Title

Cell position-based evaluation of mechanical features of cells in multicellular systems

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| Abstract

Measurement of mechanical forces of cell–cell interactions is important for studying the

emergence of diverse three-dimensional morphologies of multicellular organisms. We

previously reported an image-based statistical method for inferring effective pairwise

forces of cell–cell interactions (i.e., attractive/repulsive forces), where a cell particle

model was fitted to cell tracking data acquired by live imaging. However, because the

particle model is a coarse-grained model, it remains unclear how the pairwise forces

relates to sub-cellular mechanical components including cell–cell adhesive forces. Here

we applied our inference method to cell tracking data generated by vertex models that

assumed sub-cellular components. Through this approach, we investigated the

relationship between the effective pairwise forces and various sub-cellular components:

cell–cell adhesion forces, cell surface tensions, cell–extracellular matrix (ECM) adhesion,

traction forces between cells and ECM, cell growth, etc. We found that the cell–cell

adhesion forces were attractive, and both the cell surface tensions and cell–ECM adhesive

forces were repulsive, etc. These results indicate that sub-cellular mechanical components

can contribute to the effective attractive/repulsive forces of cell–cell interactions. This

comprehensive analysis provides theoretical bases for linking the pairwise forces to the

sub-cellular mechanical components: this showcase is useful for speculating the sub-

cellular mechanical components from the information of cell positions, and for

interpreting simulation results based on particle models.

1. Introduction

In multicellular living systems, mechanical features of cells are critical parameters for morphogenesis. For instance, polygonal epithelial cells show a tightly packed cell configuration, where both cell–cell adhesive forces and cell surface tensions are major components for regulating cell shapes, fluidity of the tissues, and tissue deformation (Bi et al., 2015; Landsberg et al., 2009; Lecuit et al., 2011). To address the roles of the mechanical components of cells in the behaviors of whole systems, several frameworks for simulating multicellular systems have been developed such as vertex models, cell particle models, cellular Potts models, phase field models, etc. (Merkel and Manning, 2017; Nonomura, 2012).

To perform simulations, mechanical parameters are required that are measured by using techniques such as atomic force microscopies (Campàs, 2016; Sugimura et al., 2016) or by using image-based force inference methods (Brodland et al., 2010; Ishihara and Sugimura, 2012; Koyama et al., 2023). The latter techniques enable us to acquire spatio-temporal information of parameter values. For instance, by fitting a vertex model to microscopic images of labeled cell membranes, cell–cell junction tensions were inferred (Ishihara and Sugimura, 2012). In the case of three-dimensional (3D) tissues, imaging cell membranes with subsequent segmentation are challenging, while we

previously reported a particle model-based force inference method where only cell

nuclear positions were used as described in detail later (Koyama et al., 2023). In other

words, this inference method is based on nuclear/cellular positions with their temporal

evolution. However, because a particle model is a coarse-grained model, it is not clear

how the forces in the particle model relate to the sub-cellular mechanical parameters

including the cell–cell adhesion forces, the cell surface tensions, etc.

The cell particle models, where a cell is described as a point particle, have been

widely applied to various cells including blastomeres, cancer cells, mesenchymal cells,

and epithelial cells (Drasdo et al., 1995; Forgacs and Newman, 2005; Guillot and Lecuit,

2013; Maître et al., 2012; Merkel and Manning, 2017; Steinberg, 2007; Yong et al., 2015).

The particle models typically assume both attractive and repulsive forces of cell–cell

interactions: i.e., mechanical potential of pairwise cell–cell interactions. Because of their

simplicity, low coding cost, and low computational load, the particle models are

advantageous for simulating larger three-dimensional systems (Delile et al., 2017; Nissen

et al., 2018). However, the origin(s) of the attractive/repulsive forces has not been

correctly clarified yet. For instance, questions to be addressed include whether the

attractive behavior of cell–cell interactions is conferred from the cell–cell adhesion forces,

etc. This question is important to correctly interpret results of simulations based on the

particle models in the context of the sub-cellular mechanical features.

In the case of isolated two cell systems (Fig. 1A-B), the cell–cell adhesion forces

should shorten the cell–cell distance, which can be described as an effective attractive

force, whereas both the cell surface tensions and excluded volume effect of the cells can

be described as an effective repulsive force, as described in text books and in some articles

(Forgacs and Newman, 2005; Merkel and Manning, 2017). Then, the summation of these

different forces may lead to distance-dependent force curves (Fig. 1C). We previously

reported that the profile of the distance–force curves is critical for morphogenesis during

early embryogenesis in mice and *C. elegan*s (Koyama et al., 2024, 2023). However, it

remains unclear whether the above relationships considered in the isolated two cell

systems are applicable to multicellular systems (Fig. 1D), because the cells in

multicellular systems can exhibit shapes far from spheres and so on.

In the present study, we aimed to extend the cell position-based force inference

framework. By using our image-based method for inferring effective distance–force

curves (Koyama et al., 2023), we theoretically evaluated the relationships between the

effective distance–force curves and the sub-cellular mechanical components. In other

words, we generated synthetic data by simulating vertex models where both the cell–cell

adhesion forces and the cell surface tensions were explicitly assumed, and then, by

applying our inference method to the synthetic data, we evaluated the relationship

between the distance–force curves and the sub-cellular mechanical components (Fig. 1D).

In addition to these components, we also consider following sub-cellular components: the

area elasticity (conservation of cell volume/area), cell growth (cell volume increase),

adhesion forces between cells and extracellular matrix (ECM), and traction forces

between cells and ECM. This comprehensive analysis provides the information whether

each sub-cellular component effectively acts as the attractive or repulsive forces, and also

provide relationships between the particle models and other models including the vertex

models.

2. Theory

2.1. Method for inferring attractive/repulsive forces of cell–cell interactions

To infer the effective attractive and repulsive forces of cell–cell interactions in

multicellular systems, we previously developed an image-based inference method

(Koyama et al., 2023). Several studies have been adopting image-based strategies for

inferring cellular mechanical forces and properties (Brodland et al., 2010; Ishihara and

Sugimura, 2012). In the case of our method, a particle model was fitted to the temporal

evolution of cell positions obtained from live microscopic imaging, which enabled us to

infer the attractive/repulsive forces between each cell–cell interaction with each time

frame as explained below. By analyzing the inferred attractive/repulsive forces, we

reported that the effective attractive/repulsive forces can be actually approximated as a

function dependent on the cell–cell distances (i.e., distance–force curves similar to Fig.

