Title

Effective mechanical potential of cell–cell interaction explains three-dimensional

morphologies during early embryogenesis

Short title

Cell–cell mechanical potential for morphogenesis

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Author contribution

H.K. designed the work, H.K., A.M.I., and H.O. contributed to the conception. H.K. and

T.F. designed experiments, and H.K. performed experiments and image processing. H.K.

and H.O. designed models, H.K. developed computational algorithms, and H.K. and K.N.

statistically analyzed the data. H.K., T.O., H.O., A.M.I., K.N., K.K., and T.F. wrote the

manuscript, and all authors contributed to the interpretation of the results.

Conflicts of interest

The authors declare no competing financial interests.

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Main text

Figure 1 to 8

Abstract

Mechanical forces are critical for the emergence of diverse three-dimensional morphologies of multicellular systems. However, it remains unclear what kind of mechanical parameters at cellular level substantially contribute to tissue morphologies. This is largely due to technical limitations of live measurements of cellular forces. Here we developed a framework for inferring and modeling mechanical forces of cell–cell interactions. First, by analogy to coarse-grained models in molecular and colloidal sciences, we approximated cells as particles, where mean forces (i.e. effective forces) of pairwise cell–cell interactions are considered. Then, the forces were statistically inferred by fitting the mathematical model to cell tracking data. This method was validated by using synthetic cell tracking data resembling various *in vivo* situations. Application of our method to the cells in the early embryos of mice and the nematode *Caenorhabditis elegans* revealed that cell–cell interaction forces can be written as a pairwise potential energy in a manner dependent on cell–cell distances. Importantly, the profiles of the pairwise potentials were quantitatively different among species and embryonic stages, and the quantitative differences correctly described the differences of their morphological features such as spherical vs. distorted cell aggregates, and tightly vs. non-tightly assembled aggregates. We conclude that the effective pairwise potential of cell–cell

interactions is a live measurable parameter whose quantitative differences can be a

parameter describing three-dimensional tissue morphologies.

Author summary

Emergence of diverse three-dimensional morphologies of multicellular organisms is one

of the most intriguing phenomena in nature. Due to the complex situations in living

systems (e.g. a lot of genes are involved in morphogenesis.), a model for describing the

emergent properties of multicellular systems has not been established. To approach this

issue, approximation of the complex situations to limited numbers of parameters is

required. Here, we searched for mechanical parameters for describing morphologies. We

developed a statistical method for inferring mechanical potential energy of cell–cell

interactions in three-dimensional tissues; the mechanical potential is an approximation of

various mechanical components such as cell–cell adhesive forces, cell surface tensions,

etc. Then, we showed that the quantitative differences in the potential is sufficient to

reproduce basic three-dimensional morphologies observed during the mouse and *C.*

elegans early embryogenesis, revealing a direct link between cellular level mechanical

parameters and three-dimensional morphologies. Our framework provides a noninvasive

tool for measuring spatiotemporal cellular forces, which would be useful for studying

morphogenesis of larger tissues including organs and their regenerative therapy.

Introduction

In multicellular living systems, various three-dimensional morphologies are

observed in tissues and organs, which are often tightly linked to their physiological

functions. Morphogenetic events are thought to be primarily dependent on the mechanical

properties of the constituent cells [1–5]. Mechanical parameters such as cell–cell adhesion

energy and cell surface tensions are involved in morphogenetic events including

compartmentalization of different cell populations, epithelial cell movements etc.

However, mechanical parameters which give rise to a variety of three-dimensional

morphologies remain to be elucidated. If such parameters are identified, we can

understand not only mechanical principles of emergent properties of multicellular

systems during morphogenesis but also easily simulate three-dimensional tissues in a

predictable manner, which may be valuable for regenerative therapy.

To search for mechanical parameters which are directly linked to three-

dimensional morphologies, we focused on mechanical potential energies of pairwise cell–

cell interactions as follows. Cell–cell adhesion forces, which are mediated by cell

adhesion molecules such as cadherin proteins, can be approximated as attractive forces in

isolated two cell systems (Fig. 1A-i and -ii), whereas both excluded volume effect of cells

and actomyosin-mediated cell surface tensions can be as repulsive forces [1,2,4,6–8]; due

to cell volume conservation, two cells cannot extremely approach each other, and the cell

surface tensions can antagonize cell–cell adhesion forces. Because the summation of

these forces would be dependent on cell–cell distance (Fig. 1A-iii), it is written by

pairwise potential energy (Fig. 1A-iv, distance–potential curve). There may be factors

other than the above affecting the pairwise potentials. In molecular and colloidal sciences,

pairwise potentials of objects such as amino acids are considered, and the profiles of the

distance–potential curves are critical for the behaviors of systems [9,10]. In multicellular

systems, the pairwise potentials are conceptually well-known [7,8,11,12]. But the profiles

have been never measured nor inferred in multicellular systems, and therefore,

researchers arbitrarily set the profiles in theoretical studies (e.g. hard- or soft-core

potentials, etc.) [13–16]. Theoretical studies related to morphogenesis did not assume

substantial differences in the profiles [17–20]. However, considering the case of

molecular/colloidal sciences, we speculated that the profiles substantially determine the

systems' behaviors or morphologies in certain multicellular systems.

To examine whether the profiles of pairwise potentials can determine

morphologies of multicellular systems, quantitative measurements/inferences of the

profiles in real tissues are inevitable. In the case of isolated two cell systems, adhesive

forces between two cells were experimentally measured (i.e. forces required to dissociate

one cell from the other) [4,21], but their pairwise potentials were not determined.

Importantly, due to complex situations in real tissues compared with isolated two cell

systems, it is unknown whether pairwise potentials are correctly defined and detectable

in vivo. On the other hand, in molecular and colloidal sciences, we found a strategy worth

considering: a top-down approach is adopted for inferring pairwise potentials, where

positions of the objects such as radial distribution functions are solely used [10,22].

