MUTATION FREQUENCIES IN A BIRTH-DEATH BRANCHING PROCESS

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Keywords: Cancer, Branching processes, Population genetics.

First, we revisit a classic two-type branching process which describes cell proliferation and mutation; widespread application has been seen in cancer and microbial modelling. As the mutation rate tends to zero and the population size to infinity, the mutation times converge to a Poisson process. This yields the number of mutants and clone sizes. Other limits and exact results are also explored. Second, we extend the model to consider mutations at multiple sites on the genome. The number of mutants in the two-type model characterises the mean site frequency spectrum in the multiple-site model. We recover a power-law distribution commonly seen in tumours.

References

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THE EFFECT OF ADULT SEX RATIO ON TRANSITIONS BETWEEN MALE AND FEMALE HETEROGAMETY

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Empirical work has shown a correlation between the mode of genetic sex determination (male heterogamety, XY, or female heterogamety, ZW) and the adult sex ratio (ASR) in tetrapods [1]. The hypothesis for this observation was that genetic factors such as meiotic drive and sex-linked deleterious mutations could be responsible for skewing the ASR. In this talk I will present theoretical work testing an alternative hypothesis; that skewed ASRs preferentially lead to a given system of genetic sex determination by biasing the probability of transition between XY and ZW. Transitions between male and female heterogamety are common in both vertebrates and invertebrates. Our recent work has demonstrated that when sex ratios are equal, genetic drift drives such transitions with a substantial bias that favours dominant sex determining chromosomes [2]. Having described this research, I will proceed to analytically show how biased ASR, combined with selection against the ancestral heterogametic sex chromosome, alters the evolutionary picture and finally interpret these insights in light of empirical data.

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Evolutionary Dynamics I

BET HEDGING MODELS: A REAPPRAISAL

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Kelly's [1] famous work on optimal gambling strategies and the financial value of information was arguably the first convincing attempt at applying concepts from information theory for analysis in a different field. Recent evolutionary bet-hedging models under fluctuating environments and environmental cues (e.g.[2]) have adhered more or less to the original economic framework. These models utilize important notions such as growth rate maximization, proportional betting and fitness matrices, while providing an operational interpretation of information in terms of increased growth rates. Here, I highlight the departures from the original economic model warranted by the shift to a biological framework, the somewhat neglected analytic and conceptual limitations of current biological models, and propose further generalizations to the information-theoretic framework to better account for evolutionary processes. I identify and analyse several implicit core assumptions of these models, such as adaptive optimization of absolute vs. relative growth rates and the targeting of asymptotic vs. finite growth rates. Crucially, I argue for more serious consideration of genetic mechanisms for developmental phenotypic randomization.

References

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Evolutionary Dynamics I

IN SEARCH OF THE GOLDILOCKS ZONE FOR HYBRID SPECIATION

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Keywords: Evolution, Speciation, Hybridization, Epistasis, Genetic architecture.

Hybridization has recently gained considerable interest both as a unique window for observing speciation mechanisms and as a potential engine of speciation. The latter remains a controversial topic. It has been hypothesized that the reciprocal sorting of genetic incompatibilities from parental species could result in hybrid speciation, when the hybrid population maintains a mixed combination of the parental incompatibilities that prevents further gene exchange with both parental populations. However, the specifics of the purging/sorting process of multiple incompatibilities have not been examined theoretically.

We here investigate the allele-frequency dynamics of an isolated hybrid population that results of a single hybridization event. Using models of 2 or 4 loci, we investigate the fate of one or two genetic incompatibilities of the Dobzhansky-Muller type (DMIs). We study how various parameters affect both the sorting/purging of the DMIs and the probability of observing hybrid speciation by reciprocal sorting. We find that the probability of hybrid speciation is strongly dependent on the genetic architecture (i.e. the order and recombination distance between loci along chromosomes), the population size of the hybrid population, and the initial relative contribution of the parental populations to the hybrid population. We identify a Goldilocks zone for specific genetic architectures and intermediate recombination rates, in which hybrid speciation becomes highly probable. While an equal contribution of parental populations to the hybrid populations maximizes the hybrid speciation probability in the Goldilocks zone, other genetic architectures yield asymmetric maxima that are unintuitive on first sight. We provide an explanation for this pattern, and discuss our results both with respect to the best conditions for observing hybrid speciation in nature and their implications for patterns of introgression in hybrid zones.