1C) in the blastomeres of the mouse and of *C. elegans* embryos (Koyama et al., 2024,

2023).

Briefly, in our method, we minimized a following cost function; $G = G_{xyz} + G_{F_0}$,

where G_{xyz} is the difference in *xyz*-coordinates of each particle between *in vivo* data and

particle simulations, and G_{F_0} is the additional cost function for cell–cell distance-

dependent weight (Koyama et al., 2023). G_{xyz} was defined so as to contain the *xyz*-

coordinates throughout all time frames:

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

where *p* is the particle ID, $P(t)$ is the total number of the particles at *t*, *T* is the total time

frames, and Δt is the time interval. x_p, y_p, and z_p are the *xyz*-coordinates of the *p*th particles

in the particle simulations. x_p^{ref}, y_p^{ref}, and z_p^{ref} are the *xyz*-coordinates of the *p*th particles

in the *in vivo* cells. The distance-dependent weight G_{F_0} means that the forces of the cell–

cell interactions should be gradually decreased as the distances of the cell–cell

interactions are increased, and ultimately, the forces become zero at the long distances.

G_{F_0} was defined as follows: $G_{F_0} = \omega_{F_0} \sum_{t=1}^{T} \sum_{i=1}^{I(t)} \psi(D_i) F_i^2 \Delta t$, where F_i is the force value of

ith cell–cell interactions, $I(t)$ is the total number of the cell–cell interactions at t, D_i is the

cell–cell distance of the ith interaction, and ω_{F0} 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, leading to that the value of F_i approaches zero around larger D_i

(Koyama et al., 2023). We numerically solved this minimization problem by using the

conjugate gradient method. Our inference method was previously validated by applying

this method to simulation data generated under pregiven forces (Koyama et al., 2023).

We had also confirmed that a unique solution was obtained by our minimization method

(Koyama et al., 2023). The code is the same as that in Koyama et al. 2023

(https://doi.org/10.5281/zenodo.7427050).

2.2. Particle model to be fitted

In our particle model, attractive and repulsive forces for pairwise cell–cell interactions

are assumed. Due to the low Reynolds number in the case of cellular-level phenomena,

the inertial force is negligible (Fletcher et al., 2014; Forgacs and Newman, 2005; He et

al., 2014; Li et al., 2017; Schötz et al., 2008). In our present study, we assumed that cells

were put on substrates, and that frictional forces between the cells and the substrates were

exerted, by which the motion of the particles was overdamped. In the case that the

substrates are fixed (i.e., non-moving), the equation of a particle motion may be written

as follows;

$$V_{C|p} = F_{C|p} / \gamma_C \qquad\qquad \text{Eq. 1,}$$

where $V_{C|p}$ is the velocity of the pth particle, $F_{C|p}$ is the summation of the cell–cell

interaction forces exerted on the pth particle, and γ_C is the coefficient of the viscous

drag and frictional forces provided from the substrates. This assumption has been used in

both particle-based models and vertex models (Honda et al., 2008; Li et al., 2017; Nissen

et al., 2017; Suzuki et al., 2017; Szabó et al., 2006).

During this inference, we assumed the simplest situation, where γ_C is constant

(=1.0). This is the same setting as that in our previous work (Koyama et al., 2023). The

dimension of the particle velocity $V_{C|p}$ was set to be μm/min for convenience, which is

typical dimension in living cells. Because we did not measure the value of γ_C in living

tissues, we cannot determine the value of the effective force $F_{C|p} (= \gamma_C V_{C|p})$ with a

specific dimension. However, under the above assumption, 1 arbitrary unit (A.U.) of F

coincides with a force which can move a particle with a velocity of 1 μm/min in tissues.

2.3. Vertex model simulation as synthetic data

As a well-defined system, we adopted the vertex model for describing epithelial cells (Fig,

2A, "Model"). This model is the standard framework for simulating epithelial cells which

typically exhibit polygonal shapes, where some sub-cellular mechanical components such

as cell–cell adhesion forces and cell surface tensions are assumed (Fletcher et al., 2014;

Okuda et al., 2015). By using the vertex model, we performed simulations, and we

considered the simulation outcomes as synthetic data (Fig. 2A, "Simulation"). In other

words, we applied our inference method to cell tracking data generated by the simulations

of the vertex model, and then obtained effective distance–force curves (Fig. 2A, "DF

curve").

The vertex model used in this study is essentially the same as that in our previous

studies (Koyama et al., 2022; Koyama and Fujimori, 2020). The potential energy in the

whole system is defined as follows,

$$ U = \sum_{<k,l>} \lambda_{\mathrm{Tot}} L^{<k,l>} + \sum_{n} \frac{1}{2} K_{\mathrm{a}} \left(\frac{a_n}{a_{\mathrm{O}}} - 1 \right)^2 a_{\mathrm{O}} . \qquad \text{Eq. 2} $$

λ_{Tot} is the line tension exerted on cell–cell junctions or on cell edges of outer boundary

(Fig. 2A, "Model"). The line tension is provided from both the cell–cell adhesion force

(λ_{AD}) and the cell surface tension (λ_{S}); the former has a negative effect on the line tension,

and the latter does a positive (Fig. 2A; $\lambda_{\mathrm{Tot}} = 2\lambda_{\mathrm{S}} - \lambda_{\mathrm{AD}}$). The potential energy on a

junction or edge is $\lambda_{\mathrm{Tot}} L^{<k,l>}$, where L is the length of the junction or edge composed of

the kth and lth vertices. The potential energy for a cell provided by the area elasticity is

$(1/2)K_{\mathrm{a}}\left(a_n / a_{\mathrm{o}} -1\right)^2 a_{\mathrm{o}}$, where a_n is the area of the nth cell and a_{o} is the natural area. The

force ($F_{\mathrm{V}|h}$) exerted on an hth vertex is calculated as follows: $F_{\mathrm{V}|h} = -\nabla U$, where ∇ is

the nabla vector differential operator at each vertex. Similar to the particle model, we

assumed that the cells were put on non-moving substrates where frictional forces were

exerted. Therefore, the motion of each vertex is described as follows: $V_{\mathrm{V}|h} = F_{\mathrm{V}|h} / \gamma_{\mathrm{V}}$,

$V_{\mathrm{V}|h}$ is the velocity of the hth vertex, and γ_{V} is the coefficient of the friction of a vertex.

