Classical sorting algorithms as a model of morphogenesis: Self-sorting arrays reveal unexpected competencies in a minimal model of basal intelligence

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Abstract

The Diverse Intelligence research seeks to understand commonalities in behavioral competencies across a wide range of implementations. Especially interesting are simple systems that provide unexpected examples of memory, decision-making, or problem-solving in substrates that at first glance do not appear to be complex enough to implement such capabilities. We seek to develop tools to determine minimal requirements for such capabilities, and to learn to recognize and predict basal forms of intelligence in unconventional substrates. Here, we apply novel analyses to the behavior of classical sorting algorithms—short pieces of code studied for many decades. To study these sorting algorithms as a model of biological morphogenesis and its competencies, we break two formerly ubiquitous assumptions: top-down control (instead, each element within an array of numbers can exert minimal agency and implement sorting policies from the bottom up), and fully reliable hardware (instead, allowing elements to be "damaged" and fail to execute the algorithm). We quantitatively characterize sorting activity as traversal of a problem space, showing that arrays of autonomous elements sort themselves more reliably and robustly than traditional implementations in the presence of errors. Moreover, we find the ability to temporarily reduce progress in order to navigate around a defect, and unexpected clustering behavior among elements in chimeric arrays consisting of two different algorithms. The discovery of emergent problem-solving capacities in simple, familiar algorithms contributes a new perspective showing how basal forms of intelligence can emerge in simple systems without being explicitly encoded in their underlying mechanics.

1. Introduction

On their respective time scales, evolutionary and developmental biology require that cognitive capabilities such as memory and goal-directed activity in the face of perturbations originate in proto-cognitive functions that existed long before complex brains came onto the scene (James, 1890; Jennings, 1906; Lyon, 2006). The gradual history of intermediate forms with different levels of competency undermines a view in which discrete natural kinds have, or do not have, binary properties such as intelligence (Fields & Levin, 2020; James et al., 2019; Keijzer et al., 2013; Levin, 2021; Lyon, 2006, 2015). Moreover, a rich continuum of intermediate forms can be created by chimerizing biological and technological material in many different combinations (Clawson & Levin, 2023; Nanos & Levin, 2022), further eroding the notion of a binary, categorical separation between engineered and biological capabilities. The nascent field

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of Diverse Intelligence seeks invariants across evolved, engineered, and hybrid systems to determine what all agents have in common, regardless of their composition or provenance, and thus better to understand the origin and scaling of embodied minds (Levin, 2019). Beyond fundamental knowledge, this is also an essential step toward being able to recognize, repair, create, communicate with, and ethically relate to an enormous space of extant and forthcoming beings ranging from human cyborgs to synthetic life forms, Artificial Intelligences (AIs), and possible exobiological beings (Clawson & Levin, 2023).

For the purposes of this study, "intelligence" refers to some degree of competency in navigating a problem space so as to meet adaptive goals despite barriers, perturbations, and unexpected challenges (James, 1890). It focuses on problem-solving as an observable behavioral competency, not on the affect, first-person perspective, or playful exploration aspects which can occur in advanced cognitive beings. The goal of using such a definition is aligned with cybernetic approaches (Rosenblueth et al., 1943) that seek frameworks in which degrees of intelligence, from passive and random behavior to high-level metacognition, can be empirically studied in a broad range of unconventional forms. Human beings have much practice and skill in recognizing conventional intelligence implemented as classic "behavior"; we easily detect it in the behavior of medium-sized objects moving at medium speeds in the 3-dimensional world. However, our evolutionary history, our outward-pointing sense organs, and our cognitive structure all make it difficult to detect unconventional intelligences that operate in novel embodiments, exist at different spatio-temporal scales, or live in unusual problem spaces such as physiological or anatomical morphospaces (Fields & Levin, 2022). In particular, while we have neuroscience and folk theory-of-mind for predicting the competencies of the collective intelligence of neural systems (i.e., animals with brains), we have no mature science that enables us to predict either the goals, or the degree of competency in pursuing those goals, of other kinds of systems.

Great strides have been made in understanding how complexity can emerge from simple local rules (Anderson, 1972; Kauffman, 1993; Kelty-Stephen & Dixon, 2012; Prokopenko et al., 2009; Ulanowicz, 2007). However, most of the emphasis to date has been on the emergence of phenomena at the lower end of degrees of the ladder of agency (Rosenblueth et al., 1943). Beyond simple emergent complexity, such as that seen in static structures like fractals, lie second-order behaviors that serve as the origins of goals, preferences, valence, memory, and other phenomena that scale up to familiar cognitive systems (Arnellos & Moreno, 2015;

Baluška & Reber, 2021; Barandiaran et al., 2009; Fields, 2014; Kauffman & Clayton, 2006; Lyon & Kuchling, 2021; Newman, 2023; Repp & Knoblich, 2007; Sultan et al., 2022). Here, in keeping with an emphasis on basal (minimal) cognition, "goal" is used not to refer to a high-order, metacognitive "known purpose" as seen in human behavior, but rather in its minimal cybernetic (Rosenblueth et al., 1943) definition of a target state that a system has some ability to reach, despite a range of challenges. Learning to predict and control the goals of collective systems—especially newly engineered systems—is likely to be of existential importance to human flourishing over the coming decades in areas ranging from swarm robotics to AI systems to bioengineered tissues (Ebrahimkhani & Levin, 2021; Gumuskaya et al., 2024).

Diverse Intelligence research includes the use of very minimal models to understand how problem-solving capacities can arise from the interaction of components at various levels (Levin, 2022). These include synthetic droplets, molecular chemotaxis, and other simple systems in addition to the study of biological pathway models and whole cells and tissues (Biswas et al., 2021, 2022; Brancazio et al., 2019; Fan et al., 2020; Hanczyc, 2014; Krist et al., 2021; McGivern, 2019; Meredith et al., 2020; Watson et al., 2010).

One such system involves the collective behavior of cells during morphogenesis, such as embryonic development, regeneration, metamorphic remodeling, and cancer suppression (Levin, 2023a; 2023b; 2023c). What all of these phenomena have in common is the ability of cells (themselves composite, agential materials (Davies & Levin, 2023)) to work collectively to achieve specific anatomical endpoints (Levin, 2023b), such as re-growing a limb and then stopping once the correct structure is complete (Birnbaum & Sanchez Alvarado, 2008), or remodeling a tail transplanted to the flank into a limb—the structure more appropriate to its new global location (Farinella-Ferruzza, 1956). Crucially, this is not just open-loop emergence, but closed-loop control and error-minimization: cellular collective behavior in anatomical morphospace exhibits numerous abilities to solve problems (that is, to meet goals despite perturbations) in ways seen in other collective intelligences (Fields & Levin, 2023; Levin, 2023b). For example, tadpoles which have the position of their facial features scrambled spontaneously re-arrange to the correct positions as they metamorphose into frogs (Pinet et al., 2019; Vandenberg et al., 2012). Examples abound of cells taking actions via molecular, cellular, and tissue-level actuators in order to reach a specific target state despite perturbations or changing circumstances (reviewed in (Levin, 2023b)). Thus, it has been proposed that morphogenesis is the behavior of a collective intelligence of cells in anatomical

morphospace, and that understanding and learning to exploit the problem-solving competencies of living tissues offers the opportunity for significant advances in regenerative medicine of cancer, traumatic injury, and birth defects (Lagasse & Levin, 2023; Mathews et al., 2023).

A large body of existing work explores the complex behavioral responses and capacities of tissues, cells (Bugaj et al., 2017; Koseska & Bastiaens, 2017), and even of molecular pathways (Biswas et al., 2021, 2022; Csermely et al., 2020). However, all of these systems and their internal subsystems are quite complex, exhibiting a likely endless variety of new details which could be responsible for the observed behaviors. To understand the necessary and sufficient dynamics for competencies to emerge requires insights from even more minimal systems—ones in which all of the components and their interactions are known and precisely trackable. Especially useful models for this research agenda leave no room to posit additional explicit mechanisms, or substrates encoding behavioral policies or goals, that have simply not been discovered yet. Thus, we are interested in toy models of collective decision-making that are entirely transparent, to gain insight into the lower bound at which unexpected behavior and problem-solving competencies can arise which may be relevant to cellular swarms.

Here, we abstract one key property of regulative morphogenesis: the ability to produce an anatomical structure with a precise order of components along one axis. For example, development or metamorphosis results in a tadpole or frog in which all of the organs are placed in a specific order along the anterior-posterior axis (Figure 1). For the purpose of modeling, we are agnostic as to whether this behavior occurs from scratch, such as during embryogenesis, or by unscrambling existing components (such as during metamorphosis and regenerative remodeling).

We abstract this task, undertaken by cells which can re-arrange the organs as needed even when starting from highly abnormal initial configurations (Pinet & McLaughlin, 2019; Vandenberg et al., 2012), as a *sorting algorithm*. We use traditional sorting algorithms, as studied by countless computer science students, as a minimal system, and we study which unexpected, novel competencies these familiar algorithms might have in order to explore the idea that novel capabilities may lie in systems that we think we fully understand because we designed them.

The use of a linear array of objects which can determine the overall direction of the collective matches the well-known ability of cells to organize and polarize a primary developmental axis (e.g., anterior-posterior, or left-right) (De Robertis et al., 1989), via mechanisms such as morphogen gradients and planar polarization (Eldar et al., 2004). To improve the fit between this model and the abilities of regulative development, we break two critical assumptions normally used with sorting algorithms. First, instead of a central algorithm operating on an array of numbers it can see and control in its entirety, we implement a distributed algorithm that is executed, in parallel, by each number (i.e., cell) with local knowledge of its environment. In lieu of a central controller, cells have individual preferences about the ordering between them and their neighbors. Second, we do not assume that each operation succeeds—that is, we (like biology) implement an unreliable substrate, in which some cells are defective and may not obey when the rules tell them to move. We then quantitatively investigate the ability of these algorithms to sort an array of integers.

Our goals here are: (1) to establish a proof of concept for taking a system which seems simple and well-understood, and for using empirical experiments to identify that system's novel capabilities, goals, behaviors, and failure modes (Abramson & Levin, 2021); (2) to gain insight into the dynamical process of establishing a linear axis, so that the relevant dynamics could be better understood by developmental biologists and synthetic bioengineers (Davies & Glykofrydis, 2020; Doursat et al., 2013; Doursat & Sánchez, 2014; Ho & Morsut, 2021; Kamm et al., 2018; Santorelli et al., 2019; Teague et al., 2016; Toda et al., 2018); (3) to understand how decentralized, agent-based systems can solve morphogenetic control tasks; (4) to determine how noise and unreliability in the medium is handled by such algorithms (robustness); and (5) to identify new behaviors and competencies that are not encoded overtly in the algorithm. Although ours is a very simple system, especially compared to any real biology, the benefit of these sorting algorithms is precisely that they are simple, easy to understand, and offer no place for additional complexity to hide (unlike in real cells). Here we show that even familiar, simple algorithms have the surprising ability to deal with perturbations in order to meet the algorithmically specified goals, and also exhibit novel behaviors that are not directly encoded in the algorithm.

2. Definitions of terms

Term	Definition
Cell	Basic element to be sorted by the sorting algorithms. Each cell has an integer value property which is used for the comparison during the sorting process.
Cell-view sorting algorithm	Every cell follows an algorithm for making decisions as to how it can swap positions with neighbors to optimize local monotonicity of the integer values. We call it a cell-view algorithm because state evaluations and move decisions are made from the local perspective of each cell, rather than from the global perspective of a single, omniscient top-down controller.
Algotype	Each cell utilizes one of several sorting algorithms to dictate its movement. This "Algotype" is constant for the life of the cell (i.e. roughly equivalent to a fixed genetic or phenotypic identity).
Cell value	The fixed integer value of each cell, which guides how it behaves in any of the algorithms (which are designed to order the cell values in sequence).
Experiment	Each sorting process starts from a randomized array of cells and runs until it meets the stop condition.
Active cell	A cell that behaves normally during the sorting process as determined by the embedded cell-view sorting algorithm.
Frozen cell	A cell that does not always move, even though the algorithm tells it to move (representing a damaged cell). There are two types. A passive Frozen Cell will not move on its own (will not initiate a move), but other cells are able to move it. A stuck Frozen Cell can neither proactively move itself nor can it be moved by another cell.
Delayed gratification	The ability to temporarily go further away from a goal in order to achieve gains later in the process. None of the algorithms have this capability explicitly coded; where present, it is an emergent property of the algorithm dynamics.
Cell aggregation	A metric of the degree to which the same type of cells cluster together (spatial proximity) during the sorting process when different Algotypes are mixed into the same sorting experiment.
Probe	The programming object which is created to monitor and record the status of the sorting process.

