Extrapolation of molecular clock to early time
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Abstract:
The further evolution of informational molecular sequences should depend on the number of viable alternatives possible for the sequences as set by selection, the unprepared mutation rate, and time. Most bio-molecular clocks are based on Kimura’s nearly neutral mutation random-drift hypothesis. This clock assumes that informational sequences are in equilibrium, i.e., the nucleotides mutate at a uniform rate and the number of nucleotides unconstrained by selection remains constant. Correcting for deviations from these assumptions should produce a more accurate clock. Informational molecules probably formed from polynucleotides having some other function such as nitrogen or nucleotide storage, thus being initially functionally unselected. At any time the rate of development of functionality in a protein may be expected to be proportional to the number of viable alternatives of sequence in its potentially interacting regions. Assuming the rate of unrepaired mutations is constant, these clocks should exponentially slow as they evolve, each with a different rate toward individual equilibria. Also if the degree of selection changes, its clock rate should change. For a more precise clock two approaches are suggested to estimate these time dependent changes in evolutionary rate. An improved clock could improve estimation of phylogeny and put a time scale on that phylogeny.