Similar to the case in the particle model, γ_{V} was set to 1.0, and the dimension of particle

velocity $V_{\mathrm{V}|h}$ was set to be μm/min. The code is the same as that given in our previous

work (Koyama and Fujimori, 2020).

The fluctuation of the line tensions (σ) was assumed as follows. Cellular edges

to be activated were selected according to p_{ED} which is the probability of activation per

unit of time. On the cellular edges selected, σ was added to the line tensions, and the

duration time of this activated state is τ as defined in the Supplementary information.

3. Results

3.1. Inference of attractive/repulsive forces in vertex model

To evaluate possible relationships between the attractive/repulsive forces and the cell–cell adhesion forces/the cell surface tensions, we applied our inference method to synthetic cell tracking data generated by our vertex model. We performed simulations containing several tens of cells (Fig. 2A, "Simulation"). Then, by tracking the centroids of each polygonal cell, we generated cell tracking data (Fig. 2B). By applying our inference method to the cell tracking data, we obtained the attractive/repulsive forces for each cell–cell interaction at each time frame (Fig. 2B, "$F_i(t)$"), and we simultaneously acquired the distances for each cell–cell interaction (Fig. 2B, "$D_i(t)$"). These paired data (i.e., $F_i(t)$ and $D_i(t)$) were plotted on a graph space below.

Fig. 2C-i shows the plots of the inferred forces ($F_i(t)$) against the cell–cell distances ($D_i(t)$). In the absence of the fluctuations of tensions (0%), the distribution of the data points was not so diverged (Fig. 2C-i, heat maps), and, by calculating the values of binned averages, a DF curve was detected (Fig. 2C-i, yellow). The binned averaged line in Fig. 2C-i is shown in Fig. 2C-ii (red line), which exhibited a typical profile with a peak of the attractive force. In the presence of the fluctuations, the distributions became wider (Fig. 2C-i, heat maps), but the DF curves were detected whose profiles were

equivalent to that without the fluctuations (Fig. 2C-ii). In conclusion, the effective DF

curves are detectable in multicellular epithelial cells.

3.2. Influence of cell–cell adhesion forces/cell surface tensions on DF curves

Next, we examined whether the microscopic features of the epithelial cells were reflected

in the effective DF curves. We performed simulations under various values of the cell–

cell adhesion forces (Fig. 3A-i); the cells showed highly deformed cell shapes or regular

hexagonal shapes under the stronger or weaker cell–cell adhesion forces, respectively.

The inferred DF curves are shown in Fig. 3A-ii, whose profiles are quantitatively

evaluated in Fig. 3A-iii. The absolute values of the maximum attractive forces were

positively correlated with the cell–cell adhesion forces (Fig. 3A-iii). These results are

consistent with the case in the isolated two cell systems.

We also evaluated the effect of the cell surface tensions (Fig. 3B), and

successfully detected DF curves (Fig. 3B-i). The maximum attractive forces were

negatively correlated with the cell surface tensions. Therefore, the effect of the cell

surface tensions was opposite to that of the cell–cell adhesion forces (Fig. 3B-i vs. 3B-ii).

If the surface tensions act as the repulsive forces, they can be emerged as the reduction of

the attractive forces in the DF curves, because the DF curves are the summation of the

repulsive and attractive forces (Fig. 1C). Together with the results in the case of the cell–

cell adhesion forces, these results indicate that the effects of the microscopic features of

the cells are conserved among the multicellular epithelial cells and the isolated two cell

systems.

Finally, we evaluated the effect of the area elasticity. Under large values of the

area elasticity, one expectation is that the slope of the repulsive region in the DF curve

becomes steeper due to its elasticity. The inferred effective DF curves and their

quantitative evaluations are shown in Fig. 3C-i and 3C-ii. The typical profiles of the DF

curves such as the peak of the attractive forces were clearly detected, but the maximum

values were not significantly affected by the area elasticity (Fig. 3C-ii). On the other hand,

although the profiles of the repulsive regions were not obtained in all conditions, the slope

under the higher value of the area elasticity (= 10.0) was steepest (Fig. 3C-i, purple line).

Therefore, the effect of the area elasticity is neutral on the attractive forces in the DF

curves, and, because the slope of the repulsive region is related to the stiffness of the cores

of the cells, the area elasticity may be correlated with the stiffness of the cores.

In summary, the cell position-based method for evaluating the mechanical

properties of multicellular epithelial cells revealed that the cell–cell adhesion forces and

the cell surface tensions showed attractive and repulsive effects, respectively. In addition,

we also tested whether these relationships were conserved in other vertex models (i.e.,

model dependency). We used another typical vertex model that assumed a potential based

on the perimeters of the cells, which increased the cell–cell junction tensions (Fletcher et

al., 2014). The definition of the potential is described in the Supplementary information.

If the coefficient of this potential was not so large, the relationships were conserved (Fig.

S1).

3.3. Influence of cell-ECM adhesion on DF curve

In real tissues, there are various types of non-cellular external factors which affect cell

behaviors; extracellular matrix (ECM), egg shells, liquid cavity, etc (Honda et al., 2008;

Kajita et al., 2003). These factors may influence inferred effective DF curves. This is

analogous to the atomic, molecular, and colloidal sciences. For instance, external

pressures increase the density of particulate objects, which is reflected in the radial

distribution function linked to the effective distance–potential curves (Atkins et al., 2018).

Another example is solvents, where hydration of particles by the solvents yields energy

barriers in the effective distance–potential curves (Israelachvili, 2011). Therefore, by

measuring the effective distance–potential curves, one can predict, at least partially, what

kind of external factors exist in systems of interest. In multicellular systems, however, it

has not been clarified how external factors influence the effective distance–potential

curves.

