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Current Opinion in Structural Biology

Genome modeling: From chromatin fibers to genes

Stephanie Portillo-Ledesma[1], Zilong Li[1] and Tamar Schlick[1,2,3,4]

Abstract

The intricacies of the 3D hierarchical organization of the genome have been approached by many creative modeling studies. The specific model/simulation technique combination defines and restricts the system and phenomena that can be investigated. We present the latest modeling developments and studies of the genome, involving models ranging from nucleosome systems and small polynucleosome arrays to chromatin fibers in the kb-range, chromosomes, and whole genomes, while emphasizing gene folding from first principles. Clever combinations allow the exploration of many interesting phenomena involved in gene regulation, such as nucleosome structure and dynamics, nucleosome-nucleosome stacking, polynucleosome array folding, protein regulation of chromatin architecture, mechanisms of gene folding, loop formation, compartmentalization, and structural transitions at the chromosome and genome levels. Gene-level modeling with full details on nucleosome positions, epigenetic factors, and protein binding, in particular, can in principle be scaled up to model chromosomes and cells to study fundamental biological regulation.

Addresses

[1] Department of Chemistry, New York University, 100 Washington Square East, Silver Building, New York, 10003, NY, USA
[2] Courant Institute of Mathematical Sciences, New York University, 251 Mercer St., New York, 10012, NY, USA
[3] New York University-East China Normal University Center for Computational Chemistry, New York University Shanghai, Room 340, Geography Building, 3663 North Zhongshan Road, Shanghai, 200122, China
[4] Simons Center for Computational Physical Chemistry, 24 Waverly Place, Silver Building, New York University, New York, 10003, NY, USA

Corresponding author: Schlick, Tamar (schlick@nyu.edu)
(Schlick T.)

Current Opinion in Structural Biology 2023, **78**:102506

This review comes from a themed issue on **Theory and Simulation/ Computational Methods (2023)**

Edited by **Turkan Haliloglu** and **Gregory A. Voth**

For complete overview of the section, please refer the article collection - Theory and Simulation/Computational Methods (2023)

Available online 26 December 2022

https://doi.org/10.1016/j.sbi.2022.102506

Keywords

Genome organization, Chromatin folding, Epigenetic regulation, Gene regulation, Gene structure.

Abbreviations

BD, Brownian Dynamics; CG, Coarse-Graining; Chip-seq, Chromatin immunoprecipitation sequencing; CpG, 5′−C−phosphate−G−3′; CTCF, CCCTC-binding Factor; CUDA, Compute Unified Device Architecture; Hi-C, High-throughput Chromosome Conformation Capture technique; HP1, Heterochromatin Protein 1; LD, Langevin Dynamics; LH, Linker Histone; MC, Monte Carlo; MD, Molecular Dynamics; mESC, mouse Embryonic Stem Cell; NCP, Nucleosome Core Particle; NFR, Nucleosome Free Region; RICC-seq, Radiation-Induced Correlated Cleavage with sequencing; TAD, Topologically Associating Domain; TF, Transcription Factor.

Introduction

How our genome is structured and regulates fundamental biological processes such as transcription, replication, and repair is central for understanding and addressing human disease. While genome sequencing has revolutionized how we perceive and can study human ancestry and disease, the study of genome organization has emphasized how profoundly epigenetic processes — structural transformations of the genome — impact gene regulation. Indeed, the activation and repression of specific genes — at precise stages of the cell cycle, and in response to internal and external factors — dictates how and when basic life processes are regulated.

While the problem of deciphering this epigenetic regulation of the genome may appear daunting, as so many levels and factors are involved, structural biologists and genomicists have developed powerful interrogatory techniques, both experimental and computational, to address these fascinating aspects of genome organization.

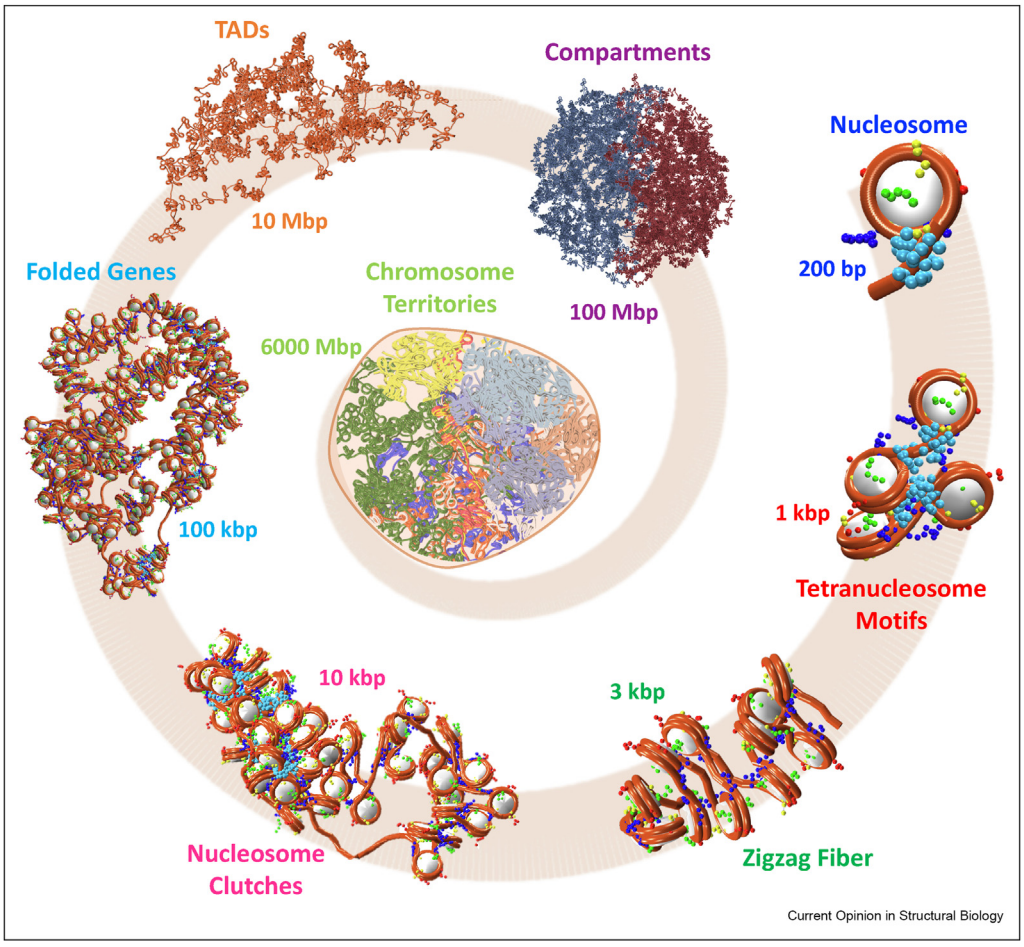
In this opinion article, we focus on computational studies that aim to scale chromatin systems from fibers to genes, simulation approaches appropriate for these systems, and biological applications, with insightful examples.