3. Methods

We developed a sorting algorithm evaluation system and implemented the cell-view sorting algorithms in *python 3*. The following sections provide more details about the model of the sorting platform, the structure of the sorting cells, the process of the evaluation, and the experimental test methods. https://github.com/Zhangtaining/cell_research

3.1. Sorting evaluation system

We designed the sorting evaluation system to consist of 2 parts: the sorting algorithm execution (which performs the sorting on a given array) and the sorting process evaluation (which oversees and analyzes the sorting across trials).

1. Sorting algorithm execution

We use three variables (Position, Value, and Algotype) to describe each cell's status. Initially, all cells are assigned values for these variables. Each cell has a unique Position (i = 0, 1, 2…L-1), while Value and Algotype may be the same as others. During sorting, Value and Algotype remain constant, and only the Position changes due to movement.

The sorting execution part chooses the specified sorting algorithm to perform the sorting experiments based on the given number of experiments and the Frozen Cells.

The execution subsystem passes a Probe object to each experiment run, and the Probe is designed to record each step of the sorting process.

After the sorting process ends, the information collected by the Probe is stored as a .npy file.

2. Sorting process evaluation

The input for the evaluation is configurable including the algorithms to evaluate, the number of Frozen Cells, and the evaluation types. The evaluation process fetches the files based on the specified inputs. The evaluation subsystem picks up the corresponding files based on the inputs that contain the sorting process info. Then the given evaluation is performed for the data in those files.

3.2. Traditional sorting algorithms

In conventional sorting algorithms, a single top-down controller implements a set of rules to move cells
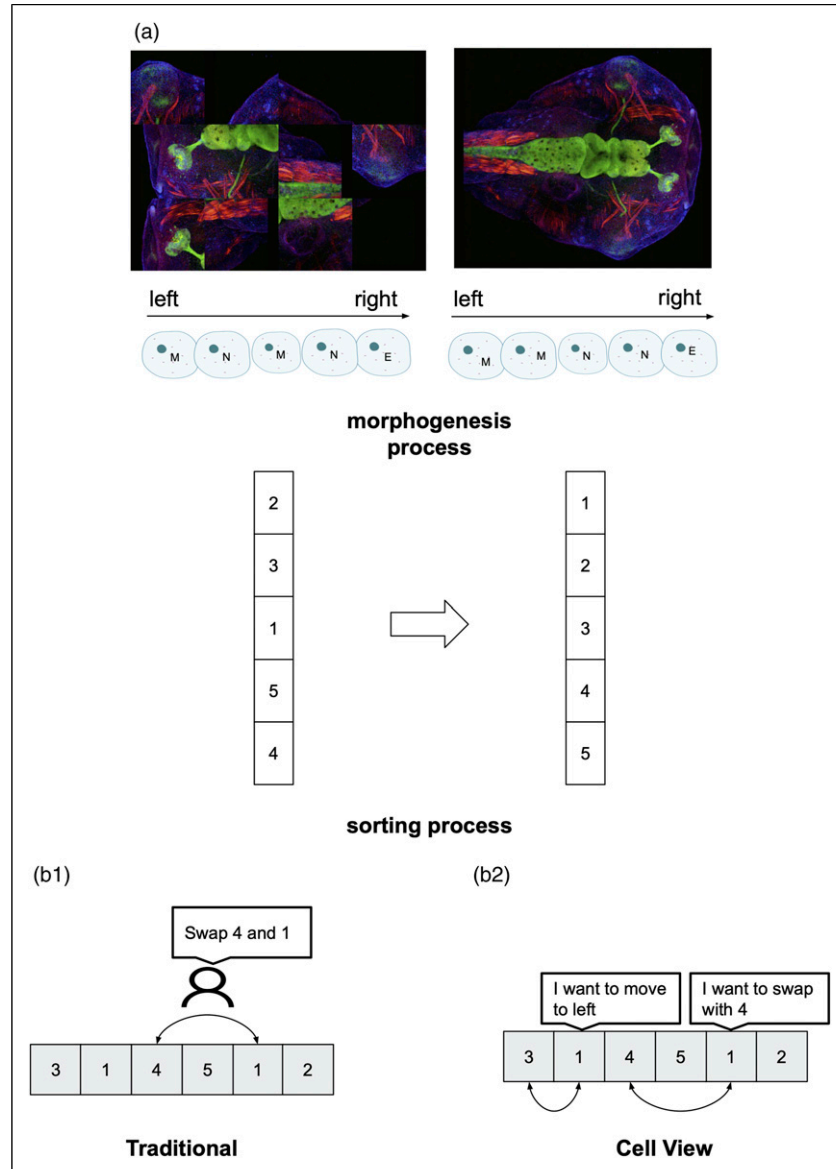
Figure 1. Morphogenesis modeled as a sorting process. In our abstraction, each element of the array was a cell, possessing an integer value that sets its final relative position along a 1-dimensional axis (simulating the correct target morphology that regulative development attempts to implement along the anterior-posterior axis). Biologically, this corresponds to the tissue identity (eye, brain, nostril, etc.) that determines which neighbors each type of tissue expects to find, and thus set the stop condition for remodeling once those neighbor relations are attained. (a) The process of morphogenesis during development, repair, and metamorphosis included cells relocating to positions at which movement would cease (as determined for a given species) (Rankin, 2015). Here, "E" = cells which will form the eyes; "N" = cells which will form the nose; M = mouth cells. (b1) Traditional sorting algorithm performs as a top-down controller that makes decisions about the actions of the elements. (b2) Our cell-view version of this algorithm delegates the decision directly to each element, and the elements act based on their embedded logic and local conditions. Tadpole head organ photo used with permission from Dr. Helen Rankin, https://www.nikonsmallworld.com/galleries/2015-photomicrography-competition/transgenic-xenopus-laevis-tadpole-head-expressing-green-neurons.

around. The traditional algorithms we used as our baseline were:

- Bubble Sort

```
procedure bubbleSort(A: list of sortable items)
    n = len(A) # Get total number of items
    swapped = False
    # Keep looping the whole list until no swapping happened.
    while not swapped
        # Check each item with its previous neighbor
        # So we start from the item on index 1 to last item (index starts from 0)
        for i in range(1,  n):
            if A[i - 1] > A[i]:
                swap(A[i - 1], A[i])
                record swap
                swapped = true
end procedure
```

- Insertion Sort

```
procedure insertionSort(A : list of sortable items)
    n = len(A) # Get total number of items
    for i in range(1, n): # Start from index 1 to end of the list (Index starting from 0)
        value = A[i]
        j = i − 1 # Start checking all the elements before the index i
        while j >= 0 and A[j] > value:
            swap(A[j + 1], A[j])
            record swap
            j = j − 1
end procedure
```

- Selection Sort

```
procedure selectionSort(A : list of sortable items)
    n = len(A) # Get total number of items
    for i in range(0, n-1):
        minIndex = i
        # go over all elements after index i and find
        # the min value to swap
        for j in range(i+1,  n):
            if A[j] < A[minIndex]:
                minIndex = j
        if minIndex != i:
            swap(A[i], A[minIndex])
            record swap
end procedure
```

3.3. Implementation of cell-view sorting algorithm

We sought to study the sorting process in a more biologically grounded (distributed) architecture, where each cell is a competent agent implementing local policies. We thus defined three bottom-up versions of common sort algorithms, where actions take place based on the cells' perspective (view) of their environment within the array. We used multi-thread programming to implement the cell-view sorting algorithms. 2 types of threads were involved during the sorting process: cell threads are used to represent all cells, with each cell represented by a single thread; a main thread is used to activate all the threads and monitor the sorting process. The cell threads were multiple instances of the same sorting class (i.e., each cell had the same Algotype, which determined which of the sorting algorithms that cell used to

guide its behavior). To ensure each cell acquires the lock randomly, regardless of the python scheduler, we ask each cell thread to generate their own random number (0–1) every time before it tries to acquire the lock. Only when the random number is smaller than 0.5 can the cell get the lock. This ensures that each cell gets the lock and performs its behavior randomly. Inspired by the 3 traditional sorting algorithms described above, we designed 3 kinds of cell-view sorting algorithms (Figure 2):

- Cell-view Bubble Sort

```
procedure run()
    while True:
        random acquire lock
        targetPosition = currentPosition + 1
        if currentValue > value at targetPosition:
            swap current cell with the cell at target position
            record swap
        release lock
end procedure
```

- Cell-view Insertion Sort

```
procedure run()
    is_enabled = False
    while True:
        random acquire lock
        if is_enabled or all left side sorted:
            is_enabled = True
            targetPosition = currentPosition - 1
            if currentValue < value at targetPosition:
                swap current cell with the cell at target position
                record swap
        release lock
end procedure
```

- Cell-view Selection Sort

```
// Each cell has an current target position and initial value is at the most left of the list.
currentTargetPosition = 0 # Expecting itself has the smallest value and deserve position 0
procedure run()
    while True:
        random acquire lock
        targetPosition = currentTargetPosition
        if currentValue < value at targetPosition:
            swap current cell with the cell at target position
            record swap
        else:
            currentTargetPosition += 1 # Lower the expectation to next right position.
        release lock
end procedure
```

The sorting process was set up in the main thread. All cells' threads were activated and killed from there.

procedure main()

```
A : list of sortable items
    cells = []
    for num in A:
        c = cell type initiation(num)
        cells.append(c)
        for cell in cells:
            cell.run()
    // Since the cell thread won't stop by themselves, we need to have the main thread keeps
    // monitoring the sorting process and stop all threads once the cells are sorted.
    while cells not sorted:
        wait(10)
end procedure
```

We also introduce the Frozen Cell concept in the following study. The implementation of this concept is in the swap function:

- Traditional sorting algorithms
  procedure swap(i, j, frozenList)
     if i in frozenList or j in frozenList:
        return
     request to swap
  end procedure

- Passive Frozen Cell
  procedure swapTo(target)
     if self is frozen:
        return
     request to swap
  end procedure

- Stuck Frozen Cell
  procedure swapTo(target)
     if self is frozen or target is frozen:
        return
     request to swap
  end procedure

3.4. Evaluation metrics

To quantify the comparison between traditional sorting algorithms and their cell-view versions, we utilized the following metrics to evaluate the performance of those algorithms.

- Total Sorting Steps, Average, and Standard Deviation

We defined each swap as a sorting step, and we used the Probe to record the total number of sorting steps for each experiment. Depending on the experiment (as stated in Results), we counted movement, or movement + comparison, as individual Steps. By comparing the average and standard deviation of the total steps, we derive the efficiency of sorting performance. We use c_i to represent for the count of the sorting steps for Experiment i, and N for the total number of sorting experiments. Then we get the equation for average sorting steps C and standard deviation s

$$C = \frac{\sum_{i=1}^{N} c_i}{N} \qquad (1)$$

$$s = \sqrt{\frac{\sum_{i=1}^{N}(c_i - C)^2}{N-1}} \qquad (2)$$

- Monotonicity and Monotonicity Error

Monotonicity is the measurement of how well the cells followed monotonic order (either increasing or decreasing). The monotonicity error is the number of cells that violate the monotonic order and break the monotonicity of the cell array. Unlike the total sorting steps, the monotonicity error can be measured at each time step. The following formula shows the calculation for the monotonicity error for increasing order sequence. V_i stands for the value of cell at position i, and n represents the total cells number. The maximum error is $n - 1$ when the list is in reverse order

$$E = \sum_{i=1}^{n-1} V_i < V_{i-1} \, then \, 1 \, else \, 0 \qquad (3)$$

- Sortedness Value

Sortedness Value is defined as the percentage of cells that strictly follow the designated sort order (either increasing or decreasing). For example, if the array were completely sorted, the Sortedness Value would be 100%. V_i stands for the value of cell at position i, and n represents for the total cells number

$$S = \frac{\sum_{i=1}^{n-1} V_i > V_{i-1} \, then \, 1 \, else \, 0}{n} = 1 - \frac{E}{n} \qquad (4)$$

- Sortedness Delayed Gratification

Delayed Gratification is used to evaluate the ability of each algorithm to undertake actions that temporarily increase Monotonicity Error to achieve gains later on. Delayed Gratification is defined as the improvement in Sortedness made by a temporarily error-increasing action. After measuring the Sortedness for each time step of the sorting process, we can get a Sortedness array. For any Sortedness mono-increasing subarray, we use S_{ii} to represent for the first Sortedness value in the subarray and use S_{ij} to represent for the last Sortedness value in the subarray. The total Sortedness change after a consecutive Sortedness value's increasing is $\Delta S_{increasing} = S_{ij} - S_{ii}$. We use S_{di} to represent for the first Sortedness value in the decreasing subarray after the increasing and use S_{dj} to represent for the last Sortedness value in the decreasing subarray. The Sortedness value decreasing starting from last peak is $\Delta S_{decreasing} = S_{di} - S_{dj}$

$$DG = \frac{\Delta S_{increasing} - \Delta S_{decreasing}}{\Delta S_{decreasing}} \qquad (5)$$

