



Morphogenesis beyond in vivo

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Abstract

Morphogenetic events during development shape the body plan and establish structural foundations for tissue forms and functions. Acquiring spatiotemporal information of development, especially for humans, is limited by technical and ethical constraints. Thus, both stem cell-based, in vitro development models and theoretical models have been constructed to recapitulate morphogenetic events during development. These in vitro experimental and theoretical models offer accessibility, efficiency and modularity. However, their physiological relevance often remains obscure, owing to their simplistic nature, which obstructs their applicability as faithful and predictive models of natural development. We examine existing in vitro experimental and theoretical models of various developmental events and compare them with the current knowledge of natural development, with particular considerations of biomechanical driving forces and stereotypic morphogenetic features. We highlight state-of-the-art methods used to construct these in vitro models and emphasize the biomechanical and biophysical principles these models have helped unveil. We also discuss challenges faced by the current in vitro experimental and theoretical models, and propose how theoretical modeling and in vitro experimental models should be combined with in vivo studies to advance fundamental understanding of development.

[H1] Introduction

During development, morphogenetic dynamics sculpts distinctive biological forms in animal bodies across species, length and time scales, and settings. Biological forms act together to support fundamental functions of life, such as breathing, moving and digesting. To decipher the mechanical forces that drive stereotypical morphogenetic events during development, substantial work has been conducted on animal models, revealing general mappings between molecular signaling and morphogenetic dynamics. Despite these successes, progress with animal studies remains constrained by the limited accessibility of spatiotemporal information in animal models, which obstructs detailed understanding of how biological signals are transduced into biophysical stimuli to shape tissue morphologies. From a pragmatic perspective, there are also uncertainties in applying animal-based knowledge for understanding human congenital disorders, owing to interspecies variations of morphogenetic dynamics. Furthermore, knowledge remains limited about how self-organization of morphogenetic cues and tissue forms can feedback to developmental signaling and cell–cell communication. Such signaling crosstalk is known to be important for controlling patterning networks to ensure the robustness and precision of development.

Beyond animal models, recent progress on development modeling based on in vitro-cultured stem cells, especially pluripotent stem cells (PSCs), provides an alternative tool to study development. These stem cell-based in vitro models generate multicellular entities that recapitulate cell lineage diversification, patterning and morphogenesis manifested in early embryonic development and organogenesis. Thus, stem cell-based models provide promising tools to study how endogenous and exogenous signals orchestrate tissue development¹⁻⁴. In parallel, theoretical and in silico models have also been constructed to rationalize morphogenetic principles.

In this Review, by juxtaposing canonical development knowledge, stem cell-based models and theoretical analysis for some representative morphogenetic processes, we argue that a conjugation between high-fidelity in vitro models and theoretical study can advance understanding of morphogenesis with quantitative specificity, for both topological and conformational morphogenesis. In particular, stem cell-based models possess modulability, which can be further consolidated by a spectrum of bioengineering tools, and are thus ideal for interrogating how endogenous scales, exogenous stimuli and boundary conditions participate in morphogenesis. We further discuss some fundamental obstacles and challenges for in vitro development modeling, from both conceptual and technical perspectives. We envision that future studies of morphogenesis should go both in vivo and beyond.

[H1] Topological morphogenesis

The intricate topologies of an animal body constitute its structural basis for essential biochemical, biophysical and biomechanical processes and functionalities. For example, cavities enable substance exchange and transportation, and joints in the skeleton facilitate motion. Three representative morphogenetic events that alter embryo topology during early development are lumenogenesis, through which tissues generate internal boundaries, segmentation, through which tissues split apart, and folding, through which tissues deform and fuse boundaries (**Fig. 1**). These processes are driven by both bulk and interfacial behaviors at both tissue and cellular scales.

[H2] Lumenogenesis

Lumenogenesis is a fundamental, cavity-generating morphogenetic process that delaminates intercellular interfaces and generates a fluid-filled  lumen **[G]**⁵. Lumenogenesis has been shown to be mediated by various mechanisms, such as hydraulic fracturing and coarsening during blastocoel **[G]** formation⁶ and mesenchymal-to-epithelial transition **[G]** (MET) during secondary neurulation **[G]**⁷. In this Review we focus on lumenogenesis of peri-implantation epiblast **[G]**, leading to amniotic cavity formation (**Fig. 1A**). Mouse studies show that both apical constriction and integrin signaling from the basal membrane are required to drive epiblast cells to undergo polarization and reorganize into a rosette-like structure with a nascent central cavity⁸⁻¹⁰. As lumenogenesis progresses, E-cadherin is removed from apical surfaces of the epiblast through endocytosis and replaced by CD34 family antiadhesins; this process reduces intercellular adhesion and facilitates cell membrane separation. In addition, epiblast cell proliferation generates intermembranous pockets at the cleavage furrow **[G]**, which fuse with the central lumen, further increasing lumen volume and propelling its expansion.⁹ Increasing embryo size has also been reported to induce apoptosis-associated formation of multi-layered and multi-lumen epiblast compartment, suggesting a size dependence in both morphology and mechanism of lumen regulation¹¹.

Epiblast lumenogenesis has been reconstituted through culturing mouse pluripotent stem cell (mPSC) aggregates in 3D Matrigel cultures (**Fig. 1A**)⁸⁻¹¹. Lumenogenic mechanisms acting in vivo appear to operate in mPSC-based epiblast models⁸⁻¹¹. In addition, an osmotic pressure gradient generated by ion pumps at the center of mPSC aggregates seems to drive lumen expansion⁹. Similar epiblast development models showing lumenogenic dynamics have also been generated using human pluripotent stem cells (hPSCs), with the lumenogenic dynamics promoted by actin polymerization but inhibited by actin contraction¹². Formation and trafficking of a subcellular structure, termed apicosome, in hPSC-based epiblast models is proposed to promote cell polarization and central lumen formation^{13,14}. Mechanical factors such as aggregate size^{11,15} and matrix mechanics^{16,17} also modulate

lumen structure and amniotic differentiation in hPSC-based epiblast development models. It remains to be explored how the location and number of lumen nucleation sites are determined within an originally amorphous epiblast or PSC cluster. This question can in principle be studied by modulating geometries of PSC-based epiblast models through bioengineering approaches.

As shown in both animal and in vitro models, epiblast lumenogenesis involves a range of cellular machineries. To regularize lumenogenic dynamics, a unified theory that integrates different mechanisms is necessary. Towards this goal, a minimalistic theory has been developed that considers both cross-membrane and paracellular transport of ions and water, highlighting the importance of pumping activities¹⁸. In another agent-based in silico model, reduced adhesion and apical repulsion at the center of epiblast compartment appear essential for lumenogenesis¹⁹. Because of the variety of mechanisms involved, an accurate account for all biophysical factors that nucleate nascent lumens and promote their expansions is non-trivial, and can benefit from quantitative characterizations on stem cell-based lumenogenesis models. Future theoretical efforts are needed to fully incorporate both subcellular mechanisms and cellular reorganization during lumenogenesis, a multiscale endeavor.

[H2] Segmentation

One of the most prominent topological features of the vertebrate musculoskeletal system is the segmentation of vertebrae by interfaces. Segmented topology of the vertebrae can be traced back to the process of somite **[G]** formation, known as somitogenesis, during embryonic development (**Fig. 1B**). Somites develop from a sequential and cyclic rostral **[G]** (R)-to-caudal **[G]** (C) segmentation process. During somitogenesis, somitic cells at the rostral presomitic mesoderm (PSM) reorganize into an epithelial rosette-like somite through MET, regulated by genetic factors, such as *TCF15*^{20,21} and *PAX3*²², and intracellular signaling molecules, such as small GTPases^{23,24}. The forming somite contracts and delaminates from the rostral PSM through a ball-and-socket separation²⁵.

In a conceptual clock-and-wavefront model, the periodicity of somite formation is attributed to a molecular oscillator, termed segmentation clock, in PSM cells. Somite size is regulated by C-to-R gradients of morphogens such as FGF8^{26,27}. The FGF8 gradient travels caudally during each segmentation clock period, and rostral PSM cells that experience FGF8 levels lower than a critical value (the ‘wavefront’ of the clock-and-wavefront model) initiate MET and form a rosette-like structure.²⁸ Animal models have provided finer molecular details of the clock-and-wavefront model. For example, in the zebrafish the segmentation clock periodically and locally inhibits Fgf/ppERK signaling and thereby dynamically modulates its relative slope to control the spatiotemporal segmentation process²⁹. Apart from intracellular developmental signals, mechanical signals such as

external strain and surface tension also regulate boundary formation³⁰, length and left–right symmetry of somites³¹.

