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A Quantitative Method for Branching Morphology of Soybeans and its Visualization Based on L-System

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Abstract: Branching morphology is a crucial factor in phenotype of soybeans and the primary tissue to transport nutrients. After the acquirement of an empirical model and distribution interval for soybeans height by nonlinear regression analysis, we, guided by the pipe model theory, quantified the main stem, branch and internode of soybeans using the taper stem equation and S-curve equation. A novel L-system was finally proposed to construct the branching form by means of the numerical nomenclature coding system and the visual simulation was performed. This technique expanded the application fields of L-systems and offered an innovative computational thinking and pattern in the research and application of the best soybeans plant type design and prediction of soybeans yield, etc.

Key words: L-system, branching morphology, pipe model, quantitative, visualization

INTRODUCTION

L-System is one of the crucial methods to model and visualize virtual plants; it is in nature a parallel character rewriting system (Prusinkiewicz and Lindenmayer, 1990). In its initial application, L-System was used to formulate morphogenesis of virtual plants with fractal features (Jaeger and de Reffye, 1992; Prusinkiewicz *et al.*, 1997). In the later few decades, L-Systems have gone through a long way in the extent and depth of application. Especially in recent years, Przemyslaw Prusinkiewicz led his team to have conducted extensive and in-depth researches on the diversity of plant morphology and structure, the molecular mechanisms of morphogenesis, plant geometric models and its quantitative computations in three dimensions. P. Prusinkiewicz, for example, probed into modeling technology and mechanism of developmental biology and presented useful and feasible methods in geometry form and molecular level (Prusinkiewicz and Rumions, 2012); he put forward a new approach to control the bud activation by means of auxin transport switch and demonstrated the branching number of *Arabidopsis thaliana* in phenotype affected by the auxin concentration (Prusinkiewicz *et al.*, 2009). Cieslak *et al.* (2008), simulated the light environment of plants by means of quasi-Monte Carlo model (Cieslak *et al.*, 2008). Palubicki *et al.* (2009), presented a method for generating realistic models of

temperate-climate trees and shrubs, in which the plants morphogenesis are influenced by the growing condition and regulated by the internal signaling mechanisms (Palubicki *et al.*, 2009).

In the studies and applications of quantitative approach to plant forms (Bucciarelli *et al.*, 2006), by employing the numerical nomenclature coding system to analyze *Medicago Truncatula* phenotypic development, documented a standardized method to characterize quantitatively the plants temporal developmental growth patterns in the way of their growth unit and the alternations of these patterns due to the absence of nitrogen and phosphorus (Bucciarelli *et al.*, 2006). However, there was no concern with the specific method to acquire and compute these quantitative results. Lars Mündermann *et al* from Canada presented a quantitative model of *Arabidopsis thaliana* which was an empirical model of phenotypic development in plants and a helpful trial to model plants phenotype by using biological experiment data effectively. Yet, they failed to reach the final shape representation and visualization of *Arabidopsis thaliana* (Mundermann *et al.*, 2005). Lauren Remmler from Canada presented a computational method to quantify the spatial patterns of growth form at the adaxial surface of leaves, in which the fluorescent particle was applied to track and record the leaves variations (Remmler and Rolland-Lagan, 2012). As for the studies of

the plants branching patterns, the emphasis has been placed on the regulation of plants hormones on the branching development (Bessonov *et al.*, 2008; Evers *et al.*, 2011).

Given the fact that L-system shows the lack of techniques for effective development and utilization of biological data, we proposed an empirical model, on the premise of analyzing the biological experimental data and in the consideration of soybeans diversity and random distribution feature in branching (Meng *et al.*, 2004; Chen *et al.*, 2006) and the developmental space constraint (Prusinkiewicz *et al.*, 2010), to quantify the branching morphology of soybeans based on the pipe model theory (Chiba, 1990, 1991). Moreover, we constructed a numerical nomenclature coding system of soybeans branching in order to formulate and computer visualize the soybean branching shape based on L-System. Eventually, we simulated this model in three dimensions which makes up for the deficiency of L-Systems in biological application.