Gene-level modeling describing how chromatin elements are defined with tailored input parameters can capture large-scale phenomena from basic physical principles, and can in principle be scaled up to model chromosomes and whole genomes to study the mechanisms that regulate gene expression associated with human disease.

Current view of genome global organization

Genomic DNA is hierarchically organized (**Figure 1**) to efficiently pack 6 billion base pairs inside the diploid

Figure 1



Hierarchical genome folding. ~147 bp of DNA wrap around the histone octamer to form the nucleosome, the chromatin basic building block. Nucleosomes fold into tetranucleosome units, and the zigzag topology appears dominant in small kb arrays. Further folding through hierarchical looping creates nucleosome clutches of different sizes and levels of compaction. Genes fold while maintaining the folding features of the lower scales. Compartmentalization at the Mb scale produces TADs, which further fold to form segregated compartments. Finally, chromosomes separate in territories in the cell nucleus.

cell nucleus and direct biological regulation of gene expression [1,2].

Hi-C contact maps have revealed that interactions between pairs of loci across the whole eukaryotic genome dictate genome segregation into open/active and closed/inactive chromatin to form distinct Mb compartments [3]. While contacts within compartments are enriched, contacts between compartments are rare. The positions of these compartments are also cell-dependent, and dictate a large range of biological phenomena related to development, differentiation, and disease progression.

At the scale of hundreds of kb, higher-resolution Hi-C maps reveal an additional level of compartmentalization involving the formation of self-interacting "Topologically Associating Domains" or TADs [4–6]. Networks of loops are supported by the protein pair of cohesin and CCCTC-binding factor (CTCF) [7,8], although cohesin might not be required for the formation or maintenance of TADs at the single-cell level [9]. TADs have been identified in many species across cell types, indicating that they are likely a conserved feature of genome organization. The importance of these domains in the regulation of genome expression, however, remains unclear. Overall, compartmentalization and loop formation appear to be two independent but related principle mechanisms of genome organization [10,8].

At the sub kb level, super-resolution microscopy and modeling at the nucleosome scale reveal that nucleosomes are organized in clusters or “clutches” [11–13]. Their size and compaction are related to the cell differentiation state [11,13], epigenetic modifications [12,14,15*], linker histone (LH) binding [15*], and cohesin binding [12].

Single-molecule force spectroscopy revealed that tetranucleosome units appear as stable secondary structure motifs in the hierarchical organization of chromatin fibers in the yeast genome [16]. Micro-C experiments combined with molecular dynamics (MD) simulations [17] show that these units organize in two basic folding motifs that favor next neighbor (i/i+2) internucleosome contacts: the α-tetrahedron and β-rhombus. While the α-tetrahedron is prevalent between the gene start and stop sites and is related to closed chromatin, β-rhombus is associated with promoters and open chromatin. In contrast, Radiation-Induced Correlated Cleavage with sequencing (RICC-seq) experiments at the sub-kb level of the human genome revealed that i/i+2 contacts, typical of two-start zigzag fibers with stacked alternating nucleosomes, are found mostly in closed chromatin, whereas non-compact solenoid structures tend to form in open chromatin [18], indicating differential folding for active and repressed chromatin. Modeling and crosslinking experiments have emphasized the prevalence of zigzag architecture [19,20].

In vitro studies have recently revealed that at high salt concentrations or presence of proteins that bind to the nucleosome, nucleosome arrays organize through liquid-liquid phase separation to form liquid droplets [21,22]. This remains somewhat controversial as chromatin behaves as a solid at the mesoscale level [23]. Similarly, in vivo experiments have provided evidence for phase separation of heterochromatin and euchromatin. For heterochromatin, phase separation is driven by repressive proteins like heterochromatin protein 1 (HP1) [24,25], and for euchromatin, transitions are driven by RNA Polymerase II [26] and transcription factors [27]. Thus, the compartmentalization of the genome into functionally chromatin compartments is emerging as a key regulatory feature.

While clearly genome organization is variable and heterogeneous when analyzed at the single-cell level [28], its hierarchical structure involves several distinct layers.

As we discuss below, each of these layers has been investigated by many computational approaches that use models of different resolutions and sampling techniques to further understand genome organization and regulation. Following our overview of molecular models and techniques in the next section, we will describe associated applications in three subsequent sections organized by genome level, followed by gene folding, and ideas regarding future directions and opportunities.

Methods across the scales

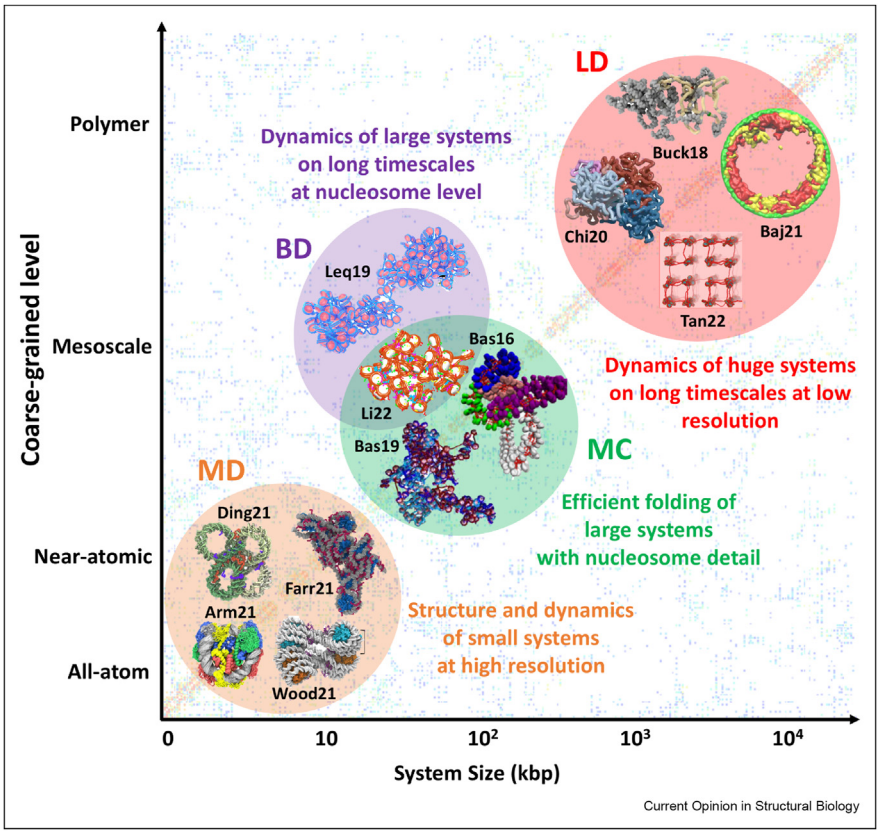
Several techniques and various multiscaling approaches are suitable for studying the different layers of genome organization by computer modeling and simulation, including nucleosomes, chromatin fibers, and chromosomes. This combination of model resolution and simulation technique restricts and defines the type of systems and which phenomena can be studied (**Figure 2**).