Studying somitogenesis requires detailed spatiotemporal information of trunk development, which is challenging to obtain using mammalian animal models. To date, it remains elusive how upstream signaling dynamics is translated into MET-associated regulators and ultimately leads to new somite boundary formation. Other questions that remain incompletely understood include the origin of drastic interspecies differences in the number of somites and thus vertebrae, and the causes of somite segmentation anomaly that leads to congenital vertebral defects^{32–34}.

Stem cell-based in vitro models have been developed to recapitulate somitogenesis (**Fig. 1B**).^{35–39} In these models, clusters of hPSCs embedded in 3D Matrigel undergo symmetry breaking and establish a R–C axis along which various somitogenesis-related dynamic events are recapitulated, including somite boundary formation, traveling waves of the oscillatory segmentation clock, spatially patterned lineage specification, and axial elongation^{36–39}. Extracellular matrix and its concentration are shown to modulate the expression of genes associated with somite epithelialization³⁸ and structure³⁶. Interaction between FGF activity and the segmentation clock is also observed in these models³⁹. However, both segmented³⁷ and unsegmented³⁸ morphologies of somitic cells are reported in somitogenesis models from *HES7*-knockout hPSC lines (*HES7* is a segmentation clock gene). Furthermore, in vivo, the PSM tissue and forming somites experience mechanical confinement by neighboring tissues, a phenomenon which is absent in current in vitro models. Engineering mechanical boundaries in somitogenesis models might help reveal intrinsic biophysical determinants in somitogenesis.

Theoretical models have been established to describe the synchronization⁴⁰, mechanosensitivity⁴¹ and clock-and-wavefront mechanism⁴² of the segmentation clock. The periodic segmentation and lineage patterning dynamics are also recapitulated in silico, based on differential adhesion⁴³ and apical tension⁴⁴ mechanisms. In the differential adhesion model, a developing rosette-like structure forms from somitic cells due to mechanical repulsion between somitic cells and PSM cells, despite a lack of explicit modeling of epithelialization and reorganization of somitic cells in the forming somite⁴³. In the apical tension model, apical constriction pulls epithelializing somitic cells away from the PSM and thus generates a new somite boundary.⁴⁴ In both models, mechanical interactions within the somite–PSM system drives new somite boundary formation and thus shares certain physical similarities with fracture in solids and the Plateau–Rayleigh instability of fluids.

Since there is limited knowledge about how intracellular signaling dynamics instructs somite boundary formation during somitogenesis, most theoretical models require empirical hypotheses and parameters to generate mechanical driving forces and induce somite boundary formation. These

limitations can now be addressed by leveraging the accessibility of stem cell-based somitogenesis models. For example, cell sorting observed in stem cell-based somitogenesis models³⁷ can be incorporated by theoretical models as a driving force for somite compartmentalization. Dynamic gene expression associated with the segmentation clock and formation of somite can also be quantified in stem cell-based somitogenesis models and compared with theoretical predictions.

[H2] Folding

During development, the embryo undergoes various folding dynamics by deforming and fusing boundaries to form cavities and thereby establish primordial organs such as the neural tube [G]. Neural tube is the embryonic precursor to the central nervous system. Following gastrulation [G], the embryonic ectoderm undergoes neural induction, giving rise to the neural plate [G] at the dorsal [G] midline abutted by non-neuroectoderm tissues. Subsequently, the embryo initiates convergent extension, with the embryo body elongating along the R–C axis and shrinking along the medial [G]–lateral [G] axis, resulting in a reduction of the distance between the two lateral edges of the neural plate and thus facilitating its folding and closure process (**Fig. 1C**). Driven by cell shape change^{45,46}, cytoskeletal dynamics⁴⁷ and mechanical forces from adjacent non-neuroectoderm tissues, the neural plate starts bending, with its lateral edges elevating and creating neural folds. In mammals, bending of the neural plate occurs at specific locations in the neural plate, termed medial and dorsolateral hinge points. At these hinge points, the neural plate is anchored to adjacent tissues: the medial hinge point is anchored to the prechordal plate mesoderm and notochord, and dorsolateral hinge points are anchored to adjacent surface ectoderm of the neural folds. Thus, hinge points stabilize the neural plate during bending. As the opposing neural folds meet on the dorsal midline, they fuse progressively and form the neural tube. Defective folding of the neural tube leads to neural tube defects (NTD), one of the most common congenital anomalies⁴⁸. To date, mechanical driving forces underlying the bending and closure of the neural plate — and the biological origin of these forces — remain debated, due to complexities in cellular mechanisms, boundary conditions and spatial heterogeneity.

Neural development models have been successfully developed based on 2D microprinted hPSC colonies, in which spatially organized neural induction and folding morphogenesis are induced. (**Fig. 1C**)^{49,50}. Geometric confinement by non-neural epithelial tissues in these models induces folding dynamics of neuroectoderm tissues⁴⁹. Greater neuroectoderm tissue size seems to hinder its folding and closure⁴⁹, supporting the importance of convergent extension of the embryo prior to neural plate folding in vivo. Defective neural plate folding occurs when either anencephaly [G] patient derived-PSCs⁵⁰ or NTD-related chemical drugs^{49,50} are used in these models. How to establish in vivo-relevant

boundary conditions such as mechanical interactions with neighboring tissues remains an open challenge for modeling the folding and enclosure dynamics of the neural plate.

Theoretical and computational models have been developed to rationalize topology-defining dynamics of neural tube formation. Discretized models⁵¹⁻⁵³, including vertex models^{53,54}, which are usually 2D, simulate the neural plate as an assembly of cell-representing elements governed by specific rules that dictate their shape, motion and force generation. Such discretized models are thus compatible with multiscale modeling. In discretized models, cells in the neuroectoderm gradually adopt a wedged or trapezoidal shape due to apical constriction, leading to dorsal bending of the neuroectoderm. However, from these discretized setups, it remains challenging to study why and how bending deformation localizes and gives rise to hinge points. The large number of parameters of these models impose additional challenges in justifying necessary assumptions and extracting principal factors.

Continuum models of neural tube formation have also been developed⁵⁵⁻⁵⁷ by abstracting cellular driving forces as intrinsic curvature, active tension and inelastic strain within the neuroectoderm. Tissue elasticity, conversely, resists folding of the neuroectoderm, owing to strain energy. Continuum models of tissue morphogenesis, in general, require inputs such as tissue stiffness, cell contractility and geometry, which can be obtained through either experimental characterization or coarse-graining of discretized models. In continuum models of neural tube formation, extrinsic forces from neighboring tissues are shown to mediate hinge point emergence and bending of the neural plate⁵⁵. Disrupted cellular force generation and tissue geometry are also confirmed in continuum models to cause neural tube closure failure⁵⁸. However, a notable difficulty in continuum models is the question of how to connect constitutive laws and parameters (especially those related to driving forces of folding) with experimentally identifiable cellular and subcellular machineries and regulatory pathways involved in tissue morphogenesis.

For both discretized and continuum modeling methods, future efforts are desired to directly connect modeling components and parameters with molecular and cellular machineries that can be perturbed either for prediction validations or identifications of potential therapeutic targets for medical intervention of NTD.

[H1] Conformational morphogenesis

During development, tissues and organs acquire their intricate conformational features, such as surface topography and aspect ratio, to define their apparent geometry and cell mass distribution. Development of such conformational features of tissues and organs often involves spatially heterogeneous and anisotropic

growth and remodeling, either at tissue surfaces or within their volumes. These conformational features are closely linked to organ functions, as exemplified by the crypt-villus morphology of the intestine, which is important for its absorptive function. A few typical conformational morphogenetic processes include wrinkling, in which tissue mass localizes quasi-periodically, branching, in which mass growth is restricted on selected sites, and axial elongation, in which mass accumulation concentrates unidirectionally within a single region. These processes all involve spatial patterns of both developmental signaling and mechanics and likely their interactions (**Fig. 2**).

[H2] Wrinkling

The intestine adopts a wrinkled crypt-villus morphology on its interior surface, with finger-like structures (villi) protruding into the intestinal lumen and flask-like structures (crypts) between the villi. This morphology effectively increases the intestine's surface area more than 10-fold⁵⁹ and serves as a mechanical basis of its absorptive function. Villus morphogenesis initiates during early intestinal development and arises from biomechanical and biochemical interactions between tissue layers lining the intestinal lumen. In chick embryos, the villus morphology is shaped by elastic mechanical instabilities during midgut development, which arise from differential growths between the epithelium–mesenchyme composite and its surrounding smooth muscle layer⁶⁰. The villus morphology of the intestine further leads to local maxima of epithelial signals such as Shh at villus tips, which restrict intestinal stem cell distribution to the base of each villus⁶¹.