The findings of the present study offer ways to quantify and visualize the optimum plant type of soybeans and simultaneously lay a certain foundation for plant morphogenesis interacting with its environment and phenotype regulating under genetic factors. It is hoped that the findings in the future will present an innovative computational thinking and mode for the practical application to gene analysis, biology breeding and yield forecast, etc.

QUANTITATIVE COMPUTING FOR PLANT HEIGHT

Soybean is the common crop in Shandong Province of China and their planting environment is divided into wild fields and fields or environment with fully automatic

room temperature. The former is mainly used in summer and the sufficiency of water should be ensured; the latter is used in the seasons when the temperature is low; soybeans are planted in the substrate of flower pots to guarantee that the temperature is controlled at 25~35°C during the day and 20~25°C at night. The planting period generally lasts four months. In this study, the study of the appropriate quantitative method for wild-field-grown soybeans is focused on.

Take the soybeans planted in wild experimental fields for example. We cultivated five categories including Jilin 35, Hedou 12, Williams 82, Zhonghuang 42 and No. 075140 on June 18, 2012. 200 of each variety were planted, with line-spacing of 50 cm and row-spacing of 10 cm. We started to measure the shoot height of soybeans on July 9 when the plants grew to about 10 cm high. Fourty of each variety were selected and the abnormal plants due to natural or factitious factors were eliminated. The distance from the ground to the top of the plant was measured every other week. Appendix A shows the measured plants heights of Williams 82.

To clarify the variations of the plant height of soybeans (h) underwent with time (t), we plotted the data in Table 1 of Appendix A. The plotted diagram showed that the nonlinear relationship between plant height (h) and time (t) is obvious. Based on Levenberg-Marquardt algorithm, a nonlinear regression analysis between plant height h and time t is conducted by applying the Logistic equation as shown in Eq. 1, in which the regression

Table 1: Statistics of probability distribution-williams 82

Statistics parameters	Average	SD	Maximum	Minimum
K	83.2964	10.3388	98.1038	48.4974
m	29.2099	7.3043	56.3963	17.4194
r	0.6615	0.0464	0.7968	0.5773

