The Origins Of Genome Architecture

The Origins of Genome ArchitectureEvolutionary Feedbacks Between Population Biology and Genome ArchitectureEvolution of Genome ArchitectureMechanisms Driving Karyotype Evolution and Genomic ArchitectureAnalysing the various layers of genome architecture using a high-throughput single-molecule techniqueNuclear, Chromosomal, and Genomic Architecture in Biology and MedicineImpacts of Genome and Nuclear Architecture on Molecular Evolution in EukaryotesModeling the 3D Conformation of GenomesThe Evolution of Organelle Genome ArchitectureGenomic Architecture HandbookDNA Rearrangements by Default Or Design?The Analysis of Genome Structure and Transcription in Dictyostelium Discoideum Using Three Recombinant PlasmidsChromosome Biology as a Key to Understand Disease Mechanisms, Genome Architecture and EvolutionCharacterization of the Interplay Between the Genome Architecture and Gene Co-expressionExperimental Evolution of Genome Architecture and Complexity in an RNA VirusStructure and Function of the Bacterial GenomeGenome Structure of Human CytomegalovirusThe Optical Mapping of GenomesHandbook of Human Molecular Evolution, 2 Volume SetMulti-scale Study of the Genome Architecture and Its Dynamical Facets Michael Lynch Tariq Ezaz Rebeca Campos Sanchez Aurora Ruiz-Herrera Jonas Huber Malgorzata Kloc Xyrus Maurer-Alcalá Guido Tiana David R. Smith Paloma Young Christine J. Shaw Karen Linnea Kindle Hartsuyker Anja Weise Audrey Baguette Anouk Willemsen Charles J. Dorman Joyce C. Tamashiro Susan Reslewic David N. Cooper Soler Vila Paula

The Origins of Genome Architecture Evolutionary Feedbacks Between Population Biology and Genome Architecture Evolution of Genome Architecture Mechanisms Driving Karyotype Evolution and Genomic Architecture Analysing the various layers of genome architecture using a high-throughput single-molecule technique Nuclear, Chromosomal, and Genomic Architecture in Biology and Medicine Impacts of Genome and Nuclear Architecture on Molecular Evolution in Eukaryotes Modeling the 3D Conformation of Genomes The Evolution of Organelle Genome Architecture Genomic Architecture Handbook DNA Rearrangements by Default Or Design? The Analysis of Genome Structure and Transcription in Dictyostelium Discoideum Using Three Recombinant Plasmids Chromosome Biology as a Key to Understand Disease Mechanisms, Genome Architecture and Evolution Characterization of the Interplay Between the Genome Architecture and Gene Co-expression Experimental Evolution of Genome Architecture and Complexity in an RNA Virus Structure and Function of the Bacterial Genome Genome Structure of Human Cytomegalovirus The Optical Mapping of Genomes Handbook of Human Molecular Evolution, 2 Volume Set Multi-scale Study of the Genome Architecture and Its Dynamical Facets *Michael Lynch Tariq Ezaz Rebeca Campos Sanchez Aurora Ruiz-Herrera Jonas Huber Malgorzata Kloc Xyrus Maurer-Alcalá Guido Tiana David R. Smith Paloma Young Christine J.*

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the availability of genomic blueprints for hundreds of species has led to a transformation in biology encouraging the proliferation of adaptive arguments for the evolution of genomic features this text explains why the details matter and presents a framework for how the architectural diversity of eukaryotic genomes and genes came to arise

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

the topic of genome architecture is of great interest to evolutionary biologists small to large chromosome rearrangements have been reorganizing the genome information including genes and heterochromatic regions such as centromeres and telomeres transposable elements tes are an essential component of the genomes of all life forms studied until now not only because of their abundance but also because of their influence on reshaping the genome architecture multiple studies have provided evidence that tes are located in particular regions of the genome e g gc rich regions for alus or at rich regions for l1s here using abundant genomic data and statistical methods as diverse as pair wise non parametric tests multiple linear regression multiple negative binomial regression multiple logistic regression interval testing procedure itp and functional logistic regression flr we addressed two questions about te biology 1 how do alus dna transposons and endogenous retroviruses ervs neighboring regions reflect integration site preferences and fixation processes for these tes what genomic features are associated with their presence genome wide 2 can we capture integration site preferences alone using data from young polymorphic or ex vivo integrations the results from the te analyses contributed to our understanding of fixation and integration site preferences genome wide providing abundant information from diverse

