

A mathematical model of the coupled mechanisms of cell adhesion, contraction and spreading

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Abstract Recent experimental work has shown that cell spreading is highly dependent on the contractility of its cytoskeleton and the mechanical properties of the environment in which it is located. The dynamic, stochastic, and cyclic nature of the development of cell spreading, as well as its role in biological processes such as wound healing, angiogenesis, and hematopoiesis, and the underlying physical mechanisms, have prompted a mathematical model for the coupling of cell spreading and contraction. The model is based on the cell edge and dynamic cytoskeleton-membrane protein (in equilibrium) enabling cell-substrate attachment. The cell's cytoskeleton is modeled as a mixture of actin filaments and microtubules, which can change mass and generate contraction. In particular, the cell's ability to contract, as well as its ability to spread, is dependent on the cell's internal state and the external environment. The model is able to predict the development of cell-substrate attachment, known as the cell's spreading, as well as the cell's ability to contract and generate force. The model is able to predict the development of cell-substrate attachment, known as the cell's spreading, as well as the cell's ability to contract and generate force. The model is able to predict the development of cell-substrate attachment, known as the cell's spreading, as well as the cell's ability to contract and generate force.

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mechanics of cells. The organization of the mechanical forces have been addressed by a series of models, some based on purely mechanical aspects (Foccardi and Venerè, 2012; Sameni et al. 2009) and some based on biochemical aspects, including signalling pathways (Cielek et al. 2005). At the cellular level, the development of global, organizational, contact and adhesion have recently been the object of a formalization (Dehpande et al. 2008) based on empirical relationships between the mechanical displacement, the organization of cells, and in equilibrium. A similar continuum approach is also introduced in the

$$\cdot + \left(\frac{v}{-} + \frac{v}{-} \right) + \cdot + \left(- + - \right) = 0 \quad (7)$$

$$\left(\frac{v}{-} + \frac{v}{-} \right) + \cdot + \left(- + - \right) + \left(- + - \right) = 0 \quad (8)$$

$$\cdot + \left(\frac{v}{-} + \frac{v}{-} \right) + \cdot = 0 \quad (9)$$

$$\cdot + \frac{1}{1+} \left(\cdot + \cdot + \cdot F \right) = 0 \quad (10)$$

the $\mathbf{I} = 1 \mathbf{1}^T$, the coupling parameter, T the partial, in the partial, c_0 keleton and T^F the partial, induced by, be. We note the ha the em, partial, c_0 keleton— a, ed on a board, en e a i-ep en, a n- mbe of po, ble componen, con- ibing o the cell elā i- . Thi incl- dē fō i- nce, mic o- b- lē, in e media e- lamen, and he memb- ane loca ed on op and he bo- om of a plana cell. A, i- ming, mall defo- ma ion (- ain a e- picall- lē, han 10 % in he p- oblem of in e-), a linea- elā i- elā ion can be, ed o dē- cibe he p- i- e c_0 keleton e- p- e:

$$\epsilon = \frac{E}{1} \frac{1}{2} (\dots) + \frac{1}{1} \dots = \dots, \text{ and } \dots = \dots, \quad (13)$$

the $\epsilon = 1$ and $\dots = \dots$. The ma- eial pa- ame e, E and - ep en he Yo- ng' mod- i- and Poi- on' - a io- e- pec- i- el- hile he- adial and ci- c- mfe- en ial linea- - ain- and a e- elā ed o he- adial d- placemen- b- = / and = / . A- d- i- ed in mo- e- de ail in [Ve ne e, and Fa, ad \(2011\)](#), he p- ial, - e, T^F of - e, - be, i- p- o- i- onal o he - ol- i- me- f- ac ion T^F and a i- e- f- om - o diffe- en - o- cē : ac- i- e- con- ac ion and p- i- e- elā i- e- p- o- e. We he- e- e- i- e:

$$T^F = T^F (E_1 + \dots) = \dots, \quad (14)$$

the e- he coef- cien E_1 deno- e- he, iffne, of, - e, - be, hile he con- ac ile - e, - e, i- he- e- l of ac- o- m- o in c- o, - b- idge d- nam- i- a- he, a- com- e- ic- le- el ([Ve ne e, and Fa, ad 2011](#)). Al- ho- gh, a- com- e- f- o- c- e- i- kno- n- o- depend on he - a- e- of con- ac ion a- p- edic- ed- b- he Hill model ([Hill 1938](#)), e- cho- e- o- neglec- h- i- a- pec- f- o- he- p- e- n, - d- and con- ide- ha- he con- ac ile, - e, i- con- an- and e- i- al o- ha- f- o- nd in a, a- e- of i- o- me- ic con- ac ion. Thi- a- i- mp- ion i- mo- i- a- ed b- he fac- ha- cell, p- eading i- a, lo- p- o- e- , compa- ed o- he- cha- ac- e- i- ic- ime- , cale of c- o, - b- idge d- nam- i- and i- he- e- f- o- e- i- n- e- i- e- o- he- a- e- of elonga- ion of, a- com- e- . Final- , fo- c- e- e- i- lib- i- m- in he mi- i- e- follo- , f- om he balance of linea- momen- i- m. Unde- a- i- mme- ic and plane- , - e, condi- ion, h- i- jeld :

$$\dots + \frac{1}{1} (\dots) - = 0 \quad (15)$$

In abo- e- e- i- a- ion, deno- e- he hicknē, of the cell and - ep en, he d- i- b- i- e- d - ac ion f- o- c- e- on he memb- ane a- i- ing f- om he in- e- ac ion - i- h- he- i- ndē- l- ing, - b- , - a- e- i- a- focal ad- hē- ion. While h- i- f- o- c- e- i- applied a- he bo- om of a cell h- o- gh i- memb- ane, i- i- e- i- alen- o- con- ide- i- a- a- angen- ial bod- , fo- c- e- applied o- he c_0 keleton b- in- oking plane, - e, a- i- mp- ion . To- all- cha- ac- e- i- e- he beha- io- of he - i- ndē- l- ing, - b- - a- e, i- i- , - e- i- l- o- no- e- ha- i- , hicknē, i- i- , all- m- ch- lā- ge- han- ha- of cell . In h- i- , i- a- ion, - e, - a- i- a- ion- a- e- e- pec- ed in a

he e μ_0

To cha a e i e he memb ane elā i c i i j i, ef i l o in, od i ce he elā ic po en ial (\mathcal{E}), i ch ha he memb ane, e, e, e ad :

$$\mathbf{T} = \frac{1}{\mathcal{E}} F \quad \text{and} \quad (\mathcal{E}) = \mathbf{T} \cdot \mathbf{T} + \frac{1}{2} (\mathcal{E})^2 \quad (29)$$

He e $F = \int_0^1$ he defo ma ion g adien, $\mathbf{T} = \int_0^1$ he p e-e i ing, i face eñ ion and i he, i ffe, of he cell memb ane. The mechanical eñ i lib i c m of he memb ane i h c, o kele on, e, e, e i hen gi en b, he, anda d eñ i a ion (Ve ne e, 2011; Ve ne e, and Fa, ad 2011):

$$\mathbf{T} \cdot \mathbf{n} = \mathbf{T} \cdot \mathbf{T} \implies \mathbf{T} = \mathbf{T} \quad (30)$$

he e \mathbf{T} i he, e, e, eñ o in he c, o kele on, n i he o i a d no mal o he cell, i he, i face g adien ope a o and $\mathbf{T} = \mathbf{T} \cdot \mathbf{e}$ i he, i face eñ ion e c o. I can be, ho n ha d, e o o i a i, mme i a, i mp ion, h i eñ i a ion e d i ced o he, imple fo m, ho n in he i gh end, ide of (30) in h i ch deno e he adial, e, e, on he bo i nda .