Molecular Dynamics (MD) is a widely used technique that allows high spatial and temporal resolutions that cannot be reached by experimental methods. Its main advantage is the intense development of robust all-atom force fields and software for general-purpose MD simulations. Because it is usually combined with atomic-resolution models, it requires significant computational resources. As recently reviewed by Huertas and Cojocaru [29], all-atom MD simulations of chromatin systems are generally limited to one ($\sim$500,000 atoms) or two ($\sim$700,000 atoms) nucleosomes. The longest simulation time achieved as of this writing for a single nucleosome system is 15 μs [30*](Arm21 in **Figure 2**), far from the 10 ns obtained by Bishop in 2005 for the first all-atom simulation of a nucleosome [31]. Some exceptions regarding system size are the works by Jung et al. on the GATA4 gene containing 427 nucleosomes and $\sim$1 billion atoms [32]; Izadi et al. on a chromatin fiber of 40 nucleosomes and $\sim$1.16 million atoms [33]; and Woods et al. on an 8-nucleosome array containing $\sim$2.75 million atoms [34*] (Wood21 in **Figure 2**). However, these simulations were restricted to only 1, 0.1, and 500 ns, respectively. It remains a challenge to sample configuration space adequately for chromatin systems via all-atom MD simulations.

To overcome this issue and close the gap between the experimental and modeling time scale, enhanced sampling techniques have been applied to nucleosome and polynucleosome systems [29], including Replica Exchange, Metadynamics, Steered MD, Umbrella Sampling, Adaptively Biased MD, and Adiabatic Bias MD (see separate literature on enhanced sampling [35,36]).

The alternative coarse-graining (CG) approaches allow longer timescales and comparison with various experimental data. Popular DNA CG models include the de Pablo three-site model 3SPN (on phosphate, sugar, and nucleotide) [37] and subsequent refinements. These models have been combined with the Wang and Takada protein CG model AICG2+ of 1 bead per residue [38], to study transcription factor binding to nucleosomes ($\sim$3000 particles) for 10 μs [39*]; with the Wolynes and Papoian protein CG model AWSEM of 3 beads per residue [40], to study chromatosome dynamics ($\sim$3000 particles) for 60 ns [41**]; and with contact potentials for the amino acids derived from a tetranucleosome crystal structure, to fold tetranucleosome arrays (8058 particles) [42**] (Ding21 in **Figure 2**). Similarly, Tan et al. combined a 3SPN model with AICG2+ and the HPS force field for disordered tails [43] to simulate a 1024-nucleosome system ($\sim$2 million particles) [44*] (Tan22 in **Figure 2**).

Figure 2



Combination of model resolution and simulation technique for chromatin systems, each with associated system sizes and phenomena. Large system sizes can be reached by reducing the number of particles (coarse-graining) with polymer models and utilizing simulation techniques like Langevin Dynamics (LD). Intermediate systems are usually studied by mesoscale models with nucleosome resolution combined with Brownian Dynamics (BD) or Monte Carlo (MC) sampling. Small systems can be studied at higher resolution with all-atom or near-atomic models by Molecular Dynamics (MD). Molecular modeling images were adapted with permission from: [42**] (Ding21); [30**] (Arm21); [50**] (Farr21); [44*] (Tan22); [59] (Baj21); and [58] (Chi20) under the Creative Commons Attribution License http://creativecommons.org/licenses/by/4.0/; [34*] (Wood21) Copyright 2021 Elsevier; [146**] (Bas19); [74] (Bas16) Copyright 2016 American Chemical Society; [63*] (Li22); and [61] (Leq19) under AIP Publishing.

The Pantano's SIRAH CG force field was recently extended for protein-DNA complexes to study DNA dynamics in a tetranucleosome array (~240,000) for 5 μs [45]. Lyubartsev, Nordenskiöld, and colleagues developed a residue-based CG model for the nucleosome core particle derived from multiple all-atom MD simulations that consider the ionic environment [46].

The rigid base pair approximation by Olson and Zhurkin treats DNA's flexibility as a harmonic oscillator with parameters extracted from experiments, accounting for sequence dependency [47]. Farr et al. recently combined this model with a residue-resolution CG model for proteins based on [48,49] to create a chemically-specific CG model [50**] (Farr21 in **Figure 2**). Similar to the multiscale used in [51] to connect all-atom to mesoscale level of chromatin, Farr et al. used two levels of coarse graining: the nucleosome all-atom model is CG into the chemically-specific model, which is then refined into a chromatin minimal model.

Eliminating the explicit representation of solvent particles in Langevin Dynamics (LD), the solvent is treated as a continuous medium surrounding the solute, leads to simulation time scales in the range of seconds. LD is generally used for simulations of polymer models in which the chromatin fiber is treated as a chain of beads connected by springs. As recently reviewed [52,53], many polymer models to investigate chromatin structure exist. These include the Nicodemi "strings and binders switch" (SBS) model, where chromatin is a self-avoiding polymer chain interacting with diffusing beads [54]; the Vaillant block-copolymer model, where chromatin is a self-interacting block-copolymer [55]; the Marenduzzo's HiP-HoP [56]; and Mirny's loop extrusion [57] models in which a loop extruding factor

anchored to the chromatin fiber extrudes a progressively growing loop until barriers along the fiber are reached.

With these models, large genomic regions can be studied. For example, the HiP-HoP and SBS models were recently used with LD to study Mbp and kbp regions equivalent to 9000 and 2640 particles, respectively [56,58] (Chi20 in **Figure 2**). Bajpai et al. used a simple polymer model in which each bead represents three nucleosomes to simulate the phase separation of a 22.4 Mbp region (37,333 particles, comparable to the X chromosome) in the nucleus (Baj21 in **Figure 2**) [59].

The appropriate version of LD for systems with large solvent interactions, Brownian Dynamics (BD), introduces generalized frictional interactions among the particles. Because the calculation of the frictional interactions among particles is computationally expensive, the system size is currently limited to a few thousand particles. The group of the late Jörg Langowski first simulated 25-nucleosome arrays by BD where chromatin was treated as an array of cylindrical segments and solid spheres attached to them [60]. Recently, the de Pablo group developed the 1CPN chromatin model for BD to simulate up to 250-nucleosome arrays over 50 μs (Leq19 in **Figure 2**) [61]. The model treats nucleosomes with implicit tails as cylinders, linker DNA as a twistable worm-like chain, and LH as flexible beads based on the Schlick LH model [62].

BD was recently developed by the Schlick group (Li22 in **Figure 2**) [63*] following early work by Beard and Schlick [64] to simulate fibers with a mesoscale model of chromatin: nucleosome cores are treated as cylinders with 300-point charges distributed on its irregular surface [65], non-uniform linker DNAs are described by 1 bead per 3 nm [66], flexible histone tails are explicitly incorporated [67,51], and flexible LHs can also be considered [62,68]. The innovation in the new BD scheme is exploiting the computational power and parallelization of CUDA for the hydrodynamics interactions, making possible simulations of systems with up to 50 nucleosomes (∼4000 particles) [63*].