In the present study, we develop a top-down method for inferring pairwise

potentials of cell-cell interactions by using movements of cells obtained from three-

dimensional time lapse imaging (Fig. 1B). Briefly, a theoretical model considering force

values of cell–cell interactions were fitted to the cell tracking data. Our method was

validated by using various synthetic data which were generated by simulations under

pregiven cell–cell interaction forces. Then, we applied our method to the blastomeres in

the *C. elegans* and mouse early embryos, and successfully detected pairwise potentials of

cell–cell interactions. We discovered quantitative differences in the profiles of the inferred

potentials among the embryos, and showed that, through simulations, the differences were

linked to the embryos' morphological features. Note that applicability of our method to

other cell types such as epithelial cells and self-migratory cells is beyond the scope of the

present study. We assume that the nearly-spherical cell shape of blastomeres may be well-

approximated by particle models, while the highly deformed cell shapes of epithelial or

mesenchymal cells may not be suitable. This issue will be discussed later in the

Discussion section with the limitations of our method.

Theory and principle for inferring effective potential

Particle-based cell models

To infer effective forces of cell–cell interactions *in vivo*, we developed a particle-

based model in which the particles interact with each other and attractive or repulsive

forces (F_i) are assumed as shown in Fig. 1B-i; i is an identifier for particle–particle

interactions. In three-dimensional cellular systems with no attachment to substrates, we

did not assume persistent random walks which originate from cellular traction forces on

substrates [23,24].

The equation of particle motions is defined below. In cellular-level phenomena,

viscous drag force or frictional force provided by the surrounding medium or tissue is

dominant, as expected from the low Reynolds number; consequently, the inertial force is

negligible in general [3,7,25–27]. The forces in such a system can be assumed to be

correlated with the velocities of the objects [3,14,25,28,29]. Thus, the velocity ($V_{C|p}$) of a

particle is calculated by the net force ($F_{C|p}$) exerted on the particle as follows (Fig. 1B-i):

$V_{C|p} = F_{C|p} / \gamma$ (Eq. 1),

where p is an identifier for particles and γ is the coefficient of viscous drag and frictional

forces. $F_{C|p}$ is the summation of cell–cell interaction forces exerted on the pth particle. We

assumed the simplest situation, i.e., γ is constant (=1.0). Thus, by giving the values of F_i

from, for instance, a distance–potential curve, a simulation can run. In addition, γ may not

be constant in real tissues, while it is challenging to measure the value with spatial

resolution at cellular level [30].

Data acquisition of time series of cell positions

To define cell positions, we focused on nuclei, because they are most easily

imaged by microscopy (Fig. 1B-ii) in a wide range of organisms from *C. elegans* to

mammals, and these data are accumulating [31–35]. We utilized publicly available

nuclear tracking data of a developing embryo of *C. elegans* [31]; nuclear tracking data of

developing mouse embryos were obtained in this study.

Development of method for inferring effective potentials/forces of cell-cell interaction

In the case of ions, molecules, etc., radial distribution functions are often used to

infer the effective potentials of their interactions [10,22]. This method is simple, but is

only applicable to thermodynamically equilibrium systems because this function reflects

the effective potentials under equilibrium states. Therefore, this method is not suitable for

non-equilibrium systems, including morphogenetic events. To infer the effective

potentials in non-equilibrium systems, we fitted the particle-based cell model to the time

series of nuclear positions, where the fitting parameters are forces between all pairs of

cell–cell interactions for each time frame (Fig. 1B-iii). We systematically searched for the

values of the effective forces between all pairs of cell–cell interactions that minimized the

differences (i.e. corresponding to least squares) between the particle positions in the

simulations and the *in vivo* nuclear positions. The differences (G_{xyz}) to be minimized are

defined as follows.

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$$G_{xyz} = \sum_{t=1}^{T} \sum_{p=1}^{P(t)} \frac{\left\{ x_p(t) - x_p^{\text{ref}}(t) \right\}^2 + \left\{ y_p(t) - y_p^{\text{ref}}(t) \right\}^2 + \left\{ z_p(t) - z_p^{\text{ref}}(t) \right\}^2}{\Delta t}$$

210   (Eq. 2)

211   Here, p is an identifier for particles, t is an identifier for time frames, and Δt is

212   the time interval between the time frames. T is the total time frame, and $P(t)$ is the number

213   of particles at each time frame. The x, y, and z coordinates of the pth particle obtained

214   from microscopic images are x_p^{ref}, y_p^{ref}, and z_p^{ref}; ref means reference. The coordinates of

215   the simulations are x_p, y_p, and z_p. Note that, because γ was assumed to be constant in

216   Equation 1, we can only infer relative but not absolute values of effective forces.

217   To determine whether our method can correctly infer effective forces, we applied

it to synthetic data generated by simulations under given potentials of particle–particle

interactions, and examined whether the inferred effective forces were consistent with the

given potentials. Unfortunately, Equation 2 did not work well: the inferred forces were

not consistent with given potentials. In particular, even around the longer cell–cell

distance, the force values did not decay (Fig. S2). Therefore, we tried to incorporate

various additional constraints into Equation 2. We found that the following cost function

worked well: the function was set so that force values approach zero at long distant

regions of cell–cell interactions as defined below:

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$$G = G_{xyz} + G_{F_0} \qquad (G_{F_0} = \omega_{F_0} \sum_{t=1}^{T} \sum_{i=1}^{I(t)} \psi(D_i)F_i^2 \Delta t) \qquad \text{(Eq. 3)},$$

where F_i is the force value of ith cell–cell interactions, $I(t)$ is the total number of the cell–

cell interactions for each time frame, D_i is the cell–cell distance of the ith interaction, and

ω_{F_0} is a coefficient for determining the relative contribution of the second term to G.