2.3 Memb ane p o, i, ion and cell g o h

Le i, no concn a e on he he phenomenon of memb ane p o, i, ion f om a ph i cal i e poin . Thi a pec of cell mechanic i kno n o in, o l e, e, e on g in e pla, be een ac in pol, me i a ion a he cell, edge and memb ane e i ane (C i elie e al. 2007; DiMilla e al. 1991; O e and Pe e j on 1985; Polla d and Bo j , 2003; Vallo n e al. 2005; Waka, i ki e al. 2003; Xiong e al. 2010). Simila o he p e, io, e, e ion, i ch chemo-mechanical co i pling can be ma hema ically add e, e, ed b, coñ ide ing he chemical eñ i lib i c m of he c, o kele on a he cell edge and ho i i affec ed

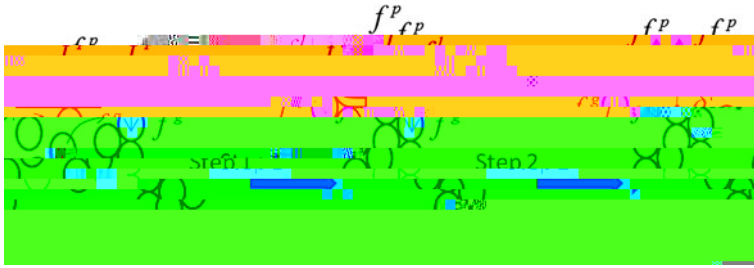


Fig. 4 A cycle of actin polymerization beneath the cell membrane: a G-actin monomer, in equilibrium

The total change of free energy during an equilibrium polymerization cycle can then be expressed by adding contributions from eqs 1 and 2. This yields:

$$\mu = (\quad 2 \quad). \quad (34)$$

2.2.2

We are now in a position to derive the chemical potential of ac in monomer, in the aggregated form accounting for the effect of membrane and in equilibrium, as follows, (Hill 1981):

$$\mu = \mu_0 + \mu = \mu_0 + (\quad 2 \quad) \quad (35)$$

Note that the change in free energy from the presence of physical forces is added to the original chemical potential μ_0 , since μ is interpreted as a free energy contributed by the ac in contact with a polymerization, eq. When the system is at equilibrium, the chemical potential of G-ac in and ac in a polymer, (aggregated ac in) are equal ($\mu = \mu$) and we obtain:

$$\mu_0 + (\quad 2 \quad) = \mu_0 + (\quad) \quad \text{if } \mu = \mu \quad (36)$$

Here, $\mu = \mu$, and the fact that the chemical potential of ac in monomer is equal to the chemical potential of ac in polymer is 0 in (31)

While the coefficient β generally a function of the magnitude of participating force (see discussion in Hill 1981), we consider here a constant ($\beta = 1/2$) for simplicity. In order to determine the physical force affecting on- and off-axis cells all using (39) and (31), it is then possible to obtain the velocity of cell spreading (or the area of activation) as a function of the membrane area:

$$v = \frac{1}{2} \left(\frac{dA}{dt} \right) \exp \left(- \frac{(\beta A)^2}{2} \right) \quad (41)$$

where v is the force dependent concentration of G-actin in a cell defined in (38). The above equation can be used to determine the area of cell spreading. In particular, one can see from (41) that the membrane area is a function of the force. Since the in equilibrium force is directly related to cell contraction, (41) can be used to determine the coupling between cell contraction and spreading: the more contraction, the faster the spreading. For the same reason, the area of

the cell membrane given in eq. of the in eq. in fac ion and and all the deformation of the, i b, a e i en i el kno n ia the kno ledge of i, adial di placem. The above eigh a iable ma be de e mined h o r gh he follo ing eigh e i a ion de i ed in he p e i o r, ec ion:

Chemical equilibrium

$$\begin{aligned} \text{S e, Be, } \mu &= \mu^F \text{ in} & (45) \\ \text{Ac in monome, } \mu &= \mu \text{ on} & (46) \\ \text{Cell membrane } \mu &= \mu \text{ in} & (47) \end{aligned}$$

Mass conservation

$$\begin{aligned} \text{C o l } \cdot + \left(\frac{v}{\rho} + \frac{v}{\rho} \right) + \cdot + \left(- + - \right) &= 0 & (48) \\ \text{M i e } \left(\frac{v}{\rho} + \frac{v}{\rho} \right) + \cdot + \left(- + - \right) + \left(- + - \right) &= 0 & (49) \\ \text{In eq in } \frac{(+)}{(\rho)} + (\rho +) \left(\frac{v}{\rho} + \frac{v}{\rho} \right) + \left(- + - \right) &= 0 & (50) \end{aligned}$$

