

Control and Integrability in Figure Skating

By Meghan Rhodes, Vaughn Gzenda, and Vakhtang Putkaradze

Figure skating is a popular athletic endeavor, even taking the prime-time slot during televised broadcasts of major sporting events like the Winter Olympic Games. The grace, precision, and elegance of the athletes—in addition to the enchanting effects of dance, music, and costumes—make this sport a perennial favorite for many viewers.

The patterns that skaters carve into the ice have intrigued a wide audience since the 19th century [2]. As a hobby, skaters designed intricate patterns and attempted to trace those designs into the ice. This pastime soon grew in popularity; the patterns became known as “figures” and the hobby was termed “figure skating.” Some of us might still remember televised broadcasts of competitions that included “compulsory figures,” during which athletes could trace patterns at any speed but were only allowed a certain number of pushes off the ice. These contests are not part of official competitions anymore; they have separated into an independent branch with its own events that differ from mainstream Olympic-style figure skating.

While the acrobatic dance programs and jump-filled free skate performances of mainstream figure skating are certainly

more spectacular for viewing—and more challenging athletically—the mathematical descriptions of continuous skating paths are just as interesting. Skaters control their motion by changing the direction of their skates and the position of their arms, legs, and torso, thus altering the moments of inertia and location of the center of mass. Such control is produced in the body’s frame, whereas the figures are traced on ice—the coordinate frame fixed in space (spatial frame). The exact nature of the mechanism that a skater employs by mapping the body to the spatial variables—which one achieves with years of careful practice—is very complex and not well understood. This lack of understanding is evident in figure skating instructional methods. For example, each figure skating element can be executed in many ways. Different body positions are considered “optimal” depending on the execution technique of the element in question. When learning a new element, skaters often experiment with technique and try to simply remember the physical feeling of a successful attempt in order to recreate the success (rather than determining the physics behind the attempt). The level to which skaters analyze their movements and the resulting impact on the physical properties varies based on the individual,

but significantly examining this relationship is not a common practice.

Though one can technically derive a full mathematical model of a skater on ice, such a model is hardly informative for theoretical understanding. The model would have to incorporate the motion of the head, torso, and every limb—all controlled simultaneously. This challenging problem is likely a good candidate for modern machine learning methods, such as reinforcement learning. However, we are interested in understanding the problem by designing the simplest realistic mechanical model as possible. We focus

on the skater’s motion without the blade’s friction with ice, which is a reasonable assumption for a description of the motion on short to intermediate time scales.

During the continuous motion of a skater on ice, the skate in contact with the ice can only move in the direction of the blade. When the skate turns with respect to the ice, the direction of motion also changes. There is thus a constraint on the velocities of the skate on ice. One cannot write the skate velocity constraint in terms of coordinates only, meaning that the mechanical system

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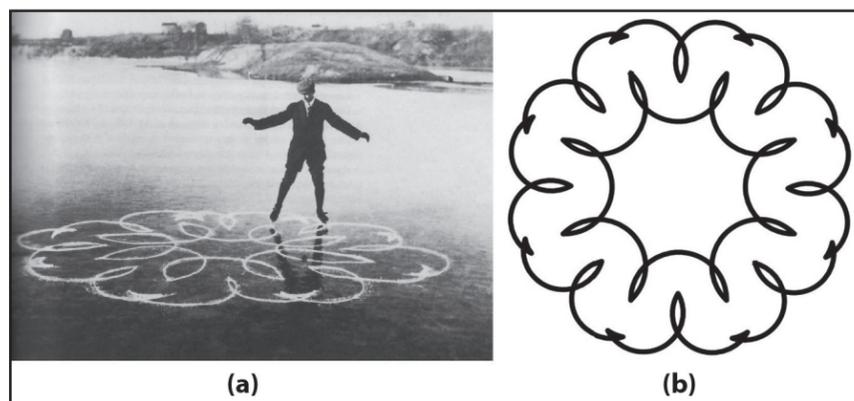


Figure 1. Original figure skating patterns both on and off the ice. **1a.** The trajectory of a skater on ice from one of the original figure skating patterns. **1b.** The same figure, computed by combining the trajectory of a controlled Chaplygin sleigh. Figure courtesy of Meghan Rhodes and Vakhtang Putkaradze.

