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~~Goldberg ML, Fischer JA, Hood L, Hartwell LH (2021) GENETICS, From Genes to Genomes, 7th edition. McGraw-Hill. Hartwell LH, Goldberg ML, Fischer JA, Hood L (2018) GENETICS, From Genes to Genomes, 6th ...~~

~~Janice A Fischer~~

~~Figure 3. Figure 3. Influence of Mutation Order on Proliferation of Stem and Progenitor Cells and Expression of Progenitor Genes. These data suggest that mutation order affects the proliferation ...~~

~~Effect of Mutation Order on Myeloproliferative Neoplasms~~

~~Arguably, the most profound impact has been in the area of cancer genetics, where the explosion ... In a tumor cell, dozens of different genes may be aberrant in structure or copy number, and ...~~

~~The genetics and genomics of cancer~~

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~~1 Department of Bioengineering, University of California, San Diego, La Jolla, CA, USA. 2 Gustave Roussy Cancer Campus (GRCC), Equipe Labellisée–Ligue Nationale contre le Cancer, Villejuif, France. 3 ...~~

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~~7 Department of Biochemistry and Molecular Genetics, University of Virginia ... defined by a reversibly quiescent state in which viral genomes are maintained, but viral gene expression is highly ...~~

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"The science of genetics is less than 150 years old, but its accomplishments within that short time have been astonishing. Gregor Mendel first described genes as abstract units of inheritance in 1865; his work was ignored and then rediscovered in 1900. Thomas Hunt Morgan and his students provided experimental verification of the idea that genes reside within chromosomes during the years 1910-1920. By 1944, Oswald Avery and his coworkers had established that genes are made of DNA. James Watson and Francis Crick published their pathbreaking structure of DNA in 1953. Remarkably, less than 50 years later (in 2001), an international consortium of investigators deciphered the sequence of the 3 billion nucleotides in the human genome. Twentieth century genetics made it possible to identify individual genes and to understand a great deal about their functions. Today, scientists are able to access the enormous amounts of genetic data generated by the sequencing of many organisms' genomes. Analysis of these data will result in a deeper understanding of the complex molecular interactions within and among vast networks of genes, proteins, and other molecules that help bring organisms to life. Finding new methods and tools for analyzing these data will be a significant part of genetics in the twenty-first century. Our seventh edition of *Genetics: From Genes to Genomes* emphasizes both the core concepts of genetics and the cutting-edge discoveries, modern tools, and analytic methods that will keep the science of genetics moving forward. The authors of the seventh edition have worked together in revising every chapter in an effort not only to provide the most up-to-date information, but also to provide continuity and the clearest possible explanations of difficult concepts in one voice"--

The 2nd Canadian edition of *Genetics: From Genes to Genomes* emphasizes not only the core concepts of genetics, but also the cutting-edge discoveries, modern tools, and analytical methods that have made the science of genetics the exciting, vibrant, and dynamic discipline that it is today. This edition continues to build upon the integration of Mendelian and molecular principles, providing students with the links between early genetics understanding and the new molecular discoveries that have changed the way the field of genetics is viewed. *Genetics: From Genes to Genomes, 2nd Canadian Edition*, takes an integrated approach in its presentation of genetics, thereby giving students a strong command of genetics as practiced today by academic and corporate researchers. Principles are related throughout the text in examples, essays, case histories, and Connections sections to make sure students fully understand the relationships between topics. McGraw-Hill Connect is an award-winning digital teaching and learning platform that helps students get better results, learn and study more efficiently; while helping instructors to increase student engagement, save time with course management, and improve overall course retention. Connect includes SmartBook, the first and only adaptive reading experience that changes reading from a passive and linear experience, to an engaging and dynamic one. Students' retain more concepts and come to class better prepared. Connect access is available for students to purchase separately, or available to package with the print text.

"*Genetics: From Genes to Genomes*" is a cutting-edge, introductory genetics text authored by an unparalleled author team, including Nobel Prize winner, Leland Hartwell. The Third Edition continues to build upon the integration of Mendelian and molecular principles, providing students with the links between early genetics understanding and the new molecular discoveries that have changed the way the field of genetics is viewed.

"*Genetics: From Genes to Genomes* is a cutting-edge, introductory genetics text authored by an unparalleled author team, including Nobel Prize winner, Leland Hartwell. This edition continues to build upon the integration of Mendelian and molecular principles, providing students with the links between the early understanding of genetics and the new molecular discoveries that have changed the way the field of genetics is viewed." -- Provided by publisher.

In the spring of 2011, a diverse group of scientists gathered at Cornell University to discuss their research into the nature and origin of biological information. This symposium brought together experts in information theory, computer science, numerical simulation, thermodynamics, evolutionary theory, whole organism biology, developmental biology, molecular biology, genetics, physics, biophysics, mathematics, and linguistics. This volume presents new research by those invited to speak at the conference. The contributors to this volume use their wide-ranging expertise in the area of biological information to bring fresh insights into the many explanatory difficulties associated with biological information. These authors raise major challenges to the conventional scientific wisdom, which attempts to explain all biological information exclusively in terms of the standard mutation/selection paradigm. Several clear themes emerged from these research papers: 1) Information is indispensable to our understanding of what life is; 2) Biological information is more than the material structures that embody it; 3) Conventional chemical and evolutionary mechanisms seem insufficient to fully explain the labyrinth of information that is life. By exploring new perspectives on biological information, this volume seeks to expand, encourage, and enrich research into the nature and origin of biological information.

This book focuses on the development and application of the latest advanced data mining, machine learning, and visualization techniques for the identification of interesting, significant, and novel patterns in gene expression microarray data. Biomedical researchers will find this book invaluable for learning the cutting-edge methods for analyzing gene expression microarray data. Specifically, the coverage includes the following state-of-the-art methods: • Gene-based analysis: the latest novel clustering algorithms to identify co-expressed genes and coherent patterns in gene expression microarray data sets • Sample-based analysis: supervised and unsupervised methods for the reduction of the gene dimensionality to select significant genes. A series of approaches to disease classification and discovery are also described • Pattern-based analysis: methods for ascertaining the relationship between (subsets of) genes and (subsets of) samples. Various novel pattern-based clustering algorithms to find the coherent patterns embedded in the sub-attribute spaces are discussed • Visualization tools: various methods for gene expression data visualization. The visualization process is intended to transform the gene expression data set from high-dimensional space into a more easily understood two- or three-dimensional space.

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