

We consider an integrative approach to studying diseases via an evolutionary model, as enforcement mechanisms for limited lifespan. We view disease signatures within the genome as a result of competition between adaptive pressures of an individual versus the individual's species. We formulate this theory mathematically in terms of dynamical systems. Among the resulting predictions will be that phylogenetically older diseases will pose proportionally greater challenges in standard GWAS studies for finding 'smoking guns', i.e., simple combinatorial genomic aberrations that are responsible for such diseases. We find in such dynamical models that there are two sources of genomic pressure towards limited lifespan. The first source is at the species level, as an enforcer of genomic versatility. The second is based on spatial localization in which local resources limit numbers of individuals with the same genome. Some consequences of these approaches result in the view of diseases as adaptive species-level traits with their own phylogenies, and in particular we examine cancers as adaptive mechanisms.