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Dependence in the survival of ancestral genome

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Brief Description

Study of the descent of genome in defined pedigrees underlies many genetic analyses, including the survival of founder DNA in the complex pedigrees of managed endangered species.

It has long been known that, across a chromosome, descent of genome through the m meioses of a defined pedigree may be represented as a random walk on the vertices of an m-dimensional hypercube.

At any single genome location, survival of a specified founder genome must decrease the probability of survival of others, the highest negative correlations in survival being between genomes in a single diploid founder, and next within a founder couple.

Across a chromosome the reverse is true.

The survival of an ancestral DNA segment from a founder greatly increases the probability of survival of a segment from an adjacent founder genome, where adjacency is in terms of the vertices of the hypercube.

Results have practical application in studying the diversity of founder genomes present in key current individuals (for example, in a clone), in studying the survival of introgressed genomes, and the effect of both breeding choices and natural selection for or against such genomes on the survival of other founder genomes.

Abstract

Study of the descent of genome in defined pedigrees underlies many genetic analyses, including the survival of founder DNA in the complex pedigrees of managed endangered species. It has long been known that, across a chromosome, descent of genome through the m meioses of a defined pedigree may be represented as a random walk on the vertices of an m-dimensional hypercube. At any single genome location, survival of a specified founder genome must decrease the probability of survival of others, the highest negative correlations in survival being between genomes in a single diploid founder, and next within a founder couple. Across a chromosome the reverse is true. The survival of an ancestral DNA segment from a founder greatly increases the probability of survival of a segment from an adjacent founder genome, where adjacency is in terms of the vertices of the hypercube. Results have practical application in studying the diversity of founder genomes present in key current individuals (for example, in a clone), in studying the survival of introgressed genomes, and the effect of both breeding choices and natural selection for or against such genomes on the survival of other founder genomes.