Here we examined the influence of ECM on the effective DF curves, that

interacts with cells. Spreading of cells on ECM is regulated by the competition between

the cell–ECM and the cell–cell adhesions; the increased forces of the cell–ECM adhesions

lead to the increase in the areas of the cells (Fig. 4-i) (Pérez-González et al., 2019; Ryan

et al., 2001; Yong et al., 2015). Because the increase in each cell area pushes the

surrounding cells, we expected that the cell–ECM adhesion forces would show a

repulsive effect on the effective cell–cell interactions (Fig. 4-i, "Repulsive force?").

Simultaneously, the increased cell areas lead to the increases in the distances between the

cells, which should be appeared as a rightward shift of the effective DF curves along the

cell–cell distances (Fig. 4-i, "Shift of DF curve?").

We modeled the cell–ECM adhesion in the vertex model used in Fig. 2. The

adhesion between cells and ECM is mediated by focal adhesions, etc (Goodwin et al.,

2016; Pérez-González et al., 2019; Yamaguchi et al., 2022). The distributions of these

adhesive structures seem to be different among tissues and conditions: some tissues show

distributions along their peripheries, while others show almost unbiased distributions.

Here we assumed the simplest case where the structures are uniformly distributed. We

defined the potential energy of the adhesion as $-E_{\mathrm{ECM}}a_n$ for each cell, where E_{ECM} is

the coefficient of the energy and a_n is the cell area as previously defined.

Under the increased cell–ECM adhesion forces, the cell areas were increased

(Fig. 4-ii, $E_{\mathrm{ECM}} = 1.0$ vs. $= 0.0$). Fig. 4-iii shows the inferred effective DF curves, and Fig.

4-iv is the quantitative evaluation of the curves. As we expected, the maximum attractive

forces were negatively correlated with the cell–ECM adhesive forces (Fig. 4-iv, left panel),

and the distances at the maximum attractive forces were increased by the cell–ECM

adhesive forces (Fig. 4-iv, right panel). These results suggest that the cell–ECM adhesive

forces are reflected in the reduction of the attractive forces in the effective DF curves.

In addition, according to Fig. 4 and Fig. 3B, both the cell–ECM adhesive forces

and the cell surface tensions showed the repulsive effects. However, the latter did not

show an increase in the distances at the maximum attractive forces (Fig. S2), suggesting

that we can distinguish the two components each other.

3.4. Influence of cell-ECM traction forces on DF curve

Next, we focused on traction forces between cells and ECM, which confer self-migratory

activities of the cells (Aoki et al., 2017; Garcia et al., 2015; Szabó et al., 2006). We

implemented the traction forces in the particle model instead of the vertex model, because

there is no general way to implement self-migratory activities in the vertex models. First,

we set the traction forces to show random directions (Fig. 5A-i, right panel), and to persist

for a given period of time (Fig. 5A-ii, "with persistency = 50.0min"). The cell–cell

interaction forces were provided by the Lennard-Jones (LJ) potential (Fig. 5A-i, "LJ").

The value of the traction forces is shown as a relative value to the maximum attractive

force of the LJ potential (Fig. 5A-ii, "1,000% of LJ"). We assumed that the friction

between the cells and the ECM, and performed two-dimensional simulations with the

friction between the cells and the ECM.

Fig. 5A-iii shows the inferred effective DF curves. In the absence of the traction

forces (0%), the inferred DF curve showed a profile similar to the given LJ potential (Fig.

5A-iii, purple line), though an inconsistency was observed at the distant region (distance

= ~7μm). In the case that the value of the traction forces was equivalent to the attractive

force of the LJ potential (100%; light blue line), the inferred curve was still consistent

with that without the traction forces, whereas the inferred curve became highly repulsive

under a larger traction force (1,000%; red line).

Fig. 5-iv shows the effect of the persistency of the traction forces. Even under

the large traction forces (1,000%), if the persistency was short (1.0min; purple line), the

inferred DF curve was consistent with the given LJ potential. In conclusion, the traction

forces can significantly modify the effective DF curves under the condition that both the

force value and the persistency are large. Otherwise, the traction forces do not affect the

profiles of the DF curves. We also found such repulsive profiles of the DF curves in

Madin-Darby canine kidney (MDCK) cells on substrates, which show highly self-

migratory activities (Fig. S3A).

3.5. Influence of cell growth on DF curve

Cell growth (i.e., increase in cell volume during the cell proliferative phase) is an

important parameter for homeostasis in multicellular systems: cell growth increases

pressure in multicellular systems, leading to contact inhibition of growth, delamination

of epithelial cells, and apoptosis (Marinari et al., 2012; Podewitz et al., 2015;

Zimmermann et al., 2016). Under the increased pressure due to cell growth, the cells

push/repel each other. In other words, the intrinsic attractive forces between the cells may

be effectively cancelled due to the cell growth. To test this hypothesis, we used a

mathematical model considering the cell growth. A well-known cell growth model is

shown in Fig. 6-i, where one cell is modeled as two particles and the growth is described

by the repulsive force (coefficient B) between the two particles (Basan et al., 2011;

Podewitz et al., 2015; Ranft et al., 2010). The repulsive force is defined as follows;

$B/(D_g + C)^2$, where D_g is the distance between the paired two particles, and C is constant.

When the distance between the two particles reaches a critical value, cell division occurs.

In our model, we set $C = 5.6$ and $D_{CR}=5.0$, and implemented that particle–particle

interactions between different cells were governed by the LJ potential that was previously

shown in Fig. 5A-iii, "LJ". The original model by Basan et al. was developed for

describing three-dimensional cell aggregates where viscous frictions between the cells

are assumed. However, we modified this model so that the cell–substrate friction was

assumed in a manner similar to Fig 2-5, instead of the frictions between the cells.

We performed simulations and, inferred effective DF curves between the cells

(Fig. 6-i, "DF curve" between the orange cells). When the coefficient of the cell growth

was set to be larger, the cell number was increased (Fig. 6-ii, $B = 4.0$ vs. 0.0). Fig. 6-iii

shows the inferred effective DF curves, and Fig. 6-iv shows their quantitative comparison.