However, in mouse embryos, neither the smooth muscle layer per se nor its confinement force is required for villus formation in the intestine⁶². Signaling molecules including Hedgehog (Hh)^{63,64} and platelet derived growth factor (Pdgf)⁶⁵ secreted by pseudostratified intestinal epithelium, and bone morphogenetic protein (Bmp)⁶² secreted by mesenchyme around the intestinal epithelium have been shown to drive mesenchymal cells to proliferate and form localized cell clusters, which might push overlying intestinal epithelium locally towards the lumen center and thus generate villi (**Fig. 2A**). However, it remains undetermined whether and how local clustering of mesenchymal cells leads to sufficient local mechanical forces for villus formation and whether a feedback loop exists between localized epithelial curvature and mesenchymal proliferation and aggregation. Given the notable interspecies differences in villus morphogenesis dynamics, it remains unclear whether similar phenomena occur during human intestine development^{66,67}.

After villus morphogenesis, crypts start to emerge between villi. Myosin II-dependent apical constriction leads to invagination of inter-villus epithelium, whereas subsequent basal constrictions on cells between villi and nascent crypts form hinges and thereby compartmentalize the crypts⁶⁸. The

intricate coupling between biochemical signals and cell mechanics that coordinates crypt-villus patterning and morphogenesis remains to be fully elucidated.

hPSC-based in vitro models have been successfully developed to recapitulate lineage specification and morphology of early-stage intestine development⁶⁹⁻⁷¹. Embedded in 3D cultures, hPSC-derived small intestine organoids show a pseudostratified epithelium surrounded by mesenchyme, which later acquires villus-like involutions that protrude into organoid lumens⁶⁹. Mesenchyme-free intestinal organoids could also be developed from hPSCs, but without obvious villus morphology⁷⁰. Mouse intestinal stem cells have also been used for organoid development with crypt formation (**Fig. 2A**)⁷²⁻⁷⁵. In mouse intestinal organoids, as in mice, myosin II-induced apical constriction, leading to local wedge-like cell shape, promotes crypt invagination⁷²⁻⁷⁴. Crypt invagination in mouse intestinal organoids occurs simultaneously with local cell fate specification events⁷³. Additionally, lumen volume reduction driven by osmotic gradient and transcellular water transport appears to promote crypt morphogenesis in mouse intestinal organoids⁷². Cell migration from crypts to villus regions, which contributes to gut epithelial renewal⁷⁶, seems to be controlled by a tension gradient around crypt boundary. However, mouse intestinal organoids could develop crypt-villus structures without a mesenchymal niche⁷⁷, despite theoretical models based on in vivo studies that ascribe villus morphogenesis to the formation of mesenchyme clusters. It will be important for future hPSC-based intestinal organoids to control and manipulate epithelium–mesenchyme interactions and examine whether morphogenetic mechanisms known to function in animal intestine development would still operate in the context of human development.

Villus morphogenesis in chick embryos has been theoretically formulated as a minimization of elastic strain energy for gut tissues under differential growth. In this theoretical model the differential growth initiates wrinkling instabilities and successfully produces lumen surface topographies at different chick embryo development stages^{60,78-81}. In contrast, murine villus morphogenesis is postulated as a Turing system in which Bmp ligands and their inhibitors develop spatial patterns via a Turing mechanism, and the Bmp pattern further drives chemotaxis and thus clustering of mesenchyme cells⁶².

Crypt morphogenesis has also been computationally modeled with both continuum^{79,81} and cell-based⁸²⁻⁸⁴ methods. It has been shown that cell proliferation, contraction and shape change could lead to local invagination and produce a crypt-like structure by deforming the epithelium^{79,81,83}. In continuum models, mechanical instability is treated as the major contributor for crypt morphology, whereas cell-based models include additional considerations of cell fate patterning, which generates localized deformation through lineage-dependent cell shape and behavior changes. Nevertheless, more biological specificity is required before juxtaposing such computational results with

experimental observations⁸⁵. Cell lineage specification and distribution have also been mathematically modeled⁸², and stem cell division in crypts is shown to minimize the time for crypt development⁸⁴.

Together, the coupling between mechanical morphogenesis, biochemical signaling and lineage patterning is still a major challenge in theoretical and computational modeling of crypt-villus morphogenesis. Signaling activity can spatially mediate cell behaviors such as contraction, proliferation and shape variation, and thus drive mechanical deformation. Reciprocally, tissue morphology and mechanics can in turn affect distributions and patterns of signaling activities. Therefore, it is necessary to simultaneously account for the biophysical and biochemical interactions between neighboring cells and tissues and explicitly address interspecies differences, in order to fully elucidate morphogenetic forces that shape the crypt-villus morphology in the intestine.

[H2] Branching

Branching morphogenesis is a ubiquitous process shared across plant and animal species. For example, it shapes the lung by establishing a fractal tree-like airway network to enable efficient air transport and exchange. Following the first branching bifurcation of the respiratory diverticulum **[G]**, which gives rise to two primary lung buds, airway branching morphogenesis continues until well into childhood and generates 300–400 million alveoli **[G]** in each mature lung⁸⁶.

At its early stage, the mammalian lung consists of an epithelium and an encasing pulmonary mesenchyme into which the epithelium branches. Patterns of branching *in vivo* have been classified either as domain branching, in which daughter branches develop in rows along the length of a parent branch, or bifurcations, in which daughter branches form on the tip of a parent branch⁸⁷. Signaling molecules and regulatory networks involved in lung branching have been studied extensively⁸⁸⁻⁹¹, and morphogens such as Fgf10, which drives lung bud growth, and Shh, a regulator of Fgf10, have been identified.

However, physical regulation of branching morphogenesis is less understood⁹². It has been shown in *ex vivo* models that a stereotypical pattern of airway smooth muscle derived from the mesenchyme at budding sites is necessary for shaping both domain branching and bifurcation, by driving the epithelium to grow only in branching directions (**Fig. 2B**)^{93,94}. Branching has also been observed for mesenchyme-free lung epithelium treated with Fgf10⁹⁵, suggesting an innate self-organizing property in lung epithelium for branching dynamics. Localized Fgf10 expression, however, has been shown dispensable for lung branching morphogenesis⁹⁶. Together, given these seemingly contradictory observations, it remains unclear how the biophysical and biochemical signals from the lung epithelium and mesenchyme and their interactions control the location and pattern of

branching sites and the number of daughter branches, and mediate their orientations after their budding.

Lung bud organoids have been derived from hPSCs to mimic early lung development with branching morphogenesis (**Fig. 2B**)⁹⁷⁻¹⁰⁰. Embedded in 3D cultures and supplemented with signaling molecules including FGFs, endodermal cells derived from hPSC clusters rapidly expand and form branching tree architectures with a minimal presence of mesenchymal cells⁹⁷, consistent with an innate branching potential in early lung epithelium. Lung bud organoids have been used for modeling diseases^{97,99} such as Hermansky–Pudlak syndrome. Although lung bud organoids do not mature in vitro, they still represent useful experimental tools to investigate early-stage airway branching development. However, efforts are needed to improve the fidelity of in vitro models, as some lung bud organoids do not produce branching morphology at all¹⁰¹⁻¹⁰³.

Various theoretical formulations have been proposed to account for branching morphogenesis. Based on the premise that branch growth pattern can be instructed by localized biochemical signaling, Turing models, in which interactions between diffusible Fgf / Shh molecules lead to patterned Fgf10 activities, have been employed to compute spatial patterns of signaling activities on the surface of a lung bud and thereby predict branch outgrowth sites^{104,105}. Nevertheless, no bi-directional coupling between signaling activities and mechanical growth has been established. It is thus unclear whether a feedback loop exists between signaling localization and growth-induced curvature.

Mechanical interpretations of branching morphogenesis have also been proposed by drawing analogies between airway branching and mechanical instabilities such as buckling¹⁰⁶, which attributes branching morphology to mechanical instability generated by the growth of lung epithelium and the confining microenvironment, and provides a viable explanation for mesenchyme-free branching. Stochastic modeling has also been adopted to analyze spatial branching morphologies, revealing that neighboring duct density might promote branching termination by inhibiting tip growth and suggesting the existence of competing interactions between neighboring branches¹⁰⁷. To date, most theoretical modeling efforts attempt to rationalize branching morphogenesis through a single source of physical driving force, yet the complex and seemingly contradictory experimental observations suggest the existence of a multilayered regulatory network — potentially with redundant or interacting components — contributing to branching patterns.