An alternative approach to these dynamics simulation techniques is equilibrium sampling by Monte Carlo (MC), generally very efficient for surveying conformational landscapes. Early MC techniques on worm-like chains by Vologodskii and coworkers showed their efficiency for sampling supercoiled and knotted DNA [69,70]. For chromatin, the Schlick group's mesoscale model uses MC sampling similarly to sample kb-range fibers [71,72]. Tailored translational and rotational moves for the nucleosome cores and linker DNA, translational moves for LH beads, regrowth moves for the histone tails, and pivot moves for short fiber segments are combined for efficient sampling of chromatin fibers [62,67,73]. The largest system reached by this approach is the GATA4 gene (Bas16 in **Figure 2**) [74], containing 427 nucleosomes (∼34,000 particles). The van Noort chromatin model with rigid body histone core and rigid base pair DNA model is also sampled with MC [75,76]. At each MC step, a sequential replacement and evaluation of every base pair in the DNA tether is performed, and MC steps for wrapping and unwrapping of DNA are also included. Similarly, Zhurkin and Norouzi use MC for a chromatin model where fixed nucleosomes can unwrap their DNA [77,78]. Finally, MC sampling is used in combination with Replica Exchange to simulate fibers with the Wedemann CG chromatin model that treats nucleosomes as spherocylindrical units connected by cylindrical segments for linker DNA, and considers LH implicitly [79]. Recently, this approach was used to study the effect of cohesin and CTCF on chromatin loops and its dependency on nucleosome positions [80].

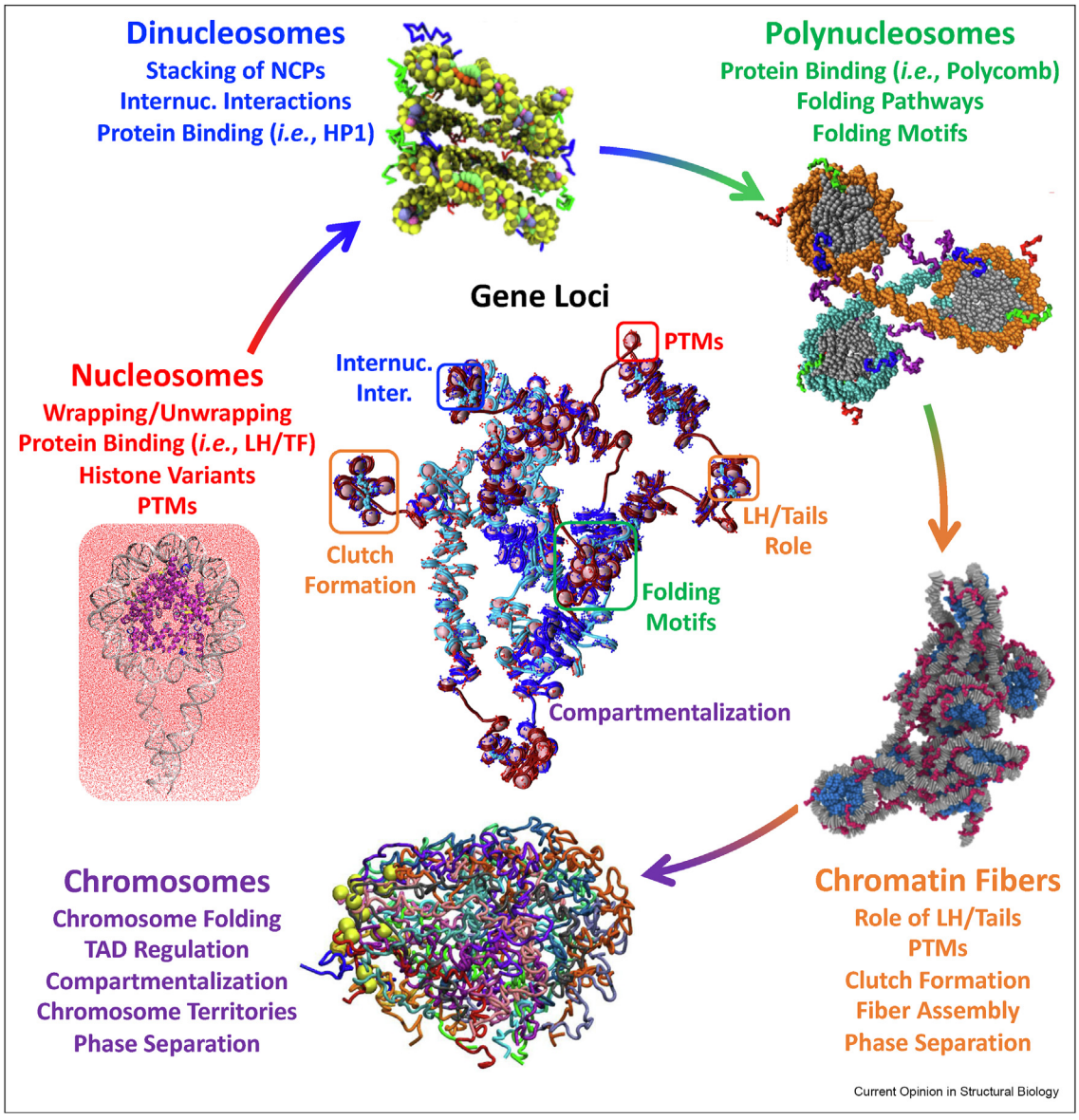
Clearly, computer simulations offer an unmatched level of resolution in addition to experiments to study chromatin folding. To investigate the structure and dynamics of chromatin fibers at the Mb and chromosome scale, the most common approach is to employ coarse-grained polymer models with LD. The structure and dynamics of nucleosome arrays of kb-range lengths has been approached with coarse-grained models at the mesoscale level with MC or BD simulations. Nucleosome all-atom MD simulations can offer more in-depth details at the atomistic level, although system size is significantly restricted. Thus, each genomic scale can provide insights at different resolution, and the details learned at a certain scale can be used to build models for the next scale. Thus, aspects at the nucleosome scale and all-atom resolution can be incorporated into mesoscale models for chromatin fibers, and features of chromatin fibers can be extrapolated to construct polymer models and study Mb systems.

Nucleosome modeling: assembly, unwrapping, positioning, and epigenetic modulation

The first nucleosome core particle (NCP) X-ray crystal structure at atomic resolution (2.8 Å) in 1997 [81] has been followed by many high-resolution structures that further revealed details on the mobile histone tails, variant core histones, binding of auxiliary proteins, ions, and solvent molecules [82]. These experimental anchors provided a platform for modeling NCP conformations and dynamics, including interactions among its elements, like DNA, histone tails, and linker histone (LH) (**Figure 3**) [29,83].

Early works of nucleosomes by all-atom and CG models focused on understanding unwrapping, assembly, and sliding, as well as their sequence dependence [84]. Recently, improved models and larger simulation times have been possible. For example, Brandani et al.