- Aggregation Value

In sorting experiments with mixed Algotypes, we measured the extent to which cells of the same Algotype aggregated together (spatially) within an array at any given
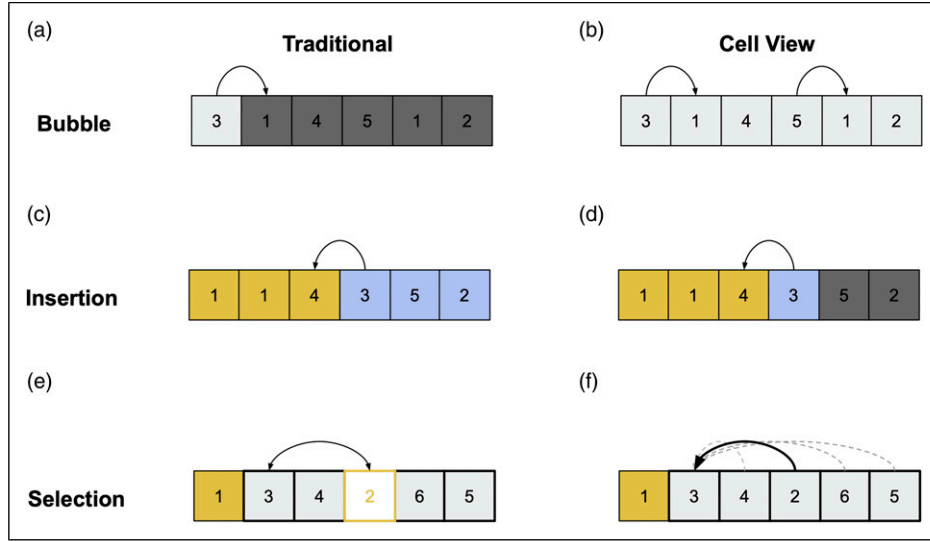
Figure 2. Traditional sorting algorithms implemented as bottom-up drivers for cell behavior. In conventional sorting algorithms, a single top-down controller implements a set of rules to move cells around. We sought to study the sorting process in a more biologically inspired architecture, where each cell is a competent agent implementing local policies. We thus defined three bottom-up versions of common sort algorithms, where actions take place due to cells' perspective (view) of their environment within the array. Shown here are examples of how cells are moved (traditional sort) or move themselves (cell-view sort) in each case. All cells have a chance to move at each time step (parallel). (a) In the traditional Bubble sort, the top-down controller chooses the first element on the left that is bigger than its right neighbor and keeps swapping it to the right until the right neighbor has larger or similar value, then repeats that process until all elements are in order. (b) For the cell-view Bubble sort, all cells (elements) run in parallel and can compare their value with their neighbors', and decide to swap to the left or right based on that value comparison. The sort is completed when no cell can move. (c) In the traditional Insertion sort, the controller splits the array into two parts: sorted and unsorted. At the beginning, only the first element on the left is considered "sorted" and all remaining elements in the array are considered "unsorted." For each step, the controller chooses the left-most element from the unsorted part, and then keeps swapping it to the correct place in the sorted part of the array. (d) In the cell-view Insertion sort, each cell knows all cells on its left, and starts to swap with its left neighbor (if its value is smaller) when all cells to its right are sorted. (e) In the traditional Selection sort, the controller finds the smallest element (for an increase sort) from unvisited elements and puts it into the next position of the sorted part of the array for each step. (f) In the cell-view Selection sort, every cell tries to swap to its own current target position. The swap will be denied if the current cell at that position has a smaller value, and then the current target position of the cell shifts the right of the original current target position.

time. We defined Aggregation Value as the percentage of cells in the array having a directly adjacent left neighbor cell that were all the same Algotype. T_i stands for the algorithm type of cell at position i and n represents for the total number of cells

$$A = \frac{\sum_{i=1}^{n-1} T_i = T_{i-1} \; then \; 1 \; else \; 0}{n} \qquad (6)$$

3.5. Statistical hypothesis test methods

We applied standard statistical hypothesis methods, z-test, to evaluate the significance of the differences we report.

4. Results

We first analyzed the results both from our Cell-View Sorting Algorithms and from the traditional versions of those sorting algorithms, with the goal of determining whether the cell-view versions worked (Figure 3), and

comparing measures of efficiency, error tolerance, and Delayed Gratification with those of their canonical counterparts. We also examined additional aspects of these algorithms' traversal of the sorting space, by characterizing their morphological structure during the process.
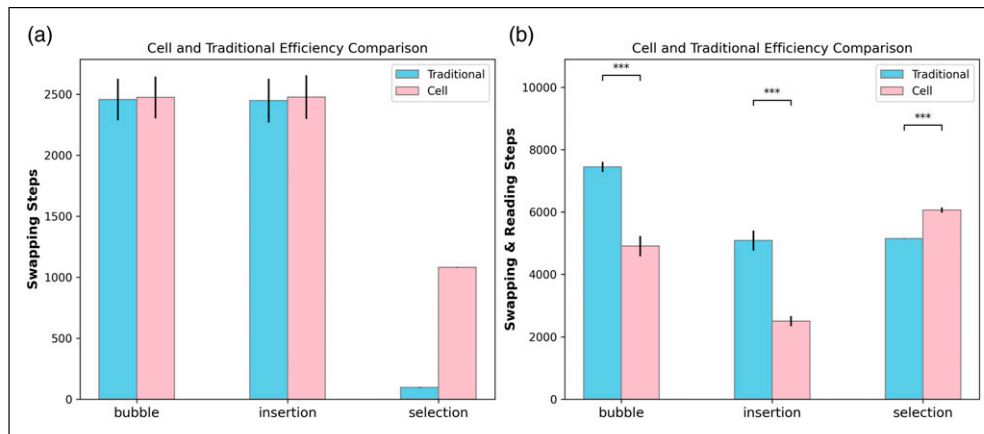
4.1. Efficiency comparison

We found that our self-sorting arrays could indeed complete the task, and proceeded to characterize their efficiency at doing so. We used the total sorting steps that each algorithm needed to complete the sorting process for 100 elements ($n = 100$) in each experiment and repeated the experiments 100 times ($N = 100$) independently for each sorting algorithm. The initial values of the elements are random permutation from 1 to 100 without duplication. Then we used the average sorting steps (C) of the 100 pairs of experiments for traditional algorithms against Cell-View algorithms with same initial values. The value of average sorting steps (equation (1)) indicated the efficiency of the algorithm (Figure 4).
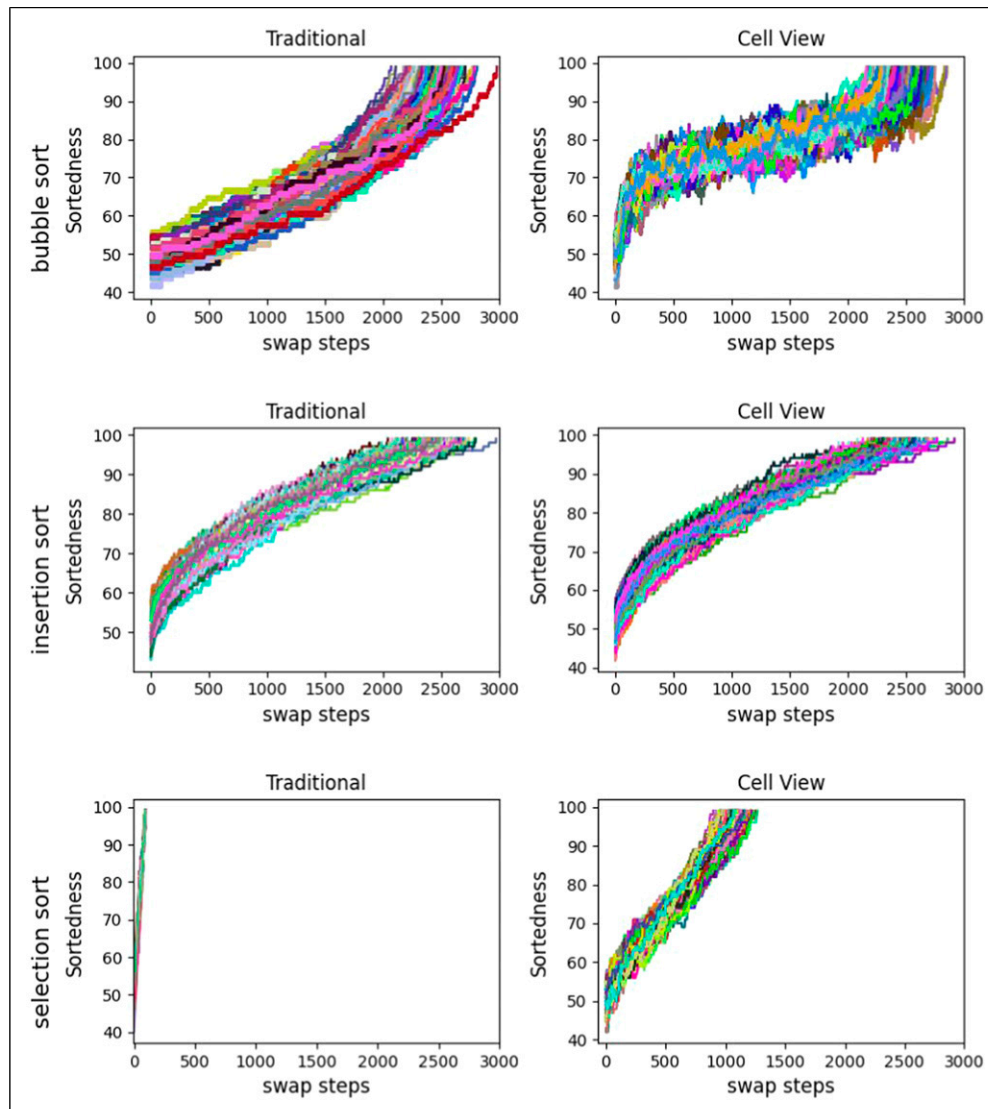
Figure 3. Visualizing the sorting process as movement through sequence space. Much as biological morphogenesis can be described as a trajectory through anatomical morphospace, here we view the progressive sorting process as the ability of traditional or cell-view sorting algorithms to navigate the state space of sequences toward the eventual goal of monotonicity. We define the degree of sequential order in the array of data, at any given time, as its *Sortedness*, here plotted on the *Y* axis. Each plot indicates the trajectory of 100 repeated experiments (sorting process on a random input number sequence, with no repeat digits). Just as their traditional counterparts do, cell-view sorts successfully completed the sorting process, navigating from a random state to the 100% fully sorted state. Top row shows the comparison of Sortedness change during the sorting process between traditional Bubble sort and cell-view Bubble sort. Middle row shows the comparison of Sortedness change during the sorting process between traditional Insertion sort and cell-view Insertion sort. The difference between the two graphs is relatively small, because the implementation of cell-view Insertion sort always keeps the left side of the array sorted and allows one cell to join the sorted side each time, which is very similar to the traditional Insertion sorting algorithm. Bottom row shows the comparison of Sortedness change during the sorting process between traditional Selection sort and cell-view Selection sort. The major difference between these two graphs is that the cell-view sorting process needs more swaps to complete the sort, because every cell can move to its current target position and be swapped away when another cell with smaller value has the same current target position.

Figure 4. Efficiency comparison between traditional and cell-view sort. 100 experimental repeats were performed in three kinds of sort, in traditional and cell-view modes, to compare efficiencies of each method. When comparing only the active moves taken (a), it is seen that cell-view sort is almost exactly as efficient as the traditional version for Bubble and Insertion sort ($p = .24$), but is less efficient for Selection sort (the Z-test statistical value is 120.43, and p-value is 0). When comparing comparisons as well as moves (corresponding to the biological cost of sensing, as well as acting), the cell-view versions are actually *more* efficient for Bubble and Insertion Sorts (Z-test statistical values for bubble and insertion sort were -68.96 and -71.19, respectively, $p \ll 0.01$), while the cell-view version is *less* efficient ($z = 106.55$, $p \ll 0.01$) for Selection sort (b).

We used 2 different ways to count the sorting steps: one counts only swaps as sorting steps; the other counts both swaps and comparisons. When we counted only swapping steps, the statistical values comparing the efficiencies of Bubble and Insertion sort were 0.73 and 1.26 (p-values were 0.47 and 0.24, respectively), revealing no significant difference between their performance. This indicates that the efficiency is very similar between traditional and cell-view versions of Bubble and Insertion sorting algorithms. However, cell-view Selection sort takes more swaps to complete sorting process than its traditional version by 11 times ($z = 120.43$, $p \ll 0.01$). Thus, we conclude that the cell-view Selection sort is less efficient than the traditional Selection sort.