The maximum attractive forces were negatively correlated with the growth forces, and

under the larger growth forces, the attractive components were absolutely diminished (Fig.

6-iv). These results indicate that the cell growth effectively decreases the attractive forces

of the cell–cell interactions.

3.6. DF curve in vertex model under steady state

In the above cases (Fig. 2-6), we assumed non-steady states: the systems are undergoing

morphological changes. Such non-steady states should be typical during morphogenesis

of multicellular systems. On the other hand, confluent epithelial monolayers would be

under steady states, that may correspond to tissues in adult organs. Under the steady states,

the motions of cells can be fluctuated, but the tissues do not experience morphological

transitions; i.e., analogous to systems under thermodynamically equilibrium states. By

using the vertex model, we then investigated the relationship between the effective DF

curves and the cell–cell adhesion forces/the cell surface tensions under the steady states.

Fig. 7A shows a confluent epithelial monolayer modeled by the vertex model

where the vertices continuously moved due to the fluctuations of the line tensions of the

cell–cell junctions defined in Fig. 2. A whole view of the simulation is shown in Fig. S4.

3.6.1. Influence of cell–cell adhesion forces/cell surface tensions on DF curve

Fig. 7B shows the inferred effective DF curves under the conditions with the different

values of the cell–cell adhesion forces. In the all cases, the DF curves showed clear peaks

of the attractive forces (Fig. 7B-i). In Fig. 7B-ii, the simulation snapshots show that the

cells exhibited either highly deformed shapes or an array of regular hexagons under the

stronger or weaker cell–cell adhesion forces (λ_{AD} = 0.9 vs. 0.0), respectively. The profiles

of the DF curves were quantitatively evaluated (Fig. 7B-iii); unlike the case in Fig. 3A,

there was a negative relationship between the cell–cell adhesion forces and the maximum

attractive forces (Fig. 7B-iii, left panel). In addition, the slopes of the DF curves at the

force = 0 —defined in Fig. 7B-iii, right panel, inset— showed a negative relationship to

the cell–cell adhesion forces (Fig. 7B-iii, right panel). We will discuss these results later.

Fig. 7C shows the inferred effective DF curves under the conditions with the

different values of the cell surface tensions. Clear DF curves were detected (Fig. 7C-i),

except that the profiles were abruptly changed between the conditions of the weaker

surface tensions and the conditions of the stronger surface tensions as follows (Fig. 7C-

i). Under the three conditions with the weaker surface tensions (Fig. 7C-i, λ_S = 0.45, 0.5,

and 0.6), the profiles of the three DF curves were almost similar, with gradual changes

among them. Under the two conditions with the stronger surface tensions (Fig. 7C-i, λ_S =

0.8 and 1.0), the two DF curves showed an additional attractive component (λ_S = 0.8) or

repulsive component (λ_S = 1.0) around the longer distances. Therefore, the profiles of the

DF curves were abruptly changed, when the surface tensions were changed from [λ_S =

0.45, 0.5, 0.6] to [0.8, 1.0]. Under the stronger surface tensions, the cells showed an array

of regular hexagons compared with the case under the weaker surface tensions (Fig. 7C-

ii). The profiles of the DF curves were quantitatively evaluated (Fig. 7C-iii); unlike the

case in Fig. 3C, there was a positive relationship between the surface tensions and the

maximum attractive forces (Fig. 7C-iii, left panel). The slopes of the DF curves at the

force = 0 showed positive relationship to the cell surface forces (Fig. 7C-iii, right panel).

We interpret the meaning of the slopes of the DF curves at the force = 0 as

follows. In Fig. 7B-C, the maximum attractive forces show a negative or positive

relationship to the cell–cell adhesion forces or the cell surface tensions, respectively. The

increased maximum attractive forces (i.e., deeper valleys in the DF curves) are usually

associated with steeper slopes of the DF curves, resulting in the steeper slopes at the

distance at the force = 0 (Fig. 7B-iii and 7C-iii). Because the state of the force = 0

corresponds to a steady state, the slope at the force = 0 relates to the stability of the state;

i.e., in the case of a system with the steeper negative slope, when the distance is slightly

changed from the steady state, the force for restoring to the steady state becomes larger

(Fig. 7C-iii, right panel, "Stability"). In other words, a system with a steeper slope

strongly prefers to keep the cell–cell distances at a unique distance equal to that at the

force = 0. This feature should lead to the formation of an array of regular hexagons as

shown in Fig. 7B-ii and 7C-ii ($\lambda_{AD} = 0$ in B-ii or $\lambda_S = 1.0$ in C-ii). In conclusion, we think

that a system that prefers a regular hexagonal array will show a steeper slope with a larger

maximum attractive force.

In addition, we also evaluated the influence of the area elasticity (Fig. S4), and

detected no significant changes in the inferred DF curves under the different values of the

area elasticities. We also inferred DF curves in MDCK epithelial cells under a nearly

stable state, and detected a clear DF curve with the attractive forces (Fig. S5).

3.6.2. DF curve in solid-liquid phase transition

As mentioned above in Fig. 7C-i, we detected an abrupt change in the profiles of the

inferred DF curves. It is possible that such an abrupt change corresponds to a certain

phase transition. In the case of multicellular systems, solid-liquid phase transitions are

well known, which are also reported in the vertex models (Bi et al., 2015; Mongera et al.,

2018; Petridou et al., 2021). We evaluated the fluidity of the cells in our vertex model-

based simulations. Fig. 8A shows the trajectories of the cell centroids under the conditions

of the different values of the cell surface tensions. Under the smaller values of the surface

tensions (λ_S = 0.45, 0.5), the cell centroids were substantially moved during the

simulations, indicating a liquid-like behavior. On the other hand, under the larger values

of the surface tensions (λ_S = 0.8, 1.0), the positions of the cell centroids were almost fixed,

indicating a solid-like behavior. Fig. 8B shows the mean square displacement (MSD). The

MSDs were continuously increased under the weaker surface tensions (λ_S = 0.45, 0.5, 0.6),

whereas the MSDs reached plateaus under the stronger surface tensions (λ_S = 0.8, 1.0).