Appendix A: Measurements of soybeans plants height---williams 82

nt	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
7-09	4.0	5.5	5.5	3.5	4.5	4.5	5.0	4.5	6.0	5.0	5.0	5.0	6.0	5.5	5.0	4.0	4.5	5.0	6.0	6.0
7-16	9.0	11.0	11.0	10.0	11.0	10.0	10.5	9.0	10.5	12.0	11.0	11.0	10.0	11.0	8.0	8.0	9.0	10.0	12.0	12.5
7-23	17.0	18.5	19.0	19.0	19.0	20.5	20.5	19.0	20.0	22.0	19.0	21.0	16.0	19.0	14.5	16.0	17.0	19.0	22.0	22.5
7-30	26.0	25.0	25.0	26.0	25.0	28.0	30.0	27.0	29.0	30.0	27.0	30.0	24.0	28.0	21.0	23.0	25.0	27.0	30.0	32.0
8-06	41.0	36.0	36.0	39.0	38.0	40.0	43.5	37.0	42.0	43.0	39.0	44.5	36.0	43.0	34.0	36.0	37.0	40.0	44.0	42.0
8-13	54.0	52.0	45.0	58.0	52.0	52.0	53.0	50.0	48.0	54.0	53.0	56.0	52.0	59.0	53.0	55.0	51.0	48.0	54.0	61.0
8-20	71.0	67.0	46.0	74.0	67.0	68.0	67.0	63.0	64.0	67.0	68.0	72.0	61.0	74.0	68.0	68.0	64.0	52.0	66.0	69.0
8-27	80.0	72.0	47.0	84.0	76.0	74.0	72.0	71.0	67.0	72.0	77.0	75.0	74.0	84.0	76.0	79.0	72.0	56.0	78.0	77.0
9-03	85.0	72.0	47.0	88.0	76.0	74.0	72.0	71.0	70.0	72.0	79.0	78.0	77.0	88.0	76.0	83.0	73.0	59.0	80.0	79.0
nt	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
7-09	5.0	5.0	4.0	6.5	5.0	4.0	5.5	5.0	4.5	6.0	5.0	6.0	4.0	6.0	5.0	4.0	6.0	5.0	4.0	5.0
7-16	9.0	9.0	9.0	11.5	9.0	9.0	10.5	8.5	8.5	9.5	10.0	10.5	9.0	11.5	11.0	9.0	10.5	10.5	8.5	9.0
7-23	16.0	17.0	16.5	20.0	17.0	16.5	19.5	16.0	16.5	18.0	19.5	19.0	17.0	22.0	21.0	17.0	20.0	21.0	17.0	16.5
7-30	22.0	26.0	25.0	28.0	25.0	22.0	27.0	23.0	23.0	24.0	28.0	28.0	25.0	30.0	29.0	26.0	28.0	31.0	24.0	25.0
8-06	34.0	40.0	36.0	38.0	37.0	34.0	38.0	37.0	36.0	36.0	38.0	41.0	38.0	42.0	42.0	41.0	41.0	45.0	37.0	39.0
8-13	47.0	53.0	49.0	54.0	49.0	49.0	50.0	50.0	53.0	47.0	50.0	59.0	51.0	58.0	55.0	52.0	56.0	57.0	51.0	55.0
8-20	62.0	66.0	63.0	65.0	58.0	62.0	56.0	64.0	65.0	59.0	64.0	71.0	65.0	71.0	72.0	69.0	70.0	70.0	65.0	70.0
8-27	70.0	76.0	70.0	74.0	60.0	72.0	56.0	67.0	75.0	66.0	71.0	82.0	79.0	80.0	77.0	77.0	79.0	80.0	76.0	79.0
9-03	73.0	80.0	72.0	76.0	60.0	78.0	58.0	70.0	79.0	69.0	75.0	88.0	79.0	80.0	77.0	80.0	79.0	82.0	80.0	84.0

coefficient is set as K, m and r separately and the regression analysis meets the significance level $\alpha = 0.05$, namely, the confidence is 95%:

$$H = K/1 + me^{-r} K, m, r > 0 \quad (1)$$

The nonlinear fitting to plants height for No. 1-4 of Williams 82 is conducted according to Logistic equation. The fitted results and corresponding confidence interval is shown in Fig. 1.

The Logistic nonlinear regression analysis of plants height for 40 different plants of Williams 82 was implemented and the 40 different sets of regression coefficients were obtained, as shown in Appendix B.

Then, we applied statistical method of Kaplan-Meier to test the three coefficients of Logistic equation and the vector of values of the empirical cumulative distribution function is uniformly distributed between 0 and 1, so we represented it as $E_i = 0.025i, i \in \{1, 2, 3, \dots, 40\}$.

The values of the empirical cumulative distribution function were compared with the theoretical values which satisfied the normal distribution with confidence level more than 95%. The values of cumulative distribution function for three coefficients K, m and r are shown in (Fig. 2a-c).

The crucial eigenvalues of probability distribution corresponding to the above three coefficients are shown in Table 1.

The same experimental analysis and computation conducted on the other four varieties of soybeans showed that the growth of the soybeans tested conforms to the Logistic curve and their coefficients all meet the