The situation changed when we considered both reading (comparison) and writing (swapping) as costly steps, simulating the metabolic cost of both measurements and actions. In this comparison, the total steps taken to complete the sorting process of bottom-up versus traditional sorting algorithms were fewer by 1.5 and 2.03 times for Bubble and Insertion sort, respectively ($z = -68.96$, -71.19, $p \ll 0.01$ in both cases). For Selection sort, the total steps of the bottom-up version were greater by 1.17 ($z = 106.55$, $p \ll 0.01$). These results indicate that the cell-view Bubble and Insertion sorting algorithms are more efficient than the traditional versions. This is likely because traditional algorithms are using each element to compare with other elements, while cell-view algorithms will stop proactively comparing with other cells when they are on the target position. In contrast, the cell-view Selection sorting algorithm is less efficient than the traditional Selection sorting algorithm.

4.2. Error tolerance

To compare the error tolerance of the cell-view sorting algorithms with that of the traditional sorting algorithms, we introduced Frozen Cells into the sorting process. We ran the sorting Experiment 100 times ($N = 100$) for 100 cells ($n = 100$) using different numbers ($f = 1, 2, 3$) of Frozen Cells and then checked the average final monotonicity errors for the experiments with a given number of Frozen Cells. A higher monotonicity error indicates lower error tolerance (Figure 5). We found that all the cell-view sorting algorithms exhibited less monotonicity error than the traditional versions, from which we conclude that cell-view algorithms have higher error tolerance than the traditional versions.

By comparing the different cell-view algorithms, we saw that with passive Frozen Cells, the cell-view Bubble sort has the least monotonicity error (average value of 100 experiments was zero with 1 Frozen Cell, 0.8 with 2 Frozen Cells, and 2.64 with 3 Frozen Cells); and the cell-view Selection sort has the highest monotonicity error (average value of 100 experiments was 2.24 with 1 Frozen Cell, 4.36 with 2 Frozen Cells, and 13.24 with 3 Frozen Cells). With stuck Frozen Cells, the cell-view Bubble sort has the highest monotonicity error (average value of 100 experiments was 1.91 with 1 Frozen Cell, 3.72 with 2 Frozen Cells, and 5.37 with 3 Frozen Cells); and the cell-view Selection sort has the lowest monotonicity error (average value of 100 experiments was 1.0 with 1 Frozen Cell, 1.96 with 2 Frozen Cells, and 2.91 with 3 Frozen Cells). In conclusion, we can see that both Cell-view and Traditional algorithms have performed with high error tolerance. The cell-view Selection sort had the highest Error Tolerance

with stuck Frozen Cells, and that the cell-view Bubble sort had higher Error Tolerance with passive Frozen Cells.

4.3. Characterization of delayed gratification

Delayed Gratification (DG) is the ability to temporarily go further away from a goal to achieve gains later in the process (Figure 6). To compare the Delayed Gratification (DG) of cell-view algorithms and traditional algorithms, we calculated the Delayed Gratification based on the results of the error tolerance experiments mentioned above (Figure 7). All the algorithms showed the ability of Delayed Gratification. It is important to note that traditional sorting algorithms encounter difficulties when encountering frozen cells. The DG metric effectively demonstrates how the level of Sortedness changes as the sorting processes encounters these frozen cells. We use the results from the experiments we have done for the error tolerance to do the analysis. The average Delayed Gratification difference between the Cell-view and Traditional Bubble sort was found to be 0.16 ($z = 34.04$, $p \ll 0.01$). The difference between the Cell-view and Traditional Insertion sort was very small - 0.03 ($z = 0.60$, $p = .55$). The average DG difference between the Cell-view and Traditional Selection sort was 2.77 ($z = 17.21$, $p \ll 0.01$). From these results, we conclude that cell-view Bubble sort performs more DG than the traditional version, cell-view Insertion sort performs very similar amounts of DG as the traditional version, and cell-view Selection sort performs less DG than the traditional version.

A random walker will also sometimes move further from its goal and thus exhibit what may at first look like Delayed Gratification; in general, perturbative experiments are needed to distinguish these cases and understand what any behavioral system is really doing. To demonstrate DG as a problem-solving strategy, it must be shown to be performed specifically in the context of barriers, not just part of a stochastic strategy without feedback or context. Thus, we next compared the amount of DG observed for each algorithm in the context of different numbers of Frozen Cells: would the algorithm tend to temporarily back-track in Sortedness *more often when there are more broken cells in its environment?* We observed a clear trend of increasing average Delayed Gratification for the Bubble and Insertion sort experiments for both Traditional and Cell-view, and the Cell-view algorithms performed more Delayed Gratification during the sorting process. The average Delayed Gratification for cell-view Bubble sort was 0.24 with zero Frozen Cell, 0.29 with 1 Frozen Cell, 0.32 with 2 Frozen Cells, and 0.37 with 3 Frozen Cells (all average values are based on 100 repetitions). For Insertion sort, we saw that the average DG value was 1.1 with no Frozen Cell, 1.13 with 1 Frozen Cell, 1.15 with 2 Frozen Cells, and 1.19 with 3 Frozen Cells. However, we did not see a clear trend for either cell-view or traditional Selection sort. This reveals that Bubble and Insertion sort deploy Delayed Gratification in a context-sensitive manner—they do more backtracking specifically when faced with defective cells.

4.4. Mixed Algotype sorting: Analyzing chimeric arrays

We next introduce the notion of an "Algotype": this refers to one of several discrete algorithms that a cell may be using to control its behavior. Algotype is meant to be distinct from data quantities like a cell's numerical value (its genotype) or its current position (its phenotype); rather, Algotype reflects a cell's behavioral tendencies. Our use of bottom-up (distributed) control in the sort process allowed a new kind of experiment: a chimeric array in which different cells use different policies to achieve their objectives, analogous to biological experiments in which cells with different genetics or cell types were mixed in the same body (reviewed in (Nanos & Levin, 2022). We wondered: would chimeric arrays still self-sort, and what would be the behaviors of individual cells when their neighbors were using different algorithms? Note that cells had no explicit provision for detecting their own or their neighbor's Algotype explicitly. Because the Algotype is a meta-property not addressed in any way in the algorithm itself, its consequences only become evident through the cells' behavior over time.

At the beginning of these experiments, we randomly assigned one of the three different Algotypes to each of the cells, and began the sort as previously, allowing all the cells to move based on their Algotype (i.e., their individual sorting algorithm). The process was considered to be completed when all the cells are sorted, or no cell can find a better position to move. When all the cells stop moving, it means that the sorting process stopped. From the programming point of view, the main thread needs to check the array status twice to decide the array is not changing and kill all the process. In control experiments, we used precisely the same code but set both of the Algotypes to the same type (Bubble sort), to rule out any spurious effects due to the implementation and ensure that whatever differences we saw could be attributed to differences in the algorithm's behavioral policies.

The first observation from these experiments was that all of the Algotype combinations can completely sort the array (Figure 8(a), blue lines), demonstrating that components with different policies but the same goal can be mixed in the same collective without abrogating the ability to complete the system-level task.

We next checked the efficiency: do chimeric arrays function as efficiently as homogenous ones? We compared the number of swapping steps in mixed-Algotype experiments with those required to reach sorted state in experiments with a single Algotype. The average steps to
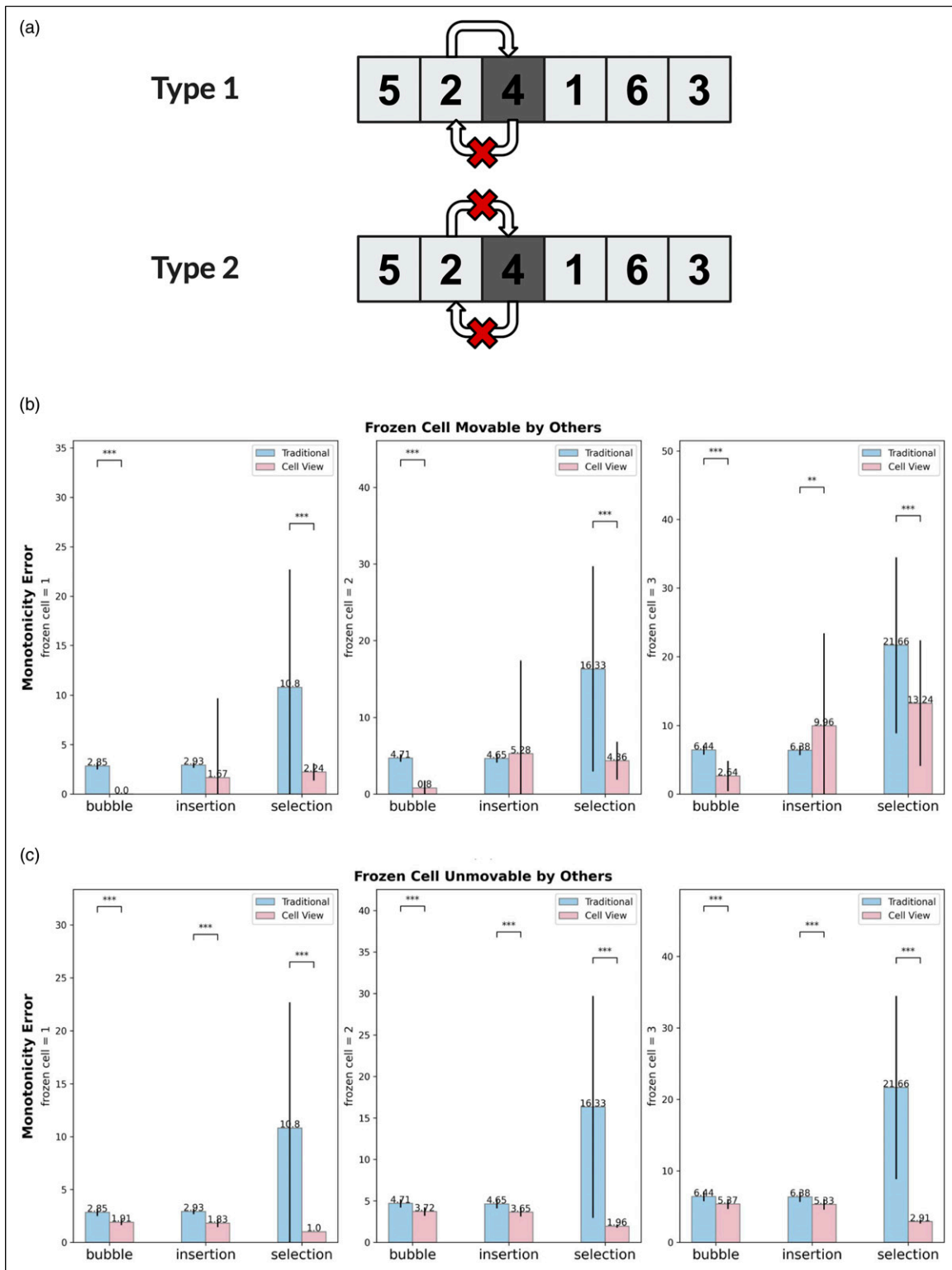
Figure 5. Cell-View algorithms have better sorting performance for sorting with Frozen Cells. Breaking the assumption of reliable media in traditional sorting algorithms enables exploration of emergent features of each algorithm in the face of errors: cells that need to move but cannot. We tested two kinds of "defects" (a): cells that can be moved by others but cannot initiate any swaps ("lack of initiative"), and cells that are completely broken and neither initiate nor participate in swaps initiated by others ("lack of motility"). (b) shows that when a Frozen Cell can be moved by others, the cell-view versions of the sorting algorithms have less monotonicity error than the traditional versions that is, the cell-view versions have higher robustness (error tolerance). The same graph also shows that among cell-view Bubble sort, Insertion sort, and Selection sort, the Bubble sort has the highest error tolerance, with the Insertion sort having next-highest and the Selection sort lowest. (c) shows that when the Frozen Cell is completely fixed, the cell-view versions of the sorting algorithms also have higher error tolerance than the traditional versions. Here, the cell-view Selection sort has the highest error tolerance.

complete a pure cell-view Bubble sort was 2448.8 ($N =$ 100 replicates). The average steps to complete a pure cell-view Insertion sort was around 2482.8 ($N =$ 100 replicates). The average steps to complete a pure cell-view Selection sort was around 1095.5 ($N =$ 100 replicates). For sorting with mixed Algotypes, the Bubble-Insertion mix took an average of 2476.02 steps to complete the sort ($N =$ 100 replicates). The Bubble-Selection mix took an average of 1740.9 steps to complete the sort ($N =$ 100 replicates). The Insertion-Selection mix took an average of 1534.77 steps to complete the sort ($N =$ 100 replicates). This revealed (Figure 8(b)) that the total number of steps used by mixed Algotypes sorts falls between the pure Algotype sort that takes the most steps and the pure Algotype sort that takes the fewest steps. Therefore, we conclude that the efficiency of a chimeric array is roughly the average of the efficiencies of its two component Algotypes (the efficiencies combine linearly).