Therefore, a solid-liquid transition occurs between λ_S = 0.6 and 0.8, and this critical point

corresponds to the abrupt change in the profiles of the inferred DF curves. We concluded

that the solid-liquid phase transition was appeared as the abrupt change in the inferred DF

curves.

4. Discussion

In the present study, we investigated how the sub-cellular mechanical components relate

to the effective attractive/repulsive forces of cell–cell interactions in multicellular systems.

By applying our particle model-based inference method to the cell tracking data generated

by some model frameworks, such as the vertex model and the 2-particel-for-1-cell model,

we related the effective attractive/repulsive forces to the various sub-cellular mechanical

components. Our comprehensive analyses are summarized in Table 1: the cell–cell

adhesion forces effectively act as attractive forces, the cell surface tensions act as

repulsive, the cell growth acts as repulsive, the cell–ECM adhesion forces act as repulsive,

the stronger traction forces with long persistency act as repulsive. In Table 1, we also

added the effect of egg-shells and liquid cavities as we previously reported (Koyama et

al., 2024, 2023). Therefore, our results indicate that some sub-cellular mechanical

components actually act as the effective pairwise forces of the cell–cell interactions. The

quantitative differences in the profiles of the inferred DF curves are critical for

morphogenesis (Koyama et al., 2024, 2023). When performing the cell position-based

force inference method, this comprehensive description would be useful to speculate the

origins of the attractive/repulsive forces.

On the other hand, under the steady states, the relationship between the effective

attractive/repulsive forces and the cell–cell adhesion forces/the cell surface tensions was

changed in the vertex model (Fig. 7). Vertex models assume many-body interactions but

not pairwise interactions (Bi et al., 2016): the potential energies are determined through

the relationship among >2 cells. We guess that the effect of the many-body interactions

become dominant under the steady states.

Our inference method may be useful for model simplification (i.e., model

reduction): models with a higher degree of freedom, such as the vertex models, are

simplified as the particle model. Because the particle models are useful to simulate three-

dimensional systems as described in the Introduction, it is worth addressing whether

three-dimensional models based on the vertex models, etc. can be simplified as the

particle models (Kajita et al., 2003; Okuda et al., 2015; Runser et al., 2024).

Some of our theoretical findings were consistent with the cases in MDCK cells

with high self-migratory activities or under the steady states (Fig. S3 and S5). To

experimentally test the effects of the sub-cellular mechanical components, we need to

prepare cells expressing different doses of related proteins such as cadherins for the cell–

cell adhesive forces, actomyosin for the cell surface tensions, integrins for the cell–ECM

adhesive forces, and so on.

Because real tissues have many mechanical components, it is challenging to

separately measure or infer each mechanical parameter value. In the case of our inference

method, it may be difficult to distinguish between the increase in the cell–cell adhesive

forces and the decrease in the cell surface tensions. To overcome this issue, simultaneous

experimental analyses are important: e.g., microscopic imaging of the proteins related to

the cell–cell adhesions or the cell surface tensions, such as cadherins, actomyosins, etc.

This is not only the case for image-based inference methods but also for invasive methods

such as laser ablation experiments, AFM, etc. For instance, by performing the laser

ablation experiments, cell–cell junction tensions are estimated (Fernandez-Gonzalez et

al., 2009; Ishihara and Sugimura, 2012; Koyama et al., 2016); because the cell–cell

junction tensions are composed of both the cell–cell adhesive forces and the cell surface

tensions, it is difficult to dissect to what extent the two mechanical components contribute

to the cell–cell junction tensions. The Young's modulus of cells can be measured by AFM,

which may be affected by cell elasticities including the area elasticities, and by the cell

surface tensions, etc. Therefore, it is important to collect information that describes how

the various mechanical components relate to each other. To this end, the theoretical

analyses presented in our manuscript, together with the measurements in real tissues, will

be invaluable. Although many techniques for measuring/inferring mechanical parameters

have been developed, it is still challenging to do in real three-dimensional tissues. This is

because of both the accessibility to the tissues and three-dimensional imaging with

subsequent image processing (i.e., segmentation). We think that our cell position-based

method can overcome these difficulties with parallel applications of the other methods.

5. Conflict of Interest

The authors declare that the research was conducted in the absence of any commercial or

financial relationships that could be construed as a potential conflict of interest.

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7. Author contribution

Conceptualization (HK, AI, HO), Data curation (HK), Formal analysis (HK), Funding acquisition (HK, TO), Investigation (HK, AI, HO, TO, KN, TF), Methodology (HK, KN), Project administration (HK), Resources (HK, TO, TF), Supervision (TF), Validation (HK), Visualization (HK), Writing – original draft (HK), Writing – review and editing (HK, AI, HO, TO, KN, TF)

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9. Declaration of generative AI and AI-assisted technologies

During the preparation of this work, the authors used DeepL in order to improve the

readability of the manuscript. After using this tool, the authors reviewed and edited the

content as needed and take full responsibility for the content of the published article.

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Figure legends

Figure 1: Attractive/repulsive forces of cell–cell interactions

A. Sub-cellular forces contributing to cell–cell interactions are exemplified in the case of

an isolated two cell system.

B. The sub-cellular forces are approximated as attractive/repulsive forces in particle

models.

C. Both the repulsive and attractive forces are provided as cell–cell distance-dependent

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

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

cells is shown.

D. The sub-cellular mechanical components in multicellular systems include the cell–cell

adhesion forces, the cell surface tensions, etc. They can be the origin of the effective

attractive/repulsive forces.

Figure 2: Inference of effective attractive/repulsive of cell–cell interaction in vertex

model

A. Vertex model. λ_{Tot} is the line tension exerted on the cell–cell junctions or on the cellular

edges along the outer boundary of the cell cluster. The potential energy on a junction or

edge is $\lambda_{\mathrm{Tot}} L^{<k,l>}$, where L is the length of the junction or the edge composed of the kth

and lth vertices. The potential energy for a cell provided by the area elasticity is

$(1/2)K_{\mathrm{a}}\left(a_n / a_{\mathrm{o}} - 1\right)^2 a_{\mathrm{o}}$, where a_n is the area of the nth cell and a_{o} is the natural area. An

example of the simulations is shown with the parameter values (right panel). In addition

to the polygonal cell contours, the cell centroids are shown as dots (See B).