[H2] Axial elongation

Early vertebrate development entails an axial elongation along the R–C axis, involving coordination of different developmental events, such as maintenance of a progenitor domain, cell proliferation, and

cell motility. After primary neurulation, a major contributor to caudal axial elongation of the embryo body comes from a pool of proliferative neuromesodermal progenitor **[G]** (NMP) cells, the maintenance of which requires both WNT and FGF signaling¹⁰⁸⁻¹¹⁴. NMP cells are bipotent and can both contribute to caudal spinal cord development and thereby drive its elongation, as well as give rise to highly motile caudal PSM cells. Motility of each PSM cell appears unoriented but shows a C-to-R (high-to-low) gradient, which is thought to cause unidirectional tissue growth, in analogy to particle diffusion under a temperature gradient (**Fig. 2C**)¹¹⁵. Interestingly, a gradient in mechanical property, from the fluid-like caudal PSM to solid-like rostral PSM, is also reported.¹¹⁶ Moreover, mechanical interactions, including compression between axial tissues and PSM, and pushing force exerted by axial tissues on caudal NMP progenitor domain, are shown to coordinate the elongation of axial tissues and PSM (**Fig. 2C**)¹¹⁷. Nonetheless, specific factors that control the rate and duration of axial elongation and therefore the body length of embryo are still unclear. How the progenies of NMP cells contribute to the development of caudal spinal cord and PSM cells in the context of human development also remains an open question. Addressing these questions requires quantitative information about the biophysical environment of NMP cells and their activities at the cellular level, which in turn requires lineage tracing and biomechanical characterization of *in vivo* tissues.

Axial elongation has been shown in many PSC-based embryoids, including gastruloids¹¹⁸⁻¹²⁰, trunk-like structures¹²¹, somite models^{36-39,122} and neural tube organoids (**Fig. 2C**)¹²³. These embryoid systems predominantly adopt gel embedding and WNT activation in their protocols, with a NMP progenitor domain localized at the elongating end, confirming its pivotal role in axial elongation. As axial elongation proceeds, the R–C axes of the embryoids are established with patterned HOX gene expression. Genetic perturbation of *TBXT*, a marker of mesodermal lineage, disrupts unidirectional elongation and caudal fate specification in neural tube organoids¹²³, consistent with mouse mutants in which *TBXT*-knockout leads to defective trunk morphogenesis^{124,125}. Given the compatibility of embryoids with live imaging, they can be used for quantitative tracking of cell proliferation, motion and organization during axial elongation. Embryoids with both neural tube-like and somite-like structures are also valuable for investigating lineage bifurcation of NMP cells. The amenability of embryoids for mechanical characterizations further facilitates extraction of mechanical parameters and studies of mechanical interactions between different elongating tissues and migrating cells.

Theoretical and computational models have been constructed to understand axial elongation of vertebrate embryos. By modeling PSM cells as Brownian particles with random motility, it is suggested that geometric confinement together with PSM cell addition from the NMP compartment can physically promote axial elongation¹²⁶. To investigate the mechanical implications of caudal Wnt signaling, tailbud cells are also modeled as self-propelled particles. It is suggested that a reduction in

cell flow coherence caused by disrupted Wnt activity could lead to cell jamming in the tailbud and thus defective elongation¹²⁷. Nevertheless, more theoretical modeling efforts are required to understand axial elongation. For example, the synergistic elongation of different caudal tissues such as spinal cord and PSM is orchestrated by cell activities and tissue–tissue interactions at the extending front. Understanding these requires considering the caudal architecture of the elongating embryo. Furthermore, coordination between local biochemical signaling and cellular behaviors also needs to be established to quantitatively recapitulate their dynamic coupling.

[H1] Deconstructing morphogenesis

Morphogenesis of a developing embryo is a highly self-regulated process in which each step is meticulously and stereotypically controlled, suggesting the existence of well-curated governing principles in each tissue to ensure their correct morphologies. In examination of morphogenesis within an individual tissue, herein we deconstruct the principles into three principal aspects, namely endogenous scales embedded in a morphing system, exogenous stimuli superimposed over tissue body, and boundary conditions enforced by the extracellular environment or neighboring tissues (**Fig. 3**). If tissue morphogenesis can be rationalized as a mathematical system $\mathcal{D}[u] = f$, in which u denotes the state of a morphing tissue, the endogenous scales effectively characterize the operator $\mathcal{D}$ that describes interactions within the tissue. Exogenous stimuli instantiate f which depicts the background signals distributing inside the tissue domain, in analogy to the body force in a mechanical system or the distributive source or sink in a diffusion system. Together with boundary conditions acting on tissue peripheries, these factors form a closed system through which tissue morphogenetic dynamics can be quantitatively studied. Note that initial conditions are excluded from discussions in this section because they arise from either preceding developmental processes or artificial system setups and thus do not pertain to morphogenesis-governing cellular or tissue mechanisms.

[H2] Endogenous scales

Arising from interactions among resident cells within each tissue, endogenous scales depict the most fundamental driving force for their self-organization. As a regulatory mechanism for morphogenesis, upstream biological activities such as gene expression first lead to spatial patterns of intercellular activities, which are further translated into local mechanical activities of cells such as proliferation, contractility and changes in cell shape or mechanical properties. Mechanical activities of cells then provide physical driving forces to deform tissues and thereby shape their morphology. Through this process, two sets of endogenous scales would emerge, one associated with signaling activities and the

other associated with mechanics, which are interconnected through mechano-transduction¹²⁸.

Endogenous scales include intrinsic length and time scales and show correlations with cell or tissue characteristics such as physical properties, geometries, and dimensions, usually through certain scaling laws. The relevance and significance of these spatiotemporal scales can also depend on the system hierarchy of interest.

Spatial and temporal scales induced by biological signaling, driven by interaction and transport of soluble factors, depend not only on tissue geometry and physical properties such as transport rates, but also on interactions between cells and signaling molecules and the structure of signaling regulatory network (**Fig. 3A**). If the signaling mechanism involves two species of counter-interacting molecules, namely an activator with low transport rate and an inhibitor with high transport rate, the activator tends to accumulate locally and thus generates a heterogeneous pattern called a Turing pattern, which has been theoretically studied and reviewed extensively¹²⁹⁻¹³¹. As a reaction–diffusion model, the Turing mechanism introduces intrinsic length scales such as the ratio between diffusivity and reactivity. Such intrinsic length in zebrafish germ layers is reported to be scalable with tissue dimension, rather than a constant, to ensure a proportional embryo pattern and normal development¹³². Therefore, extended Turing and reaction–diffusion models have been developed to investigate the emergence of robust size-insensitive patterning¹³²⁻¹³⁴. Turing patterns are associated with a variety of pattern formation in biological structures such as seashells¹³⁵, fish skin¹³⁶, and fingerprints¹³⁷, and is conceived as a governing mechanism of many spatially repetitive morphogenetic events such as villification⁶² and branching¹³⁸. Differential signaling behaviors between cells on tissue boundaries and those in bulk also introduce a length scale. For example, BMP signaling is restricted to border cells in mouse epiblast development due to BMP receptor localization on their basolateral surfaces¹³⁹, which leads to an edge-sensing length scale. Signaling activities can also result in time scales. For example, the rates of molecular regulation at the cellular level may provide a temporal pace for cellular activity, whereas the rates of long-range signaling interaction, such as molecular transport and degradation, could introduce characteristic time scales at the tissue level. The leading difficulties in justifying signaling-induced scales, however, include identifying associated signaling molecules and their interactions, quantifying their biophysical and biochemical parameters such as intercellular transport rates and intracellular regulation, and elucidating emerging crosstalk between signaling activities from different sources across different scales, which require experimental models accessible for both genetic manipulation and high-resolution live imaging.

Mechanical scaling, which describes the transition from mechanical driving forces to tissue shape, is sensitive to tissue mechanical properties and geometries (**Fig. 3A**). Within a mechanically stimulated biological body, mechanical energy is generated both on the surface, characterized by

properties such as surface energy, and in the bulk, characterized by properties such as modulus or viscosity. The ratios between surface and bulk quantities naturally define some length or time scales related to processes involved in topological boundary formation such as segmentation³¹ or fracture in biological structures¹⁴⁰. When polarized cells adopt a wedge-like shape, as in neural plate folding^{45,46} and intestinal crypt invagination⁶⁸, an intrinsic curvature and therefore a length scale are activated. If elastic instabilities are triggered, tissue mechanical properties together with tissue dimensions would introduce a characteristic wavelength into the system. A common scenario where this length scale dominates is differential or inhomogeneous tissue growth, exemplified by villus formation in chick intestine⁶⁰ and looping of chick gut tube¹⁴¹. Together these length scales describe how cells are spatiotemporally displaced and sculpt tissue structures. The major difficulty in examining these underlying scales is in identifying the corresponding driving forces, which requires visualization of dynamic cellular behaviors at the single-cell resolution and biomechanical perturbations and characterizations in situ. Implementing these experimental methodologies on mammalian embryos in vivo remains a significant challenge.