genomic features this information is of great importance to direct studies of insertional mutagenesis and gene therapy additionally we provided a set of statistical tools to analyze complex genomic datasets moreover we explored the genes on the y chromosome of gorilla we performed this by first generating y specific transcripts from testis rnaseq data second by evaluating their structure in the y chromosome assembly third by using these transcripts to scaffold the y chromosome assembly finally we predicted novel genes from the assembly that could have been transposed from other chromosomes this project allowed us to create a workflow to assemble y transcripts from testis samples this protocol will be applied in future studies in addition we proved the usefulness of transcriptome data to scaffold genomes

understanding of the origin of species and their adaptability to new environments is one of the main questions in biology this is fueled by the ongoing debate on species concepts and facilitated by the availability of an unprecedented large number of genomic resources genomes are organized into chromosomes where significant variations in number and morphology are observed among species due to large scale structural variants such as inversions translocations fusions and fissions this genomic reshuffling provides in the long term new chromosomal forms on which natural selection can act upon contributing to the origin of biodiversity this book contains mainly articles reviews and an opinion piece that explore numerous aspects of genome plasticity among taxa that will help in understanding the dynamics of genome composition the evolutionary relationships between species and in the long run speciation

this volume reviews the latest research on the functional implications of nuclear chromosomal and genomic organization and architecture on cell and organismal biology and development and progression of diseases the architecture of the cell nucleus and non random arrangement of chromosomes genes and the non membranous nuclear bodies in the three dimensional 3d space alters in response to the environmental mechanical chemical and temporal cues the changes in the nuclear chromosomal or genomic compaction and configuration modify the gene expression program and induce or inhibit epigenetic modifications the intrinsically programmed rearrangements of the nuclear architecture are necessary for cell differentiation the establishment of cell fate during development and maturation of tissues and organs including the immune muscle and nervous systems the non programmed changes in the nuclear architecture can lead to fragmentation of the nucleus and instability of the genome and thus cause cancer microbial and viral infections can lead to a clustering of centromeres telomeres and ribosomal dna and alter the properties of the nuclear membrane allowing large immobile macromolecules to enter the nucleus recent advances in next generation sequencing technologies combined with nucleus chromosome conformation capture super resolution imaging chromosomal contact maps methods integrative modeling and genetic approaches are uncovering novel features and importance of nuclear chromosomal and genomic architecture this book is an interesting read for cell biologists researchers studying the structure and function of chromosomes and anyone else who wants to get an overview of the field of nuclear chromosomal and genomic architecture