We next looked for unexpected behaviors at the level of individual cells and groups of cells (corresponding to chimeric tissues within an organism) by examining the spatial location of cells with different Algotypes. Specifically, we computed the tendency of individual Algotypes to cluster together within the array as a way to determine if the Algotype has any influence on *how* those cells travel throughout the morphological space (Fields & Levin, 2022; Raup & Michelson, 1965; Stone, 1997) making up the array structure, during the array's travel through its sorting space. To check whether the same Algotypes tended to gather closely together during the sorting process (Figure 8(c)), we tracked the position of different Algotypes and repeated the experiment multiple times to check the average Aggregation Value during the sorting process. It is important to note that this is not something that we could have predicted a priori since none of the algorithms access the Algotype information of their own or neighboring cells—there are no explicit steps implementing clustering or any other kind of distribution.

As a negative control, we first ran the experiments using Algotypes that were in fact identical algorithms, as a sanity check to exclude the presence of irrelevant factors in the code (Figure 8(a), light pink line). We found that the peak mean Aggregation Value of the Bubble-Insertion mix was 0.61 (std dev 0.04, $N =$ 100), the peak mean Aggregation Value of the Bubble-Selection mix was 0.65 (std dev 0.05, $N =$ 100), and the peak mean Aggregation Value of the Insertion-Selection mix was 0.57 (std dev 0.04, $N =$ 100) (Figure 8(a)), revealing the baseline that corresponds to significant aggregation ($p \ll 0.01$) among arbitrary elements following precisely the same algorithm.

However, when we analyzed the aggregation values in arrays with chimeric Algotypes (consisting of cells using distinct algorithms to guide their behavior), we observed a remarkable and unexpected effect (dark red lines in Figure 8(a)). At the beginning, the aggregation was 0.5 in all cases, as befits the random assignment of Algotypes to cells. At the end, they were also 0.5 because the final state is a fully-ordered array, and the random assignment of Algotypes to initial values means that is impossible to maintain non-random Algotype assortment when sorting on the cells' values (which are randomly related to their Algotype). However, during the sorting process itself, we observed a significant ($p \ll 0.01$) difference of the aggregation values from the negative control: distinct Algotypes cluster together, to aggregated peak means of 0.72, 0.65, 0.69, and 0.62 in experiments mixing Bubble and Selection; Bubble and Insertion; Selection and Insertion; and all three, respectively. The maximum segregation occurs at 42, 21, 19 and 22% of the way through the process for Bubble and Selection; Bubble and Insertion; Selection and Insertion; and all three, respectively. We conclude that the different Algotypes exhibit aggregation (spatial clustering) during the sorting process even though the cells have no way to directly read each other's type and none of the algorithms refer to that property explicitly.

Why does this happen? Based on the above data on algorithm efficiencies, we first hypothesized that cells with a more efficient Algotype would move to the desired positions first, and as the sort continues, the cells with less efficient Algotypes would "catch up" and move the aggregated cells to their final position, splitting up the initial clusters. This hypothesis predicted that the aggregation would be entirely due to differences in the Algotypes' efficiency (as defined in Figure 4). On the other hand, there could be a more general phenomenon at play. To analyze this, we performed similar experiments as above but allowed assignment of duplicated values to cells (100 cells each individually given a value from 1 to 10 and guaranteed each value has 10 cells). Thus, there was no explicit reason for one cell of value "5" (for example) to appear before or after another cell of value "5" by the time the whole array was sorted. In other words, this version of the experiment allows any clustering to be maintained through to the end of the sorting process because a set of numbers could now be at the correct position in terms of their value and yet be arranged in any degree of clustering according to Algotype within that region (Figure 8(e)).

In the duplicate-value case, we observed that the Aggregation Values rose and did not decrease for the Bubble-Selection mix and the Insertion-Selection chimeric arrays. The average final Aggregation Values for Bubble-Selection and Insertion-Selection mixes were 0.65 and 0.7 (repeated 100 times), which is higher than the highest Aggregation Values of Bubble-Selection and Insertion-Selection mixes with non-duplicate values. This suggests that the efficiency hypothesis can be the explanation for the segregation, because the Selection algorithm is more efficient than Bubble and Insertion while the efficiency is similar between Bubble and Insertion based on our previous analysis.
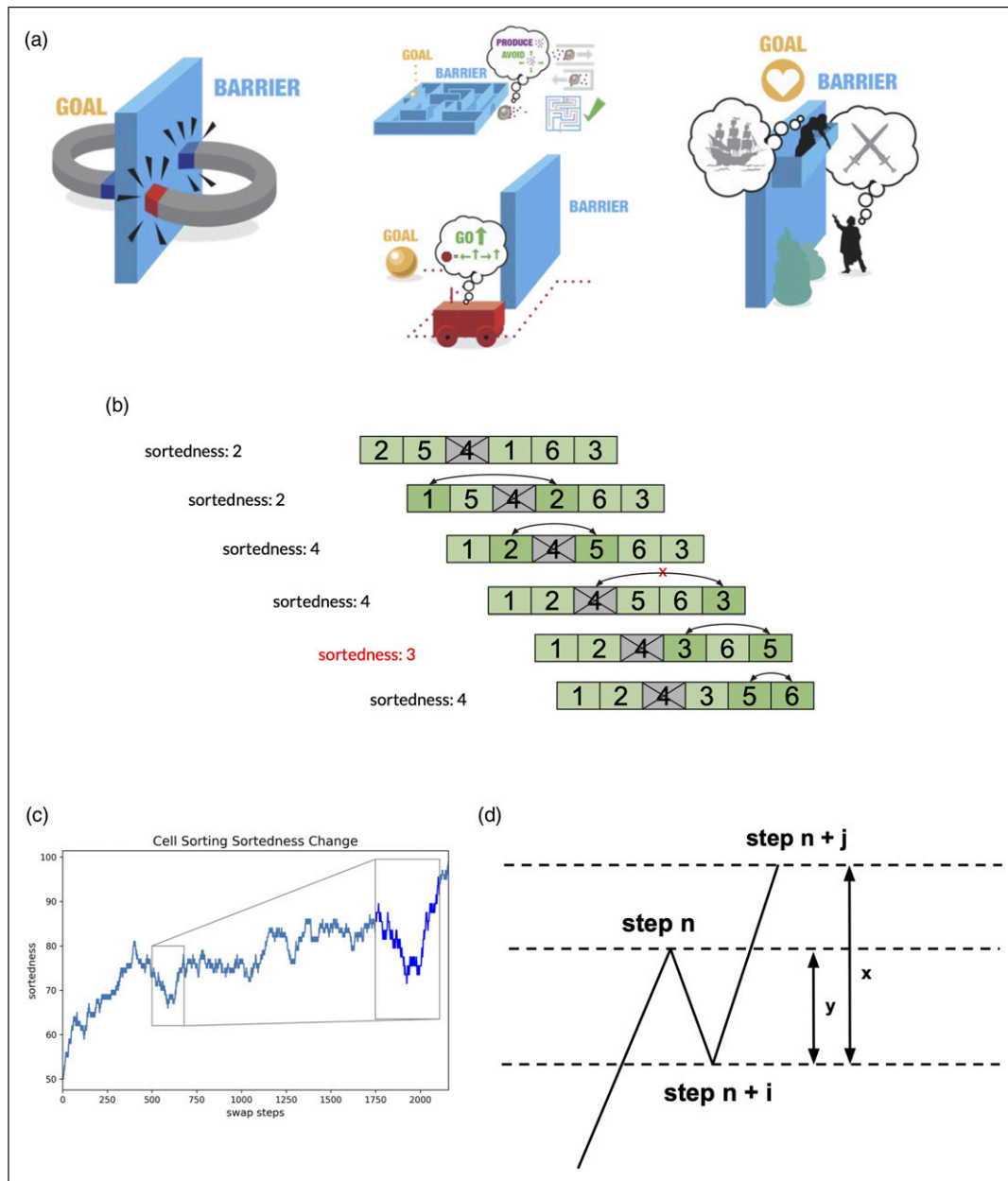
Figure 6. Characterization of delayed gratification during the sorting process. The ability of any agent to navigate towards its goal may include the property of *Delayed Gratification:* being able to temporarily go further away from its goal to achieve gains later in the process. (a) An illustration of William James' example of intelligence expressed as the ability to back-track from one's goals, which is not seen in simple energy-minimizing systems like magnets that will never go around a barrier to get closer (left-most panel). By contrast, temporary movement against their preference gradient is extensively seen in mammalian systems which can do complex planning (such as the Shakespearean story of Romeo and Juliet, who had to navigate complex physical and social barriers and affordances, in pursuit of their goals, right-most panel). This capacity exists to intermediate degrees in cells, tissues, and various autonomous vehicles (middle panel). This has been proposed as a key parameter for defining a generic notion of intelligence (James, 1890), and is seen in our self-sorting cellular agents able to go around Frozen Cells. Artwork in panel (a) is courtesy of Jeremy Guay of Peregrine Creative. (b) An example of going around a Frozen Cell (broken cell) using a short array, in which the cell with value 3 wants to swap to third position but it can't, so it swaps to fourth position, which is the next possible alternative, because all positions before third position should be occupied by smaller values and only positions after third position are possible to put 3 while fourth position is the most left position after third. This move temporarily decreases the Sortedness, until the cells with values 5 and 6 have swapped and caused Sortedness to increase again. (c) In the arrays with more Frozen Cells, there were multiple local reductions of Sortedness during the process. (d) Such backtracking and the subsequently realized gains can be used to define a *Delayed Gratification* index during the sorting process, which is calculated by using the total consecutive increasing value (x) of Sortedness after the drop minus the total consecutive decreasing value (y) as the numerator, and the total consecutive decreasing value (y) of Sortedness before the increase as the denominator.

The experiments in which repeated cell values were allowed also enabled us to ask another question. If we release the pressure of needing to be numerically sorted at the end, how high would the aggregation go? In the unique-value experiments, cells clustered with their same Algotype would eventually get pulled apart at the end to establish the correct final sort order. But, if there were multiple versions of each value with different Algotypes, they could remain next to each other while the whole cluster was in its numerically proper position. Thus, we could see how high the natural tendency for emergent aggregation is, when not artificially limited by the explicit algorithm's need to sort the values. We performed these experiments (Figure 8(d)) and observed maximal levels of 0.69, 0.63, and 0.71 in experiments mixing Bubble and Selection, Bubble and Insertion, Selection and Insertion, respectively. The maximum segregation occurred at 100, 13, and 100% of the way through the process for Bubble and Selection, Bubble and Insertion, Selection. This illustrates how the explicit goals of a mechanism, and its emergent behaviors, can be tested separately, and shows the ability for these emergent behaviors to aim for a specific parameter value (e.g., a segregation value of 0.69, not simply "maximize segregation").

The availability of chimeric arrays gave us one more interesting opportunity: what happens when the two different Algotypes are at cross-purposes in their traversal of sorting space—that is, when elements in the same array do not have the same goal? This corresponds to biological problems such as chimeras made of animals with different target morphologies (Levin et al., 2019; Nanos & Levin, 2022): what will the cells end up building? To test this in our model, we performed experiments using two mixed Algotypes, where one was made to sort in *decreasing* order while the other sorted in *increasing* order. We ensured that all 3 combinations started from random configurations of similar Sortedness, ~50%. At the end of the sorting process, none of them reached 100% sorted; instead, they ended with Sortedness values of 42.5, 73.73, and 38.31 in experiments mixing (a) Bubble sorting decreasingly and Selection sorting increasingly, (b) Bubble sorting increasingly and Insertion sorting decreasingly, and (c) Selection sorting decreasingly and Insertion sorting increasingly, respectively. We observed (Figure 9) that the sorting trajectories of these 3 combinations were very different. For Bubble and Selection, the Sortedness dropped sharply at the beginning of the sorting process, then increased for a short period. After the Sortedness value reached around 48, it dropped again and stopped at the value below 44. For Bubble and Insertion, the Sortedness value monotonically increased and stopped above 50, while for Selection and Insertion, the Sortedness value almost monotonically decreased during the sorting process and stopped below 50. Thus, the different Algotypes battle each other for some time but eventually reach a global equilibrium. This reveals how

competition among chimeric subunits with different emergent local goals can be studied in the context of a collective system with explicit algorithmic goals, and the overall stable states that can be achieved. The same experiment using repeated numbers (10 copies each of 1…10) gave similar results (Figure 10).