A Measure of Morphodynamics

By Mattia Serra and L. Mahadevan

One of the grand challenges of modern biology is understanding the way in which a complex, multicellular organism arises from a single cell via spatiotemporal patterns that are repeatable and reproducible across the tree of life. As the organism grows, its cells change their number, size, shape, and position in response to genetic, chemical, and mechanical cues (see Figure 1a). Four-dimensional microscopy (three spatial dimensions and time) is beginning to illuminate how these cues impact the fate of cells and the geometric form of tissues and organs that constrain and enable function at multiple scales [3]. Even though individual cells might seem to move chaotically, the large-scale, collective cell movements within tissues resemble a choreographed ballet and raise a few natural questions:

- (i) How can we quantify the patterns and predict the formation of different organ systems?
- (ii) How can we understand these patterns from a biophysical and biochemical perspective as a function of the way in which cells divide, grow, and move in response to environmental cues?
- (iii) How can we control these movements to intervene and correct pathological development or guide tissue development in situations like organoid formation?

Here we focus on the properly invariant quantification of large-scale cellular movements and draw inspiration from the study of objective transport barriers in hydrodynamics [2, 5]. Just as it is more meaningful to focus on the large-scale coherent structures in a complex flow rather than track individual particles, we believe that it is useful to quantify the large-scale motions that characterize tissue morphogenesis. Any framework that aims to analyze spatiotemporal trajectories in morphogenesis requires a self-consistent description of cell motion that is independent of the choice of reference frame or parametrization. This objective (frame-invariant) description of cell patterns ensures that the material response of a deforming continuum—e.g., a biological tissue—is independent of the observer [7].

One can quantify this idea mathematically by considering two reference frames that describe cellular flows and are related to each other via the transformation $\bar{x}(t) = Q(t)x(t) + b(t)$, where $Q(t)$, $b(t)$ are a time-dependent rotation matrix and translation vector respectively. A quantity is objective (frame invariant) if the corresponding descriptions in both frames transform appropriately: scalars $c(t)$ (e.g., concentration) must remain the same with $\bar{c}(t) = c(t)$; vectors $v(t)$ (e.g., velocity field) must transform via the rule $\bar{v}(t) = Q(t)v(t)$; second-order tensors $A(t)$

(e.g., strain rate) must transform via the rule $\bar{A}(t) = Q(t)A(t)Q^T(t)$; and so forth [7]. It is thus immediately apparent that objects like velocity fields, streamlines, and vorticity—which are typical outputs from microscopy following some elementary image analyses—are frame dependent. Therefore, any metrics that are based on these objects for comparative purposes are likely erroneous, owing to their inability to remove dependence on artifacts that are associated with variations in the choice of reference frames (see Figure 1b). Indeed, most Eulerian approaches that characterize fluid or cellular flows suffer from this flaw, despite having served as workhorses for a long time [1, 5]. So, how can we do better?

A Lagrangian view that integrates over the history of cellular movements in time can clearly distinguish the way in which cells move apart or together, and ultimately provides a better perspective on cellular and tissue fate. This approach has successfully unraveled the complexity of passive fluid flows in problems that range from microfluidic mixing to atmospheric polar vortices using the notion of Lagrangian coherent structures (LCSs) [2]. Hyperbolic LCSs are time-evolving attracting and repelling manifolds that shape the overall spatiotemporal patterns in complex dynamical systems. In the context of morphogenesis, the *dynamic morphoskeleton* is the collection of attracting and repelling LCSs. From a practical perspective, we can compute these structures in terms of the largest finite-time Lyapunov exponent (FTLE), which is defined as

$$\Lambda_{t_0}^t(x_0) = \frac{1}{|T|} \ln \left(\max_{\delta x_0} \frac{|\nabla F_{t_0}^t(x_0) \delta x_0|}{|\delta x_0|} \right)$$

Here, $F_{t_0}^t(x_0) = x_0 + \int_{t_0}^t v(F_{t_0}^\tau(x_0), \tau) d\tau$ is the Lagrangian flow map that is induced

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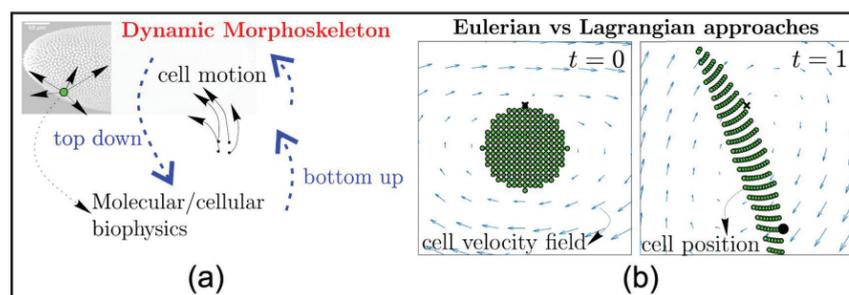