the traditional view of genomes suggests that they are static entities changing slowly in sequence and structure through time e g evolving over geological time scales this outdated view has been challenged as our understanding of the dynamic nature of genomes has increased changes in dna content i e polyploidy are common to specific life cycle stages in a variety of eukaryotes as are changes in genome content itself these dramatic genomic changes include chromosomal deletions i e paternal chromosome deletion in insects goday and esteban 2001 ross et al 2010 developmentally regulated genome rearrangements e g the v d j system in adaptive immunity in mammals schatz and swanson 2011 and the specialization of a distinct somatic genome through epigenetically regulate dna elimination during development found in protists and some animals coyne et al 2012 prescott 1994 wang and davis 2014 wyngaard et al 2011 what likely allows genomes to be highly flexible is the separation of germline i e heritable and somatic i e functional material even in the context of a single nucleus germline soma distinctions have been best described and most easily seen in lineages of multicellular eukaryotes e g plants animals and fungi due to obvious sexual structures germline genomes of these taxa are restricted to specialized cells e g gametes for example pollen grains eggs and spores and remain undifferentiated and often transcriptionally inactive whereas the somatic cells e g skin leaves hyphae provide the basis for ensuring organismal survival to reproductive life stages sequestered germline and somatic genomes are not restricted to these well known multi cellular lineages but are also well described among ciliates the focus of this dissertation and some foraminifera however in these protists germline and somatic genomes are not isolated into distinct cells and tissues but rather are isolated into distinct nuclei that share a common cytoplasm ciliates are a diverse and ancient clade of eukaryotes 1 1 2 gya old and their study has led to the discovery of broad uniting eukaryotic features such as telomeres blackburn and gall 1978 and self splicing rnas kruger et al 1982 as in the macrobial eukaryotes the somatic genome macronucleus mac is transcriptionally active transcribing all the genes necessary to maintain the cell while the germline genome micronucleus mic remains transcriptionally inactive during the asexual portions of the life cycle while the germline chromosomes in ciliates are physically similar to other traditional eukaryotic chromosomes e g being multi mbp with centromeres the physical structure of the somatic chromosomes is highly variable for example in the model ciliate tetrahymena thermophila the somatic genome is composed of 225 unique chromosomes most of them being 200 400kbp with each at approximately 45 copies whereas oxytricha trifallax s somatic genome is composed of 16 000 gene sized chromosomes 2 3kbp with each chromosome at its own independent copy number average copy number 2 000 despite dramatic differences in somatic genome architecture in ciliates the development of a new somatic genome involves for all ciliates studied to date this metamorphosis from traditional germline chromosomal architecture to the incredibly variable somatic genome architecture includes large scale genome rearrangements and dna elimination this transformation involves the epigenetically guided retention of somatically destined dna from the background germline genome while genomic rearrangements in most other eukaryotes are often fatal and are symptoms of well known diseases e g some cancers this traditionally catastrophic event is a fundamental part of ciliate life cycles although studies of

ciliate germline genomes have largely been restricted to only a few genera there appear to be broad similarities in gene organization that may be phylogenetically conserved ciliate germline genome architecture has been categorized as either non scrambled or scrambled where non scrambled architectures are often defined as possessing macronuclear destined sequences mdss soma that are separated by germline limited dna and remain in consecutive order e g 1 2 3 4 figure 3 1a and figure 4 4a scrambled germline architectures are highly variable but are broadly defined as mdss being maintained in non consecutive order e g 1 3 4 2 and or on opposing strands of dna figure 3 1 b d and figure 4 4b the germline genomes of chilodonella uncinata the main focus of this dissertation possess a combination of scrambled and non scrambled architectures before my thesis work only those ciliates with gene sized chromosomes have been demonstrated to have scrambled germline loci interestingly previous work has implicated somatic genome architecture impacting the observable accelerated rates of protein evolution in ciliates where the proteins of those ciliates possessing gene sized chromosomes experience the greatest evolutionary rates these observations highlight the need for further work exploring the evolutionary impacts of different germline genome architectures as the germline structure itself has direct impact on the development of the somatic genome while this dissertation aims to elucidate some aspects of the evolution of germline soma distinctions and the impact of genome and nuclear architecture chapters 2 4 there remain several fundamental questions that we can start addressing for instance in this work we observe that the most expanded gene families in chilodonella uncinata are composed of genes that are disproportionately found at scrambled germline loci chapter 3 a major step future step will be to explore the functional implications of this increased paralog diversity through forward and reverse genetics techniques similarly it will be incredibly valuable to better understand the nuclear architecture of the differing genomic contents of the three distinct nuclei present during ciliate development i e the degrading parental mac the new mic and the developing mac there may be observable compartmentalization that is exploitable or critical to the accurate rearrangement of the germline genome into a functional somatic genome finally with the increasingly apparent utility of single cell omics techniques which we use in chapters 3 and 4 there is opportunity to probe into taxonomic groups where physical germline soma separations exist which will provide a far more expansive understanding of the evolutionary and functional impacts of harboring multiple distinct genomes inside of a single cell organism

this book provides a timely summary of physical modeling approaches applied to biological datasets that describe conformational properties of chromosomes in the cell nucleus chapters explain how to convert raw experimental data into 3d conformations and how to use models to better understand biophysical mechanisms that control chromosome conformation the coverage ranges from introductory chapters to modeling aspects related to polymer physics and data driven models for genomic domains the entire human genome epigenome folding chromosome structure and dynamics and predicting 3d genome structure

a genome includes all of the genetic information of an organism it is made up of the nucleotide sequences of dna the complete set of non random arrangements of functional elements within the