$\Psi(D_i)$ is a distance-dependent weight that exponentially increases and eventually becomes

extremely large, leading to that the value of F_i approaches zero especially around larger

D_i (Fig. S1A-iii). We show validations of this cost function in the next sections. Detailed

procedures are described in Supplementary Information (Section 4).

Results

Systematic validation of inference method using simulation data

We systematically validated our inference method using simulation data. We

used the Lenard–Jones (LJ) potential as a test case of the given potentials (Fig. 2A-i), and

generated simulation data under LJ potential, to which we applied our inference method.

Importantly, we assumed cell-intrinsic mechanical activities that were introduced as

fluctuations of the forces relative to the LJ potential (Fig. 2A-i, "fluctuation (% of LJ)"),

because the cells rapidly stop movements without such activities.

In Fig. 2A-i, the particles were initially scattered to some extent, and then

assembled. The inferred effective forces for each pair of particles for each time frame

were plotted against particle–particle distances (Fig. 2A-ii, heat map), and by calculating

binned averages, we obtained distance–force (DF) curves (Fig 2A-ii, yellow). In the

absence of the fluctuations, the data points were located around the DF curve (Fig. 2A-ii,

standard deviation (SD) = 0%), and the DF curve showed a similar profile to that from

the LJ potential (Fig. 2A-iii, LJ vs. 0%). In the presence of the fluctuations (SD = 100 or

1,000%), although the data points were widely distributed (Fig. 2A-ii), the resultant DF

curves were equivalent to that of the LJ potential and of that under SD = 0% (Fig. 2A-iii).

We also quantitatively evaluated the differences of the force values between the inferred

DF and the LJ potential by calculating L2 norm which is described in the legend; i.e., L2

norm = $\{F_{\text{inferred}}(D) - F_{\text{LJ}}(D)\}^2$, where F_{inferred} and F_{LJ} are the force values from the

inferred DF and the LJ potential, respectively. These results suggest that our method is

correctly applicable for assembling process even under large fluctuations of the forces.

Effect of ω_{F_0} in Equation 3 is shown in Fig. S2. In addition to the LJ potential, we also

tested other potentials (e.g., Morse potential) and the inferred DF curves were similar to

the given potentials (Fig. S2 and S3).

In Fig. 2B, effective DF curves were inferred in systems under steady states

where particles continuously moved due to the force fluctuations (SD = 1,000%). The

inferred DF curves showed an almost similar profile to that of the LJ potential (Fig. 2B-

ii, sampling interval = 1min), but increased sampling intervals caused inconsistency with

the LJ potential (sampling interval = 5 min).

In Fig. 2C, effective DF curves were inferred in systems with cell proliferation

where cell numbers were increased from 38 to 47; handling of cell proliferation/division

is described in the Supplementary information with the case of dead/lost cells. The

inferred DF curves showed a similar profile to that of the LJ potential (Fig. 2C-ii), and

the influence of the sampling interval was similar to Fig. 2B.

These results suggest that our method can correctly infer the forces of cell–cell

interactions in three-dimensional cell aggregates. Note that long sampling intervals cause

incorrectness of the inference in practice. In addition, around longer cell–cell distances,

the inferred DF curves showed slight inconsistencies with the LJ potential in the case of

Fig. 2B and 2C but not 2A. This may be caused by crowding, because the particles in Fig.

2A were sparsely distributed compared with Fig. 2B and 2C.

Spatial constraints had no influence on effective forces

Next, we assessed the applicability of our method to systems with spatial

constraints resembling the zona pellucida or eggshells, which the mouse and *C. elegans*

embryos possess. The particles with the LJ potential were put into spherocylindrical

constraints (Fig. 3-i). In longer lengths of spherocylinders, inferred DF curves were well

consistent with the DF curves from the LJ potential (Fig. 3-ii; length of spherocylinder ≥

25μm). These results indicate that DF curves are correctly inferred under spatial

constraints.

By contrast, under shorter spherocylinders, the profiles of inferred DF curves

were shifted leftward along the distance (Fig. 3-ii; length of spherocylinder ≤ 20μm). In

these cases, the particles were compressed, and their movements were significantly

restricted as follows. The mean diameter of the particles roughly corresponds to the

distance providing the potential minimum (Fig. 1A-iii and -iv). In Fig. 3-i, the particle

diameters were depicted to be equivalent to the mean diameter of cells, and, under the

condition of the length = 16μm, the distances between the adjacent particles seemed to be

less than the diameter of the particles. Moreover, the positions of the particles were not

changed but fixed throughout the simulations (Fig. 3-i, 16μm), and showed a well-aligned

array resembling a closed-packed state (Fig. 3-i, broken lines). Compressive states are

observed in real tissues such as spheroids [29,36,37], whereas we do not know the

existence of tissues where cell movements are absolutely restricted by spatial constraints;

if such tissues existed, DF curves could be affected by the constraints.

Effective pairwise potentials were detected in C. elegans early embryo

We next investigated whether effective potential could be detected as a function

of cell–cell distance in three-dimensional *in vivo* systems. The nematode *C. elegans*

exhibits well-defined embryogenesis: cell movements in early embryos are almost

identical among different individuals, and the time series of nuclear positions have been

reported previously [31]. During early *C. elegans* embryogenesis, a fertilized egg (i.e. one

cell) repeatedly undergoes cell division and cell differentiation in a stiff/undeformable

eggshell, ultimately forming an ovoid embryo containing ~350 cells (Fig. 4A-B, and

Movie S1A). The cells become smaller through cell division [38], and the total volume

of the embryo remains constant. Thus, the volume of each cell is reduced by a factor of

350 relative to the original egg, meaning that mean cell diameter is reduced by a factor of

7 (Fig. 4B; e.g., the diameter at t (time frame) = 195 is ~28% of that at t = 16). Because

the mean diameter of particles is approximately reflected on a DF curve (Fig. 1A-iii and

-iv), we expected that inferred DF curves should be gradually shifted to the left side of

the distance–force graph throughout embryogenesis.