Figure 1. Frame-invariant description of cellular flows. **1a.** Sketch of bottom-up and top-down approaches to cell motion. Bottom-up approaches study local mechanisms that drive cells, while top-down approaches study patterns of cell motion that are caused by local and global driving mechanisms. The dynamic morphoskeleton uncovers the centerpieces of cell trajectory patterns in space and time. **1b.** Snapshots of a simple analytic velocity field (blue) and its Lagrangian particle positions (green). The black dot marks the position of a particle that began at the black x marker at time 0. The frame-dependent velocity field suggests the presence of a vortical structure while the tissue undergoes exponential stretching. Figure courtesy of [6].

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SIAM Celebrates Mathematics and Statistics Awareness Month

By Jillian Kunze

April is Mathematics and Statistics Awareness Month!¹ Each year, the Joint Policy Board for Mathematics—a collaboration between SIAM, the American Mathematical Society, the American Statistical Association, and the Mathematical Association of America—holds a month-long celebration to enhance public understanding and appreciation of mathematics and statistics. Both subjects have real-world societal impacts in nearly every imaginable field, such as medicine, biotechnology, energy, manufacturing, and business. Throughout the month of April, universities, high schools, student groups, research institutions, public information offices, and other related organizations host math-related activities. These activities often include workshops, competitions, departmental open houses, festivals, lectures, art exhibits, poetry readings, and other events centered around

¹ <https://www2.amstat.org/mathstatmonth/index.html>

themes related to mathematics and statistics. Due to the ongoing pandemic, participants are encouraged to celebrate virtually this year and use the hashtag #MathStatMonth on social media to share their festivities.

Mathematics and Statistics Awareness Month originated in 1986 as Mathematics Awareness Week under then-U.S. president Ronald Reagan, who noted that enrollment in U.S. mathematical programs was declining. Mathematics Awareness Week initially focused on national-level events, such as a mathematics exhibit at the Smithsonian Institution and a reception on Capitol Hill. It became Mathematics Awareness Month in 1999 and began to shift its emphasis towards local, state, and regional activities. In 2017, the name changed to Mathematics and Statistics Awareness Month to recognize important research in both fields. Though the number and breadth of celebrations have grown throughout the years, the event has remained dedicated to increasing the visibility of mathematical and statistical research across a wide audience.

University department chairs, high school teachers, public policy representatives, and other professional leaders can access and share resources that help educate the public about the importance of mathematics and statistics in ongoing scenarios like sustainability, internet security, disease, and climate change. Mathematical and statistical research drives technological innovation and leads to discoveries of broad societal importance across many scientific fields. Here, several members of the *SIAM News* Editorial Board detail the ways in which they utilize mathematics to solve engaging problems.

Hans Kaper (Georgetown University), editor-in-chief of *SIAM News*: “I am an applied mathematician by training and profession, and my interests lie in the mathematical modeling of natural phenomena. Mathematical modeling combines the laws of nature with observational data and expresses them into the language of mathematics. A mathematical model is an

abstraction; it reflects reality but should not be thought of as “reality.” It reveals the essential mechanism that drives the phenomenon of interest and allows us to explore various scenarios, whether theoretically or computationally.

Among the natural phenomena that have fascinated me in the past are reaction-diffusion phenomena in combustion systems, vortex formation and transport in high-temperature superconductors, and pattern formation in magnetic materials. I have recently become interested in climate issues and modeling the effects of human activities on Earth’s climate system. Some of my current work is related to the dynamics of glacial cycles during the Pleistocene, problems that concern food systems and food security, and mathematical approaches to resilience.”

Korana Burke (University of California, Davis): “Anyone who has tried to enter or exit a massive lecture room, music hall, or other large venue has likely been stuck in a crowd. This scenario is not a pleasant

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Morphodynamics

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by cell velocities. $\Lambda_0^t(\mathbf{x}_0)$ characterizes the maximum rate of separation of points in a neighborhood of \mathbf{x}_0 —denoted by the infinitesimal vector $\delta\mathbf{x}_0$ —during the time window $[t_0, t]$ (see Figure 2). The FTLE has a natural interpretation in continuum mechanics and is related to the largest eigenvalue of the Cauchy-Green strain tensor [7], therefore serving as a natural invariant measure of deformation in a continuous medium.