genome is known as the genomic architecture the architecture of the genome is crucial in gene regulation utilizing high throughput techniques for 3d interaction mapping and chromatin profiling produces extensive experimental data sets that describe the structure and dynamics of the genome the study of genomic architecture is currently a very prominent area of research that has significant applications in the study of processes such as cell development differentiation and carcinogenesis this book explores all the diverse aspects of genomic architecture it presents researches and studies performed by experts across the globe the extensive content of this book provides the readers with a thorough understanding of the subject

this topic has been realized and is in collaboration with dr constanze pentzold post doctoral researcher at the institute of human genetics university hospital jena

the relation between the structure of the genome and gene regulation is critical to normal and disease development but the molecular details of how they are interconnected are still unknown chromatin conformation capture hi c studies discovered several layers of chromatin organization however the way those structures impact or are impacted by regulation is unclear we thus wanted to clarify the links between chromatin architecture and transcription regulation in this study we use two types of domains one having a structural definition and the other a functional definition and compare them to find their differences and similitudes topologically associating domains tads have been selected to represent the genomic architecture they have a more static nature and their boundaries have been suggested to limit the spread of regulatory signals co expression domains cods were chosen to represent the aspects of gene regulation cods are defined as domains within which genes have correlated expression by definition cods are thus very dynamic and more likely to change from cell to cell in this study we analyze the effect of tad boundaries on nearby genes here we show that tads and cods have distinct functions and are delimited by different boundaries we confirm that tad boundaries disrupt co expression we also characterize cod boundaries and find that they seem to be marked by a switch of strand on which genes are located and they are independent of structural proteins we use expression quantitative trait loci eqtl data to confirm the observations and find that genes affected by the same eqtl are preferentially located on the same strand and are less likely to be separated by barriers such as tad boundaries we thus propose a model for human cells in which the gene conformation impacts gene co regulation we suggest that strand position of genes affects their co expression probability and the introduction of barrier elements further disrupts it that model would serve as a simple principle to which more complex mechanisms may rely

presents an integrated view of the expression of bacterial genetic information genome architecture and function and bacterial physiology and pathogenesis this book blends information from the very latest research on bacterial chromosome and nucleoid architecture whole genome analysis cell signaling and gene expression control with well known gene regulation paradigms from model organisms including pathogens to give readers a picture of how information flows from the environment to the gene modulating its expression and influencing the competitive

fitness of the microbe structure and function of the bacterial genome explores the governance of the expression of the genes that make a bacterium what it is and updates the basics of gene expression control with information about transcription promoter structure and function the role of dna as a regulatory factor in addition to its role as a carrier of genetic information small rnas rnas that sense chemical signals ribosomes and translation posttranslational modification of proteins and protein secretion it looks at the forces driving the conservation and the evolution of the dynamic genome and offers chapters that cover dna replication dna repair plasmid biology recombination transposition the roles of repetitive dna sequences horizontal gene transfer the defense of the genome by crispr cas restriction enzymes argonaute proteins and brex systems the book finishes with a chapter that gives an integrated overview of genome structure and function blends knowledge of gene regulatory mechanisms with a consideration of nucleoid structure and dynamics offers a dna centric approach to considering transcription control views horizontal gene transfer from a gene regulation perspective assesses the opportunities and limitations of designing synthetic microbes or rewiring existing ones structure and function of the bacterial genome is an ideal book for graduate and undergraduate students studying microbial cell biology bacterial pathogenesis gene regulation and molecular microbiology it will also appeal to principal investigators conducting research on these and related topics and researchers in synthetic biology and other arms of biotechnology