Mechanical equilibrium

$$\begin{aligned} \text{Cell } \frac{\sigma}{\rho} + \frac{1}{\rho} (\sigma \sigma) + \frac{F}{\rho} + \frac{1}{\rho} (F F) - &= 0 & (51) \\ \text{S i b a e } \frac{\sigma}{\rho} + \frac{1}{\rho} (\sigma \sigma) + &= 0 & (52) \end{aligned}$$

The e e i a ion a e complemen ed b he e bo nda condi ion (co e ponding o he above e i e diffe en ial e e i a ion) and ini ial condi ion , pecif ing he a e of he cell a he beginning of he, im i a ion . The e condi ion a e, i ch ha he cell and i b a e a e ini ial, i nde fo med and i np e, i i ed:

$$i (, 0) = 0 \quad i (, 0) = 0 \quad (, 0) = 0 \quad (53)$$

In addi ion, i i a, i med ha he compo i ion of he cell con i , of 25 % ol i me f ac ion of elemen, comp i ing he p a i e c o ke lon, 5 % ol i me f ac ion of ac in monome, and no ini ial, e, Be, (e fe en e f o he e n i mbe, a e gi en in Table 1).

$$(, 0) = 0.25 \quad (, 0) = 0.05 \quad F(, 0) = 0 \quad (54)$$

and all in eq in a e o i ginal, in he i lo af ni a e (ee Table 1 fo e fe en e):

$$(, 0) = 5^{-15} \quad (, 0) = 0 \quad (55)$$

Conce ning he bo nda condi ion , e a, i me ha he e a e no i e of c o ol and ac in monome, ac o, he cell memb ane and no lo af ni in eq in a e allo ed o en e he, em. In o king Eq. (11) and (26), e can h, i e:

Table 1 Pa ame e, i, ed in he, im; la ion

| De ni ion | S mbol | Val; e | Uni | Refe encę |
|-----------|--------|--------|-----|-----------|
|-----------|--------|--------|-----|-----------|

C; o; ol; me f ac ion

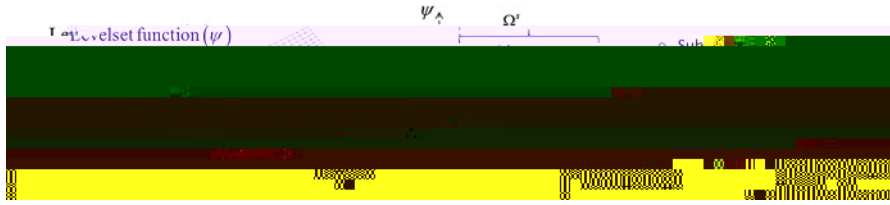


Fig. 6 Illustration of the level set function defining the cell boundary and the degree of freedom associated with the node in the computational domain

Let ψ_i and ψ_j be defined as the element, e , in the membrane. Finally, the above definition of the level set function is coupled with the global level set function (41) in order to determine the motion of the cell boundary in time. The numerical approach, outlined in (48–52) is described below.

3.1 Cell boundary evolution

In order to determine the partial and time evolution of the material, the physical domain (epithelial cell and cell boundary) is discretized in a finite number of elements and nodes. A potential issue with the previous problem is the cell

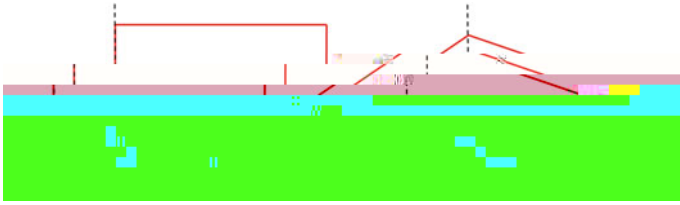


Fig. 7 a

Here $e = 1, 2, 3$ denote the local node number for each element and the element \bar{u} and \bar{u} correspond to longitudinal and shear degrees of freedom respectively for non-enriched elements. Substituting the finite element polynomials (58) in the equilibrium and linearizing the equations, one can show that the problem reduces to solving the following algebraic problem:

$$C\dot{U} + K U + F = 0 \tag{63}$$

Here U denotes the vector containing global degrees of freedom, while C , K and F are the damping matrix, stiffness matrix and force vector respectively (see Appendix A.2 for a more detailed explanation). Equations (63) are solved at each time step, using a Newmark-Raphon procedure and a backward Euler integration method, to compute the unknown field at each time step, as follows:

$$U = \dot{U}. \tag{64}$$

Here e denotes the time increment. Upon obtaining a solution at time increment n , the method consists of computing the average \bar{U} at the next time step $n+1$:

$$\bar{U}(n+1) = \bar{U}^{-1}(n+1) + \dot{U} \tag{65}$$

Here the average \bar{U} is computed for each element by substituting Eqs. (64) and (65) into Eq. (63). This leads to the following equation:

$$\left(C_{+1}^{-1} + K_{+1}^{-1} \right) \cdot \dot{U} = \left(F_{+1}^{-1} + C_{+1}^{-1} \cdot \bar{U}_{+1}^{-1} \right). \tag{66}$$

The average is then repeated until the norm of the vector U is smaller than a small tolerance.

3.2 Cell growth and leucocyte egression

To model cell growth, from the equilibrium equations at each time step can be considered to imagine the partitioning and membrane expansion of cells appearing in (41). Since the cell adhesion is defined in terms of the leucocyte function, the rate of change in time can implicitly be expressed in terms of the additional leucocyte egression equation (Dodd et al. 2008):

$$\dots = \dots + \dots = 0 \tag{67}$$

Here the cell boundary velocity is computed in (41). Defining the leucocyte adhesion function (i.e. $\dots = 1$), one can find the expansion of the leucocyte function at time step $n+1$ as:

$$\dots + \dots = \dots + \dots \tag{68}$$

Go h picall, in ol_e he ç ea ion of ne ma e ial poin, , ho e compo i ion i
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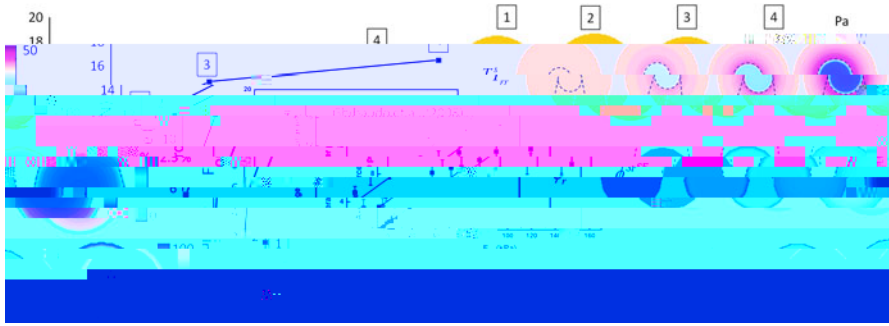


Fig. 8 Relationhip between cell contraction and cell adhesion forces. The model predicts a nonlinear relationhip between contraction and adhesion forces in agreement with experimental data (Ghibaudo et al. 2008). For comparison purposes, the initial adhesion force in the dynamic equilibrium is also compared in equilibrium conditions by the numerical simulation and the experimental data. The evolution of adhesion force in the adhesion force field of the cell is shown in the adhesion force field and the concentration of high affinity in equilibrium, however, different adhesion forces.



