Figures

Figure S1: Distribution of relative length of new wall.
**Figure S2:** Distribution of areas after as compared to before cell division. The ratio of the area after cell division to the area before cell division is shown.
**Figure S3:** Comparison of our model with that of Besson and Dumais [1]. Histograms show $\log |\Delta V|$, the difference between the predicted and actual potential used by the cell, for each model. The negative of the slope corresponds to inverse temperature, the parameter $\beta$ in the Besson-Dumais model.
**Figure S4:** Definition of cell coordinates in local frame (left) and various parameters used in the definitions of fitness measure (right). The reference axes for definition of angles are the principal components of the segmentation.
Figure S5: Example of potential function landscape, shown for cell 25 using a weight vector $w = (1,1,0,0)$. Darker regions correspond to higher altitudes, light regions to valleys. The global minimum is shown with an open circle and the actual wall endpoints by a dot. The two axes give the angle of $\theta_1$ and $\theta_2$ in degrees, and the inset shows an outline of the actual and predicted cell walls.
Figure S6: Results of optimization of the 4-dimensional weight vector \( w = (A, L, E, G) \), where A, L, E and G represent the relative weight of the area, length, extension and growth direction potential in three-dimensional sub-spaces. (a) Along the ALE axes with \( \varepsilon_e = 1 \); (b) along the ALE axes with \( \varepsilon_e = 0 \); (c) along the ALG axes with \( \varepsilon_g = 1 \); (d) along the ALG axis with \( \varepsilon_g = 0 \). Colors represent percentile, with the lowest percentile (1%) corresponding to least optimal value.
Figure S7: Simulated z-projection of meristem grown from a single cell in Cellzilla after 1000 cell divisions. (a) The modern interpretation of Errera’s Rule used for cell division. (b) Optimized potential model using \( w = (0.1,1,0) \) (area, length, cell extension).
Figure S8
(a) Solid line indicates the quantity of cells dividing within a given period. Dotted line indicates the mean ratio of cell expansion within a 2 hour period.
(b) Heat map on the left shows the amount of cell expansion between the time points at 2 and 4 hours as a ratio. Stars indicate cells that divided during this time period.
(c) Histogram on the right shows the mean expansion of cells that divided during any 2h period compared to cells that did not divide.
Figure S9
Relationship between growth axis and plane of cell division. Top pane shows all 207 cell divisions. Bottom pane shows data in 15 degree bins.
Figure S10
Comparison of our potential model with the Besson-Dumais model. A lower Hausdorf fitness is a better fit. Potential model: mean is 1.53, standard deviation is 0.85 and skewness is 0.57. Besson-Dumais model: mean is 1.62, standard deviation is 0.84 and skewness is 0.84.
Image Segmentation

Z-stacks in LSM format were first converted into TIF series using ImageJ[2] and the LSMToolbox plugin. These series of TIF images were then imported into MorphoGraphX[3]. The surface of the meristem was extracted using the Closing, Edge_Detect, and Marching_Cubes_Surface functions. The surface mesh was then smoothed and subdivided to around 500,000 vertices. The fluorescent signal from 0 to 3um below the surface was projected onto the surface mesh. Segmentation seeds were added by manually clicking in the center of each cell. The surface image was then segmented using the seeds. Cells were created from the segmented boundaries with a minimum of 1um between vertices. For the full Python code used to automate this method

The Python code to generate the 3D mesh was as follows:

```
Stack.Resize_Canvas("Yes","Yes",0,0,20)
Stack.Shift_Stack(0,0,10)
Stack.Average(1,1,1,1)
Stack.Closing(15,15,3)
Stack.Edge_Detect(50000,2,0.3,30000)
Mesh.Marching_Cubes_Surface(5,5000)
Mesh.Smooth_Mesh(1)
Mesh.Subdivide()
Mesh.Smooth_Mesh(3)
Mesh.Subdivide()
Mesh.Smooth_Mesh(1)
Mesh.Subdivide()
Mesh.Subdivide()
Mesh.Subdivide()
Mesh.Project_Signal("No",1,2,0,50000)
```

Manual seeding of each cell in the image was then performed followed by this Python code

```
Mesh.Segment_Mesh(20000)
count = 0
while count < 2:
    try:
        Mesh.Make_Cells(1)
        break
    except:
        Mesh.Fix_Corners()
        Mesh.Smooth_Mesh(1)
        Mesh.Segment_Mesh(20000)
    count += 1
```

The cells generated by this were exported to a text file for further analysis.