Figure 3



Examples of recent modeling applications, from nucleosomes to chromosomes, and gene loci. Nucleosome simulations provide insights into dynamical phenomena like assembly, wrapping and unwrapping, and sliding, the effect of LH and TF binding, and role of post-translational modifications and histone variants. Dinucleosome systems are used to study the regulation of internucleosome interactions and binding of repressing proteins like HP1. Polynucleosome studies reveal folding motifs and pathways, and the effect of repressive proteins like polycomb. Chromatin fibers at the kb-level reveal typologies, nucleosome clutches, role of linker DNA, LH, and histone tails, and phase separation. Modeling of chromosomes provides insights into folding and TAD formation/regulation, compartmentalization, chromosome territories, and phase separation. For gene loci, the elements and phenomena studied at each genomic scale are combined to obtain a high-resolution structure. Molecular modeling images were adapted with permission from: chromatin fibers [50**] and chromosomes [142**] under Creative Commons Attribution License http://creativecommons.org/licenses/by/4.0/; dinucleosome [118] https://pubs.acs.org/doi/10.1021/acscentsci.1c00085 and under Creative Commons Attribution License https://creativecommons.org/licenses/by-nc-nd/4.0/, polynucleosome [119] Copyright 2022 Elsevier, and gene loci [146**].

characterized nucleosome intermediates during nucleosome assembly [85], finding a high sequence (A/T-rich signals) and salt dependency. In agreement with previous modeling studies on nucleosome sliding [86] and unwrapping [87], genomic sequence alone likely controls nucleosome positioning.

The regulation of nucleosome dynamics by histone tails, epigenetic modifications, and histone variants have been extensively studied by molecular modeling. For example, Armeev et al. recently reported the longest all-atom MD simulation (15 μs) of the NCP (Arm21 in **Figure 2**) [30*], suggesting that the unwrapping of

DNA ends is mediated by H3 and H2A histone tails, and coupled to the destabilization of the DNA near the dyad. Fu et al. similarly noted that H3 tail acetylation enhances DNA mobility, which could facilitate DNA repair [88], echoing previous simulations reporting that methylation and acetylation of H3 produce a more open DNA [89,90]. DNA methylation, instead, produces more compact nucleosomes, resistant to unwrapping, as shown by Li et al. [91*]. Histone variants also modulate NCP dynamics, as shown by Peng et al. for the H2A.B variant [92], and by Pitman et al. for heterotypic nucleosomes containing both H3 variants CENP-A and H3.3 [93*]. Epigenetic modifications and histone variants likely regulate chromatin architecture and gene expression through modulation of the NCP.

LH, with variants specific to distinct species or tissues, regulates chromatin architecture and is implicated in many functions [94]. Because of its important role, many modeling studies have investigated chromatosome structure and dynamics, as recently reviewed by Öztürk et al. [83]. Early studies performed molecular docking and modeling to understand the LH interaction with DNA and its relative position to the nucleosome [83]. Later, Wade, Cojocaru, and collaborators highlighted on/off dyad binding modes [95], conformational plasticity of the nucleosome [96], and effect of LH mutations and post-translational modifications on chromatosome structure [97].

Recent modeling studies have focused on the role of LH variants and the disordered N- and C-terminal domains. Woods et al. studied chromatosomes containing the globular domain of two LH variants, *Xenopus laevis* generic H1 and *G. gallus* H1.0 [98*]. While the on-dyad binding appears enthalpically favored by both variants, especially H1.0, the off-dyad was relatively more entropically stabilized. However, the large globular domain dynamics suggested that both binding states might simultaneously occur, in agreement with what has been proposed by the Wade group [99]. Wu et al. found that the *X. laevis* generic H1 displays disorder for both N- and C-terminal domains [41], while still producing a compact and rigid chromatosome. In contrast, for this variant, Sridhar et al. suggested a disorder-to-order transition of the N-terminal domain upon nucleosome binding [100]. Finally, Zhou et al. studied chromatosomes containing the globular domain of human LH variants H1.0, H1.10, and H1.4 [101]. A more open chromatosome was found for H1.10, which highly interacts with nucleosomal DNA compared to H1.4 and H1.0, which mostly interact with linker DNA.

Overall, these various modeling studies indicate that the LH variants and binding modes lead to chromatosome heterogeneity, which is context specific. Moreover, they agree with prior work by Perišić et al. demonstrating how LH variants and binding modes affect chromatin compaction, and suggesting that combinations of on and off-dyad binding result in different levels of chromatin compaction, from relatively open to condensed arrays [68]. Earlier work by the Schlick group also revealed mechanisms of condensation by LH via DNA stem formation [62,68,73,102].

Transcription factor (TF) binding to nucleosomes has recently started to be studied by molecular modeling. The Cojocaru group, reported the first simulation of a nucleosome with a TF [103]. They show that DNA local flexibility mediates Oct4 binding, and that nucleosome breathing and twisting increases with the number of TF binding sites, indicating that nucleosome dynamics facilitates TF binding. Tan et al. proposed an allosteric mechanism for the simultaneous binding of the TFs Oct4 and Sox2 [39*] in which one TF modulates the nucleosome structure to promote binding of a second TF. As recently reported by Peng et al., histone tails, in particular H3 and H4, regulate the binding of regulatory proteins to the nucleosome as they occupy the same regions in the nucleosomal or linker DNA [104]. Finally, Ishida et al. found torsional stress induced by protein binding as the mechanism regulating DNA unwrapping [105]. Thus, nucleosome stability and DNA accessibility can be tuned by the binding of regulatory proteins to control gene expression.

Despite the vast number of applications of nucleosome simulations, larger systems are needed to further understand the scaffold of genome folding. Next we discuss coarse-grained models for simulation of systems containing several nucleosomes.

From dinucleosomes to polynucleosome arrays: internucleosome interactions, structural heterogeneity, and protein binding

Favorable stacking interactions between NCPs provide the basis for chromatin fiber folding. Not many studies have focused on genome organization at this level.

Experimentally, the most interesting structural insights come from high-resolution X-ray structures of LH-bound dinucleosomes [106], tetranucleosomes [107,108], and LH-bound 6-nucleosome arrays [109], as well as from Cryo-EM structures of dinucleosomes [110], trinucleosomes [110,111], and 12-nucleosome arrays [112].

Modeling of 2- to 16-nucleosome arrays has provided insights into stacking, internucleosome interactions, and protein binding, as well as folding pathways and motifs (**Figure 3**). Pioneering work from the Orozco and Schlick groups used a multiscale approach to study the role of internucleosome interactions in fiber folding [51]. Their all-atom MD simulations of wild-type and H4-acetylated dinucleosomes revealed that H4 and H3 tails mediate most of the internucleosome interactions,

and that H4 acetylation impairs internucleosome interactions due to a decrease in tail disorder. In agreement, subsequent modeling works showed that H2A and H4 form most of the NCP-NCP stacking contacts [113–116], that H4K16Ac directly reduces internucleosome interactions [117], and that H4 tail and its acetylation strongly contributes to the strength and shape of the dinucleosome interaction landscape [118]. As recently suggested by Lequieu et al., besides histone tails, the linker DNA in dinucleosome systems tightly regulates the interaction landscape (Leq19 in **Figure 2**) [61]. Different conformations emerge depending on the linker DNA length, and while some conformations are favored by short linkers, all conformations are equally possible for medium linkers. Similarly, Kenzaki et al. showed that the folding of trinucleosomes strongly depends on the linker DNA length, finding 5 distinctive configurations [119]. These results extend earlier works on chromatin structure showing that variations of DNA linker lengths trigger fiber polymorphism [66,120].