this splendid compendium will be the standard reference work for years to come a handbook to browse to consult to look things up in and to read with pleasure wonder and post darwinian exhilaration richard dawkins this is a marvellous book it should be in every university library preferably in several copies and every reader of this journal should add it to their next grant application it really is that good i have already found this book to be invaluable for many years to come these two volumes will be the starting point for anyone wishing to find out about virtually any subject relating to human genetics any scientist working on humans or other animals will find many things in these pages that will stimulate inform and inspire the authors editors and publishers are to be congratulated for their work order a copy now human genetics the publishers and editors deserve to be congratulated for publishing this major book which coincides with the 200th anniversary of the birth of charles darwin the book is well timed with biologists theologians and sociologists engaged in intense debate on the darwinian theory on the origin of species evolution and natural selection there is little doubt that this marvellous publication should be in the library of universities and academic institutions dealing with basic and applied biology research and education it will not be surprising if the individual academic or researcher decides to invest in this resource and enrich their personal collection of leading books in genetics and genomics genomic medicine a unique collection of high quality articles derived from the acclaimed encyclopedia of life sciences the revolution in human molecular genetics which has taken place over the last three decades has yielded a wealth of information not only on the structure and function of our genes but also on gene expression mutation and polymorphic variation over the last five years the focus has moved from genes to genomes even though the annotation of our 30 000 genes is still in progress genome wide studies have already yielded

abundant evidence for the signatures of past selection and adaptive evolution within human gene sequences further the completion of the sequencing of the 3 billion base pair human genome coupled with the increasing availability of other vertebrate genome sequences has ushered in a new era of comparative genomics we are now able to identify many of the molecular events from the chromosomal level down to the single base pair that have occurred during vertebrate mammalian primate and hominid evolution indeed the detailed comparison of the human and chimpanzee genomes has begun to reveal some of the genetic changes that have been involved in the development of human lineage specific traits we are thus acquiring the ability to ask searching questions about our origins about the demographic processes associated with the global radiation of humankind as well as some of the unique adaptations that make us human evolutionary biology has become so broad that its impact may be felt across the spectrum of the biological sciences the aim of the handbook of human molecular evolution is relatively straightforward to bring together under the same cover the many and varied strands of our knowledge of human primate vertebrate molecular evolution hence the 282 chapters that comprise this essential reference work have been thematically arranged into twelve sections covering the whole scope of research into human molecular evolution general concepts in evolutionary genetics mutation adaptation and natural selection evolutionary and population genetics human evolution human genome evolution evolution of human gene structure and function evolution of gene expression mitochondrial genome evolution chromosomal evolution comparative genomics evolution and disease susceptibility analysis of ancient dna this conceptual outline informed the selection of the chapters themselves and the connections between them some of these chapters are intended to be introductory aimed at undergraduates and non specialists they provide basic information and a list of recommended further reading to encourage the reader to explore a topic in more depth this approach helps the student reader progress from textbook material to primary literature some chapters are overviews that address topics of broad interest and importance while others focus on quite specialized topics these chapters are written for postgraduate students and research workers they contain more detailed information and key references allowing the reader to investigate a specific area in more depth this format allows professionals to use the books as a quick reference source the chapters are richly supplied with website information to allow access to relevant data sources over the internet the self contained peer reviewed articles in this unique handbook have been written by leading scientists in each field key topics include the evolution of enzyme function the use of nucleic acid divergence as a molecular clock the origin of non functional or junk dna the role of gene duplication in the emergence of novel gene function and the identification of molecular changes responsible for various human characteristics especially those pertaining to infection cognition disease and disease susceptibility the handbook of human molecular evolution has adopted an integrated approach to the study of human evolution and seeks throughout to emphasize the interplay between molecular genetic concepts and principles on the one hand and information acquisition and interpretation on the other in this way it is hoped that the documents of evolutionary history written into the fabric of our genome will become accessible to the widest possible audience

high throughput chromosome conformation capture 3c techniques have provided a comprehensive overview of the genome architecture hi c a derivative of 3c has become a reference technique to study the 3d chromatin structure and its relationship with the functional state of the cell however several aspects of the analysis and interpretation of hi c data remain a challenge and may hide a potential yet to be unveiled in this thesis we explore the structural landscape of multiple chromatin features we developed an integrative approach combining in situ hi c data with nine additional omic layers and revealed a new dynamic and transitional genomic compartment enriched in poised and polycomb repressed chromatin this novel intermediate compartment plays an important role in the modulation of the genome during b cells differentiation and upon neoplastic transformation specifically in chronic lymphocytic leukemia cll or mantle cell lymphoma mcl patients we also developed tadpole a computational tool designed to characterize the hierarchy of topologically associated domains tads using hi c interaction matrices we demonstrated its technical and biological robustness and its capacity to reveal topological differences in high resolution capture hi c experiments

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