Figure 4C are snapshots at different time points, that show nuclear positions with

inferred effective forces where the color of the lines corresponds to the values of the

forces (Movie S1B). Note that, in our inference in this system, we confirmed that this

inference problem has essentially a unique solution (Fig. 4D); the uniqueness of solutions

is important to judge whether the inferred result is plausible in fitting problems as

previously discussed [39,40]. We divided the whole embryogenesis into segments

containing different time frames, and examined whether DF curves were detectable. Fig.

4E is an example of the DF curve (binned average) at t = 76-115 with all data points

shown as a heat map. Although the data points were widely distributed similar to the

previous figures (Fig. 2A-ii), a clear DF curve was detected as shown by yellow. The DF

curve exhibited a typical profile with regions of repulsive and attractive forces (Fig. 4F, t

= 76-115). Similarly, we successfully detected the DF and DP (distance–potential) curves

for each period (Fig. 4F, t = 16–55, 36–75, 76–115, 116–155, and 156–195). These curves

were gradually shifted toward the left side, as we had theoretically expected, indicating

that the inferred effective potentials were quantitatively consistent with the reduction in

cell volume during embryogenesis. To evaluate differences in mechanical properties

among the periods, we normalized both the distances and potentials by the distances at

the potential minima (Fig. 4G); the potentials were divided by the square of the distances

at the potential minima. The curves were almost unchanged during the periods, suggesting

that the mechanical properties of cell–cell interactions are not drastically modulated

during the development except for the cell sizes. Although slight deviations were

observed for the stages t36-75 and t76-115, whether this represents changes in the

mechanical properties in the embryo requires further investigation.

We also compared the profiles of the inferred DP curves with previously used

ones. The framework of the Morse potential is often considered (e.g. Fig. S3) [13,18,20],

while other frameworks were presented [14,16,20,29,41]. We fitted these frameworks to

our inferred DP curves. The Morse potential often fitted with small discrepancies,

whereas the potential presented by Delile et al. [20] usually showed larger discrepancies

(Fig. S7). This is because the Morse potential is quite flexible (i.e., various profiles are

generated according to their parameter values), while the Delile's potential sets a narrower

range of cell–cell distances where attractive forces can be exerted.

Model dependency of inference in C. elegans embryo

Next, we evaluated a model-dependency. In our particle model, the viscous

frictional forces were assumed to be proportional to the absolute velocities of the particles

as previously presented (Eq. 1). On the other hand, some papers argued that the viscous

frictional forces should be determined by the velocities relative to surrounding particles

[29,36].   The   equation   of   motions   in   this   model   is   as   follows;

$F_{C|p} = \sum_{m=1}^{N} [\{\omega_g(D_{pm})\gamma\}\{(V_{C|p} - V_{C|m})\bullet e_{pm}\}e_{pm}]$, where m is the ID of particles interacting

with the pth particle and $V_{C|m}$ is the velocity of the mth particle; see the Supplementary

information in detail. The difference between the two models comes from whether the

viscous frictional forces originate from non-moving objects (e.g., liquid medium,

substrate) or moving objects (e.g., neighboring cells). Fig. S8 shows the comparison of

the inferred DP curves between the two models, which were almost similar profiles each

other. We guess that, in systems where cell populations exhibit collective migration (i.e.,

similar velocities among the cells), the model choice may become significant, and, during

the developmental stages in the early *C. elegans* embryo, collective migration may rarely

occur.

Effective pairwise potentials were detected in mouse pre-implantation embryos

368   To further investigate whether effective forces were detectable in three-

dimensional real systems, we focused on mouse pre-implantation embryos, including the

8-cell and compacted morula stages (Fig. 5A, illustration). In 8-cell stage embryos before

compaction, cell–cell adhesion is weak, and individual cells can be easily discerned (Fig.

5A, bright field). In the compaction-stage embryos composed of ~16-32 cells, cell–cell

adhesion becomes stronger due to elevated expression of cadherin proteins on cell

membrane, and the cells are strongly assembled [42]. The surface of the embryo becomes

smooth, and the embryonic shape becomes more spherical (Fig. 5A, bright field). We

performed cell tracking (Fig. 5A, tracking) and inferred effective forces. We successfully

detected effective DF and DP curves for the two stages (Fig. 5B and S9 for other embryos),

which showed typical profiles with regions of repulsive and attractive forces.

Compaction-stage embryos include inner and outer cells differentiating to different cell

types [43]. We calculated DF curves for three pairs of interactions (inner–inner, outer–

outer, and inner–outer), and found that the profiles of the curves were different each other

(Fig. S10).

Effective potentials were capable of describing morphologies

To examine whether effective pairwise potentials can be a parameter for

determining morphologies, we performed simulations based on the inferred potentials

from the *C. elegans* and mouse embryos. In simulations of multicellular systems, the

simulation outcomes are determined by both DF curves and initial configurations,

because energetic local minimum states (i.e. metastable state) as well as global minimum

states are meaningful. To find stable states under the DF curves, we performed

simulations starting from various initial configurations of the particles (Fig. 6A, two

different initial configurations are shown), and the systems were relaxed.

From the DF curves of the *C. elegans* embryos, we observed a tendency that the

particles form an aggregate with an ovoid or distorted shape (Fig. 6A). These results may

be consistent with experimental observations: the embryonic cells can keep a cell

aggregate even when the eggshell is removed, and subsequent culture leads to a cell

aggregate with an ovoid or distorted shape, except for very early stage of development (<

~20 cells) [44,45]. From the DF curves of the mouse 8-cell stage embryos, an aggregate

was generated (Fig. 6B). From the DF curves of the mouse embryos at the compaction

stage, a spherical aggregate was generated (Fig. 6B); this morphology is consistent with

the *in vivo* situation. Therefore, the effective potentials from the *C. elegans* and mouse

embryos yielded different morphologies. These results suggest that all of the DF curves

are capable of recapitulating the basic morphological features of the systems.