Appendix 2: Parameters of the logistic equation---williams 82

CN	K	m	r	CN	K	m	r
1	93.6531	35.9826	0.6631	21	83.2950	31.7694	0.6275
2	81.1433	28.3976	0.6558	22	88.1503	30.8612	0.6456
3	48.4974	17.4194	0.7968	23	79.6479	30.7675	0.6596
4	98.0092	38.3360	0.6687	24	85.6358	22.0912	0.5989
5	86.3622	28.7808	0.6377	25	63.9653	28.9073	0.7515
6	82.0134	26.1486	0.6561	26	88.8718	33.1239	0.6151
7	77.5358	24.4509	0.6879	27	60.3756	21.8185	0.7444
8	78.9763	26.1452	0.6459	28	75.2106	35.3723	0.7136
9	73.6422	23.4784	0.6940	29	87.3810	37.2705	0.6671
10	78.2240	21.6139	0.6617	30	77.2216	22.9467	0.6026
11	89.3079	26.9033	0.6205	31	83.5885	22.8297	0.6004
12	83.5311	25.7958	0.6780	32	98.1038	29.0306	0.6203
13	87.6008	28.5409	0.6083	33	90.0363	32.3004	0.6333
14	97.6749	31.2912	0.6465	34	89.1869	24.3034	0.6363
15	83.9926	56.3963	0.7578	35	85.2406	26.6191	0.6647
16	91.5146	45.0721	0.6942	36	87.5567	34.5273	0.6774
17	80.7687	31.7610	0.6710	37	88.6876	27.5088	0.6469
18	59.7084	21.0625	0.7361	38	89.3132	25.0240	0.6444
19	89.9211	19.6410	0.5773	39	90.2069	34.9405	0.6406
20	85.4307	21.8764	0.6459	40	92.6722	37.2881	0.6675

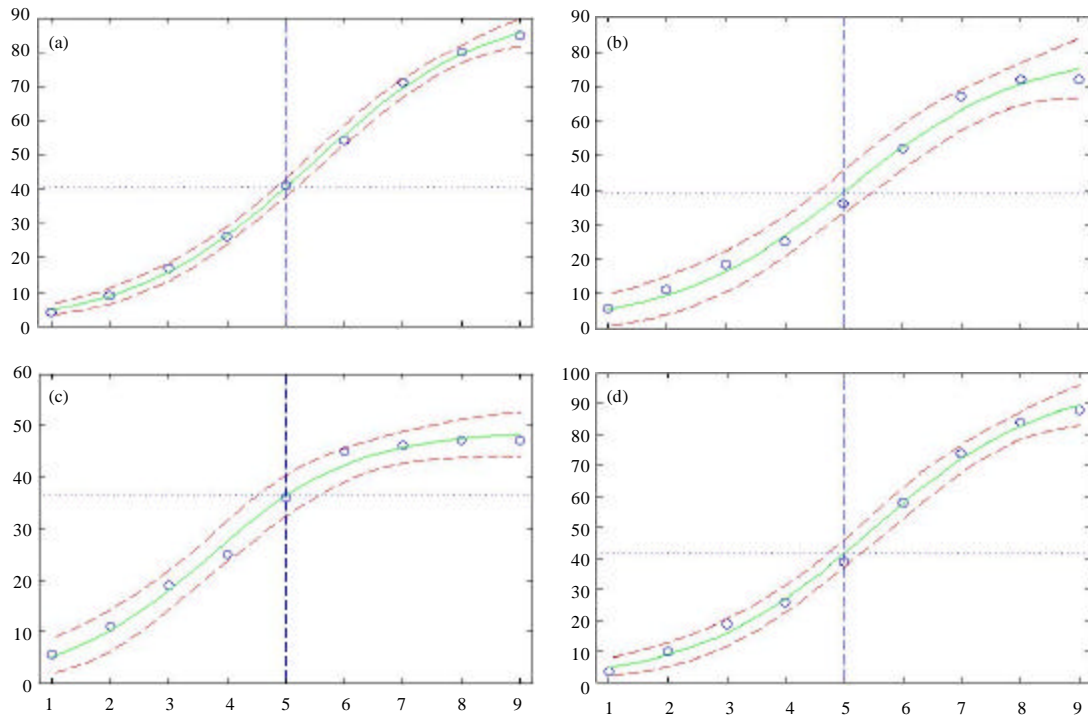


Fig. 1(a-d): Plot of the plant height (Williams 82: No. 1-4)