Compared to their in vivo counterparts, embryoids and organoids usually provide superior manipulability and therefore stand out as promising systems to probe endogenous scales (**Fig. 3A**). With tissue dimension being an easily controllable parameter, size effects have been demonstrated on lineage development trajectory¹⁴² and morphogenesis in embryoids and organoids (such as epiblast lumenogenesis, neural tube closure and intestinal crypt formation)^{11,49,72}. With regard to signaling-driven scales, a BMP-stimulated spatial pattern of hPSC differentiation, as a 2D model of human gastrulation, has been demonstrated to occur through a reaction-diffusion mechanism¹⁴³. Furthermore, using the same system, the edge-sensing length scale of BMP signaling can be mathematically modeled with a diffusion theory^{139,144}. Similarly, cell mechanics has been shown to induce an edge-sensing length scale in a hPSC-derived neuroectoderm patterning model¹⁴⁵. As another example of mechanics-induced scaling, biomechanical characterizations and theoretical analyses of mouse intestinal organoids reveal basic mechanical scaling laws between crypt morphology and geometric parameters of intestinal lumen such as spontaneous curvature, lumen volume and tissue thickness⁷². In terms of time scale, dynamics of the segmentation clock has been recapitulated and quantified across different species using species-specific PSCs¹⁴⁶⁻¹⁵⁰. Interspecies difference in segmentation clock period appears to correlate with biochemical reaction rates¹⁴⁸ and thus metabolic rates¹⁴⁶ and ultimately the embryogenesis timespan¹⁴⁷, which may provide hints about the fundamental timescale governing embryo development. However, the physiological relevance of endogenous scales embedded in in vitro models, which can be sensitive to the model architecture, is yet to be determined. It will be of interest for future work to elucidate the conditions for each scale to be

dominant through theoretical modeling, targeted modulations of in vitro models, quantitative comparisons between in vitro and in vivo phenotypes, and as such demonstrate the applicability of endogenous scales derived in vitro.

[H2] Exogenous stimuli

Exogenous stimuli such as extrinsic morphogens or mechanical cues can also instruct morphogenesis (**Fig. 3B**). In developing embryos, morphogens are synthesized by specialized cells or tissues within specific regions, generating spatial morphogen gradients in their environments through transport^{151,152}. Morphogen gradients essentially provide a coordinate system with length scales to instruct spatially informed cell lineage development and morphogenetic movements through its slope and local intensity, which is also referred to as positional information¹⁵³. For example, WNT and FGF signals generated at the embryo caudal tail bud result in C-to-R gradients of these potent developmental signals^{108,154}. In parallel, somites in the trunk synthesize retinoic acid, the concentration of which is thus highest in the trunk and become lower towards the rostral and caudal ends of the embryo^{155,156}. These morphogen gradients instruct lineage patterning along the R–C axis and are involved in regulations of morphogenetic dynamics such as embryo elongation and somitogenesis by inducing spatially graded cell activities such as motility, polarization and proliferation^{108,115}. Similarly, positional information shapes the development of a limb along its proximal–distal axis, imposed by FGF signaling, and along its R–C axis, imposed by retinoic acid and SHH signaling^{157,158}. Extrinsic mechanical stimuli such as tissue stiffening¹⁵⁹ and stiffness gradients¹⁶⁰ have also been reported and correlated to morphogenetic cell migration^{159,161}. Nonetheless, given the technical difficulty in modulating their heterogeneity in in vivo models, it remains challenging to quantitatively characterize exogenous stimuli and establish spatial mapping between stimulus patterns and local morphogenetic events.

In vitro models have been successful in directly recapitulating heterogeneous exogenous stimuli (**Fig. 3B**). When luminal hPSC cysts on coverslips are exposed to exogenous uniform BMP4 stimulation, the lateral cyst wall obstructs permeation of BMP signals, leading to a medial–lateral (low–high) BMP activity gradient on its bottom surface. This graded BMP activity results in patterning of the non-neural epithelium on the periphery and neuroectoderm at the center of the cyst bottom, where neural folding dynamics is further induced⁴⁹. Exogenous morphogen gradients have also been generated by microfluidics for modeling amnion–epiblast symmetry breaking¹⁶², germ layer patterning¹⁶³ and neural plate patterning¹⁶⁴. Thus, in vitro models with controlled exogenous stimuli can be useful for inferring dynamic formation of embryo body axes¹⁵¹. Exogenous mechanical stimuli with predefined spatial patterns have also been superimposed on 2D embryoids. For example, cell

fate can be spatially regulated in 2D gastruloids¹⁶⁵ and patterned neuroectoderm tissues¹⁴⁵ through local stretching and mechanotransduction. In these systems, patterns of exogenous stimuli are directly controllable, thereby enabling quantitative mapping between local mechanical stimuli and cellular behaviors, a significant technical advantage compared with in vivo models.

[H2] Boundary conditions

Molecular and mechanical interactions often take place at tissue boundaries, which define another component regulating morphogenetic dynamics within a tissue (**Fig. 3C**). Biochemically, a tissue boundary can provide a local source or sink for signaling molecules. Mechanically, tissue boundaries can define a spatial domain within which tissue morphogenetic activities proceed¹²⁸. For example, physical confinements from the neural tube, epidermis, intermediate mesoderm and endoderm underpin the unidirectionality in PSM elongation¹²⁶. Active force signals can also develop on tissue boundaries, such as the tensile margin between embryonic and extraembryonic tissues which drives gastrulation in avian embryos.¹⁶⁶

In in vitro tissue cultures, boundary conditions are highly modifiable, which facilitates investigations of their roles in tissue morphogenesis. The most prevalent boundary conditions implemented for in vitro models hitherto can be roughly categorized into three types (**Fig. 3C**). First, under a free boundary condition, both tissue growth and morphogen diffusion are unconstrained, as seen in free-floating tissue cultures. This boundary condition is probably most relevant to pre-implantation embryo development¹⁶⁷⁻¹⁶⁹. Second, under a tractile boundary condition, tissues experience mechanical interactions at tissue boundaries while chemical signals can still diffuse freely, as in 3D tissue cultures using natural or synthetic ECM. Such 3D tissue cultures provide an anchoring environment required for cellular activities such as migration, contraction and mechanotransduction without prohibiting exogenous chemical signal modulation. Third, under a solid boundary condition, neither tissues nor morphogens can pass through the boundary, as exemplified by tissues cultured on a solid surface. Such solid boundaries enforce spatial confinement and/or guidance for tissue development. Combinations of different boundary conditions have also been implemented^{15,162,170}. Based on their modifiability, different boundary conditions can be tested on the same tissue to uncover how they mediate tissue development and morphogenesis. Notably, none of the three boundary conditions, either individually or combined, fully recapitulates the biomechanical and biochemical complexity at tissue–tissue interfaces in vivo. To address this limitation, tissue–tissue co-culture models and multi-tissue embryoid systems have been developed^{121,171}. It remains to be determined what the functional roles are of tissue–tissue interfaces in mediating tissue morphogenetic dynamics and how they can be effectively recapitulated in vitro.

[H1] Engineering morphogenesis

There are many bioengineering tools available for adoption in in vitro models for high-precision modulation, opening new possibilities for probing morphogenetic mechanisms². Unlike conventional cultures in which cell colonies or 3D tissues are surrounded by uniform biochemical and biomechanical cues, it has now become possible to apply bioengineering tools to engineer tissue geometry, exogenous stimuli and extracellular environment, with designed spatiotemporal specificities down to the scale where morphogenesis is relevant. Doing so not only enables multiscale mechanistic investigations but also effectively improves experimental throughput and reduces variability between assays (**Fig. 4**).

[H2] Engineering geometry

One of the most effective and straightforward approaches to probe endogenous spatial scales is to modulate tissue geometry. Controlling tissue geometry can define the dimension and shape of cell colonies and thereby provide an initial and/or boundary condition for progressive morphogenetic dynamics. Based on soft lithography^{172,173}, the most common bioengineering methods to regulate tissue geometry include surface pre-patterning and micro-well confinement. In surface pre-patterning, adhesive islands with pre-designed patterns are generated on 2D surfaces onto which cells can adhere and thereby form colonies with desired geometries^{49,165,174,175}. An example of surface pre-patterning is micro-contact printing (μ CP), which facilitates customization of adhesive island patterns on a variety of cell culture surfaces such as glass coverslips, polystyrene dishes and polydimethylsiloxane (PDMS) (**Fig. 4A**)^{172,176,177}. To develop stamps required by μ CP, prepolymer of elastomer such as PDMS is poured and cured over a master with relief surface features fabricated by microlithography. Next, the stamps are coated with adhesive molecules and pressed against an activated surface to enable transfer of adhesive molecules from the stamps to cell culture surfaces to produce adhesive patterns.