Robustness of simulation outcomes

As shown above, the ovoid/distorted shape or spherical shape were generated in a manner

dependent on DF curves. We examined whether our inference robustly results into the

same simulation outcomes. During the minimization of the cost function G, we sampled

DF curves before reaching the minimum of G. Fig. 6B shows the DF curves for the *C.*

elegans embryo t36-75 (left panel), and their values of G are plotted against the maximum

attractive force in the DF curves (right panel); the colors in the two panels correspond

each other. Before reaching the minimum (a red line in left panel and a red circle in the

right), the DF curves exhibited some differences in their profiles (red vs. light blue or

purple). Then, simulations were performed from an initial configuration which shows a

cuboid shape (bottom panel, "start"). For all the DF curves tested, the particles were not

spherically assembled but the initial cuboid shape was almost sustained. By contrast, in

the case of the mouse compaction stage shown in Fig. 6C, the particles were spherically

assembled for all the DF curves except for an intermediate sample (light blue) which

shows two isolated aggregates. These results suggest that simulation outcomes resulting

from our inference are robust, and the DF curves are sufficient to explain morphologies

among different tissues.

Effective pairwise potentials were different between compacted and non-compacted

mouse embryo

425   To evaluate the predictive capability of the DF curves inferred by our method,

we performed perturbation experiments. In the mouse compaction stage, the cells are

tightly assembled to form a spherical and symmetric embryonic shape. In other words,

we think that there are two morphological features, 1) increase in symmetry of the

embryos, and 2) smoothing of the embryonic surfaces. The embryos are surrounded by

external structures called zona pellucida which have negligible effects on morphogenesis

[46 and reference therein]. Because both E-cadherin and actomyosin are essential for the

compaction process [42,47,48], we inhibited these proteins by chemicals: EDTA

(ethylenediaminetetraacetic acid) for E-cadherin, cytochalasin D for F-actin, and

blebbistatin for non-muscle myosin II (Fig. 7A).

435   The effective DP curves were inferred under these drugs (Fig. 7B and S12 with

enlarged views). Then, we quantitatively evaluated the differences among the DP curves,

and found that the distances at the potential minima were increased under the three

inhibitors (Fig. 7C, left panel). Because the distances at the potential minima are related

to the mean diameters of cells (Fig. 1A-iv), this result predicted that the distances between

adjacent cells were increased. This prediction was supported through histological

observations: each cell exhibited a nearly spherical shape and seemed that the cells were

not so densely assembled especially under the condition of EDTA compared with the no-

drugs condition (Fig. 7D). The embryonic and cellular shapes are schematically depicted

in Figure 7E. In addition, we found another quantitative difference among the DP curves,

related to decay of attractive forces. We measured distances at 10% energy of potential

minima as relative values to the distances at the potential minima, and found that the

relative distances were decreased under EDTA and blebbistatin (Fig. 7C, right panel, and

S14A). This result means that attractive forces of long-range interactions were reduced

under these drugs.

Effective pairwise potential described compacted and non-compacted morphologies in

mouse embryo

Simulations under the DP curves from the drugs-treated embryos were

performed. The cell particles were spherically or almost spherically assembled under the

potentials of the normal embryos or the cytochalasin D-treated embryos, respectively (Fig.

8A). By contrast, the cell particles were not spherically assembled under the potentials of

the EDTA or blebbistatin-treated embryos. All simulation data are provided in Figure

S15A from which representative results are shown in Fig. 8A.

To uncover what kinds of the profiles of the DP curves are linked to

morphological changes in the compaction process, we first introduced two indices for the

morphologies as follows. Sphericity ($=(36\pi V^2)^{1/3}/S$) is essentially defined as the ratio of

volume (V) to surface area (S) so that the value becomes 1.0 for spheres. Shapes other

than spheres show values less than 1.0. Thus, both the increases in symmetry and in

smoothness of surfaces contribute to this index. Aspect ratio is defined as the ratio of the

length of the longest axis to that of the shortest axis in an ellipsoid which is fitted to an

object of interest. The increase in symmetry leads to that the aspect ratio becomes 1.0,

and otherwise the aspect ratio shows more than 1.0. The sphericities of all simulation

outcomes in Figure 8A and S15A were measured, and we found that the sphericities were

decreased under EDTA and blebbistatin (Fig. 8B, left panel). Similarly, the aspect ratios

were increased under EDTA and blebbistatin (Fig. 8C, left panel).

We searched for parameters which can describe the sphericities or aspect ratios.

Among several parameters tested, the distances at potential minima measured in Figure

7C showed a tight relationship to the sphericities (Fig. 8B, right panel). The sphericities

showed an abrupt change along the x-axis. These results indicate that the sphericity is the

order parameter for the morphological transition of the compaction process and that the

distance at the potential minimum is the control parameter. On the other hand, the relative

distances at 10% potential minima showed a clear relationship to the aspect ratios (Fig.

8C, right panel). Thus, the morphological transitions of the compaction process are

induced by the quantitative changes in the DP curves.

Discussion

In this study, we developed a top-down method for statistically inferring

effective potentials of cell–cell interactions using cell tracking data. We then

demonstrated that effective potentials are detectable as a function of cell–cell distances

in real tissues. Our findings provide for the first time the experimental quantification of

effective potentials, which have been recognized conceptually [7,8]. Furthermore,

effective potentials with quantitative differences in their profiles can be a critical

parameter for morphologies; ovoid vs. spherical, compacted vs. non-compacted.

Moreover, the experiments using inhibitors suggest that effective potentials can be a

measure for evaluating mechanical properties of cells including mutants in a noninvasive

manner.

