Mitochondrial DNA as a Molecular Marker. Mol Biol Evol 34, 2762-2772, 171 doi:10.1093/molbev/msx197 (2017). 172 17 Phillips, N. L. H. & Roth, T. L. Animal Models and Their Contribution to Our Understanding of 173 the Relationship Between Environments, Epigenetic Modifications, and Behavior. Genes-174 Basel 10, doi:ARTN 4710.3390/genes10010047 (2019). 175 18 Dalia, A. B. & Dalia, T. N. Spatiotemporal Analysis of DNA Integration during Natural 176 Transformation Reveals a Mode of Nongenetic Inheritance in Bacteria. Cell 179, 1499-1511 177 e1410, doi:10.1016/j.cell.2019.11.021 (2019). 178 19 Fox, T. D. Mitochondrial genes in the nucleus. Nature 301, 371-372, doi:10.1038/301371a0 179 (1983). 20 180 McCutcheon, J. P. & von Dohlen, C. D. An interdependent metabolic patchwork in the nested 181 symbiosis of mealybugs. Curr Biol 21, 1366-1372, doi:10.1016/j.cub.2011.06.051 (2011). 182 21 Roossinck, M. J. The good viruses: viral mutualistic symbioses. Nat Rev Microbiol 9, 99-108, 183 doi:10.1038/nrmicro2491 (2011). 184 22 Dawkins, R. The selfish gene. (Oxford University Press, New York, 1974). 185 23 Chen, Q., Yan, W. & Duan, E. Epigenetic inheritance of acquired traits through sperm RNAs 186 and sperm RNA modifications. Nat Rev Genet 17, 733-743, doi:10.1038/nrg.2016.106 (2016). 187 Wray, G. A. et al. Does evolutionary theory need a rethink? - COUNTERPOINT No, all is well. 24 188 Nature 514, 161-+ (2014). 189 25 Corning, P. A. Beyond the modern synthesis: A framework for a more inclusive biological 190 synthesis. Prog Biophys Mol Biol 153, 5-12, doi:10.1016/j.pbiomolbio.2020.02.002 (2020). 191 26 Bonduriansky, R., Crean, A. J. & Day, T. The implications of nongenetic inheritance for 192 evolution in changing environments. Evol Appl 5, 192-201, doi:10.1111/j.1752-193 4571.2011.00213.x (2012). 194 27 Laland, K. et al. Does evolutionary theory need a rethink? - POINT Yes, urgently. Nature 514, 195 161-164, doi:DOI 10.1038/514161a (2014). Baedke, J., Fabregas-Tejeda, A. & Vergara-Silva, F. Does the extended evolutionary synthesis 196 28 197 entail extended explanatory power? Biol Philos 35, doi:ARTN 2010.1007/s10539-020-9736-5 198 (2020). 199
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