Projection to Local Euclidean Plane

A local Euclidean plane was fit to each cell before division, and to the pair of cells after division. The least squares fit to $z = Ax + Byz + C$ is described by the normal equations:
Each raw data point \((p_i, q_i, r_i)\) was then projected to the local Euclidean by dropping a perpendicular. Let the nearest point in the projection be \((x_i, y_i, z_i)\), where \(z_i = Ax_i + By_i + C\); the coordinates \((x_i, y_i)\) are found by minimizing the square distance function

\[
f = (p_i - x_i)^2 + (q_i - y_i)^2 + (r_i - Ax_i - By_i - C)^2
\]

which can be reduced to solving the linear system

\[
\begin{bmatrix}
A^2 + 1 & AB \\
AB & B^2 + 1
\end{bmatrix}
\begin{bmatrix}
x_i \\
y_i
\end{bmatrix}
= \begin{bmatrix}
Ar_i + p_i - AC \\
Br_i + q_i - BC
\end{bmatrix}
\]

Once the point \((x_i, y_i)\) is known, \(z_i = Ax_i + By_i + C\). Both the normal equations for the least squares fit and the projection to the plane are solved using the Mathematica function LinearSolve.

**Alignment of Principal Axes**

After translation to the local coordinate system each cell is represented by a matrix of data points

\[
X = \begin{bmatrix}
x_1 - x_c & y_1 - y_c \\
\vdots & \vdots \\
x_n - x_c & y_n - y_c
\end{bmatrix}
\]

where \(x_c\) and \(y_c\) are the means of the \(x\) and \(y\) coordinates. The covariance matrix is calculated using the Mathematica function Covariance as

\[
M = \frac{1}{n-1} X^T X
\]

The eigenvectors of this matrix give the principal directions.

Each cell is rotated into a new coordinate system with \(x'\) oriented along the eigenvector first principal component (the one with the larger eigenvalue), \(y'\) along the second principal component, and oriented so that \(x' \times y'\) points outward from the meristem. The angle of rotation between the before and after coordinate systems is

\[
\tan \theta = \frac{x'_A \cdot y'_B}{x'_A \cdot x'_B}
\]

in terms of the unit vectors \(x'_A, y'_A, x'_B, y'_B\) in the after and before Euclidean planes. The after-cells can be aligned with the before-cells by rotating through an angle \(\theta\). Finally, each cell is translated to the center of mass frame[4],

\[
x_i = \frac{1}{6} \sum_{j=0}^{n} (x_j + x_{j+1})(x_j y_{j+1} - x_{j+1} y_j)
\]

\[
y_i = \frac{1}{6} \sum_{j=0}^{n} (y_j + y_{j+1})(x_j y_{j+1} - x_{j+1} y_j)
\]

where the vertices are numbered counter-clockwise and vertex 0 is associated with vertex \(n\).

**Cell Expansion and Division in Space and Time**
It is known that cells must expand and divide to maintain the amount of tissue in the SAM as groups of cells are incorporated into flower primordia around the periphery and exit the SAM. To quantify this phenomenon we measured the expansion of each cell over each 2 hour period. The cell expansion occurs in waves as can be seen in Figure S8a. This wave phenomenon is also observed in the quantity of divisions over time. Over the observed 38 hours the average expansion rate and quantity of divisions gradually decreases, possibly due to the exposure to laser light, dissection of surrounding flowers, or the repeated submersion in water all of which effect the health of the plant. It should be noted that while the waves of expansion and division are approximately in phase with each other, the cells that are dividing are not necessarily the same cells that expand the most during any 2 hours.

As shown in Figure S8b, cells in the center of the meristem expand very little and in some cases shrink between time points. This phenomenon is observed at all time points and does not fluctuate with the waves of expansion observed elsewhere in the meristem.

