UNIVERSITY of WASHINGTON

Undergraduate Research Symposium May 17, 2019 Mary Gates Hall

Online Proceedings

SESSION 1L

MATHEMATICAL MODELING IN THE SCIENCES

Session Moderator: Elizabeth Thompson, Statistics
MGH 271
12:30 PM to 2:15 PM

* Note: Titles in order of presentation.

How do Mean and Variance Affect Gene Survival and Gene Frequencies?
Jueyi Liu, Senior, Economics, Applied & Computational Mathematical Sciences (Scientific Computing & Numerical Algorithms)
UW Honors Program
Mentor: Elizabeth Thompson, Statistics

Mutation produces new variation in populations, and in each generation these variants are copied from parents to offspring. While almost all variants of genes are lost, they may remain in the population for many generations. We use branching process models to analyze counts of gene copies. In a population of constant size, on average, a gene copy produces one offspring copy at the next generation. An advantageous mutant will have a mean greater than 1, and a deleterious one will have a mean less than 1. It is thought that most mutations are slightly deleterious, and with high probability those variants become extinct rapidly. Nonetheless, the few deleterious mutants that are not yet extinct may achieve high numbers. Thus, we have a particular interest in those with a mean slightly less than 1. We use different probability models for the offspring distribution and consider the mutant's survival about: the extinction probability over k generations, the expected copy count conditional on survival, and the probability of survival additional k generations conditional on surviving k already. We find that variances in addition to means of offspring distributions closely relate these statistics. By adjusting parameters of distributions, we let the mean and variance be approximately the same across distributions. Based on our simulations, when k is large and the mean and variance of offspring are the same, the mutant's survival condition is uniform throughout. In other words, those statistics above can be estimated by the mean and variance exclusively, and the specific distribution does not affect much the conditional population dynamics. However, at the first few generations, these statistics are different for each distribution. Thus, if we know the mean and variance of a mutant, we can predict the long-term population behaviors conditional on survival without knowing the true distribution of the mutant.

POSTER SESSION 3

Commons West, Easel 8
2:30 PM to 4:00 PM

Assessing DNA Damage by Single-Cell Gel Electrophoresis (Comet Assay)
April Lenae Suarez, Senior, Microbiology
Nicholas Patton (Nick) Shugart, Senior, Microbiology
Mentor: Ernie Tolentino, nursing research
Mentor: Hilaire Thompson, Biobehavioral Nursing and Health Informatics

Single-cell gel electrophoresis, or a Comet Assay, can be used to assess DNA damage in cells as it liberates single-strand DNA breaks (SSB), alkali labile sites (ALS), and DNA cross-links, then uses microscopy to determine levels of chromosome damage. Various methods have been used to detect DNA damage; advantages of this assay include its capacity to detect low levels of DNA damage, the small number of cells required, low cost, and the ability to utilize various cell types. Our lab used lymphocytes withdrawn from elderly patients as we targeted quantifying the effects on an individual's DNA due to aging, stress, and drugs. Lymphocytes were suspended in low-melting point agarose and placed on a slide pre-coated with regular agarose. Once cells were fixed on the slide, they were placed in lysis solution to remove membranes and liberate DNA. Lymphocytes then went through an alkaline treatment to unwind DNA super-coils. The assay has been tried under neutral conditions however, we used the alkaline method because it is known to increase reproducibility and specificity. The cells were then placed in an electrophoresis chamber at 5 V/cm for 30 minutes, the SSB's, ALS's, and DNA cross-link fragments traveled towards the anode, forming a comet like appearance behind the cell. The cells were then neutralized, stained with ethidium bromide, and the comets were visualized. Data can be quantified using software provided by Instem Technologies. A comparison of Comet values derived from varying cell densities as well as untreated control samples are also presented, confirming good reliability using this technique.

POSTER SESSION 3

Commons West, Easel 7

2:30 PM to 4:00 PM

Determination of Human Telomere Length by Quantitative RT-PCR

Nicholas Patton (Nick) Shugart, Senior, Microbiology
April Lenae Suarez, Senior, Microbiology
Mentor: Ernie Tolentino, nursing research
Mentor: Hilaire Thompson, Biobehavioral Nursing and Health Informatics

Telomeres represent the structural ends of genomic chromosome molecules and are composed of hexamer repeats of the form [TTAGGG] which play a protective role against DNA damage and genetic information loss. The telomere length of normal diploid cells decreases over time and can be correlated with issues related to cancer and the aging process. Our preliminary work utilizes methods developed initially by Cawthon and O'Callaghan and is applied to DNA samples obtained from research studies involving the elderly as well as those with aneurisms. In contrast to standard measurements which use real-time PCR in order to calculate relative telomere lengths, our method uses absolute quantification through the use of standard curves generated with a synthetic 84-mer telomere (control gene) and another synthetic oligomer (36B4 'housekeeping gene'). Through the use of both synthetic standards in a typical RT-PCR experiment utilizing SybrGreen and specific primers for either telomere sequence or housekeeping gene, the true length of a diploid telomere can be calculated by extrapolation from standard curves. Telomere lengths obtained through this method have been compared to results derived from commercially available test kits which used relative RT-PCR as a quantification measure. Results obtained through the use of this technique can be incorporated in research studies encompassing cell apoptosis, processes involved with aging. This technique can also be used to ascertain the effects of environmental impacts involving DNA damage on plants, bacteria, and animal cells.