Fig. 9 Evolution of cell force, membrane force and cell adhesion force

C Cell adhesion is provided by the clustering of integrins in ligand complexed with the chemical equilibrium described in Sec. 2.2. Cell contraction, in the adhesion, is a function of the membrane and the internal force, which has the adhesion force, each a maximum of the cell's perimeter. When ligand is present, in equilibrium, the adhesion force is reduced to the equilibrium force in the region, which leads to the adhesion force [according to (22)]. This explains the adhesion

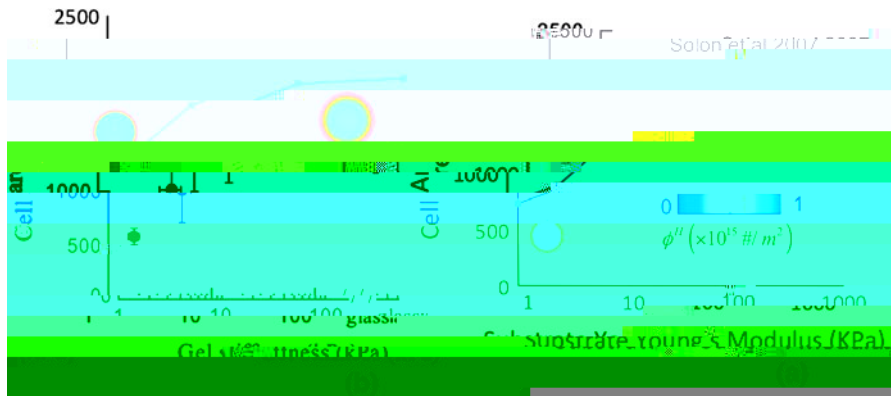


Fig. 10 Change of cell area and high-affinity in equilibrium concentration, adhesion force difference, stiffness, and composition in the peripheral cell, of Solone et al. (2007)

The effective permeability and membrane elasticity are depicted as a function of time. In the present study, the permeability of the difference between and which has been analyzed (the occurrence), the velocity of permeability becomes negligible. Another effect of the permeability is to increase the area of permeability by increasing the action energy. The model hypothesizes, as seen in both cell area and permeability in concentration and, therefore, a non-biomechanical cell area becomes large and one more of the high in Fig. 8.

The model predicts that the above mechanical parameters are nonlinearly related and dependent on the stiffness and ligand density. We note that the order of the model by comparing numerical prediction and experimental measurement from the literature.

4.2 Effect of stiffness on cell area

Experimental studies on fibroblasts have shown that cell area (Solone et al. 2007) increases with stiffness in a nonlinear fashion (Fig. 10). The effective permeability dependence by considering an elastic force of ligand concentration in the cell, as $(\rightarrow \infty)$ on the cell, permeability is only affected by stiffness. To increase cell permeability, a form of an original cell concentration of surface area $A_0 \approx 600 \mu^2$ in which no force, force, and high affinity in equilibrium. Since high permeability is originally of equilibrium, the effective permeability is formed in equilibrium ligand adhesion and cell permeability has been affected by

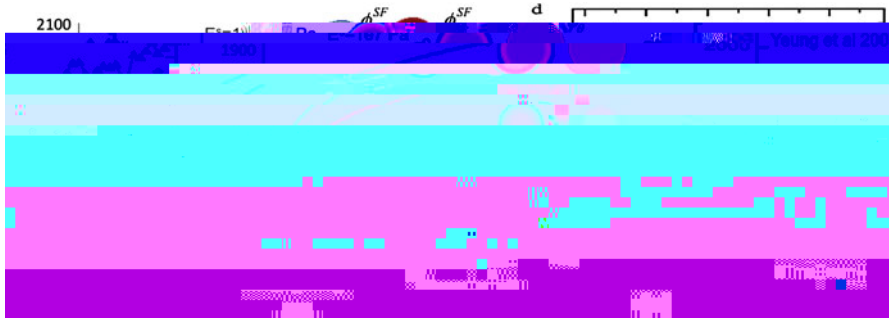


Fig. 11 **a** Change of cell area and volume fraction over time for different cell types, **b** schematic of cell, and **c** dependence of cell area and volume fraction on time, of Young et al. (2005)

a limit, which depends on the mechano-elastic properties of the polymer. First, ϵ_c , ϵ_e , ϵ_b , ϵ_{en} all depend on the maximum concentration, which limits the concentration a cell can experience depending on its volume fraction and hence the packing force. Second, according to (41), the area of packing is controlled by the competition between packing and the cell's packing force. As observed in Fig. 9, the cell's packing force, while originally weak, increases as a mechanical force is applied and eventually becomes the dominating factor; hence, an end of cell packing.