B. Structure of the data obtained by our inference method. $F_i(t)$ is the inferred force of

the ith cell–cell interaction at t, where the distance is $D_i(t)$.

C. Inferred effective distance–force (DF) curves under various values of the fluctuations

of the line tensions, σ. i) The inferred forces are plotted against the cell–cell distances,

and the values of the binned averages of the forces are shown in yellow. The width of the

bins for the distances (D) is 0.27 µm. The procedure is detailed in the Supplementary

information. ii) The inferred DF curves were shown, which were obtained by linearly

connecting the plots of the binned averages in (i).

Figure 3: Effective attractive/repulsive forces in vertex model

A. Inferred DF curves under various values of the cell–cell adhesive forces, λ_{AD}. i)

Simulation outcomes are shown where the cell cluster tends to form a circular colony

under the increased values of the adhesive forces ($\lambda_{AD} = 0.9$). ii) Inferred DF curves. iii)

Quantitative comparison of the DF curves. The maximum attractive force (F_{max}) is

defined.

B. Inferred DF curves under various values of the cell surface tensions, λ_S. i) Inferred DF

curves. ii) Quantitative comparison of the DF curves.

C. Inferred DF curves under various values of the area elasticities, K_a. i) Inferred DF

curves. ii) Quantitative comparison of the DF curves.

Related Figure: Figure S1 (inferred DF curves in the presence of the potential derived

from the cell perimeters).

Figure 4: Effective attractive/repulsive forces in the presence of cell-ECM adhesion

The cell–ECM adhesion potential energy was assumed in the vertex model used in Fig.

2-3. i) The potential for a cell is $-E_{ECM}a_n$, where E_{ECM} is the coefficient of the potential.

ii) Simulation outcomes are exemplified where the cell areas are increased under the

larger values of E_{ECM}. The left and right panels are shown at the same scale. iii) Inferred

DF curves. iv) Quantitative comparisons of the DF curves. The insets illustrate DF curves,

where F_{max} and D_x are defined.

Related Figure: Figure S2 (The effect of the cell surface tensions on the distances at the

maximum attractive forces is shown. See Fig. 4-iv and Fig. S2.).

Figure 5: Effective attractive/repulsive forces in the presence of cell-ECM traction forces

A. The traction forces between cells and ECM were assumed in the particle model under

two-dimensional conditions. i) The cell–cell interaction forces were provided by the LJ

potential. The directions of the traction forces were assumed to be random. ii) An example

of the simulations is shown. iii and iv) Inferred DF curves under various values of the

traction forces and under various values of the persistency, respectively. The distance–

force curve provided by the LJ potential is also shown (broken black lines).

B. The traction forces were assumed to have the same vector (i.e., the same value and the

same direction). i) An example of the simulations is shown. Due to the same vector, the

particles migrated unidirectionally. ii) Inferred DF curves under various values of the

traction forces. The distance–force curve provided by the LJ potential is also shown.

Related Figures: Figure S3 (inference in the self-migratory MDCK cells on substrates)

Figure 6: Effective attractive/repulsive forces in growing cells

i) Model of cell growth. Orange, a cell; green, a particle. The growth was expressed as a

repulsive force between the two particles as defined in the main text ($C = 5.6$ and $D_{CR} =$

5.0). The distance–force curve provided by the LJ potential was set to have the maximum

attractive force = 0.005. When $B = 0.5$ and $D_g = 4.4$, the repulsive force given from the

growth becomes 0.005, equivalent to the attractive force of the LJ. ii) Examples of the

simulations under different values of B, where the particles but not the cells are visualized.

iii) Inferred DF curves. iv) Quantitative comparison of the DF curves.

Figure 7: Effective attractive/repulsive forces under steady state

A. Examples of vertex model simulations under steady state. The vertex model is the

same as that in Fig. 2-3. The cell centroids are shown as crosses. The whole view of the

simulation is shown in Fig. S4.

B. Inferred DF curves under various values of the cell–cell adhesive forces, λ_{AD}. i)

Inferred DF curves. ii) Simulation outcomes. iii) Quantitative comparisons of the DF

curves. The insets illustrate DF curves.

C. Inferred DF curves under various values of the cell surface tensions, λ_S. i) Inferred DF

curves. ii) Simulation outcomes. iii) Quantitative comparisons of the DF curves. The

slope (dF/dD) is related to the stability of the state with D at $F = 0$.

Related Figures: Figure S4 (whole view of the simulation, and inferred DF curves under

various values of the area elasticities, K_a), Figure S5 (inferred DF curves in MDCK cells

under the steady states)

Figure 8: Solid-liquid phase transition in vertex model

A. The trajectories of the cell centroids in the vertex model in Fig. 7 are shown under

various values of the cell surface tensions. The sizes of each window correspond to those

in the simulation snapshots in Fig. 7.

B. The mean square displacements (MSD) are shown under various values of the cell

surface tensions.

Table 1: Effect of cellular and non-cellular factors on effective force of cell−cell interaction

	Influence on force (attractive or repulsive)		Figures
Cellular factors			
cell−cell adhesion	attractive		3A
cell surface tension	repulsive		3B
area elasticity	neutral	core stiffness increased?	3C
cell growth	repulsive		6
Non-cellular factors			
cell-ECM adhesion	repulsive		4
cell-ECM traction force			
i. random direction	neutral/repulsive		5A
ii. uniform	neutral		5B
egg-shell	neutral		Ref. 1
cavity			
i. expanding	repulsive		Ref. 2
ii. non-expanding	neutral		Ref. 2

Ref. 1; (Koyama et al., 2023). Ref .2 ; (Koyama et al., 2024)

828
829

A **Two cells**
Cell — Nuclei

Adhesion

Surface tension + Volume effect

Distance

B **Description by particles**

Attractive

Balanced

Repulsive

: a cell (mean size)

C **Distance-force (DF) curve**

Force of cell-cell interaction (F)

repulsive ← → attractive

summa­-tion

repulsive force

attractive force

cell-cell distance (D)

mean diameter of cell

D **Origins of effective attractive/repulsive forces**

cell-cell adhesion force
cell surface tension
etc.