Morphology of embryo

For the generation of spherical/circular tissues, tissue surface tension is involved

in [1,29,49,50]. The surface tension reduces surface area of tissues in analogy to liquid

droplets. Therefore, when non-spherical cell aggregates are provided, they show a

tendency to round up to spherical shapes, where tissue surface tension contributes to the

dynamics (i.e., the speed of the rounding-up) [49,51]. Although the presence of tissue

surface tension may be a typical property of tissues [1,29], tissues do not always exhibit

spherical shapes including the *C. elegans* embryos whose eggshells are removed [44,45].

Similarly, the drugs-treated mouse embryos showed a morphological transition from a

spherical shape to a non-spherical shape after adding the drugs (Fig. S11). These data

mean that tissue surface tension is not a sole determinant, but there are other factors

significantly contributing to tissue shapes which can overcome the effect of the tensions.

Note that cell–cell adhesion forces contribute to both tissue surface tension [26,50] and

the pairwise potential of cell–cell interactions (Fig.1), suggesting that the pairwise

potential relates to tissue surface tension.

In addition, the EDTA-treated mouse embryos harbor intercellular spaces (Fig.

7D and S13), in which we do not think that tissue surface tensions are correctly defined.

Our result identified a parameter which explains sphericity of such tissues (Fig. 8B).

Similar tissues with intercellular spaces are also known in other species and tissues

including zebrafishes [52].

Comparison of other inference methods with other models

To understand morphogenetic events, mechanical states and simulations based

on those states are essential. Models such as vertex, Cellular Potts, and phase field models

are often utilized, especially for epithelial cells [3,53–56]. These models successfully

recapitulated various morphogenetic events, including cell sorting, epithelial cell

movements/rearrangements, the formation of the mouse preimplantation embryos [53,57],

and very early embryogenesis in *C.elegans* [58]. However, it is still challenging to

measure cellular and non-cellular parameters in three-dimensional systems with high

spatiotemporal resolution, although high-resolution inferences of parameters such as cell–

cell junction tensions and stresses have been performed in two-dimensional situations by

fitting a vertex model to experimental observations [40,59]. In addition, because the

assumptions of the vertex model are based on epithelial cells, its application to other cells

is limited including blastomeres and mesenchymal cells. On the other hand, particle

models are mainly used for cell aggregates and mesenchymal/self-propelled cells [12,14],

while some papers applied particle models to epithelial cells [15,18,19,60], meaning that

the applicability of particle models is expanding. Due to its simplicity of particle models

(i.e. low degrees of freedom), our method can provide a framework for quantitatively

connecting model parameters to *in vivo* parameters under three-dimensional situations.

Possibilities of image-based inference methods are expanding under three-dimensional

situations [61].

Limitation and perspective of our inference method

In the present study, we applied our inference method to blastomeres.

Applicability of our method to other cell types including epithelial and mesenchymal cells

will be evaluated. Epithelial cells are usually modeled by the vertex models where each

cell is assumed to be polygonal, and many-body (i.e. ≥ 3 cells) interactions but not

pairwise ones are considered [62,63]. By using the vertex model, the highly deformable

features of epithelial cells are well reproduced. It remains unknown whether pairwise

potentials can be a good approximation of epithelial cells, though three-dimensional

epithelial cells were modeled by particle-based models, which enabled one to simulate

three-dimensionally large tissues [15,18,19,64]. In deformable objects such as cells, cell–

cell interaction forces show hysteresis; i.e., the forces at the same distance become

different between the cases when two cells are approaching and dissociating. This effect

may be expressed by different profiles of DF curves between the two cases. In the vertex

models, this hysteresis is implemented through its high deformability. Because our

inference method contains temporal information of cell–cell interaction forces, it may be

possible to examine whether systems show hysteresis. It would be worth investigating

whether the framework of two DF curves based on the hysteresis can expand the

capability of particle models for describing various phenomena.

In our inference method, the coefficient of viscous frictional forces is considered

as described in Equation 1. Typically, this coefficient is assumed to be constant in

multicellular models. However, the values of this coefficient and its spatiotemporal

distributions in real tissues remain poorly understood [30]. There can be many factors

affecting the coefficient; e.g., cell–cell contact area, cell size, the number of contacting

cells per one cell, cell–cell adhesion molecules including cadherins, surface structures of

cells [65–67]. In the second model presented in the *C. elegans* embryos (Fig. S8), the

number of contacting cells per one cell is effectively considered. Influence of cell–cell

adhesion molecules means that the coefficient is different among cell types (e.g.,

differentiated vs. undifferentiated cells, etc.). Unfortunately, experimental measurements

of the coefficient with spatiotemporal resolution are lacking.

A serious issue to be considered is possible influence of external factors on

inference results. We showed that spatial constraints such as eggshells were negligible.

On the other hand, there are many external factors in real tissues such as expanding liquid

cavities in cystic structures such as the mouse blastocysts, traction forces exerted between

cells and extracellular matrices (ECM) which leads to self-migratory activities, cell–ECM

adhesions which leads to cell spreading, and so on [53,68,69]. It is important to evaluate

whether these factors affect inferred results or not, and this issue holds true about other

inference methods based on model fitting approaches (e.g. the vertex model-fitting

described above). Unfortunately, it is often technically challenging to directly measure

the spatiotemporal effect of the external factors on cell movements, otherwise, we can

correctly infer cell–cell interaction forces by subtracting the effect of the external factors.

Although overcoming this situation with many degrees of freedom is challenging, we

speculate that the analogy to molecular and colloidal sciences can be helpful. In these

fields, systems including external factors (e.g. solvents, pressures, etc.) can be

successfully approximated as effective pairwise potentials of particle–particle

interactions to some extent which are informative for predicting the systems' behaviors.

We are planning to examine what kinds of external factors can be approximated as effective pairwise potentials, leading to establishment of a framework for simulating larger tissues/organs in a minimal model.