To regulate tissue geometry in 3D, microwells in which cells can form 3D aggregates with target size and shape are widely used (**Fig. 4A**)¹⁷⁸⁻¹⁸³. Apart from commercial sources, microwells can be produced with elastomers via techniques like those used for μ CP stamps. Microwells can also be fabricated with biological gels through micro-molding, in which elastomeric stamps with desired tissue architecture in bas-relief are used to mold gels^{179,183,184}. Such geometrical regulation can be extended to develop 3D scaffolds with complex interior structures (**Fig. 4A**)^{185,186}. Furthermore, bioprinting offers a powerful approach to generate initial tissue geometry with arbitrary conformation and topology (**Fig. 4A**)¹⁸⁶.

Geometric regulation on in vitro models allows efficient probing of endogenous scales encoded in morphing tissues. In 2D hPSC cultures, modulating colony geometry helps identify the

tension-mediated gastrulation-like phenotype¹⁶⁵. By embedding mammary epithelial cells in 3D trenches of various shapes inside collagen gels, it has been shown that tissue geometry could instruct distribution of autocrine inhibitory morphogen signals and as such determine locations of and spacing between branching sites¹⁷⁹. With similar geometric regulation methods, local geometry of mouse intestine tissues is found to induce a gradient in cell spreading and associated YAP activity, leading to crypt-villus lineage patterning and morphogenesis¹⁸³. Via direct control of tissue size and shape, it is now possible to expose morphogenetic mechanisms that respond to or originate from tissue geometry and scale.

[H2] Engineering stimuli

The impact of exogenous stimuli can be simulated and investigated through various engineering approaches. Signaling stimuli can instruct local cellular activities and convey inter-tissue communications during morphogenesis. To recapitulate spatiotemporal patterns of biochemical and biomechanical signals, a variety of bioengineering tools have been employed in organoid and embryoid cultures (**Fig. 4B**). To introduce localized sources of morphogens, morphogen-loaded microbeads have been incorporated into embryoid bodies to drive heterogeneous differentiation of PSCs^{187,188}. Microfluidic technologies have also been used to generate defined morphogen gradients within cell cultures by engineering molecular diffusion patterns^{163,164,189-191}. In these microfluidic platforms, cells are usually cultured in a confined space while different molecules are supplemented from different boundaries of the culturing space, forming a stable morphogen gradient pattern in the cell culture via passive diffusion. For example, when hPSCs are cultured in a micro-chamber with its two opposing sides adjacent to two channels, one supplemented with BMP4 and the other with SHH agonist, dorsal–ventral **[G]** (D–V) patterning is imposed on neuronal cells differentiated from hPSCs, mimicking neural patterning along the D–V axis¹⁹⁰. Another microfluidic device for generating a linear morphogen gradient uses a serpentine channel gradient generator to create a quasi-linear WNT activator gradient over hPSC-derived neural tissues for their R–C regionalization¹⁶⁴. To create a more drastic morphogen gradient, hPSC clusters can be anchored on the interface of two micro-channels supplemented with different morphogens. With BMP4 supplemented in one of the channels and no morphogen in the other, a spontaneous amniogenesis-like symmetry breaking in the hPSC cluster is induced¹⁶². However, confined space within microfluidics can lead to undesired mechanical interactions between developing tissues and device boundaries, a non-trivial limitation that precludes the use of microfluidics for long-term tissue cultures. More recently, optogenetic tools have also been used to locally control morphogenetic processes such as apical constriction in organoid cultures, with high spatiotemporal specificity¹⁹².

Given the roles of mechanical stimuli in instructing lineage specification and morphogenesis^{30,193-196}, there are substantial efforts in integrating biomechanical tools that allow controls of mechanical stimuli with embryoid and organoid cultures. For cell colonies cultured on a 2D elastomeric substrate, mechanical stimuli can be introduced by changing the mechanical properties of the substrate, which are modulable through either controlling elastomer constituents^{197,198} or by introducing surface microstructures such as microposts, the rigidity of which is controlled by their height and hence independent of effects on adhesive and other material surface properties¹⁹⁹. To investigate the impact of exogeneous strain and stress, mechanical loading has been explicitly incorporated into in vitro cultures using bioengineering tools (**Fig. 4B**). Conventional cell or tissue straining devices generate a homogenous macroscopic strain field on a substrate or matrix through motor or pneumatic-driven displacements and thereby transmit mechanical loading to cells or tissues attached to the substrate or embedded in the matrix²⁰⁰. However, these methods often provide limited throughput and cannot model complex or heterogeneous loading dynamics. To improve throughput and facilitate mechanical screening, microfabricated platforms for both tensile and compressive loading have been developed²⁰¹⁻²⁰³ to investigate independent or integrative effects of loading parameters such as strain magnitude, rate and period²⁰⁴. To model the effect of shear stress, shear flow can be introduced over cell culture surfaces²⁰⁵⁻²⁰⁷. Technologies such as acoustic tweezing cytometry further enable force applications on a cellular scale without continuum strain by actuating microbubbles anchored to cell surface receptors such as integrins, and therefore decouple mechanical activation from cell deformation^{208,209}. To establish a spatially patterned heterogeneous loading, inflatable PDMS microchambers are placed beneath 2D hPSC colonies at designated locations and, with increased chamber pressures, induce regional biaxial stretching of the overlying 2D hPSC colonies. This method has been applied to instruct neural¹⁴⁵ or mesodermal¹⁶⁵ lineage patterning, and can potentially be extended to stretch a 2D colony at arbitrary regions with desired shapes.

[H2] Engineering extracellular environment

Engineering properties of the extracellular environment has proved effective for inducing morphogenetic activities and therefore also provides an opportunity for investigating boundary conditions of morphogenesis (**Fig. 4C**). For cells embedded in a 3D bioengineered tissue scaffold, cell fate and morphogenesis could be mediated by matrix mechanical properties such as elasticity^{16,193} and viscoelasticity^{17,210}. Extracellular matrix can also be conjugated with chemical signals, such as growth factors, to create a biochemical interface for embedded tissues²¹¹. Furthermore, recent developments of stimulus-responsive biomaterials enable spatiotemporal control over the structural, mechanical, and biochemical cues in the extracellular matrix through light, ultrasound or

electromagnetic stimulations^{212,213}. For embryoid and organoid cultures, animal-derived biological gels, such as Matrigel, have been used extensively as conductive 3D environments that facilitate spontaneous morphogenesis and lineage patterning^{15,16,36-39,49,69,121,170,181,185,186,214,215}. However, the ill-defined and variable biochemical constituents in animal-derived biological gels could hinder the rationalization of morphogenetic activities manifested by embryoids and organoids in such 3D cultures²¹⁶, as is exemplified by the delicate dependence of somite-like tissue morphology on Matrigel concentration in the hPSC-based somitogenesis model³⁶. To address this issue, many naturally derived and synthetic gel matrices with chemically defined components like ECM-based proteins²¹⁷ or polyethylene glycol (PEG)²¹⁸ have been developed^{216,219}. More demonstrations of morphogenesis-inducing potentials of these fully defined gel matrices are required before they can be widely adopted in embryoid and organoid research.

[H1] Outlook

Stem cell-based, in vitro development models are being rapidly developed with favorable accessibility, efficiency and modularity. These in vitro development models are promising experimental tools to supplement canonical in vivo models. However, there are fundamental challenges that need to be fully addressed before in vitro development models can fully achieve their potential. The first crucial conceptual question is how to assess similarities between in vitro morphogenetic events and their in vivo counterparts. It might be difficult to expect molecular and mechanical similarities between in vitro and in vivo models at every stage of dynamic morphogenetic processes, because in vivo complexity remains to be fully understood and characterized. As a slightly lower standard, in vitro models can also be evaluated by certain critical morphogenetic phenotypes, which then requires careful scrutiny of which part of in vitro dynamics pertains to in vivo phenotypes of significance.

If the standard of in vivo relevance is clearly defined, an imminent challenge is to fully optimize the faithfulness of existing in vitro models, which can be particularly challenging if relevant in vivo knowledge is limited. To improve model fidelity, it might be necessary to increase model complexity by, for example, incorporating additional cell lineages or combining different tissues. Yet it is also important to ensure that system complexity does not overshadow the most essential morphogenetic mechanism or phenotype of interests, or negatively impact model accessibility or modularity. As one possible solution, we envision that incorporating high-precision bioengineering tools can help modularize different aspects of morphogenesis and therefore selectively target different dimensions of complexity with spatiotemporal controls. Additionally, the use of bioengineering controls can substantially improve in vitro throughput, and therefore facilitates model iteration and optimization.