To quantify the relation of expansion and division we measured the expansion ratio of cells that divided and cells that did not divide separately, the results of which are shown in the Figure S8c. The mean expansion ratio of the 207 dividing cells barely different from that of the nondividing cells: the variance of both populations is too large to differentiate statistically. This suggests that expansion and division are not directly coupled, at least in the two hours prior to division. Given that the cells are all of similar sizes, expansion over the entire cell cycle must be correlated with division.

While rapidly expanding cells have no correlation to dividing cells, there is a bias in the spatial location of the rapidly dividing cells. As seen in the Figure S8b, cells towards the top of the meristem are dividing more slowly than those toward the bottom, but there is no clear boundary between rapidly and slowly expanding regions. This phenomenon was observed at all time points.

**More Heuristics**

These heuristics are a continuation of the three heuristics covered in section “Heuristics” of the main text.

*Heuristic: The cell divides perpendicular to the main axis of growth (Hofmeister’s Rule)*

The difficulty with applying this rule is that it is difficult to calculate the main axis of growth without a fine time-resolution set of live images. Hofmeister (1863) emphasized that the axis of growth is not necessarily the longest diameter of the cell. The instantaneous direction of growth can be defined mathematically as the principal axis of the velocities of the vertices (corresponding to the eigenvector with largest eigenvalue of the covariance matrix of the velocities of the vertices)[5]. Alternatively, one might conjecture that since more material will accumulate in the principal direction of growth, that the cell will be extended primarily along that direction. This would imply that the principal axis of the cell (corresponding to the eigenvector with the largest eigenvalue of the covariance matrix of the vertices of the cell, or of the segmentation points, or the principal axis of inertia) should be used to define this main axis of growth. It is challenging to measure the instantaneous direction (despite the algorithm given by [5]) because (1) matching vertices at two different time points assumes that the material at the vertex at one time point should be matched to the vertex at the succeeding time point; and (2) we have observed that cells often shrink (see cell growth heuristic, below) during the time around cell division so it is difficult to assign a meaning to the growth direction in these cells.
Because the change in area over the few hours around cell division is very small, and sometimes negative, small errors in segmentation can lead to significant differences in determination of the velocity axis.

Hofmeister’s rule (using cell elongation for principal axis) is supported by a change in the distribution of the isoperimetric ratios before and after cell division. This ratio is $i = 4\pi A^2/P^2$, where $A$ is the area and $P$ is the cell perimeter. It gives a size-independent measure of the elongation of a polygon. A value of $i = 1$ indicates that the cell is nearly circularly shaped; all other closed curves will have a value of less than 1. The further away from 1, the more elongated the cell is. The inequality $4\pi A^2 \leq P^2$ has been attributed to the ancient Greek geometer Zenodorus, in the sense that a circle has greater area than any other regular polygon of equal perimeter. Using the Calculus of Variations it was proven for any closed curve by Jakob Steiner 1836[6]. The typical distribution of isoperimetric ratio in the L1 layer is illustrated in Figure 4a. In Figures 4b and 4c we compare the isoperimetric ratios before and after cell division. Statistically there is very little difference in the average value of $i$ before and after cell division, but the distribution is tighter after division ($i = 0.78 \pm 0.07$), identical to the global surface average, than before ($i = 0.76 \pm 0.10$). Furthermore, the skewness of the distribution as evident in the overall data is reproduced by the cells after division, but is not as evident in the cells before division. In other words, cells that are about to divide are shaped differently than typical cells. However, this difference does not indicate any particular body shape as the data spread is fairly wide.

The angle between the new cell wall and the principal axis is heavily weighted towards perpendicularity (90 degrees), with a differentiation from perpendicular of less than 10 degrees in 30% of the data; less than 20 degrees in 55% of the data; and less than 30 degrees in 75% of the data. This supports the notion that cell elongation should be used to determine new cell wall direction. The actual distribution of these angles is shown in Figure 4d. The principal axis is determined as the eigenvector, corresponding to the largest eigenvalue, of the covariance matrix of the projection of the segmentation to the least-squares local Euclidean plane. The direction of the cell wall is found from a least-squares parabolic fit to the new cell wall, as illustrated in Figure 4e.