Materials and methods

Details of experimental procedures, mathematical modeling, and statistical methods are described in Supplementary Information.

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Figure 1: Overview of strategy for inferring the effective potential of cell–cell interactions

A. Relationship between microscopic forces and attractive/repulsive forces in isolated

two cell systems. i) Microscopic forces are exemplified. ii) The microscopic forces are

approximated as attractive/repulsive forces where cells are described as particles with the

mean size. iii) Both the repulsive and attractive forces are provided as cell–cell distance-

dependent functions, and the summation (black broken line) is the distance–force curve

of the two particles. The relationship between the curve and the mean diameters of the

cells is shown. iv) A distance–potential curve is shown where the mean diameters of cells

correspond to the distance at the potential minimum.

B. Strategy for inferring effective forces of cell–cell interactions. i) Particle model. A blue

sphere corresponds to a cell. Attractive or repulsive force between the particles (blue

spheres #1–4), was considered; vectors of cell–cell interaction forces (F_i) are illustrated

by black arrows in the case of particle #3. The net force ($F_{C|p}$) of particle #3 is shown by

a red vector. The summation of F_i results in $F_{C|p}$ which determines the velocity ($V_{C|p}$) of

pth particle. ii) Nuclear tracking data were obtained and used as a reference data during

the inference. iii) Effective forces of cell–cell interactions were inferred by fitting. Red

line, attractive; blue line, repulsive. iv) From the inferred effective forces, we examined

whether distance–force/potential curves are detected.

Related figure: Figure S1 (inference method).

Figure 2: Validation of inference method using simulation data

Simulations were performed on the basis of a distance–force (DF) curve obtained from

the Lenard-Jones potential (LJ). The DF curve is shown in A-i. The simulation conditions

contain "Assembling process" (A), "Steady state" (B), and "Cell proliferation" (C). For

A-C, snapshots of the simulations are shown where the particles are of the mean size of

cells (i). In A-ii, the procedure of data analyses is exemplified, where a colored heat map

representing the frequencies of the data points (Frequency index (FI)). Averaged values

of the forces are shown in yellow (binned average). In A-iii, B-ii, and C-ii, the resultant

effective DF curves are shown with the DF curves from the LJ potential. Normalized L2

norms = $\{F_{\text{inferred}}(D) - F_{\text{LJ}}(D)\}^2 / (F_{\text{LJ\_max}})^2$ were calculated along D, and then the mean

values along D were calculated; $F_{\text{LJ\_max}}$ is the maximum attractive force in the LJ potential,

and the range of D was set that the absolute values of attractive forces at D are $\geq (0.1 \times$

$|F_{\text{LJ\_max}}|)$. The normalize L2 norms are: in A-iii, 0.035 (0%), 0.034 (10%), 0.033 (100%),

and 0.024 (1000%); in B-ii, 0.032 (1min), 0.046 (3min), and 0.15 (5min); in C-ii, 0.068

(1min), 0.035 (3min), and 0.095 (10min).

Related figures: Figure S2 and S3 (in the case of other given potential and random walk).

Figure 3: Influence of external constraints to effective forces of cell–cell interaction

Spherocylindrical constraints corresponding to eggshells are assumed in the particle

model used in Fig. 2. i) An example of simulations with labeling three cells (red, yellow,

and green). For the condition of the spherocylindrical length = 16μm ("compressive"),

the array of particles is marked by broken lines. ii) Inferred DF curves. The normalize L2

norms defined in Fig. 2 are: 0.062 (40μm), 0.066 (30μm), 0.077 (25μm), 0.16 (20μm),

and 0.29 (16μm).

Related Figures: Figure S4 (inference under spherical constraints) and S5 (inference in

spherocylindrical constraints).

Figure 4: Inference of effective force of cell–cell interaction in *C.elegans* embryos

A. Snapshot of the nuclear positions in the *C.elegans* embryo with cell lineages at time

frame = 76.

B. Mean diameters of cells at each time frame estimated from cell numbers. Given that

the volume of the embryos is constant (= *Vol*) during embryogenesis, the mean diameters

were estimated from the cell numbers (N_c) at each time frame as follows: mean diameter

= $\{Vol / (4/3 \pi N_c)\}^{1/3}$. The diameters relative to that at time frame = 16 are shown with

cell numbers. The sizes of the circles reflect the diameters, whose colors roughly

correspond to the colors in the graph in F.

C. Snapshots with inferred effective forces with the force values described by colored

lines at *t* = 16, 76, and 195. Forces are depicted in arbitrary units (A.U.); 1 A.U. of the

force can move a particle at 1μm/min. The nuclear tracking data were obtained from a

previous report [31].

D. Uniqueness of solution of effective force inference was examined. The minimizations

of the cost function *G* were performed from different initial force values as described in

the x- and y- axes, and the inferred values of each cell-cell interaction were plotted by

crosses.

E. The inferred effective forces of cell–cell interactions were plotted against the distance

of cell–cell interactions with binned averages at *t* = 76-115.

F. Inferred DF and DP curves at various time frames.

G. DP curves normalized by the distances at the potential minima at various time frames.

Related figure: Figure S6 (uniqueness of solution was examined), S7 (the inferred DP

curves were fitted by previously used frameworks such as the Morse potential), and S8

(inferred potentials under the relative velocity-based model).

Related movies: Movie S1A (tracking data) and S1B (force map).

Figure 5: Inference of the effective force of cell–cell interaction in mouse pre-

implantation embryos

A. Eight-cell and compaction stages of mouse embryo are illustrated, and their confocal

microscopic images are shown: bright field, maximum intensity projection (MIP) and

cross-section of fluorescence of H2B-EGFP. Snapshots of nuclear tracking are also

shown; blue spheres indicate the detected nuclei. Scale bars = 15μm.

B. Inferred DF and DP curves.

Related figures: Figure S9 (data from other embryos) and S10 (DF and DP curves in the

outer and inner cells in the compaction stage).