5. Discussion

Morphogenesis—the self-assembly of complex anatomies during development or regeneration—can be understood as collective behavior of cells traversing morphospace (Fields & Levin, 2022; Levin, 2023b). We constructed a simplified model of how cells or organs sort themselves along an axis during regulative development and regeneration (Pinet et al., 2019; Pinet & McLaughlin, 2019; Vandenberg et al., 2012) as being functionally similar to the task of sorting numbers along a number line. Organisms perturbed during development (for example, by moving cells out-of-place), or dissociated cells allowed to re-aggregate, often find their way to the specific target morphology (Levin, 2023b; Pezzulo & Levin, 2016). We used conventional sorting algorithms as a very minimal component of this repair process, and looked for behaviors from those algorithms that might be new to students of computer science who routinely utilize those algorithms. This strategy is part of the field of Diverse Intelligence in that it helps to recalibrate our intuitions about the complexity of underlying mechanisms that may be sufficient for basal competencies normally expected of advanced or even neuronally based systems, and also helps us see navigation of diverse kinds of problem spaces as bona fide *behavior* that can be probed via interventional strategies. This approach is relevant to other efforts addressing optimization problems in collectives of in silico agents or in morphological computation by materials (Daly et al., 2023; Lamport et al., 1982; Zampetaki et al., 2021).

We analyzed three such algorithms in their classical form, as well as in a new implementation where we discarded two ubiquitous assumptions in favor of more bio-realistic scenarios. First, instead of top-down algorithms that control an entire process as a single agent with a single algorithm (behavioral policy), we implemented the same algorithms from the cell's-eye view, as a local, distributed system in which each cell has preferences for what neighbors it will have, and has some capacity to move around in order to implement those preferences (Friston et al., 2015). While biology does have important examples of global control and top-down signaling (reviewed in (McMillen et al., 2021; Pezzulo & Levin, 2016)), many biological outcomes result from the activities of distributed, local agents. This perspective is implemented in many examples (Bessonov et al., 2015; Dalle Nogare & Chitnis, 2020; Doursat et al., 2013; Glen et al., 2019; Newgreen
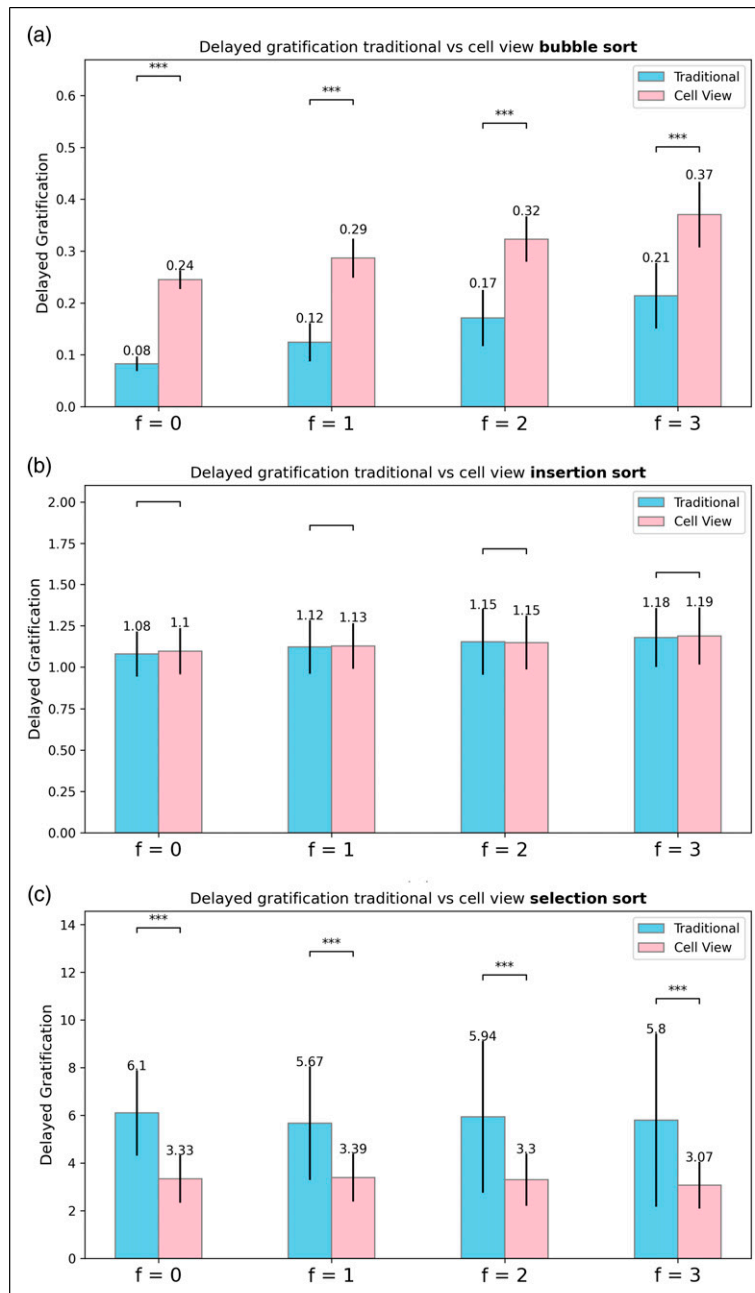
Figure 7. Delayed Gratification Comparison between Traditional and Cell-View Sort. Delayed Gratification is a characteristic shown in all the sorting algorithms for both traditional and cell-view, because all the experiments show some degree of Delayed Gratification. However, the Delayed Gratification is not merely evaluating the inefficient movements that occasionally go backwards, because the figures reflect the increasing trend of Delayed Gratification as the number of Frozen Cells increases. We use f stands for the number of stuck Frozen Cell in the figures. (a) shows that the cell-view Bubble sort gets more Delayed Gratification than the traditional algorithm ($Z = 34.04$, $p<<0.01$). (b) shows that the cell-view Insertion sort gets slightly more Delayed Gratification than the traditional algorithm ($Z = 0.60$, $p = .55$). Panels (a) and (b) show that the Bubble and Insertion sorts get more Delayed Gratification as the number of Frozen Cells increases. Panel (c) shows that the cell-view Selection sort has less Delayed Gratification than the traditional algorithm ($Z = -17.21$, $p<<0.01$) and has no clear relation between Delayed Gratification and the number of Frozen Cells. Comparing (a), (b), and (c), the Selection sort does the best in Delayed Gratification ($Z = 40.81$, $p<<0.01$), and the Insertion sort does better than the Bubble sort for both traditional and cell-view algorithms ($Z = 98.04$, $p<<0.01$).

et al., 2013; Pascalie et al., 2016; Thorne et al., 2007) of using agent-based modeling in biology (although the actual agency possessed by those components is typically assumed to be low).

There exist conventional parallel sorting algorithms, such as multi-threaded merge sort and multi-threaded bubble sort (Figure 2). However, these sorting algorithms closely resemble traditional single-perspective sorting algorithms. They distribute the sorting tasks among multiple threads to enhance performance, but still fundamentally operate in a top-down manner, in the sense that individual entries in the list have no algorithm of their own. By contrast, our approach gives each entry in the list the ability to "sort itself" according to its particular algorithm. Random sorting networks use a stochastic process to determine the order in which elements are compared and swapped. The implementation of our Cell-View sorting algorithms could be considered part of the random sorting algorithm class, because random threads can gain the lock to perform their own logic during the sorting process.

Second, we introduced the notion of damaged or malfunctioning cells that cannot move even when the algorithm says they should. While unreliable computing is an existing field (Armstrong, 2003; Brown et al., 2015; von Neumann, 1952; Wang, 2014), the standard study of sorting algorithms assumes that the steps are followed correctly. By contrast, biology excels at managing a highly noisy, unreliable media at every scale (Noble, 2021; Noble & Noble, 2018), utilizing this condition as an important aspect of evolving problem-solving machines (not unique solutions) (Levin, 2023c). In biology, the noisiness of the microenvironment is a feature, not a bug, because it forces evolved architectures to be highly competent at pattern completion and repair, in physiological, anatomical, and behavioral contexts. The ability to overcome novelty and error (Levin, 2023b; Pezzulo & Levin, 2016), within the developmental layer between the genome and behavioral/functional phenotypes, hides structural information from selection and encourages evolution of multi-scale competency mechanisms that can do their jobs despite errors in the genome. This fascinating ratchet of continuously increasing problem-solving capacities, and the resulting de-coupling between selection and the genomic hardware specifications (Frank, 2013, 2018, 2019; Shreesha & Levin, 2023), could likely be exploited in future bio-inspired computational platforms.

We evaluated the Sortedness of the input array as a measure of the traversal of the algorithm through its problem space, and performed experiments which illustrate how even minimal, deterministic systems can be tested for novel behavioral competencies. First, we found that a cell-level version of algorithm does, in fact, work: it completes the task.

We also assayed an important aspect of intelligence: the ability to, when faced with a Frozen Cell, go around it in a manner that temporarily takes one further from the goal (Delayed Gratification) (Fields & Levin, 2022; James, 1890). Pure strategies that seek to minimize error (like the magnets separated by a small piece of wood in William James' example (James, 1890)) cannot do this, and different creatures have different tolerances for this way of navigating the problem landscape. The possibility of this behavior in sorting algorithms has not to our knowledge been considered, possibly because in their traditional implementation, there are no Frozen Cells for them to go around. Here, we included "damaged cells," which were in effect a Frozen Cell in sorting space—the algorithm simply could not move a cell when it needed to, to continue its trajectory. We found that when their path in sort space is analyzed, it is seen that cell-view sorting algorithms do indeed exhibit this rerouting behavior, temporarily allowing Sortedness to decrease (moving away from their goal) in order to find a new set of steps that would solve the problem and ultimately improve monotonicity. This was shown to be context-dependent; that is, Delayed Gratification was a function of the number of Frozen Cells.

This is especially significant because our cell-view algorithms contained no explicit steps for what to do in case of a disobeying cell, or even any steps for assaying whether any of their actions have had the desired effect in the first place. In other words, our cells' explicit algorithms were purely open-loop with no feedback. The fact that our systems nonetheless exhibited implicit goal-seeking with Delayed Gratification highlights two paths to robust biological goal-seeking: stochasticity *or* distributed components with fault-tolerance. While our simulations here only studied the latter, in future work, we plan to investigate how behavior changes when both techniques can be utilized simultaneously.

We find it notable and surprising that these simple algorithms solve unexpected problems in their space, given that the algorithm itself has no "metacognitive" steps that monitor the sorting progress. We believe these results, like the maze navigation exhibited by microbial cells and even simple chemical droplets (Adamatzky, 2012; Adamatzky et al., 2020; Nakagaki, 2001; Nakagaki & Guy, 2007; Reid et al., 2013; Tero et al., 2007), imply the need for experimental exploration even of systems whose simple, transparent nature can lull us into a false sense that we understand their capabilities just because we understand (or even created) their parts. This goes beyond first-order (static) emergent complexity (e.g., fractals or cellular automata) and draws attention to a next level: emergent behavioral competencies and the beginnings of minimal agency.