**Heuristic: The new cell wall forms in a plane that is perpendicular to existing cell walls**

To quantify how often the new cell wall forms in a plane perpendicular to existing cell walls the angle between the new cell wall and the existing wall was measured (Figure 5). Because the segmentation is pinched in around the intersection, a short arc of the segmentation (up to around 30 degrees central angle in either direction) was fit with a parabola, and the intersection between that parabola and a similar quadratic least squares fit to the new cell wall was used to determine the angle of intersection. The measure used was the smaller of the two interior angles formed by the intersection of the two tangent lines. Some 25% of the intersections were within 5 deg of perpendicular; 52% within 10 deg of perpendicular, and 84% within 20 deg of perpendicular when measured in this manner. This is consistent with Sachs’ observation that cell walls tend to form along orthogonal trajectories, as an emergent property in a statistical sense[7].

**Heuristic: The cell continues to grow immediately after cell division**

In only 65% of the 207 cell divisions was the area, as measured in the first time point after cell division, greater than the area as measured at the last time point before cell division. The ratio of the area after cell division (
\[ A_{after} = A_1 + A_2 \] where \( A_1 \) and \( A_2 \) are the areas of the sibling pair) to the area before cell division \( (A_{before}) \) is illustrated in Figure S2. While this may be partially due to an artifact of the image segmentation algorithm (which may favor “pinching” in the corners near the new wall), it may also indicate that perhaps the additional tension added by the new wall may inhibit additional growth for a short period of time after cell division. The various heuristics fall into two categories (list them): those that determine the cell wall completely, and those that put constraints on the optimization process, but do not fully determine wall position on their own.

**Cell Division - Potential Model**
The cell division model defines a potential function[8, 9]
\[ V(\theta_1, \theta_2) = \sum_{\{A_i, e_i, g_i\}} w_i V_i(\theta_1, \theta_2) \] (S9)
where \( \theta_1 \) and \( \theta_2 \) gives the central angles of the end points of the new wall measured from the cell center of mass (figure 1), \( w \) is a weight vector, and \( V_i \) represents each contributor to cell division.

Four components were included in the sum (9): an area potential, a length potential, a perpendicularity potential and a growth direction potential.

1. The area potential \( V_A \) is minimized when the two daughter cells are equal in area:
\[ V_A = \left( \frac{A_1 - A_2}{A} \right)^2 \] (S10)
The function is squared to improve computational stability near the minimum (which would otherwise have a non-differentiable corner there). The disadvantage of this potential is that it does not have a unique global minimum, i.e., any line of cell division will that divides the area in half will give a value of zero. Thus the area potential must be tempered by either an additional potential function (such as the perpendicularity and/or length potential) or an additional heuristic to select the desired minimum value that does not require a unique minimum (e.g., randomly select division direction from amongst all equivalent minima).

2. The length potential \( V_L \) is
\[ V_L = \frac{(d - d_{min})^2 + c_i \Delta^2}{(d + d_{min})^2} \] (S11)
where \( d \) is the actual wall length and \( d_{min} \) is the minimum length diameter. Thus \( V_L \) will be minimized when the cell wall is most closely aligned with the shortest possible diameter.

3. The extension potential \( V_e \) is minimized when the new wall is perpendicular to the direction of maximal cell extension \( e \):
\[ V_e = (w \cdot e)^2 + \frac{e \Delta}{d} \] (S12)

4. The growth direction parameter \( V_g \) is minimized when the new wall is perpendicular to the vector of maximal cell growth \( g \):
\[ V_g = (w \cdot g)^2 + \frac{g \Delta}{d} \] (S13)
Maximal cell growth direction is calculated using the method described in [5].
The parameter \( \Delta \) in (S11), (S12) and (S13) gives the shortest distance between the wall and the cell center, with weighting factors \( \varepsilon_e \) and \( \varepsilon_g \). In (S12) \( d \) is the actual wall length. The purpose of the \( \Delta \) term is to help distinguish between different walls of the same length (for \( V_L \)) or direction (for \( V_g \)): one that passes closer to the center is more likely than of the same length (or direction) that skirts the edge of the cell; such “skirting” walls would otherwise be predicted by \( V_L \) or \( V_g \), especially in more oblong cells.