Related movies: Movie S2A-B (tracking data) and Movie S2C-D (force maps)

Figure 6: Outcomes of simulations based on inferred distance–force curves

A. Simulations results under the DF curves derived from *C. elegans* and mouse embryos

are exemplified.

B and C. DF curves sampled before reaching the minima of G, and simulation outcomes.

DF curves, left panels; the values of G and the maximum attractive forces in the DF curves,

right panels; simulation outcomes for each DF curve with the initial configuration

("start"), bottom panels. The values of G are relative to that in the case of all forces = 0.

The colors in each three panels in B and C correspond each other. In the right panels, the

numbers of the data points are 14 and 12 in B and C, respectively, and the representative

ones (colored circles) are selected for presenting the DF curves and the simulation

outcomes.

Figure 7: Inference of effective potentials of cell–cell interaction in compaction-inhibited

mouse embryos

A. Microscopic images of embryos under chemicals. CytoD, cytochalasin D; Bleb,

blebbistatin.

B. Inferred DP curves in the drug-treated embryos. N=6~10 for each condition.

C. Quantitative differences in the DP curves. Distances at the potential minima in the DP

curves, left panel; Distances providing 10% energy of the potential minima as the relative

value to the distances at the potential minima, right panel. Mann–Whitney–Wilcoxon tests

were performed and the resultant p-values for "No Drugs" vs. "EDTA", vs. "CytoD", and

vs. "Bleb" are 0.011, 0.23, and 0.00040, respectively, in the left panel. In the right panel,

distances providing other % energies instead of 10% are shown in Fig. S14B.

D. Confocal microscopic images of cell shapes. Cell shapes were visualized by staining

F-actin or E-cadherin.

E. The embryonic and cellular shapes illustrated based on D.

Related figures: Figure S11 (experimental design), S12 (enlarged view of DP curves), S13

(histological images of other embryos), and S14 (details of quantification of DP curves).

Figure 8: Simulations under inferred distance–potential curves in drug-treated embryos,

and identification of parameters explaining morphological transition

A. Simulation results for the drug-treated embryos. All simulation data are provided in

Figure S15A, and the representative results which nearly showed the mean values of the

sphericities for each condition are chosen here.

B. Sphericities in the simulations of the drug-treated embryos (left panel), and the

sphericities plotted against the distances at the potential minima calculated in Figure 7C.

Mann–Whitney–Wilcoxon tests were performed: p-values for "No Drugs" vs. "EDTA",

vs. "CytoD", and vs. "Bleb" are 0.011, 1.0, and 0.00080, respectively.

C. Aspect ratios in simulations of the drug-treated embryos (left panel), and the aspect

ratios plotted against the relative distances providing 10% energy of the potential minima

calculated in Figure 7C. Mann–Whitney–Wilcoxon tests were performed: p-values for

"No Drugs" vs. "EDTA", vs. "CytoD", and vs. "Bleb" are 0.21, 0.97, and 0.33,

respectively.

Related figures: Figure S15 (all simulation outcomes).

A Distance-force/potential curve in isolated two cells system

i. Two cells

Cell   Nuclei

Adhesion

Surface
tension
+
Volume
effect

Distance

**ii. Description
by particles**

Attractive

Balanced

Repulsive

 : a cell
(mean size)

iii. Distance-force (DF) curve

summa-
tion

repulsive force

attractive force

cell-cell
distance (D)

mean diameter
of cell

Force of cell-cell interaction (F)
(repulsive / attractive)

equivalent

iv. Distance-potential (DP) curve

$$U(D) = -\int_{+\infty}^{D} F(D)dD$$

cell-cell
distance (D)

mean diameter
of cell

Potential of cell-cell interaction (U)

B   Strategy for inference

i. Particle model

$V_p = F_{C|p}/\gamma$

$(F_{C|p} = \Sigma F_i)$

Cell

ii. in vivo (reference data)

nuclei

cell positions (xyz-t)

iii. Fitting (statistical inference)

attractive
or
repulsive

analogy with
atomic/molecular
/colloidal sciences

iv. Distance-force/potential curves

Whether distance-force curves
are detected?

Whether the curves describe
the properties of systems?

mechanical property
morphology

Fig.1 Koyama et al.

A   Assembling process

i. Simulation

Radius of particle
=2.5 μm

t = 100 min   t = 1000

LJ
+
fluctuation
(% of LJ)

ii. Plot & binned average of inferred effective force

SD value of force fluctuation (%)

Effective force of cell-cell interaction [A.U.]
repulsive — attractive

0   100   1000

cell-cell distance [μm]

binned average

frequency index
>2.5
>0
0

iii. Inferred effective distance-force curve

Effective force of cell-cell interaction [A.U.]
repulsive — attractive

cell-cell distance [μm]

- - - LJ (given)
— 0 %
— 10
- - - 100
— 1000
SD value of force fluctuation given to LJ

B   Steady state

i. Simulation

t = 200 min   t = 700

ii. Inferred effective distance-force curve

Effective force of cell-cell interaction [A.U.]
repulsive — attractive

cell-cell distance [μm]

- - - LJ (given)
— 1 min
- - - 3
— 5
sampling interval

C   Cell proliferation

i. Simulation

t = 200 min   t = 500
cell number = 38   = 47

ii. Inferred effective distance-force curve

Effective force of cell-cell interaction [A.U.]
repulsive — attractive

cell-cell distance [μm]

- - - LJ (given)
— 1 min
— 3
— 10
sampling interval

Fig.2 Koyama et al.

Fig.3 Koyama et al.

Fig.4 Koyama et al.

Fig. 5 Koyama et al.

Fig.6 Koyama et al.

Fig.7 Koyama et al.

A Simulation

No drugs   EDTA   CytoD   Bleb

B Sphericity

C Aspect ratio

Fig.8 Koyama et al.