Lastly, we note that the use of bottom-up distributed algorithms allows the testing of something that is impossible in the classic version: a chimeric scenario in which some cells utilize a different sort algorithm than other cells. Chimerism at different scales (Nanos & Levin, 2022) is
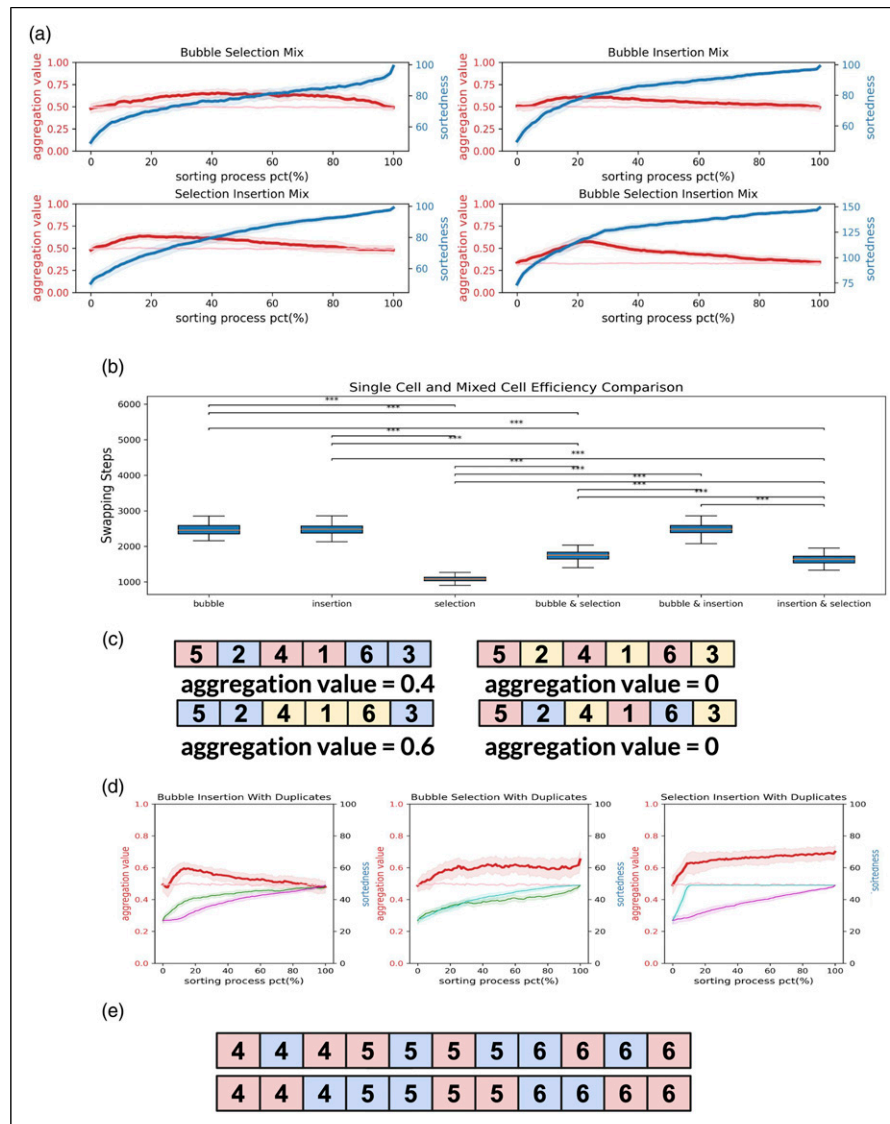
Figure 8. Unexpected aggregation of Algotypes occurs in chimeric arrays. A cell-view (local) implementation of sorting policies enables an experiment that cannot be done in traditional top-down sorting: chimeric arrays in which individual cells follow their own distinct policies ("Algotype", which can be different among the cells of the array) for how to move (corresponding to chimeric embryos consisting of cells of 2 different lineages (Nanos & Levin, 2022)). Panel (a) shows the results of each possible combination of sort algorithms within an array. The blue lines indicate the progress of the sort itself (the Sortedness value). We also computed aggregation—the tendency of cells with similar Algotypes to cluster together spatially. To study how such chimeric collectives behave, we investigated 100 repeats of scenarios where each combination of the 3 sort algorithms was represented equally; note that the algorithms were not modified in any way and thus do not have any provision for knowing their own Algotype or that of their neighbors. Remarkably, significant aggregation was observed during the sorting process, reaching >60% (with peaks that occur at slightly different times during the sorting process for each of the chimeric combinations). The pink lines indicate the Aggregation Value when two identical sorts (Bubble Algotype) are used—this negative control shows, as expected, that there is no significant deviation from 50% chance. The red line indicates the Aggregation Value of each kind of sort. As expected, at the beginning the Aggregation Value is 50%, since types are assigned to cells randomly. Likewise, at the end, the Aggregation Value is back to 50% since the array is sorted only by each cell's Value, with no regard for Algotype, and the Algotypes were randomly assigned. Panel (b) quantifies the efficiencies of such chimeric individuals. (c) To understand the relative spatial distribution of cells executing each algorithm within the array during the sorting process, we defined *aggregation value*: the probability that a cell's neighbor is of the same type as itself. Algotypes were assigned to each cell randomly in each experimental array and did not change during the course of the sort. (d) We then allowed duplicate digits in the arrays, so that some instances of each number would be of each of the types, in order to see what maximum aggregation could be achieved if the explicit (monotonic numbers) and implicit (aggregation of types) goals were made compatible. We use purple lines, green lines, and teal lines to represent for the Sortedness change for Insertion Algotype, Bubble Algotype and Selection Algotype respectively. The red lines represent the aggregation value change. We observed that the final Aggregation Values in (d) were larger than the final Aggregation Values in (a), showing the system is able to reach greater aggregation values when the pressure of having to sort on unique number values (which can conflict with the goal of identical adjacent Algotypes) is released by allowing duplicate valued cells. Panel (e) shows two examples of the cell aggregation after the sorting process when the list contains duplicate values. Different colors represent different Algotypes. For cells with the same value, the first example shows no clustering while the second example shows clear clustering.

often used in biology to address the role of the genome in the collective decision-making that determines large-scale form and function. Yet despite much progress on the molecular genetics guiding individual cell properties, the field generally has no models that make predictions on morphological outcomes from chimeric experiments in development or regeneration. That is, while we have a good understanding of the molecular hardware, we do not have good frameworks for understanding the collective decision-making of cells with different policies ("biological algorithms" for systems with multi-scale competency) with respect to how they will navigate anatomical space. Simple models like ours which map the behavioral competencies of chimeric systems onto large-scale problem-solving are important for developing an understanding of the principles involved.

We define the notion of the Algotype, referring to the behaviors of a given cell under various circumstances. We intend this concept to be significantly different from genotype (specification of the explicitly observable hardware) and from phenotype (outcomes that can be detected in a single observation, such as geometric or physiological states and properties). Note that in denoting the time-extended "personality" of cells, the Algotype consists of two components: the expected behavior overtly encoded in the algorithm (the sorting), and possible emergent tendencies not obvious from the mechanics and not explicitly assigned (e.g., the clustering). Thus, Algotypes include behavioral tendencies (such as preferring to associate with their "kin" during their journey through morphospace) that may not be explicitly encoded anywhere in the algorithm and can only be observed as a holistic dataset encompassing many scenarios and situations (Goldstein, 2021). In biology, multiple Algotypes can be instantiated by the same genetics, and multiple different genomes can result in hardware with similar Algotypes. We believe this notion will be useful to understand plasticity and scaling of competencies in biology (Fields & Levin, 2019, 2020, 2022, 2023; Arias Del Angel et al., 2020; Fields et al., 2020; Kuchling et al., 2022; Newman, 2019a, 2019b, 2023; Niklas et al., 2019) far beyond the toy model of multi-scale problem-solving explored here.

We found that chimeric arrays consisting of distinct Algotypes still manage to get sorted; there is no need for each cell to be following the same algorithm as long as they have the same goal. However, if they are set to cross-purposes (one sorts for increasing, and the other sorts for decreasing), they reach a dynamic equilibrium at a mixed, intermediate state in which the large-scale demographics of the array (with respect to Algotype) no longer changes, but the individual cells can still move (akin to extensive biological turnover at the molecular and cellular scale while the large-scale anatomy is maintained over years).

This is, as far as we know, the only model that implies a prediction of what will happen when, for example, different species' stem cells (neoblasts) are mixed within one flatworm body. Given that each set of stem cells knows how to undergo division and metamorphosis until a specific head shape is completed, it is entirely unclear what will happen in a chimeric worm: will one type be dominant over the other, or will an intermediate shape result, or will there be endless remodeling because neither set of cells ever reaches its stop condition with respect to the morphology? Our model showed that despite no explicit affordance made for this scenario in the algorithm, the sort process included many islands within each array where cells of similar Algotypes clustered together within the space of the overall array. This suggests the testable hypothesis that what will occur in a chimeric biological body is the establishment of a set of tissue-level islands, each of which has the identity of one of the parent species (a patchwork of local neighborhoods that possess a tissue-wide but not organism-wide identity). Because our model did not include explicit mechanisms for cells to behave differently with neighbors of different Algotypes, we suggest that this biological clustering should occur even in the absence of, for example, distinct adhesion molecules present on the cells of different genomes or any other hardware-encoded mechanisms for cell sorting.

Finally, we found a most unexpected behavior in these chimeras. During the sorting process, cells with similar Algotypes (and thus the same sorting behaviors) tended to aggregate together spatially within the array. Eventually they are pulled apart by the necessity to sort themselves according to their positional (numerical) value (rather than by algorithm type), but before that happens, they act as though they have a strong affinity for each other despite the fact that the algorithm says nothing about aggregating, and has no explicit provision for a cell determining the Algotype of any given neighbor (or itself). We suggest that this simple model can be used to ask basic questions about large-scale outcomes in chimeric systems in which components have different explicit and implicit Algotypes. These kinds of analyses can begin to provide principled answers to currently open questions in biology, such as how to predict the morphogenetic outcomes in cellular chimeras consisting of different species' cells or engineered components that extend functional reach outside the standard body envelope (Clawson & Levin, 2023; Levin et al., 2019; Lobo et al., 2012; Nanos & Levin, 2022). This may also be usable as a way to increase the utility of computation per unit cost, as the aggregation happens "for free" as part of the sorting process (requires no additional computational steps). It may be possible to harness this type of byproduct effect for useful functionality that requires no extra execution steps.