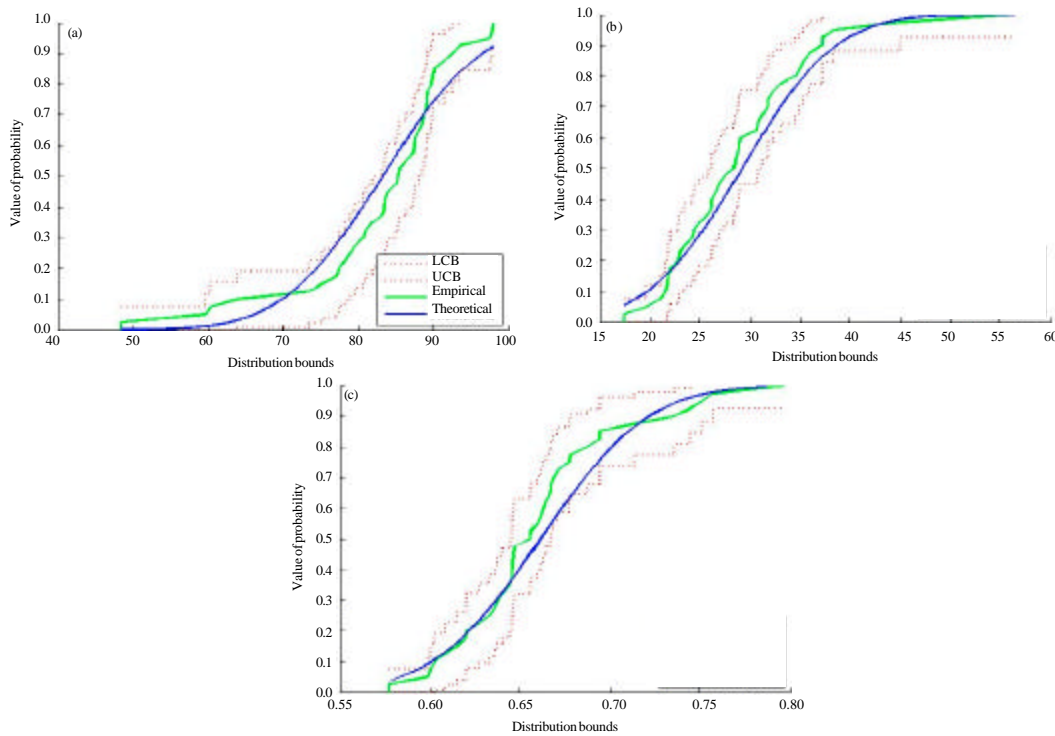


Fig. 2(a-c): Contrast between empirical value and theoretical value in CDF

normal distribution within the permissible error range $2(<0.05)$. However, the crucial eigenvalues of probability distribution for three coefficients of Logistic are different from the other kinds of soybeans.

Therefore, the characteristics of probability distribution for the soybean plant height are satisfied, then we can get the relevant coefficients of Logistic equation according to the uniform normal distribution and eventually we can compute and predict the plant height in any time, to any individuals. This is the basis for the branching morphology of soybeans.

QUANTITATIVE REPRESENTATION OF BRANCHING

The number of branches is one of the important factors in the plant type and yield per plant of soybeans. Therefore, accurate quantification and evaluation of the number of branches is essential which is the basis for soybean production forecast (Dun *et al.*, 2009; Leyser, 2009).

The branching number of soybeans is the number of effective disposable branches on the main stem which has more than two internodes and at least one of them grows pods. Figure 3 shows a harvested plant of Williams 82 planted in our wild experimental fields. It is observed



Fig. 3: Shape of the grown soybean---williams 82

clearly that: The branching form of soybeans is composed of a number of branches grown from the main stem and each of the branches includes at least two or more internodes. From the investigation of the actual growth of the soybeans, we can draw the conclusion that the secondary branches from the initial branch are completely negligible.

In our study, attention was paid to the statistical analysis of the experimental data for the quantitative representation of soybeans branching including the plant

height, the number of internodes on the main stem, branching numbers and the number of internodes on each branch. Other factors, such as the environment, were assumed to be in the ideal state.