By choosing to integrate either forwards or backwards in time, one can delineate manifolds that are zones of attraction or repulsion over a given time interval; doing so establishes an organizing skeleton for the flow pattern (see Figure 2). The resulting dynamic morphoskeleton is frame invariant, easy to compute, and robust to noise and loss of local data because of its (integrated) averaging property [6].

When deploying this approach on light-sheet microscopy data from the embryo of a normally-developing chick that involves $\sim 10^5$ cells (see Figure 3a) [4], we see that the dynamic morphoskeleton consists of two repellers—critical boundary regions across which cells will likely assume different fates—and one attractor (see Figure 3b). Repeller 1 marks a dynamic boundary between the embryonic and extra-embryonic regions. By contrast, repeller 2 marks the anterior-posterior boundary of a characteristic feature that is known as the primitive streak (PS): a zone of strong cellular convergence (an attractor) during early embryogenesis. First, we note that repellers remain invisible to Eulerian and Lagrangian tools that researchers use in multicellular flows.¹ This fact may explain why repellers appear to be undocumented in the literature, despite their relevance for cell fate acquisition.

Second, we notice that just an hour after cells have barely started to move, the dynamic morphoskeleton captures the PS’s

¹ See the online version of this article for a corresponding animation.

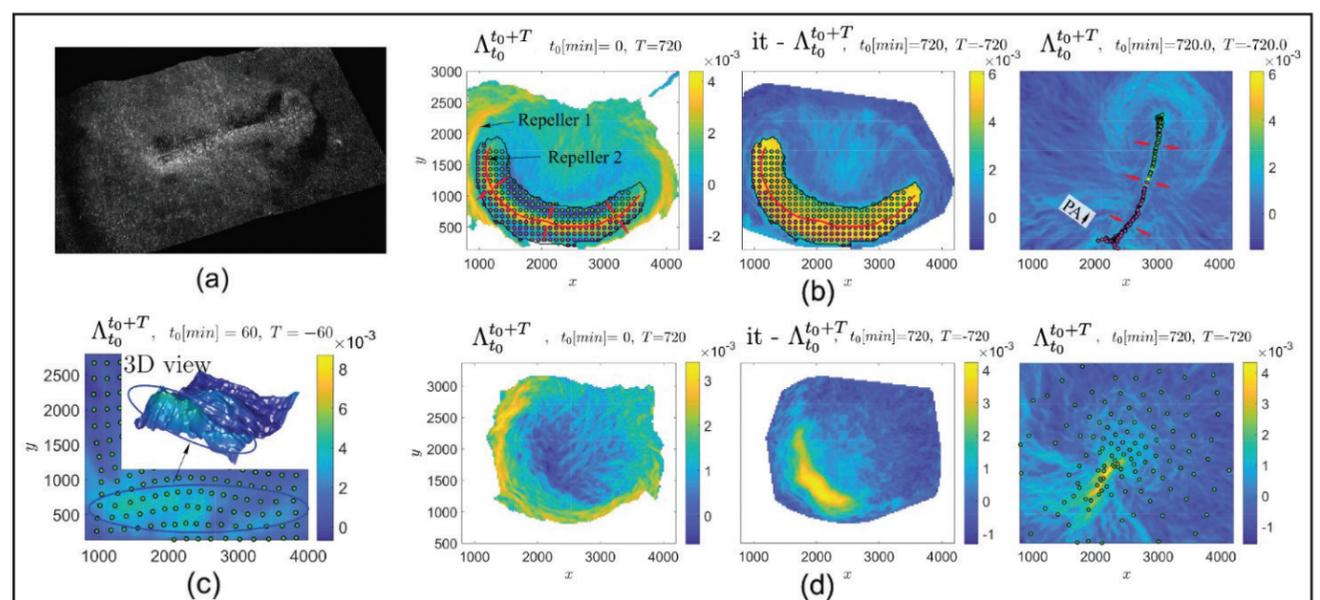


Figure 3. Dynamic morphoskeletons in chicken gastrulation. **3a.** Light-sheet microscopy image of a chick epiblast during the primitive streak (PS) formation. **3b.** Left: FW $FTLE_0^{12h}$ highlights two repelling Lagrangian coherent structures (LCSs). Right: BW $FTLE_0^{12h}$ highlights the attracting LCS that corresponds to the formed PS. Center: BW $FTLE_0^{12h}$ field in the right panel is passively transported to the initial time; this marks the initial position of the mesendoderm precursor cells—bounded by the solid black line—that eventually form the PS. Cells that begin on different sides of repeller 2 form the anterior and posterior part of the PS. The finite-time Lyapunov exponent (FTLE) has units $1/\text{min}$, and the axis units are in μm . The time evolution of the FTLE fields and cell positions for different T are available in an online animation. The lower panels of this animation depict the time-averaged velocity, cell positions, and a deforming Lagrangian grid. **3c.** BW $FTLE_0^{1h}$ ridge highlights the PS’s early footprint (blue ellipse) using only the first hour of data when the cells (green dots)—initially released on a uniform rectangular grid—have barely moved. **3d.** The same situation as 3b for a chick embryo that is treated with a critical diffusible morphogen (FGF) receptor inhibitor. An online animation shows the time evolution of the FTLE fields and cell positions for different T . Figure 3a courtesy of Cornelius Weijer, 3b-3d adapted from [6].

