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This eBook presents all 10 articles published under the Frontiers Research Topic "Evolutionary Feedbacks Between Population Biology and Genome Architecture", edited by Scott V. Edwards and Tariq Ezaz. With the rise of rapid genome sequencing across the Tree of Life, challenges arise in understanding the major evolutionary forces influencing the structure of microbial and eukaryotic genomes, in particular the prevalence of natural selection versus genetic drift in shaping those genomes. Additional complexities in understanding genome architecture arise with the increasing incidence of interspecific hybridization as a force for shaping genotypes and phenotypes. A key paradigm shift facilitating a more nuanced interpretation of genomes came with the rise of the nearly neutral theory in the 1970s, followed by a greater appreciation for the contribution of nonadaptive forces such as genetic drift to genome structure in the 1990s and 2000s. The articles published in this eBook grapple with these issues and provide an update as to the ways in which modern population genetics and genome informatics deepen our understanding of the subtle interplay between these myriad forces. From intraspecific to macroevolutionary studies, population biology and population genetics are now major tools for understanding the broad landscape of how genomes evolve across the Tree of Life. This volume is a celebration across diverse taxa of the contributions of population genetics thinking to genome studies. We hope it spurs additional research and clarity in the ongoing search for rules governing the evolution of genomes.

A groundbreaking introduction to vectors, matrices, and least squares for engineering applications, offering a wealth of practical examples.

For many researchers, Python is a first-class tool mainly because of its libraries for storing, manipulating, and gaining insight from data. Several resources exist for individual pieces of this data science stack, but only with the Python Data Science Handbook do you get them all—IPython, NumPy, Pandas, Matplotlib, Scikit-Learn, and other related tools. Working scientists and data crunchers familiar with reading and writing Python code will find this comprehensive desk reference ideal for tackling day-to-day issues: manipulating, transforming, and cleaning data; visualizing different types of data; and using data to build statistical or machine learning models. Quite simply, this is the must-have reference for scientific computing in Python. With this handbook, you ' ll learn how to use: IPython and Jupyter: provide computational environments for data scientists using Python NumPy: includes the ndarray for efficient storage and manipulation of dense data arrays in Python Pandas: features the DataFrame for efficient storage and manipulation of labeled/columnar data in Python Matplotlib: includes capabilities for a flexible range of data visualizations in Python Scikit-Learn: for efficient and clean Python implementations of the most important and established machine learning algorithms

Calculations for Molecular Biology and Biotechnology: A Guide to Mathematics in the Laboratory, Second Edition, provides an introduction to the myriad of laboratory calculations used in molecular biology and biotechnology. The book begins by discussing the use of scientific notation and metric prefixes, which require the use of exponents and an understanding of significant digits. It explains the mathematics involved in making solutions; the characteristics of cell growth; the multiplicity of infection; and the quantification of nucleic acids. It includes chapters that deal with the mathematics involved in the use of radioisotopes in nucleic acid research; the synthesis of oligonucleotides; the polymerase chain reaction (PCR) method; and the development of recombinant DNA technology. Protein quantification and the assessment of protein activity are also discussed, along with the centrifugation method and applications of PCR in forensics and paternity testing. Topics range from basic scientific notations to complex subjects like nucleic acid chemistry and recombinant DNA technology Each chapter includes a brief explanation of the concept and covers necessary definitions, theory and rationale for each type of calculation Recent applications of the procedures and computations in clinical, academic, industrial and basic research laboratories are cited throughout the text New to this Edition: Updated and increased coverage of real time PCR and the mathematics used to measure gene expression More sample problems in every chapter for readers to practice concepts

Monthly. Bibliography of MEDLARS-based journal articles that describe perturbations in the ecosystems important to health. For the most part, genetic and clinical literature not included. Index medicus format; author, subject sections.

Traumatic brain injury (TBI) remains a significant source of death and permanent disability, contributing to nearly one-third of all injury related deaths in the United States and exacting a profound personal and economic toll. Despite the increased resources that have recently been brought to bear to improve our understanding of TBI, the development of new diagnostic and therapeutic approaches has been disappointingly slow. Translational Research in Traumatic Brain Injury attempts to integrate expertise from across specialties to address knowledge gaps in the field of TBI. Its chapters cover a wide scope of TBI research in five broad areas: Epidemiology Pathophysiology Diagnosis Current treatment strategies and sequelae Future therapies Specific topics discussed include the societal impact of TBI in both the civilian and military populations, neurobiology and molecular mechanisms of axonal and neuronal injury, biomarkers of traumatic brain injury and their relationship to pathology, neuroplasticity after TBI, neuroprotective and neurorestorative therapy, advanced neuroimaging of mild TBI, neurocognitive and psychiatric symptoms following mild TBI, sports-related TBI, epilepsy and PTSD following TBI, and more. The book integrates the perspectives of experts across disciplines to assist in the translation of new ideas to clinical practice and ultimately to improve the care of the brain injured patient.

Neuropathology of Drug Addictions and Substance Misuse, Volume One: Foundations of Understanding, Tobacco, Alcohol, Cannabinoids, Opioids and Emerging Addictions provides the latest research in an area that shows that the neuropathological features of one addiction are often applicable to those of others. The book also details how a further understanding of these commonalities can provide a platform for the study of specific addictions in greater depth, all in an effort to create new modes of understanding, causation, prevention, and treatment. The three volumes in this series address new research and challenges, offering comprehensive coverage on the adverse consequences of the most common drugs of abuse, with each volume serving to update the reader ' s knowledge on the broader field of addiction, while also deepening our understanding of specific addictive substances. Volume One addresses tobacco, alcohol, cannabinoids, and opioids, with each section providing data on the general, molecular/cellular, and structural/functional neurological aspects of a given substance, along with a focus on the adverse consequences of addictions. Provides a modern approach on the pathology of substances of abuse, offering an evidence based ethos for understanding the neurology of addictions Fills an existing gap in the literature by proving a one-stop-shopping synopsis of everything to do with the neuropathology of drugs of addiction and substance misuse Includes a list of abbreviations, abstracts, applications to other addictions and substance misuse, mini-dictionary of terms, summary points, 6+ figures and tables, and full references in each chapter Offers coverage of preclinical, clinical, and population studies, from the cell to whole organs, and the genome to whole body