Another major challenge associated with in vitro development models is how to derive mechanistic insights relevant to in vivo settings. Despite uncertainties of their applicability and predictive capacity, in vitro platforms, together with theoretical models, possess the unique potential of providing quantitative mechanistic knowledge. Animal models have been instrumental in establishing correlations between single factors, such as specific developmental genes and tissue organization. In vitro and theoretical models, conversely, allow probing combinatorial and crosstalk effects of multiple factors and thus filling the gap within in vivo derived knowledge. When combined, the quantitative power of in vitro and theoretical models can hopefully elucidate the applicable scope of observed mechanisms and phenomena, which can not only help explain contradictory experimental results but also clarify necessary conditions for normal morphogenesis. In terms of human morphogenesis and disease modeling where in vivo knowledge is limited, in vitro models might provide the most human-relevant systems to capture both the specificity and diversity among human genetic background. Nevertheless, a general research paradigm is yet to be established to organically integrate existing in vivo knowledge, in vitro models and theoretical analyses to generate systematic insights of morphogenetic principles.

In this review, we discuss about how in vivo, in vitro and theoretical models have contributed knowledge towards understanding of morphogenesis. We argue that developing in vitro and theoretical platforms opens new possibilities to improve insight into the biomechanical and biophysical principles underlying morphogenesis. With emerging stem cell technologies and bioengineering tools available for reconstituting morphogenesis in vitro, it is expected that more opportunities from in vitro and theoretical models would arise to help rationalize biological forms with new understanding that can feedback to and be integrated with in vivo knowledge.

Glossary

Lumen: a cavity or inner space enclosed by cells or tissues.

Blastocoel: A fluid-filled cavity inside pre-implantation embryos called blastocysts.

Mesenchymal-to-epithelial transition: A biological process during which loosely connected mesenchymal cells re-organize, establish apical-basal polarity and transition into an assembly of closely packed epithelial cells. Its reverse process is called epithelial-to-mesenchymal transition.

Neurulation: Formation of neural tube, which involves two different morphogenetic processes. In primary neurulation the neural plate folds inward until opposing edges come into contact, fuse, and give rise to the neural tube. In secondary neurulation, cavities form in caudal neural precursors and later merge with the neural tube formed by primary neurulation.

Epiblast: Pluripotent cells derived from inner cell mass in a blastocyst. It locates between hypoblast and trophoblast, and gives rise to three definitive germ layers.

Cleavage furrow: The indentation of a cell's surface that begins the progression of membrane separation during cell division.

Somite: Segmented, block-like structures flanking the neural tube. They are the precursors to vertebrae, part of occipital bones of the skull, skeletal muscles, dermis, cartilage, and tendons.

Rostral: Towards the head.

Caudal: Towards the tail.

Gastrulation: A morphogenetic process through which epiblast cells reorganize, differentiate, and ultimately form three spatially organized germ layers, namely (dorsal to ventral) ectoderm, mesoderm, and endoderm.

Neural tube: A tubular neural tissue and the precursor of central nervous system.

Neural plate: A region of ectoderm which contains a flat layer of columnar neuroepithelial cells.

Dorsal: Towards the back.

Medial: Towards the body midline.

Lateral: Away from the body midline.

Anencephaly: A congenital defect in the formation of neural tube, in which a baby is born without parts of the brain and skull.

Respiratory diverticulum: A ventral outpouching structure that develops from the endodermal foregut and bifurcates into left and right lung buds. Lung buds are rudiments of two lungs and the left and right primary bronchi, and the diverticulum stem forms the trachea and larynx.

Alveoli: Hollow, distensible cavities in lungs where the exchange of oxygen and carbon dioxide occurs.

Neuromesodermal progenitor: a population of bipotent progenitor cells in the caudal region of the embryo. It contributes to both spinal cord and presomitic mesoderm development.

Ventral: Towards the front.

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Acknowledgements

Studies in the Fu research group are supported by the Michigan-Cambridge Collaboration Initiative, University of Michigan Mcubed Fund, University of Michigan Mid-career Biosciences Faculty Achievement Recognition Award, National Science Foundation (PFI-TT 2213845, I-Corps 2112458, CMMI 1917304, CBET 1901718, and CMMI 2325361), and National Institutes of Health (R21 NS113518, R21 HD100931, R21 HD105126, R21 NS127983, R21 HD109635, R21 HD105192, R33 CA261696, R01 GM134535, and R01 NS129850). The authors apologize to colleagues whose work they could not cite owing to space restrictions.

Author contributions

Y.L. and J.F. wrote the article text. Y.L. generated the figures. All authors contributed to the conceptualization of the article.

Competing interests

The authors declare no competing interests

Peer review information

Figures

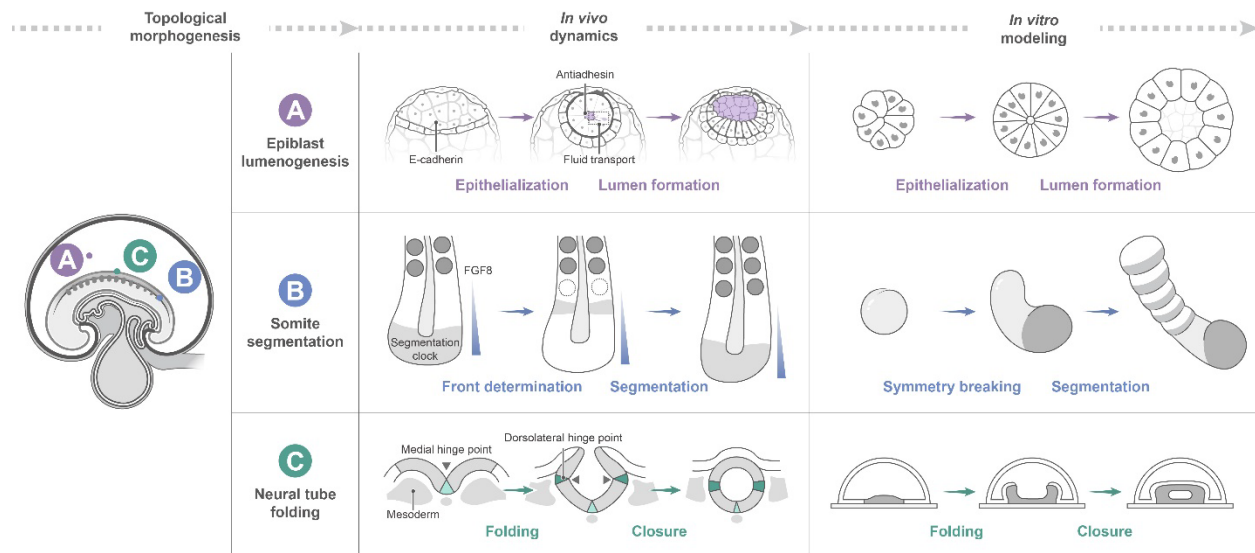


Fig. 1 | In vivo knowledge and in vitro modeling of three topological morphogenetic events. a, Epiblast lumenogenesis. **b,** Somite segmentation. **c,** Neural plate folding. Embryo schematics adapted with permission from Ref².

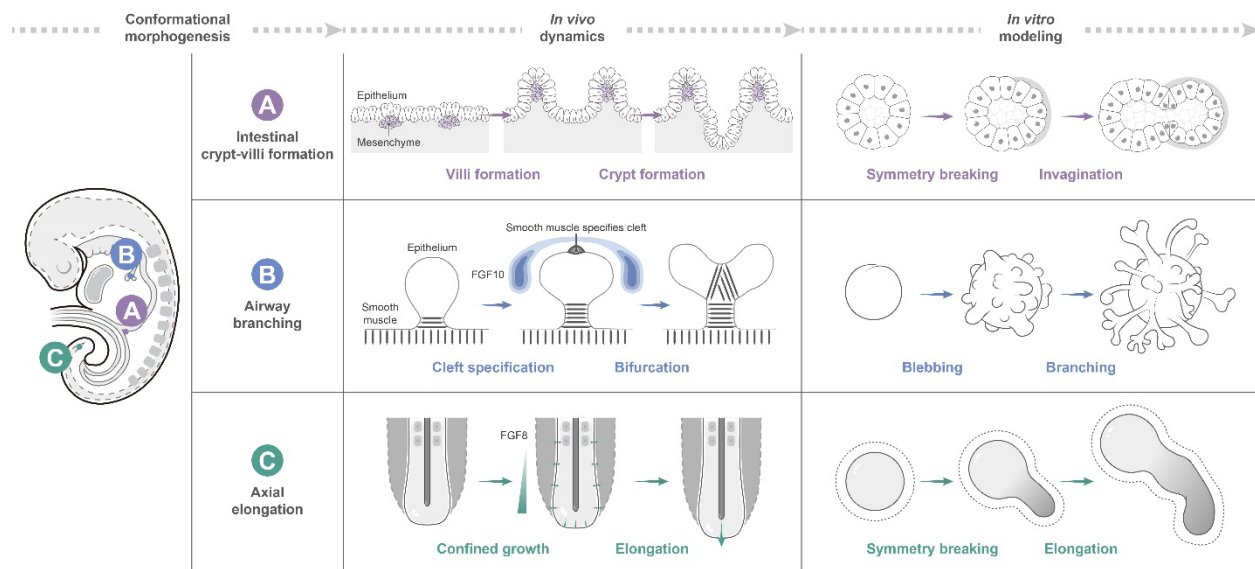


Fig. 2 | In vivo knowledge and in vitro modeling of three conformational morphogenetic events. a, Intestinal crypt-villi formation. **b,** Airway branching. **c,** Axial elongation. Embryo schematics adapted with permission from Ref². Part **b** adapted with permission from Ref.⁹⁰