**Fitness Functions**

We asked the question whether any weight vector \( w \) could be found such that \( V(\theta_1, \theta_2) \) is minimized when the predicted angle pair matches the actual cell division plane. To determine the weights we performed a coarse global search on the first quadrant of the global hyper-sphere \( |w| = 1 \). For each \( w \) value, the location of the minimum potential in \((\theta_1, \theta_2)\)-space was determined and subjected to a fitness measure. For any given cell \( i \), the following fitness measures were considered:

1. Error in distance between endpoints of actual and predicted wall, as measured along the circumferential path of the boundary, measured relative to the maximal cell diameter:

\[
 f_{i, \text{boundary}} = \sum_{j=1}^{n} \frac{d_1 + d_2}{d} \tag{S14}
\]

where \( d \) is the maximal cell diameter, \( d_1 \) and \( d_2 \) are the circumferential distances between the actual and observed end points;

2. Actual distance between endpoints of actual and predicted cell wall, relative to maximal cell diameter:

\[
 f_{i, \text{distance}} = \sum_{j=1}^{n} \frac{D_1 + D_2}{d} \tag{S15}
\]

3. Area of the convex hull of the four endpoints of the actual and predicted cell wall, relative to the total cell area, \( f_{i, \text{area}} = A_{\text{convex hull}} / A_{\text{cell}} \);

4. Smaller of the two angles between the diagonals of the convex hull of the four endpoints, divided by 90 degrees; if one of the endpoints falls inside the convex hull of the other three points, this devolves to the angle between the actual and predicted cell wall, \( f_{i, \text{angle}} = \phi / 90 \);

5. Relative Euclidean distance in angle space; if the actual and predicted walls have endpoints at central angles \((\theta_{A,1}, \theta_{A,2})\) and \((\theta_{P,1}, \theta_{P,2})\) measured in degrees, then

\[
 f_{i, \theta} = \frac{\sqrt{(\theta_{A,1} - \theta_{P,1})^2 + (\theta_{A,2} - \theta_{P,2})^2}}{90\sqrt{2}} \tag{S16}
\]
6. The Hausdorff distance between the actual and predicted cell division line. The Hausdorff distance between two sets gives the maximum distance in the first set to the nearest point in the second set. Hausdorff distances were estimated numerically by computing distances at 100 equally spaced points along each wall.

Each fitness measure was averaged over all 207 cell division. The results were sorted by fitness (lower is better) and clustered by location in \( w \)-space to find a best fit vector, which could be used to, e.g., to predict cell division, as implemented in Cellzilla.

**Cellzilla Growth Model**

Cell growth is described by a Hooke's law spring potential \( \phi = \frac{1}{2} \sum k_{ij} (|\Delta x_{ij}| - \ell_{ij})^2 \) applied to each pair of vertices, and summed over all adjacent vertices. Here \( k_{ij} \) is a constant assigned to the wall joining vertex \( i \) with vertex \( j \), and \( \Delta x_{ij} \) is an extension or compression of a virtual spring beyond its equilibrium length \( \ell_{ij} \). The net force will pull vertex \( v_i \) towards \( v_j \) if the spring is extended, and push the vertices apart if the spring is compressed, as described below by equation 17. Pressure is described as a force per unit wall length, so that it can be applied equally at each vertex.

Cellzilla[9] is a two-dimensional tissue growth simulation extension for Cellerator[10]. Each cell is described as a single polygonal compartment. Growth occurs via dynamics assigned to each vertex \( v_j \) as

\[
\frac{d v_i}{dt} = -\sum_j k_{ij} \left( \frac{v_i - v_j}{|v_i - v_j|} \right) (|v_i - v_j| - \ell_{ij}) + \frac{1}{2} P \sum_a \sum_{ij} n_{ij,a} |v_i - v_j| \tag{S17}
\]

where the sums over \( j \) are over all vertices that are connected to \( i \) and the sum over \( a \) is over all cells that abut the edge connecting vertices \( i \) and \( j \). The first term describes a weak spring dynamics, where \( k_{ij} \) and \( \ell_{ij} \) are the spring relaxation constant and resting length for the edge connecting vertices \( i \) and \( j \). The second term describes an internal turgor pressure \( P \) in each cell that is applied normal to the cell wall (normal vector \( n_{ij,a} \) and divided equally between the vertices. (Similar dynamics have been used by others, e.g.[11, 12].)