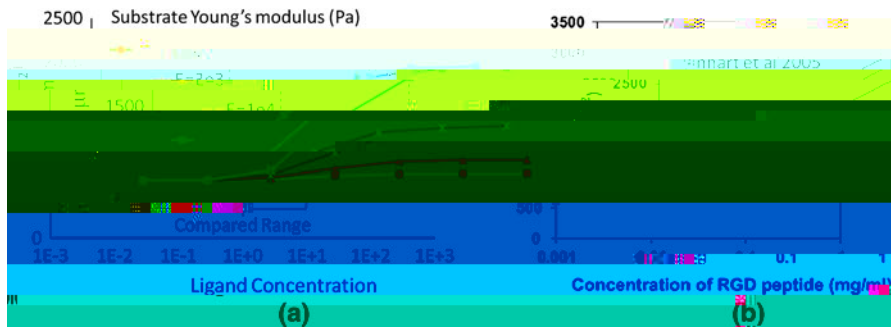


Fig. 12 Change of cell area, adhesion force for different ligand concentration, and comparison in the peptide immobilization of Reinhart-King et al. (2005)

the cell area is a linear function of ligand density in this concentration range from 0.001 to 1 mg/ml. To know the behavior of the proposed model compared to the experimental data, we considered a cell lying on a substrate of given stiffness, and varied the ligand concentration from 0.001 to 1,000 ligand/ μm^2 . As depicted in Fig. 12, the model predicts a nonlinear relationship between ligand density and cell area. While this is a major contradiction with the experimental data, the area of the plane for the observed displacement, Fig. 12, should be noted that the range of ligand concentration considered in the immobilization method chosen here is significantly higher than in the experimental data. In fact, if one compares the same concentration range, the model predicted increase in cell area is close to the linear relationship seen in the experiment. For the most obvious of this range, model prediction is a perfect order and it is known that cell area cannot increase and decrease each a maximum, regardless of the concentration of ligand. Similarly, when no ligand is present, cell area must converge to a small value. This is the fact that cell area has a minimum value for a ligand density, and order and in this. Finally, the increase of cell area with ligand concentration can be explained on the basis of (22). On the one hand, when ligand density is high, in equilibrium cannot achieve the substrate; the probability of the presence of a peeling force and the associated increase in cell area. On the other hand, when ligand density is high, cell cannot achieve the substrate and generate a contraction; the probability of the area, and so on.

ligand attachment on the plasma membrane is promoted by the increase in phospholipid concentration and endocytosis of the cell membrane and adhesion, respectively. Finally, the phenomenon of proliferation of the cell is due to the increase in the number of cells at the edge of the cell and the stretching and bending of the cell membrane. The above mechanism has been presented in this paper as a mathematical model of the coupled mechanism of the cell.

and enforcing the fact that $\dot{\gamma} = \dot{\gamma}$, we obtain the following expression for $\dot{\gamma}$:

$$\dot{\gamma} = \frac{1}{1} \left[\frac{1}{E} (1 + \nu)(1 - 2\nu) (\dot{\epsilon} + \dot{\epsilon}) \right] \quad (71)$$

where E and ν are the Young's modulus, and Poisson's ratio of the actin filament network. The relationship between the Lamé constants, appearing in (70) is given below:

$$E = \frac{\mu'(3 + 2\mu')}{1 + \mu'}; \quad \text{and} \quad \nu = \frac{\mu'}{2(1 + \mu')} \quad (72)$$

We now consider the divergence of the velocity field \mathbf{v} for a bi-ionic in the equilibrium of mass balance (4-6). For a homogeneous problem, the divergence of $\mathbf{v} = \dot{\epsilon} + \dot{\epsilon} + \dot{\gamma}$ where $\dot{\epsilon}$ is the imposed deformation rate of the actin filament. Using the fact that:

$$\dot{\gamma} = \frac{1}{1} \left[\frac{1}{E} (1 + \nu)(1 - 2\nu) (\dot{\epsilon} + \dot{\epsilon}) \right] \quad (73)$$

from (71), we can write:

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