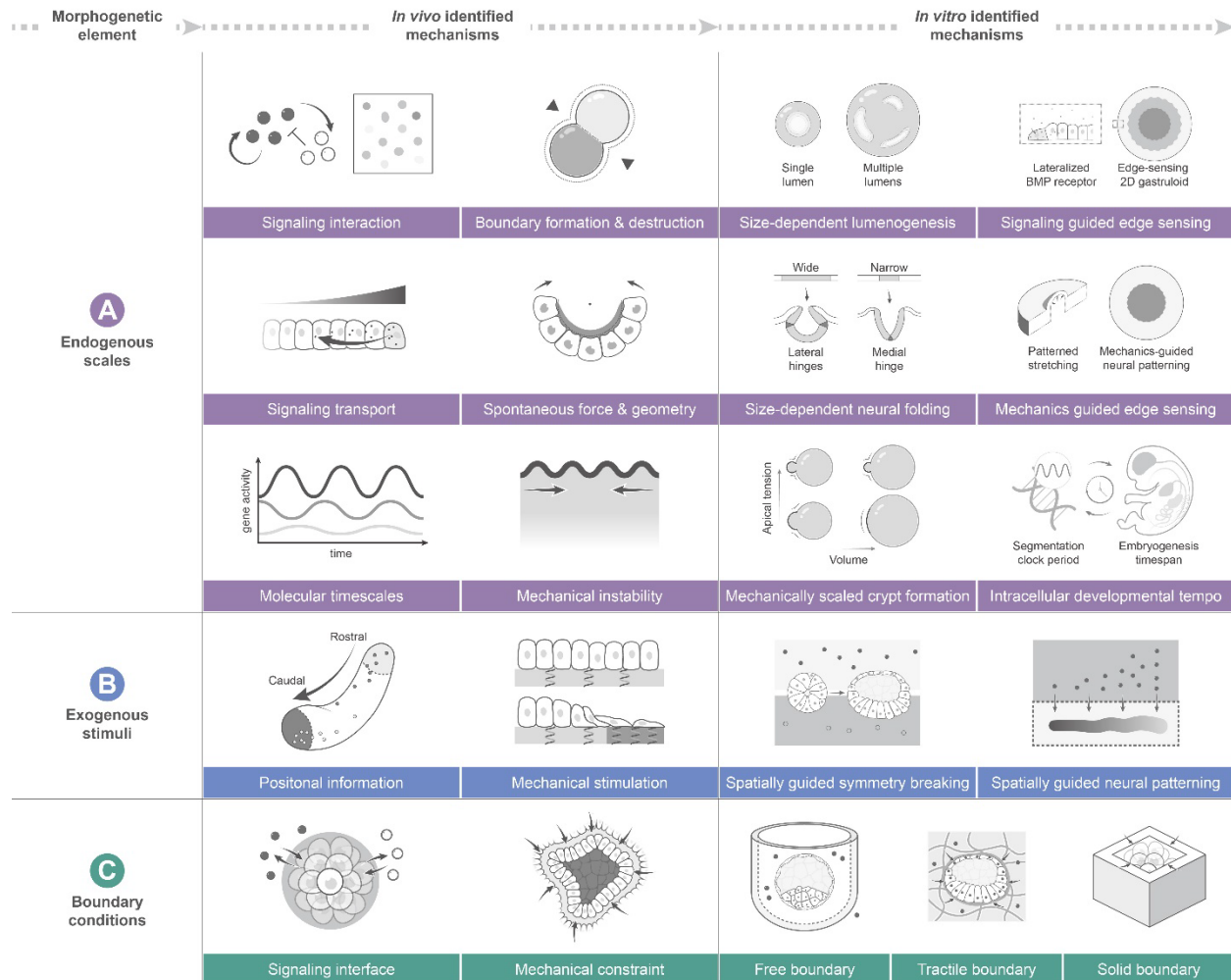


Fig. 3 | Essential aspects of morphogenetic dynamics with selected *in vivo* and *in vitro* examples. a, Endogenous morphogenetic scales. b, Exogenous stimuli. c, Boundary conditions. Part a adapted with permission from Ref.²

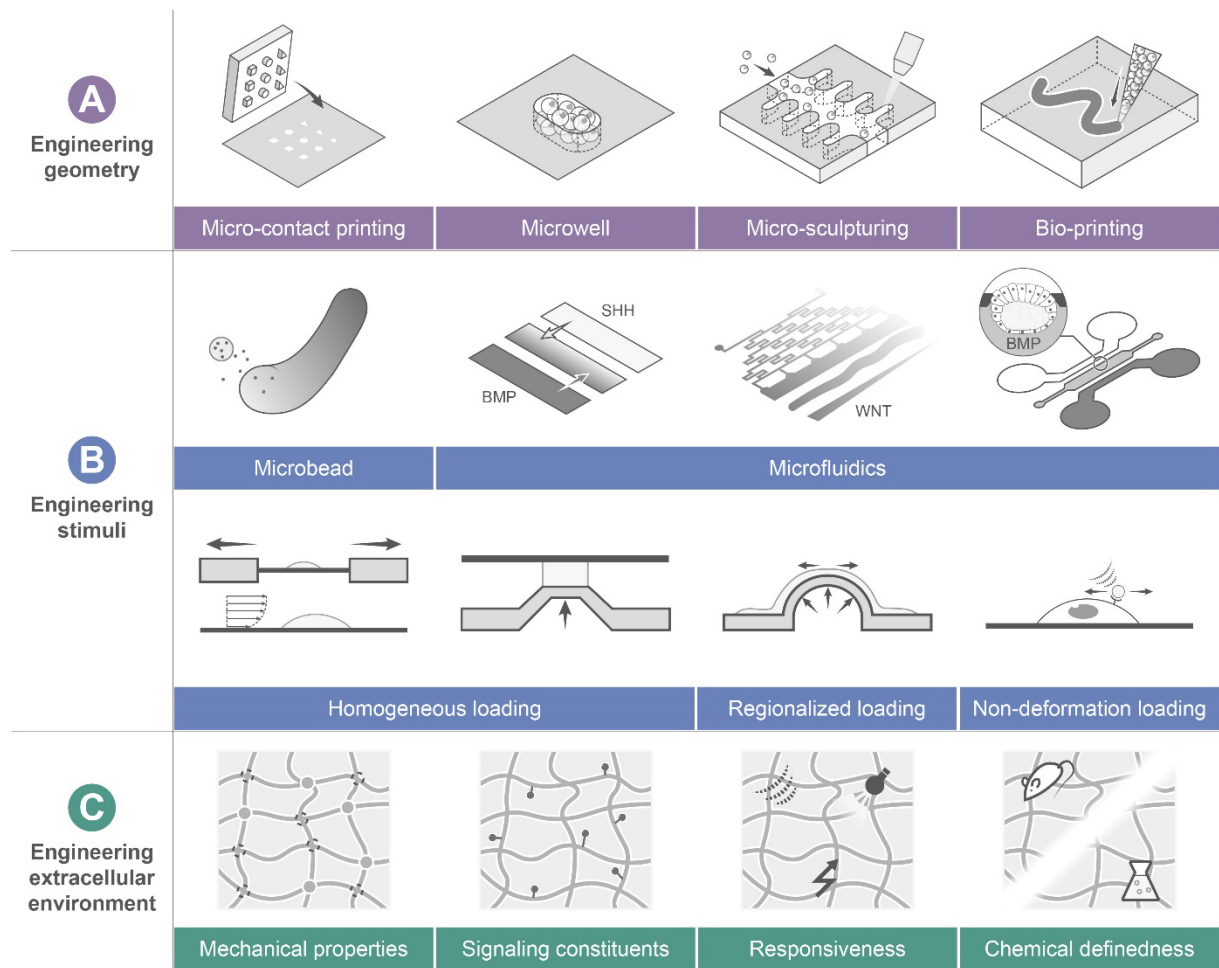


Fig. 4 | Bioengineering tools and methods to model and study morphogenesis in vitro. **a**, Modulation of tissue geometry. **b**, Application of exogenous stimuli. **c**, Modification of extracellular environment of embryoids and organoids.