Isotropic linear growth is described by increasing the resting length of cells:

\[
\frac{d \ell_{ij}}{dt} = \mu \Theta (|v_i - v_j| - \ell_{ij}) \tag{S18}
\]

where

\[
\Theta(x) = \frac{x + |x|}{2} \tag{S19}
\]

Cell division occurs when the cell passes a mass threshold. Each cell is randomly assigned a unique mass threshold at creation, with the population of thresholds distributed normally. The placement of the new cell wall may be assigned either by the modern interpretation of Errera’s rule or a potential model as described elsewhere in the paper.

In the first optimization we assumed that the fourth component (dependence on cell growth direction) was zero \((w_4=0)\) and optimized and the remaining 3-dimensional subspace. The optimum fitness results were
clustered around a weight vector of \(w=(0.68,0.73,0,0)\), where the four values represent the relative importance of area equalization, length minimization, perpendicularity to cell elongation, and parallelism to growth direction (Figure S6). Variations in the first component have very little effect, except as \(w_1 \rightarrow 1\) (area). As the heat map in figure S6 illustrates this region of low fits is confined to the region near \((1,0,0,0)\) for \(e_a=1\), while it spreads along the entire area/extension plane when \(e_a=0\) (figure S6b). In the latter case, there is a second cluster of optimality around \((0.02, 0.81, 0.58, 0)\), though there is wide spread along the entire extension/length plane that is nearly as optimal. These results would indicate that the area, length, and cell extension potentials contribute are all potential predictors of cell division.

We also optimized the fourth component of the weight vector, growth direction, under the assumption that the direction of maximal extension did not contribution (e.g., by setting \(w_3=0\), using the protocol of (Goodall and Green [5]) to determine cell growth direction over a 2 hour period. The optimal weight vector remained at \(w=(0.68, 0.73, 0, 0)\), regardless of the value of \(e_a\). The region of optimality was noticeably smaller (figures S6C and D) than in the case when \(w_3\) was optimized, with the fitness values rapidly increasing as one moves away from the \(w_4=0\) plane. This would indicate that the actual instantaneous direction of growth (as measured over a two-hour period) is not a significant predictor of cell division.

This result would, indeed, suggest that when the different predictors are dissociated in this manner, that the best predictor is the shortest length wall that passes near the center. This prediction is very similar to the modern interpretation of Errera’s rule, that the wall will form in the shortest path that divides the cell in half. To compare these statements, the predicted wall locations according to this rule were computed for all 207 cell divisions. The distribution of fitnesses for a potential function minimization with \(w=(0.68,0.73,0,0)\) were slightly better than for the modern interpretation of Errera’s rule (Figure 6). Thirteen of the 14 worst cases were the same cells for both methods. Visually there is very little difference between the two methods of prediction. Using a distance fitness measure, the potential method gave a better fit in 68 of the 207 cell division, the modern interpretation of Errera’s method in 40 cases, and both had identical fitnesses in 2 cases. In the hindsight model the numbers were 36 (Errera); 2 (tie) and 72 (potential).

Simulation results for both the modern interpretation of Errera’s model and the optimized potential model are illustrated in Figure S7 after 1000 cell divisions have occurred (see also the movies in supplemental material 4 and 5). The tissues were grown in-silico from single quadrilateral cells and projected onto a parabolic surface. The resulting cell division patterns in both cases are evocative of observed data.