As discussed above, tetranucleosomes can arrange in α-tetrahedron and β-rhombus configurations [17]. Recently, Alvarado et al. revealed the spontaneous formation of the two α and β configurations in 4- and 16-nucleosome arrays, which appear as metastable states in the free energy surface [121*]. Similarly, Ding et al. studied the folding pathway of tetranucleosome arrays (Ding21 in **Figure 2**) [42**], finding many metastable configurations, in which some shapes were similar to the α and β motifs. Woods et al. emphasized their stabilization by LH in octanucleosome arrays (Wood21 in **Figure 2**) [34*].

The binding of repressive proteins to polynucleosome arrays has also been investigated by coarse-grained simulations. Watanabe et al. showed that HP1α binds to two sites in adjacent nucleosomes, bridging the two nucleosomes [122]. Leicher et al. showed the simultaneous binding to non-adjacent nucleosome pairs of the Polycomb repressive complex 2 [123], demonstrating how it can bridge non-contiguous chromosomal segments.

Overall, molecular modeling studies on nucleosome arrays have emphasized the role of histone tails and linker DNA on internucleosome stacking and interactions, energetically favored the formation of tetranucleosome units, and the regulation of dinucleosome and tetranucleosome units by protein binding. Fiber modeling at the kb level and beyond is essential for providing further details on genome organization.

Fiber modeling by mesoscale and polymer models: zigzags, hierarchical loops, and structural transitions

Understanding chromatin 3D architecture is essential to interpret the epigenetic regulation of the genome and relate genome organization to function and human disease.

Usually, fibers of up to 100 kb are modeled at the mesoscopic level with approaches that coarse grain the chromatin elements from their atomistic structures. These are first-principle models in which the simulations aim to predict genome folding with a mechanistic basis. When systems are very large (Mb), polymer models may be preferred. These models generally aim to generate configurations that reproduce experimental contact maps rather than generating folding from first-principles, although many polymer models use only a few parameters and are more mechanistically oriented.

For recent comprehensive reviews on chromatin modeling at the mesoscale and polymer level see [71,124–128]. Here, we focus on recent applications of mesoscopic and polymer models (**Figure 3**).

The Schlick group's mesoscale model for MC sampling of chromatin fibers has evolved as experimental data emerged [72], and applied to simulate fibers in the kb range [71]. Early applications focused on electrostatic mechanisms of folding [64], role of tails [67], and LH and divalent ion-driven compaction [73]. Later, the model helped explain that fibers fold mostly with a zigzag topology and moderate solenoid features, producing a hybrid structure [20]. These zigzag dominant chains further fold to form higher-order hierarchical loops, that are LH-dependent and explain interphase and metaphase folding [19,72,129]. Fiber heterogeneity also emerged from non-uniform linker DNA lengths, which create fluid fibers [20,66,120].

In recent efforts, the role of LH on chromatin architecture, binding of antibodies [130], and nucleosome clutches were investigated. As discussed above, Perišić et al. found that combinations of LH on and off-dyad binding, and LH density produce different levels of compaction, tuning chromatin architecture [68]. The C-terminal domain flexibility and disorder, in particular, appeared modulated by post-translational modifications, which in turn affect chromatin architecture. Yusufova et al. showed that a decrease in LH density produces a chromatin structural transition from a straight/rigid to a globular/loose structure [131], which might be involved in the upregulation of gene expression during lymphoma development. Portillo-Ledesma et al. recently suggested that such a transition occurs at an LH density $\sim$0.5, and is tightly regulated by linker DNA length, epigenetic modifications, and salt conditions [132].

In a recent study by Portillo-Ledesma et al., the formation of nucleosome clutches, or clusters, emerged in chromatin fibers with nucleosome-free regions (NFRs) [15*], in agreement with super-resolution microscopy

studies [11]. Clutch size and compaction appeared regulated by LH density and acetylation levels. Such heterogeneous clusters were also found by Bajpai et al. using a mesoscale chromatin model that considers the implicit binding of non-histone proteins [133].

The role of linker DNA on chromatin architecture was recently studied using the 1CPN chromatin model by the de Pablo group (Leq19 in **Figure 2**) [61], the rigid base pair chromatin model by van Noort [75,76], and the Wedemann chromatin CG modeled [80]. Overall, their results show how the free energy of chromatin assembly and folding/unfolding mechanisms strongly depend on linker DNA length, in agreement with previous findings [66,78].

Recently, Collepardo-Guevara and coworkers' coarse-grained model of 125 independent 12-nucleosome chromatin arrays (300 kb) suggested that nucleosome breathing favors the liquid-liquid phase separation of chromatin due to an increase in the transient nature and heterogeneity of nucleosome−nucleosome contacts (Farr21 in **Figure 2**) [50**]. Sridhar et al. found that the LH-disordered C-terminal domain leads to an asymmetric and dynamical nucleosome conformation, promoting chromatin structural flexibility and long-range hierarchical loops [134].

Several polymer models at nucleosome resolution or coarser have been used to study larger systems, such as domains, chromosomes, or whole genomes. Wiese et al. showed with a nucleosome resolution model that nucleosome spacing in yeast strongly affects domain structure and dictates chromatin interactions and domain boundaries, being the only input parameter needed to reproduce experimental contact maps [135]. The Spakowitz nucleosome-resolution polymer model was used to predict how epigenetic marks control the 3D organization, revealing that binding of HP1 to methylated regions drives the segregation of heterochromatin from euchromatin [136], and that heterochromatin preferentially positions at the nuclear periphery [137].

Polymer models with coarser resolution revealed that chromatin can exist as both a fluid or gel state, depending on the level of TAD compaction [138**]; that cell-to-cell variability on chromatin structure can be explained by phase separation [139]; and that loop extrusion and phase separation mechanisms rather than compete, co-exist to fold chromatin fibers [140**].

Interesting developments of polymer models based on Hi-C data are the MiChroM model by Di Pierro, Wolynes, Onuchic, and collaborators [141] that uses Hi-C to incorporate active and silent chromatin types and loops positions; the Orozco's group whole-genome 3D model [142**], with chromosomes built as chains of beads representing a genomic region corresponding to a bin from the Hi-C map; and the Sanbonmatsu and Lee 4DHiC model [143], that uses harmonic constraints to simulate cross-linking distances. MiChroM has been applied to study the effect of condensin II on genome folding [144**], suggesting that chromosomes separate in territories with condensin, but produce mixed centromere clustering without condensin. The Orozco group's model was used to study the effect of DNA methylation on genome organization, finding that it increases chromatin condensation in peri-centromic regions and favors heterochromatin state [142**].

