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INF 501

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Comparative Genomics and the Evolution of Cancer Suppression

Research Topic Overview

The knowledge of bio-information has evolved substantially today, incorporating advanced methods for analyzing the whole genome sequencing data and comparative genomics method. It has been shown that now genomic data are more meaningful to investigate the diversity of life. Comparative genomics is a useful tool in finding the mechanism of tumor suppression in different species. Dr. Marc Tollis's research is focused on how these genome sequencing data can be used to consider similarity and differences between complete different genomes to find the mechanism of tumor suppression. In the long history, many species have taken advantage of natural selection to modify their gens structure to suppress tumor. Professor points out that there is no particular relationship between cancer and the type of species. This observation is known as Peto's paradox in evolutionary biology. For example, the African savannah elephant, which is the largest land-living mammal, has much lower cancer rates than humans or a mouse as an animal with small body mass is involved with cancer more than humans.

The professor also reviews theory and methods of comparative cancer genomics and highlights highlight species whose biology evolved mechanisms of tumor suppression and discuss related genomic efforts to understand the basis of this tumor suppression. Each type of cell has its lifespan, and when it dies off, it will be replaced by the new one, which makes replication of DNA essential. DNA replication is the biological process of producing two identical replicas of DNA

from one original DNA molecule. Cancer results from the somatic accumulation of mutations in cells which means the replication of DNA in somewhere are wrong. Current sequencing efforts of cancer genomes have revealed that many kinds of cancers contain mutations in DNA damage response pathways and genes, including the p53 pathway.

Research Connections

I was able to distinguish some critical connections between my study and that of Dr. Marc Tollis's. As a CS student, such genetic knowledge arms the biomedical fields with clues to the origins of cancer are similar as the theory of move and copy file in the Linux operating system (see Figure 1). While most DNA replicates with reasonably high fidelity, mistakes(mutations)do happen which can lead to cancer. However, in computer science, even file replicates also with sufficiently high accuracy, mistakes(mutations)do happen. When there is an error in the file move and copy, then we have to open two files, compare each word and find the mistakes. Hence, if there are mutations in DNA replicates, we need to analyze this two DNA and check each nucleotide which means comparative genomics.
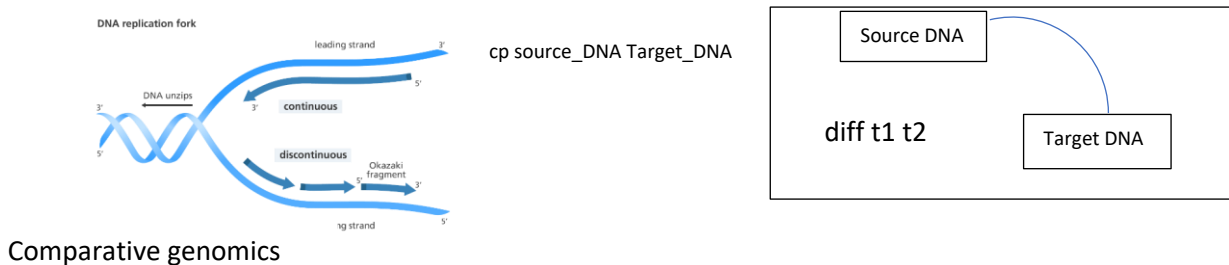

Comparative genomics

Figure 1: DNA replication VS move and copy file

Comparative genomics is a powerful tool to be used to consider similarity and differences between complete different genomes and discover these unique and shared molecular adaptations concerning cancer suppression. In computer science, the *diff* is a powerful function to analyzes

two files and prints the lines that are different. When diff is describing the differences between these two files, it is telling you how to change the first file to make it match the second file. However, when Comparative genomics is describing the differences between these two genomes, it can't tell you some particular conclusion.

<u>Conclusion</u>

As discussed previously, Dr. Marc Tollis's research seeks to use comparative genomics to find the mechanism of tumor suppression in different species. As he considered, there are some significant challenges to be addressed before this concept will become realized, and researchers can mutually benefit from being continually interconnected. Such as the effect of body mass on the incident of cancer over different types of species or a specific variety of species was interesting for me. It has been shown that there is no correlation between the occurrence of cancer and the number of cell or the longevity in different types of species. This observation is known as Peto's paradox in evolutionary biology.