*Cell Division is a Boltzmann Distribution*

Following the work of Besson and Dumais[1] we evaluated the hypothesis that selection of cell division surface may follow a Boltzmann distribution

\[
\Pr_{\text{surface}} = \exp(-\beta \Delta V_{\text{surface}}) / Z(\beta)
\]

(S20)

where \(Z(\beta)\) normalizes the distribution and beta is the inverse of temperature) in a phenomenological potential function, rather than actually minimizing the potential function for each cell all the time. In the limit of zero temperature such a model is equivalent to minimizing the potential; nonzero temperatures (finite betas) record departures from minimality. In this analysis we applied the prior authors' concept of a thermodynamic model to our data; we applied their model to our data to see how their potential function \(\Delta V = l p\) compared with ours (equation S9) in a thermodynamic analysis. We evaluated the Besson & Dumais model against our data, as our model use straight lines for cell division and theirs uses arcs of circles. When
we evaluated their model we used arcs of circles. Figure S3 supports this hypothesis with quantitative evidence from SAM cell images, both for our potential function (equation S9 and Figure S3A) and for the Besson-Dumais potential function (equation S13 and Figure S3A), though with a substantially lower effective temperature for our proposed potential function.

**Comparison to the Besson-Dumais Model**

We evaluated the Besson-Dumais model on our data set by calculating the most likely wall location from among all allowed wall locations, where a wall location was allowed if its endpoints subtend a minimum central angle, as measured from the cell centroid, of 135 degrees (a restriction we have justified by the histogram in Figure 4C). In figure S3 we compare the results of our model with the Besson-Dumais model. In order to make a valid comparison we computed the log-histogram of $|\Delta V|$, the difference between the predicted and actual potential used by the cell, for each model. For our model, we plotted the log-histogram of $|\Delta V|$ where $V$ is computed by equation S9; for the Besson-Dumais model, we plotted the log-histogram of $|\Delta V|$ where $V = l/\rho$. In each case we computed the weighted least squares fit:

$$\log N = a |\Delta V| + b$$  \hspace{1cm} (S21)

where the slope $b$ and intercept $a$ are solutions of the normal equations

$$\begin{bmatrix} \langle |\Delta V|^2 \rangle & \langle |\Delta V| \rangle \\ \langle |\Delta V| \rangle & 1 \end{bmatrix} \begin{bmatrix} a \\ b \end{bmatrix} = \begin{bmatrix} \langle |\Delta V| \log N \rangle \\ \langle \log N \rangle \end{bmatrix}$$ \hspace{1cm} (S22)

The expectations are computed by defining a normalized weight vector $w = \frac{1}{N} n$, where $n$ is the vector of counts in each bin, and $N = \sum n_i$. Then

$$\langle |\Delta V| \rangle = \sum w_i |\Delta V|_i$$ \hspace{1cm} (S23)

$$\langle |\Delta V|^2 \rangle = \sum w_i |\Delta V|^2_i$$ \hspace{1cm} (S24)

$$\langle |\Delta V| \log N \rangle = \sum w_i |\Delta V|_i \log n_i$$ \hspace{1cm} (S25)

$$\langle \log N \rangle = \sum w_i \log n_i$$ \hspace{1cm} (S26)

The negative of the slope corresponds to inverse temperature, the parameter $\beta$ in the Besson-Dumais model. As can be seen the resulting distributions are similar. The corresponding fits (the straight lines in Figures S3 A and B) have slope -10.4 (Besson-Dumais) and -62.1 (Potential Model). When a similar least squares fit was computed without the weighting the corresponding slopes were -9.0 (Besson-Dumais) and -45.9 (Potential Model). By comparison, the similar empirical fits by (Besson-Dumais) of a Boltzmann distribution with energy function $V_{BD} = l/\rho$, on their data in their figure 6B for four species Coleochaete, Microsorum, Dionaea, and Zinnia, resulted in a slope of with a “universal” or cross-species best fit slope $\beta$ of 20.6. This difference of results for the potential function $V_{BD}$ may be accounted for by the different ways we and (Besson-Dumais) use the same potential function. (Besson-Dumais) consider just a few cell division surfaces between pairs of cell sides, allowing arcs; we consider straight lines, specified by two continuous intersection angles finely discretized into 10000 angle pairs, and restricted by central angle as above. Thus, in the direct comparisons that have been made, we find a substantially lower effective temperature $1/\beta$ and thus substantially less randomness, using our proposed potential function rather than that of (Besson-Dumais).