By allowing repeated digits, we were able to partially dissociate the pressures of the explicit algorithm (to sort elements based on numerical value) from the tendencies of the emergent aspect of the Algotype (to cluster with like-minded elements within the string). Existing real-world biological examples of releasing sub-agents from explicit control, to ask what they
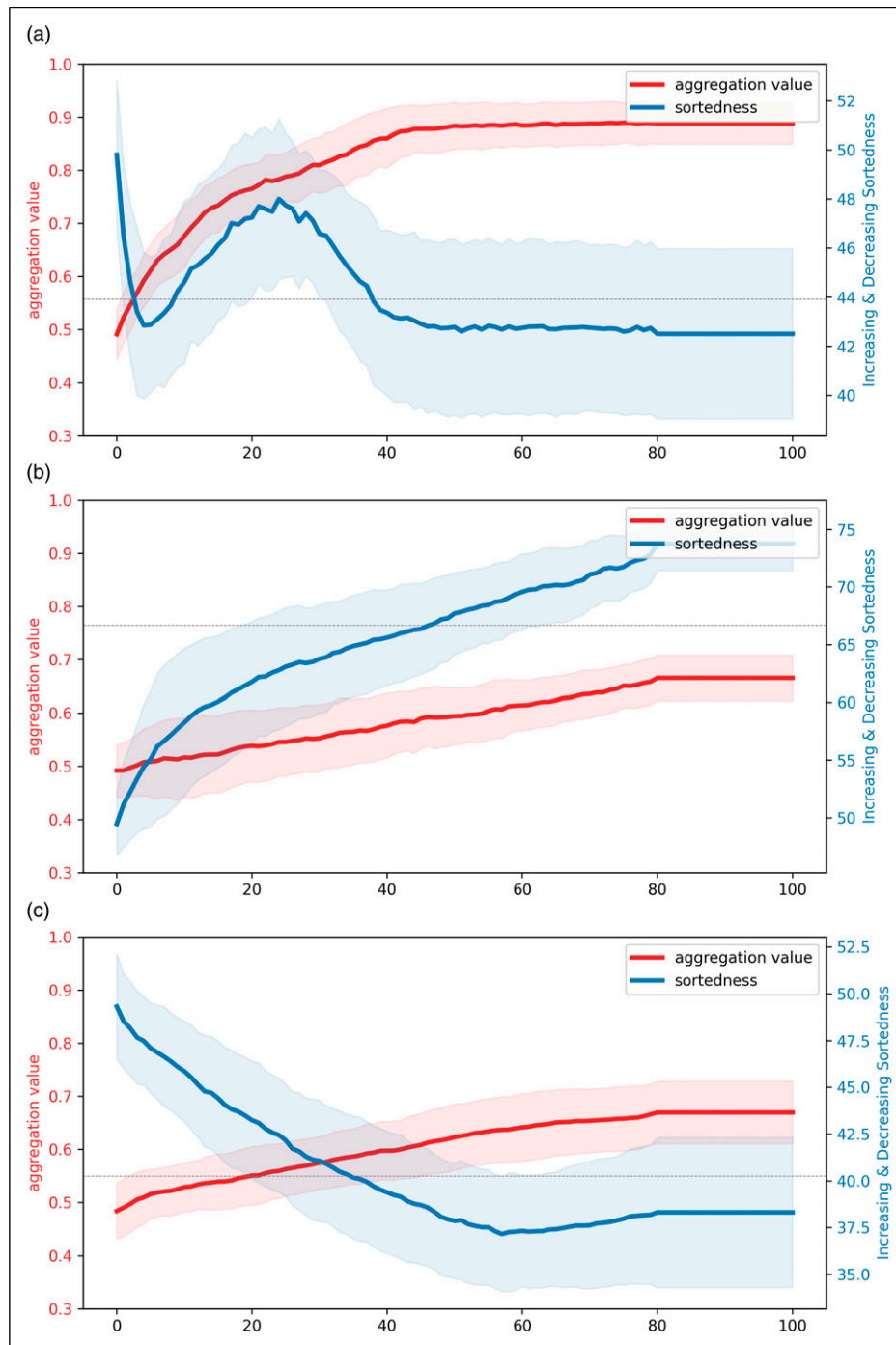
Figure 9. Cell aggregation for unique cells with different sorting directions. In biological chimeras made from the cells of different species, those cells not only use different policies for their activity, but they are actively working to build different anatomical patterns. Thus, we asked what chimeric sorts would do if the two types of cells were trying to sort in opposite directions (monotonic increasing vs. decreasing). For each combination of sort types, there is a consistent but not linear dynamic of conflict between the 2 algorithms. The horizontal gray dotted lines in the middle of the plots indicate the average final Sortedness value of all experiments. In (a), we set Bubble cells to sort decreasingly and Selection cells to sort increasingly. In (b), we set Bubble cells to sort increasingly and Insertion cells to sort decreasingly. In (c), we set the Insertion cells to sort increasingly and the Selection to sort decreasingly. After some initial back-and-forth, Sortedness flattens out (reaches a stable point after which nothing will change), with algorithms "winning" (being more effective than their competitors) in this order: Bubble > Selection > Insertion. The Aggregation Values rise and also flatten out: the final Aggregation Values were all higher than the starting averages, which were ~0.5. The data shown here are from experiments with arrays of digits 1..100, with no repeated digits.
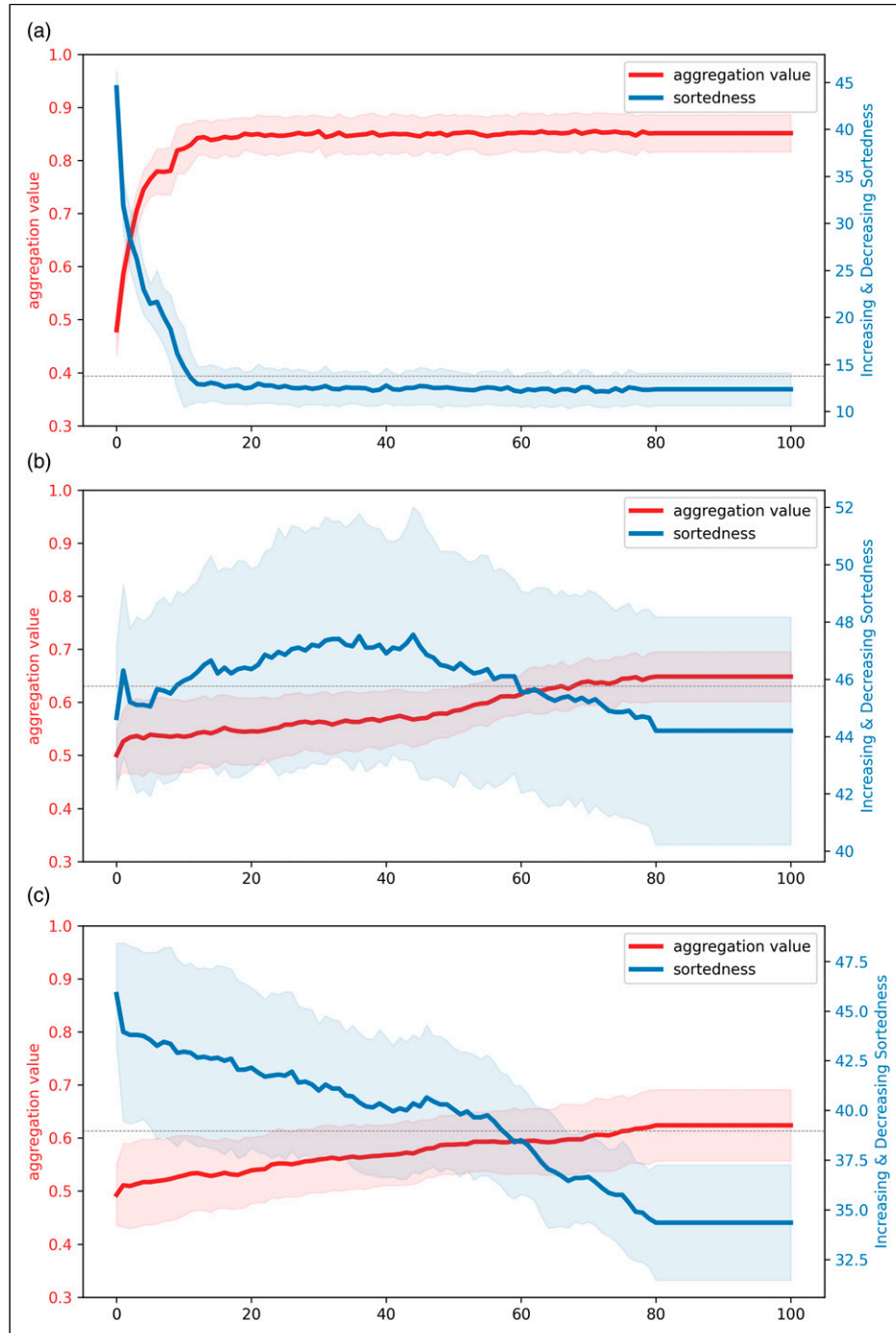
Figure 10. Cell aggregation for repeated cells with different sorting directions. In biological chimeras made from the cells of different species, those cells not only use different policies for their activity, but they are actively working to build different anatomical patterns. Thus, we asked what chimeric sorts would do if the two types of cells, with duplicates (multiple copies of cells with the same value) allowed, were trying to sort in opposite directions (monotonic increasing vs. decreasing). For each combination of sort types, there is a consistent but not linear dynamic of conflict between the 2 algorithms. The horizontal gray dotted lines in the middle of the plots indicate the average final Sortedness value of all experiments. In (a), we set Bubble cells to sort decreasingly and the Selection cells to sort increasingly. In (b), we set Bubble cells to sort increasingly and Insertion cells to sort decreasingly. In (c), we set Insertion cells to sort increasingly and Selection to sort decreasingly. After some initial back-and-forth, Sortedness flattens out (reaches a stable point after which nothing will change), with algorithms "winning" (being more effective than their competitors) in this order: Bubble > Selection > Insertion. The Aggregation Values rise and also flatten out: the final Aggregation Values were all higher than the starting averages, which were ~0.5. The data shown here are from experiments with arrays of digits 1..10, with 10 repeated copies of each digits.

would do if allowed, include the engineering of biobots. It has recently been shown that un-modified, genetically normal cells self-assemble into constructs with novel behaviors when freed from the instructive influence of their neighbors (Blackiston et al., 2023; Gumuskaya et al., 2024), revealing baseline competencies not apparent from their standard role within default developmental algorithms. The minimal model shown here represents a first step toward the development of more general strategies to study emergent goals in collective systems and ways in which those goals cooperate with, compete with, and alter the performance of explicit goals we (or evolution) instantiate via hardware or software mechanisms.

There is no magic here, of course: everything that happens is, in some way, a consequence of the rules being followed. In the same way, truly cognitive behavior of living systems must be consistent with the physics of their smallest components. However, while such behaviors do not contradict the laws of physics of their world and can be explained after they are observed, they often require a different set of conceptual tools to effectively predict and exploit them than physics and chemistry (Noble, 2008a, 2008b, 2009, 2010, 2011, 2012; Arias Del Angel et al., 2020; Ellis et al., 2011; Levin, 2022; Newman, 2019b, 2023). We believe advances in our understanding will result from when we will be able to identify and predict *in advance* the preferences and behavioral competencies of novel collective systems we engineer. Note also that we observed not only capabilities related to the solving of the problem which the algorithm explicitly addressed (sorting numbers) but new behaviors (clustering) that do not seem related to the intended purpose for which their algorithm was written. This aspect goes beyond the well-known realization that simple rules can give rise to unexpected emergent behaviors, emphasizing the need to be able to predict and control the properties that such novel behaviors actively seek to maximize.

This model can be expanded in numerous ways. For example, what happens with cells that are not permanently broken, but have the ability to unfreeze given specific (or merely repeated) nudges by their neighbors? Also, we plan to investigate how general these findings are to algorithms for 2-dimensional ordering problems and others. Another interesting direction would be to mix distributed and top-down controls—to monitor the behavior of a classical algorithm working on an agential material that also moves in ways that it was not instructed to. This is the situation in biology, and the evolutionary and cognitive impacts of an agential medium are just beginning to be understood (Davies & Levin, 2023; Levin, 2023c). Understanding what changes should be made to a top-down algorithm to facilitate and exploit the competencies of its medium would, for example, assist the design of multi-scale robotics.

One limitation of the current analysis is that we looked at only one emergent behavior (aggregation); other interesting things could be happening that we do not yet know to test for, even in this system. More broadly, we believe it is necessary to develop frameworks for looking for novel competencies in systems, with an increased emphasis on broad, unbiased analyses to help human scientists find those goal-directed behaviors which our cognitive biases do not readily facilitate.

We suggest that the study of these kinds of dynamics is potentially of broad significance. In both science and everyday life, we deal with a wide range of systems along the spectrum stretching from passive matter (and mechanisms made thereof) to the complex metacognitive capacities of adult human beings (Rosenblueth et al., 1943). Especially interesting are the intermediate cases, such as cells, organs, swarms, artificial intelligences, autonomous vehicles, synthetic organisms, constructs made of active matter, and other increasingly prevalent systems that have never existed in the evolutionary stream, all of which display a diverse range of capacities (Clawson & Levin, 2023). It is not enough to aim for minimizing estimates of agency (Morgan's Canon (Morgan, 1894), often favored by scientists), because sub-optimal efficacy of prediction and control can result when we treat advanced reprogrammable systems as dumb machines and fail to appreciate their unexpected competencies. There are, of course, also downsides to over-estimating agency (Davies & Levin, 2023; McShea, 2012, 2013, 2016; McShea & Hordijk, 2013). The latter (false positives) result in low efficiency, while the former (false negatives) are associated with opportunity cost in engineering and regenerative medicine (Lagasse & Levin, 2023; Pezzulo & Levin, 2015, 2016), not to mention serious ethical lapses; it is therefore both practically and ethically valuable to get our estimates of agency correct, not just low.

Indeed, this problem has only gotten thornier with time. During the early days of computers, we could accurately treat machines as passive (non-agentic) and humans as smart. However, with improvements in bioengineering and AI, it is becoming harder and harder to rely on such simple heuristics (Bongard & Levin, 2021). The field of Diverse Intelligence seeks principled frameworks for being able to recognize, predict, control, create, and ethically relate to a wide range of unconventional systems across the intelligence spectrum (Levin, 2022; Rosenblueth et al., 1943). Algorithms are increasingly seen as open dynamical systems interacting with other algorithms, physical systems, and agents (Dörfler et al., 2024; Goldstein, 2021); as such, they are good candidates, alongside genes, thermodynamic cycles, and passive information, for an abstraction of the minimal unit of agency in the biotic and abiotic world.

Classical thinkers such as William James (James, 1890) were prescient enough to define intelligence in a cybernetic way, not tied to specific hardware (e.g., brains) or evolutionary origins. Definitions such as "competency to reach the same goal by different means" provide a sufficiently general, but empirically testable, way to define a spectrum of cognitive capacities. This drives hopes of being able to infer the design principles by which cognitive systems of different levels can be built, by creating novel active agents

and studying the rich examples provided for us across the web of life (Baluška & Levin, 2016; Vallverdu et al., 2018). We strongly support (Bongard & Levin, 2023; Rahwan et al., 2019; Rouleau & Levin, 2023) a definition of basal intelligence as problem-solving, utilizing an objectively observable, third person perspective to distinguish these highly tractable and empirically testable questions from the thorny debates around first-person consciousness (Friston et al., 2020; Frith & Metzingher, 2016; Tononi & Koch, 2015).

Minimal chemical systems such as active matter are being explored (Čejková et al., 2017; Dine et al., 2018; Khademi et al., 2019; Oakey & Gatlin, 2018; Points et al., 2018; Qiao et al., 2017; Serwane et al., 2017; Shin et al., 2017; Suzuki et al., 2017), as are basal competencies of "lower" organisms (Boisseau et al., 2016; Boussard et al., 2019; Dussutour et al., 2010; Reid et al., 2012, 2013; Vallverdu et al., 2018; Vogel & Dussutour, 2016; Vogel et al., 2015, 2018; Zabzina et al., 2014). Here, we sought to produce an even more minimal, digital version of a system in which baseline expectation would not normally suggest any degree of intelligence. One advantage over biology, even at its lowest scales, is simplicity and transparency that guarantees that observed competencies of these algorithms are not due to an as-yet undiscovered explicit mechanism. Our goal is to show how an empirical stance, in which we use experimental tools of behavioral science and other disciplines to determine (rather than to make assumptions about) the level of cognition in a system, leads to interesting novel findings and discovery of capabilities we did not expect in a small, well-defined, deterministic, fully transparent system created entirely by us. Prior examples of this approach include dynamical systems such as models of gene-regulatory networks, which exhibit not only complexity but several types of unexpected learning capacity (Beer, 1995, 2004, 2014, 2015; Agmon et al., 2016; Beer & Williams, 2015; Biswas et al., 2021, 2022; Izquierdo et al., 2015; Katz & Fontana, 2022; Katz, Goodman, et al., 2008; Katz & Springer, 2016; Katz, Springer, et al., 2008; Manicka & Harvey, 2008). We suggest that the discovery of unexpected problem-solving competencies (such as Delayed Gratification and segregation) that are not apparent from the component policies and algorithms themselves is a critical research program. The impacts of this effort, a central component of the emerging field of Diverse Intelligence, will have implications ranging across evolutionary developmental biology, philosophy of mind, AI alignment, and human flourishing via the safety of engineered composite systems.

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Declaration of conflicting interests

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