early footprint—well before it is actually visible to conventional tools (see Figure 3c). This approach can also detect preliminary signatures of abnormal development. Use of a drug to inhibit the presence of a critical diffusible morphogen (FGF) that is required for early gastrulation causes the PS formation to fail (see Figure 3d) and results in a lack of anterior-posterior cell differentiation, which is quantified by the loss of repeller 2 (evident in the left panels of Figure 3b and 3d).² Similar analysis of a whole curved embryo of a developing fruit fly with roughly 6,000 cells allows us to visualize how the attractors and repellers characterize the motions that lead to gastrulation in both normal and pathological development [6].

² An animation in the online version of this article depicts the time evolution of the dynamic morphoskeleton for the FGF receptor inhibitor embryo.

The enormous amounts of data that are rapidly becoming available from large-scale imaging of biological development require properly invariant methods of analysis. The aforementioned approach—which integrates local (cell-based) and nonlocal (neighborhood/tissue-based) cues—provides a step in the right direction. The dynamic morphoskeleton sets the geometric stage for uncovering the dynamic organizers of cellular movements and tissue form; it also provides a lens for uncovering the underlying relevant mechanisms at play. When we combine the morphoskeleton with the ability to track and manipulate gene expression levels, mechanical forces, etc., perhaps we will be able to determine the biophysical mechanisms that underlie normal and pathological morphogenesis and move a little closer to answering one of the grand questions of modern biology.

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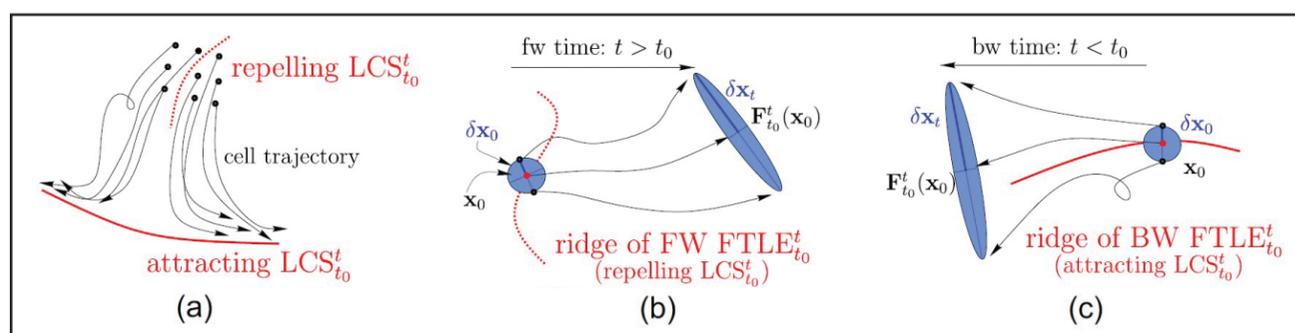


Figure 2. Attractors and repellers organize cell motion. **2a.** Illustration of the attracting and repelling Lagrangian coherent structures (LCSs) over the time interval $[t_0, t]$. **2b.** The forward finite-time Lyapunov exponent (FTLE) measures the maximum separation $\delta\mathbf{x}_t$ over the time interval $[t_0, t]$ between two initially close points in the neighborhood \mathbf{x}_0 . A forward-time FTLE ridge—a set of points with high FTLE values—marks a repelling LCS; nearby points from opposite sides of the ridge experience the maximum separation over $[t_0, t]$, $t > t_0$. **2c.** A backward-time FTLE ridge demarcates an attracting LCS—i.e., a distinguished curve at the final time that has attracted initially distant particles. Figure adapted from [6].