Finally, in a breakthrough development, the group of Luthey-Schulten created a whole-cell kinetic model of a minimal cell with a reduced genome of 493 genes [145**] in which one circular chromosome of 543 kbp, treated as a self-avoiding polymer, is created from cryo-electron tomograms and 3C maps.

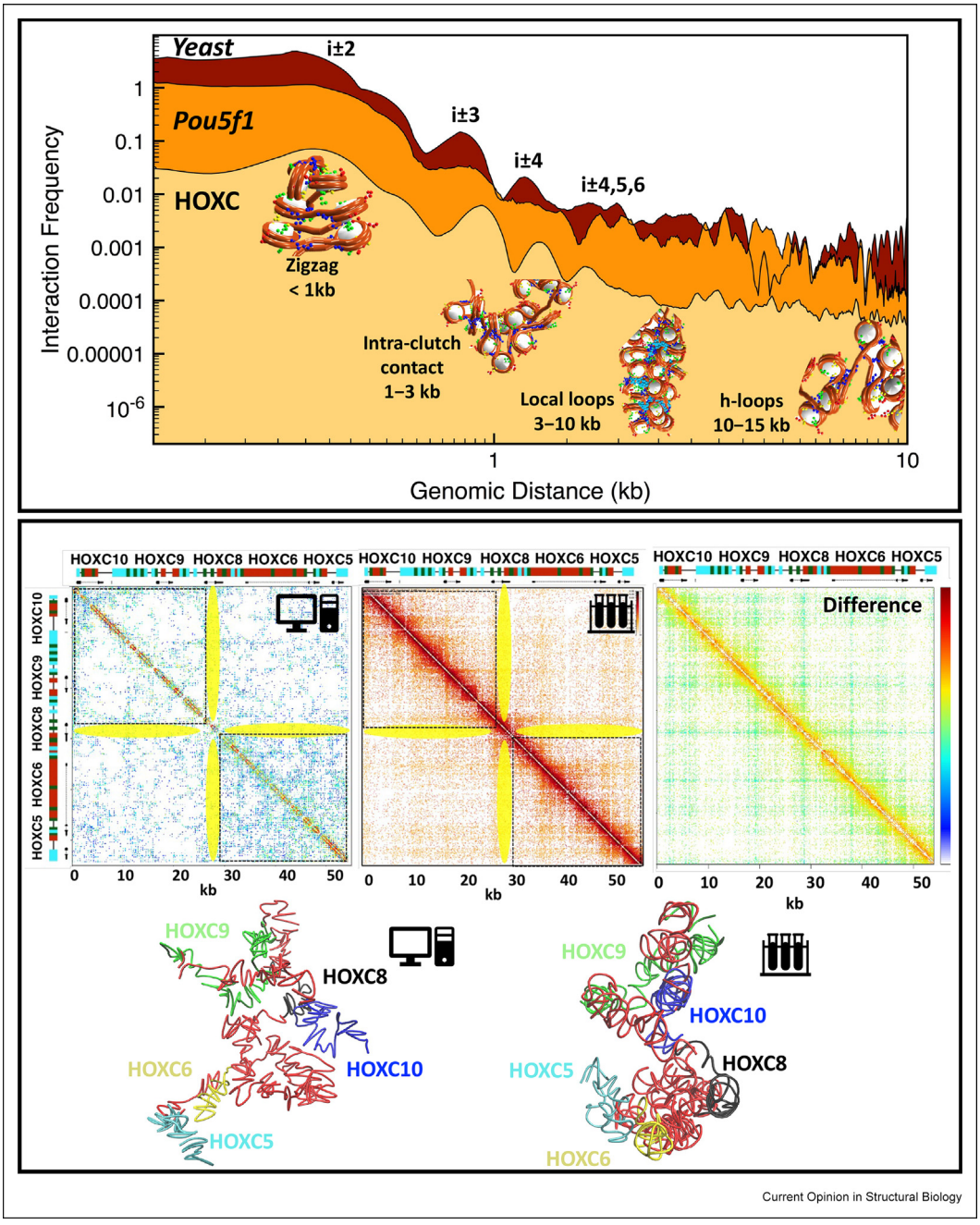
Clearly, these studies of chromatin fibers in the kb or Mb-range by mesoscale and polymer models provide insights into the role of LH and histone tails, formation of nucleosome clutches, fiber assembly and its regulation by nucleosome breathing, chromosome folding, phase separation, and chromosome territories, among others. However, as we discuss below, further efforts are needed to describe the folding of gene loci. In particular, to understand the relationship between genome aberration and disease development, it is important to build high-resolution 3D structures of gene loci that incorporate all the interacting elements and capture large-scale phenomena, such as transitions and domain formation.

Scaling up to genes to interpret gene regulation

To describe how chromatin elements are defined at the gene locus level, different models and input parameters need to be tailored for these important studies to capture physical interactions between genes, promoters, and enhancers, and predict the detailed structure of gene loci and associated mechanisms.

The GATA4 gene locus was first built by a mesoscale model using 3C internucleosome contact data (Bas16 in **Figure 2**) [74]. Five loop restraints mimicked 3C contact data. Although a uniform DNA length of 44 bp and average LH densities of 0, 0.5, and 1 LH per nucleosome were used, the model suggested a gene repression mechanism in which hierarchical looping, produced by the combination of the 5 loops, occludes the transcription start site. This motif involves elevated long-range contacts by the formation of "loops of loops" while maintaining local zigzag geometry, and was identified by modeling combined with crosslinking experiments [19]. Later, the GATA-4 mesoscale model was used to build the first 1 billion atom model of a gene [32].

Figure 4



Conserved structural motifs and life-like folding by in silico gene folding. **Top:** Internucleosome interaction contact frequencies for HOXC [146**], Pou5f1 [13], and yeast 30 kb genome region [149]. Structural peaks are annotated as follows: short-range contacts (<1 kb) measure next-neighbor interactions common in zigzag fibers; contacts in the 1–3 kb range arise from intra-clutch interactions; chromatin loops between neighboring clutches account for 3- to 10-kb contacts; and hierarchical loops [19] account for 10- to 15-kb contacts. **Bottom, left to right**: Computational contact map of the modeled HOXC from [146], experimental Micro-C map of mESC from [148], and the difference map between the computational and experimental maps. The HOXC gene locations are marked alongside the maps, with acetylation and LH-rich regions colored red and turquoise, respectively. Stripe regions are highlighted in yellow. At bottom, from left to right, are the HOXC configurations obtained in [146**] and from the Micro-C map from [148]. For the latter, we created a polymer model of 508 beads (equal to the length of the HOXC region in the Micro C map) corresponding to ~51 kb, and positioned the beads using the nucleosome and DNA beads coordinates in the initial configuration of HOXC in [146**]. Experimental Micro-C interactions from [148] were used directly to form harmonic "bonds" between connected and non-connected beads, the latter 1.5 times longer, similar to Lappala et al. [143]. A cutoff was used to retain major Micro-C interactions. The structure was then energy minimized subject to those harmonic bond restraints. See details in [154].