?

multicellular systems (epithelia etc.)

Fig.1 Koyama et al.

Fig.2 Koyama et al.

Fig.3 Koyama et al.

Cell-ECM adhesion energy

i. Vertex model with cell-ECM adhesion

a_n nth cell

ECM

E_{ECM}

Cell-ECM adhesion

potential = - E_{ECM} a_n

Particle

DF curve ?

E_{ECM}

Cell area

Repulsive force?

Shift of DF curve?

ii. Simulation

coefficient of cell-ECM adhesion, E_{ECM}

1.0   0.0

iii. Inferred effective distance-force curve

Effective force of cell-cell interaction, F [A.U.]

repulsive   attractive

0.004

0.000

-0.004

0   5   10

cell-cell distance, D [μm]

0.0
0.2
0.5
0.7
1.0

coefficient of cell-ECM adhesion, E_{ECM} [A.U.]

iv. Quantitative comparisons

Mean ± SD, N = 4 simulations

Maximum attractive force ($|F_{max}|$, × 10^{-3} [A.U.])

8.0

0.0

0   0.6   1.2

coefficient of cell-ECM adhesion, E_{ECM} [A.U.]

F_{max}

Distance at maximum attractive force, D_x [μm]

8.0

0.0

0   0.6   1.2

coefficient of cell-ECM adhesion, E_{ECM} [A.U.]

D_x

Fig.4 Koyama et al.

A Traction force of random direction between cell-ECM

i. Particle model with traction force

cell-cell interactions   traction force
(random direction)

ii. Simulation (2-dimension)

t = 100 min   t = 200

maximum attractive
force of LJ = 0.01

traction force
= 0.1
(1,000% of LJ)
with persistency
= 50.0 min

iii. Inferred effective distance-force curve
effect of traction force value

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

cell-cell distance [μm]

persistency
= 50 min

--- LJ (given)
— 0 %
— 100
— 1,000

value of
traction
force,
(% of LJ)

iv. Inferred effective distance-force curve
effect of persistency of traction force

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

cell-cell distance [μm]

traction force
= 1,000 %
of LJ

--- LJ (given)
— 1.0
— 10
— 50

persistency
of traction
force,
(min)

B Traction force of uniform vector

i. Model & simulation

traction force
(uniform vector)

traction force = 3,000% of LJ

start line

t = 100 min   t = 200

ii. Inferred effective distance-force curve

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

cell-cell distance [μm]

--- LJ (given)
— 0 %
— 1,000
--- 3,000

value of
traction
force,
(% of LJ)

Fig.5 Koyama et al.

Cell growth

i. Model: 2-particles for 1-cell model

1-cell

growth force
(coefficient, B)
$F = B/(D_g + C)^2$

at critical distance, D_{CR}

division
(random direction)

cell-1   cell-2

cell (orange)

LJ   LJ

DF curve ?

particle (green)

ii. Simulation (2-dimension)

coefficient of growth force, B

0.0   4.0

t = 90 min   t = 390
cell
number = 36   36

t = 90 min   t = 390
48   117

iii. Inferred effective distance-force curve

Effective force of cell-cell interaction, F [A.U.]

repulsive / attractive

0.01

0.00

−0.01

0   5.5   10

cell-cell distance, D [μm]

coefficient of growth force, B [A.U.]
— 0.0
— 0.5
— 1.0
— 2.0
— 3.0
— 4.0

iv. Quantitative comparisons

Attractive force at $D = 5.5$ μm
($-F(5.5)$, × 10^{-3} [A.U.])

10.0

−10.0

0   2.0   4.0

coefficient of growth force, B [A.U.]

$D = 5.5$
$F(5.5)$

Mean ± SD,
N = 4 simulations

Fig.6 Koyama et al.

A Vertex model under steady sate

Simulation

$\lambda_S = 0.5$
$\lambda_{AD} = 0.8$
$K_a = 1.0$

t = 0 min   t = 300 min

Thick lines:
elevated tension due to
fluctuation

B

Cell-cell adhesion force

i. Inferred effective distance-force curve

$\lambda_S = 0.5$
$K_a = 1.0$

Effective force of cell-cell interaction, F [A.U.]

cell-cell distance, D [μm]

cell-cell adhesion force, λ_{AD} [A.U.]
— 0.9
— 0.8
— 0.5
— 0.2
— 0.0

ii. Simulation snapshots

$\lambda_{AD} = 0.9$ $\lambda_{AD} = 0.0$

iii. Quantitative comparisons

Maximum attractive force ($|F_{max}|$, × 10^{-3} [A.U.])

F_{max}

cell-cell adhesion force, λ_{AD} [A.U.]

Slope at $F = 0$, $|dF/dD|$ [A.U.]

cell-cell adhesion force, λ_{AD} [A.U.]

DF curve

dF/dD

Mean ± SD,
N = 6 simulations

C

Cell surface tension

i. Inferred effective distance-force curve

$\lambda_{AD} = 0.8$
$K_a = 1.0$

Effective force of cell-cell interaction, F [A.U.]

cell-cell distance, D [μm]

cell surface tension, λ_S [A.U.]
— 0.45
— 0.5
— 0.6
— 0.8
— 1.0

ii. Simulation snapshots

$\lambda_S = 0.45$ $\lambda_S = 1.0$

iii. Quantitative comparisons

Maximum attractive force ($|F_{max}|$, × 10^{-3} [A.U.])

F_{max}

cell surface tension, λ_S [A.U.]

Slope at $F = 0$, $|dF/dD|$ [A.U.]

dF/dD

cell surface tension, λ_S [A.U.]

Stability
depends on slope.

Mean ± SD,
N = 6 simulations

Fig.7 Koyama et al.

A

Trajectory of cell centroid in vertex model

Simulation

$\lambda_S = $ 0.45 0.5 0.6 0.8 1.0

$\lambda_{AD} = 0.8$
$K_a = 1.0$

B

Mean square displacement

— 0.45
— 0.5
— 0.6
— 0.8
— 1.0

cell surface
tension,
λ_S [A.U.]

Fig.8 Koyama et al.