From the overall shape of soybeans, there is no clear distinction in the growth process between the crown and trunk, only a main stem and a number of branches on it. Meanwhile, there are a quantity of internodes on the main stem and its branches. As such, according to the pipe model theory (Chiba, 1990, 1991; Jelonek *et al.*, 2008), based on the Main-Axis Cutting Method, the plant height of soybeans H could be obtained by Eq. 2:

$$H(t) = \int_0^L (M(t) + B(t) + R(t)) dt \quad (2)$$

where, $1 \leq i \leq N_m$, t is length cutting along the main stem, N_m is ideal nodes number on the main stem, obtained by Eq. 8; M(t) is unit nodes number on the main stem; B(t) is unit branch number on the main stem; R(t) is unit total nodes number of all branches split from the main stem and there are certain restrictions among M(t), B(t) and R(t).

From the biological observation of the planting process, the soybeans stems form was of tapered distribution. Then, being subject to M(t), B(t) and R(t), not infringing the pipe model theory as the premise, the stem taper equation was used to compute quantitatively the actual plant height of soybeans (Kurinobu *et al.*, 2007; Hjelm, 2013), as in Eq. 3:

$$\frac{d^2}{DBH^2} = b_0 + b_1 \left(\frac{h}{H} \right) + b_2 \left(\frac{h^2}{H^2} \right) \quad (3)$$

where, d is the diameter outside the bark, h stands for the stem height, DBH is the diameter at breast height and H is the plant height of soybeans. In accordance with the Logistic distribution in Part 2, $b_i (i = 1, 2, 3)$ is the statistical coefficients to be calculated.

For any of the soybeans, we applied the Maximum Likelihood Estimator (MLE) proposed by R.A. Fisher was applied for the statistical analysis of the distribution of the nodes number and the location of the internodes in branches on the main stem because they possess a certain stochasticity.

In general, the internode number and branch number are all in line with the characteristics of discrete stochastic variable and then the likelihood function was used to calculate them, as in Eq. 4:

$$L(?_1, ?_2, \dots, ?_k; x_1, x_2, \dots, x_n) = \prod_{i=1}^n f(x_i; ?_1, ?_2, \dots, ?_k) = \prod_{i=1}^n P(X = x_i) \quad (4)$$

Table 2: Probability distribution of branch in internode along the main stem

No.	I1	I2	I3	I4	I5	I6	I7	I8	I9	I10	I11
MLEs	1	1	0.725	0.725	0.85	0.675	0.725	0.475	0.425	0.15	0.025

Taking Williams 82 for example, we estimated the values of the maximum likelihood probability whether a branch had grown in any of the internodes according to the data collected from the planting record. The final results are shown in Table 2.

Therefore, the ideal number of branches on the main stem may be calculated by Eq. 5:

$$B_m = \sum_{i=1}^n I_i P_{MLE_i} \quad (5)$$

There is at most one branch on each of internodes on the main stem of the soybeans. Thus, $I_i = 1$ and $B_m = 6.05$ and it is similar to the average value of the height of the lowest legume 5.61 cm.

The branch number of soybeans is the crucial factor that determines the size of its diameter at breast height and then B_m is placed with the parameter DBH in Eq. 3. For this reason, we assumed $DBH = B_m = 6.05$ as the ideal value of the diameter at breast height of the soybeans.

The whole main stem of soybeans is divided into two parts by the internode position (denoted by z_B) in which no branch will grow out. This is because it has the feature of taper stem form when cutting the stem by main-axis. The growth modes of the stem diameter conform to the distribution feature of "S-curve" (Chiba, 1990), as in Eq. 6:

$$\frac{1}{S(z)} = \frac{1}{S_0 \exp(z/\alpha)} + \frac{1}{S(z_B) \exp(|z - z_B|/\beta)} \quad (6)$$

where, z is the number of internodes on the main stem and $1 \leq z \leq N_m$, N_m is the ideal value of the internodes number on the main stem calculated by Eq. 7. Taking Williams 82 for example, the maximum likelihood probability distribution of the internodes number on the main stem is shown in Table 3:

$$N_m = \text{int} \left(\sum_{i=1}^n \eta_i P_{MLE_i} \right) \quad (7)$$

where, n is the distribution interval length of the internodes number on the main stem, the ideal value of the internodes number on the main stem for Williams 82 computed by Eq. 7 is $N_m = 20$.