For a more accurate gene description, the specific positions of nucleosomes, LHs, and epigenetic marks are needed. The folding of the 55-kb HOXC gene locus from the ground up was based on experimental information (Bas19 in **Figure 2**) [146**]. To build the HOXC system, acetylation islands were modeled based on Chip-Seq data, NFRs were identified and positioned using MNase-seq data, nucleosomes were positioned using a linker DNA length distribution obtained from chemical mapping in mouse embryonic stem cells (mESC), and LHs were placed to mimic trends seen in mESC. The simulations revealed how distinct epigenetic features cooperate to form a spontaneous contact hub that bridges promoters in the gene locus and creates two separate domains, an acetylation and LH-rich domain, emphasizing how epigenetic factors are coordinated to influence chromatin architecture. Thus, elements at the nucleosome level, such as tail acetylation and LH binding, stacking of nucleosomes, and kb-range elements like zigzag and hierarchical looping motifs, as well as nucleosome clutches converge into a complex folding (**Figure 4, top**) that cannot easily be generalized at all genomic scales. As commented by Di Pierro, this work advanced the field "*by pushing the resolution of chromatin modeling to a level that allows us to study the inner workings of individual genes*" [147]. This complex folding recapitulates the life-like folding (**Figure 4, bottom**). The calculated contact map resembles the experimental Micro-C map from mESC [148], showing stripes (yellow regions) arising from promoter interactions, and the contacts between the acetylation and LH-rich regions. Moreover, the 3D structure is similar to that obtained from the constrained optimization of a polymer model using experimental interparticle distances from the Micro-C map (see **Figure 4** caption). However, as seen from the difference contact map (**Figure 4, bottom**), some structural features, like other stripes and microdomains close to the diagonal produced from loop extrusion, are not captured; this implies a more open structure compared to the one corresponding to the Micro-C map. Thus, incorporation of structural proteins like CTCF and cohesin is important for capturing all experimental factors and thus gene folding.

This HOXC study served as an inspiration to model other genes. For example, the *Pou5f1* gene was modeled using experimental data to study the formation and regulation of nucleosome clutches during mouse cell differentiation [13]. Similarly, MNase-seq data were used to position nucleosomes, and experimental values were used for LH density and acetylation levels, as found in mESC and neural progenitor cells. Results showed that the *Pou5f1* gene folds into nucleosome clutches, with larger and more compact clutches in differentiated cells than in stem cells, recapitulating experimental results obtained at a genome-wide level [11]. Moreover, these clutch changes appeared accompanied by enhanced hierarchical looping in differentiated cells, providing a mechanistic explanation for the trends found in the experiments. Later, the differential folding in growing and quiescent or non-proliferating yeast cells was studied by modeling a 30 kb region of the yeast genome [149]. MNase-seq data were used to position nucleosomes, and Chip-seq to locate LHs and tail acetylations. Higher tail interactions of H3 and H4 with non-parental nucleosome cores were found in quiescent cells, emerging as a mechanism at the kb-range level for repressing gene expression during quiescence. Moreover, basic folding motifs, such as zigzag topology, clutches, loops, and hierarchical loops observed for HOXC, are also present in the *Pou5f1* and yeast systems (**Figure 4, top**), underscoring common gene folding principles.

Although without nucleosome resolution, polymer models have also been used to simulate gene loci. For example, the Marenduzzo group's polymer HiP-HoP model uses experimental ATAC-seq data for positioning transcription factors and Chip-seq data for cohesin/CTCF and epigenetic marks [56]. Application to the Pax6, globin, and SOX2 loci showed that epigenetic marks recapitulate complex genomic loci in 3D [56]. The Nicodemi SBS model was used to predict the structure of the HoxB locus containing 28 genes by defining the genomic position of CTCF binding sites and gene promoter states based on the presence of RNA polymerase [150]. Later, it was used to study the α-globin locus in embryonic stem cells (Chi20 in **Figure 2**) [58].

Clearly, the genome organization modeling field has advanced over the past few years. Detailed structures of gene loci are now emerging frequently. However, as shown by our comparison of the HOXC computed and experimental contact maps and structures in **Figure 4**, while these studies provide models for studying gene structures, chromatin interacting elements and epigenetic features must be incorporated to fully recapitulate life-like folding. For instance, the combination of DNA CpG methylation, transcription factors, CTCF/cohesin, and LH binding, as well as tail modifications, plays an important role in modulating genome architecture. In addition, inference of folding based on contact maps averaged over heterogeneous cell populations may not translate directly to single gene folding. Advances in both models and experiments and their combination will be important for moving the field forward to achieve higher-resolution views of genes and genome architecture. The recent MiOS approach [151] is a promising combination of super-resolution microscopy and Hi-C data with polymer and coarse-grained modeling in this goal.

Looking ahead

Living chromatin depends on nucleosome density and occupancy, chromatin loops of varied sizes, gene density and orientation, activating marks like histone tail acetylation and remodeling proteins like transcription

factors, repressive marks like DNA methylation, and protein regulators like LH and HP1, folding mechanisms, and compartmentalization.

In this perspective, we have discussed many modeling studies that aim to understand genome folding, from the nucleosome to the chromosome level, and provide insights into the mechanisms that regulate gene expression. While each study considers different chromatin elements and genomic scales, as well as employs different approaches for combining model and simulation technique to reach large system sizes and study specific biophysical phenomena, modeling chromosomes from the ground up has not yet been achieved.

How to create models that allow us to study larger systems without losing resolution is still a work in progress, although some strategies are emerging [50,136**,146**, 151]. Physics-based models are likely necessary to provide mechanistic insights into folding and structural transitions, even though machine learning (ML) approaches may soon allow us to automatically approximate folded gene models from aggregate Hi-C maps (e.g., [141]). Given the spectacular recent success of Deep Mind's Alpha Fold in folding the structures of millions of proteins, there is no doubt artificial intelligence and ML approaches will only increase in the near future, as we recently described in perspectives for the field of biomolecular modeling and simulation [152,153].

Yet, as experimental techniques move toward the single-cell level and nucleosome resolution, biophysical studies with new models benefiting from multidisciplinary collaborations among mathematicians, physicists, chemists, biologists, engineers, and computer scientists will drive genome research further. We thus expect many exciting innovations in the near future, integrating the best of both worlds from physics-based and ML approaches, and separating aggregate cell populations from single-cell structures.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Data availability

Data will be made available on request.

Acknowledgements

This work was supported by the National Institutes of Health (NIH), National Institute of General Medical Sciences, grant MIRA R35-GM122562; National Science Foundation Rapid Award 2030377 and DMS-2151777 from the Division of Mathematical Sciences and Division of Chemistry; and Philip-Morris/Philip-Morris International, awarded to T. Schlick. We thank Jill Hoffman for preparing the Micro-C map image used in Figure 4.

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