$S(z)$ is the diameter of the main stem, S_0 is the stem diameter per unit length over z_B , S_B is the stem diameter

Table 3: MLEs for the internode numbers of main stem---williams 82

z	13	17	18	19	20	21	22
MLEs	0.025	0.025	0.2	0.05	0.3	0.375	0.025

per unit length from z_b down to the position of the diameter at breast height and its approximate value is $DBH/[Z-Z_b]$, DBH/z_b , respectively. In terms of the individual soybean, a and b are all constant.

If $d = S(z)$, then the diameter outside bark is approximately equal to the stem diameter. The growth length of stems is computed by Eq. 3. Meanwhile, the distribution law of branches on the stem meets the regulation in Table 2 and the distribution law of internodes numbers on each branch is computed by the maximum likelihood probability.

L-SYSTEMS AND BRANCHING MORPHOLOGY OF SOYBEANS

Numerical nomenclature coding system: L-system is essentially a character system. In order to visualize the quantified branching morphology of soybeans and keep the consistency of the simulated results with the quantitative data, the numerical nomenclature coding system of soybeans (Hanan *et al.*, 2007) has to be utilized to get the relevant system conforming to the L-system grammar.

Bending representation of branches by L-system: The flexible modeling feature of B-spline curve is in accordance with the soybean characteristic of bending branches. Therefore, one branch of the soybean is represented by a sub-L-system converted from a B-spline according to the de Boor-cox algorithm (Prusinkiewicz and de Reuille, 2010). Meanwhile, we applied the plant height H and the stem length h in this sub-L-System and then got the quantitative results of H or h in Part 2 and 3.

According to the recursive algorithm of de Boor-cox with the corresponding sub-L-system, we got the B-spline curve as follows:

$$\begin{aligned}
 &\text{Sub-L-System: B-Spline} \\
 &\omega: P(v_0), P(v_1), \dots, P(v_n) \\
 &p1: B(t): k \leq j \leq n \rightarrow P_{i,k}(t) \\
 &p2: P_{i,0}(t) \rightarrow P(v_i) \\
 &p3: P(v_{i-k}) < P_{i,r+1}(t) < P(v_{i-k+1}): r > 0 \\
 &\quad \rightarrow P(u_1 v_{i-k} + u_2 v) P(u_2 v + u_1 v_{i-k+1})
 \end{aligned}$$

Here, $u_1 = (t_{i+k,r+1}-t)/(t_{i+k,r+1}-t_i)$, $u_2 = (t-t_i)/(t_{i+k,r+1}-t_i)$, meeting the distribution of knots vector U for B-spline curve.

Representation of branching angles in L-system: Fibonacci sequence was applied to represent uniformly

the branching angles. That is, the first and the second branching angle of internodes on the main stem are $a_1 = 25^\circ$, $a^2 = 25^\circ$, respectively and the next branching angle is $a_i = a_{i-1} + a_{i-2}$. In three dimensions, the Fibonacci rules were applied for computing the branching deflection angles α , β along x-axis, y-axis, respectively in the devised L-systems.

DESIGN AND SIMULATION EXPERIMENT OF SOYBEAN BRANCHING MORPHOLOGY

We have designed the branching morphology of soybeans according to the object-oriented method. The visualization of soybeans growth is an iterative process: Select the main stem as reference axis and start from the initial growth point and it can develop an internode during each iteration and the length of an internode is the stem height quantified in Part 3 so as to determine the starting position in the next developmental internode. The iterative process comes to the end when the individual soybean grows to the quantitative plant height after a number of iterations. The visualization of branches applies the same iterative process as the preceding one, but its initial growth point is the position, where a branch grows on the main stem and abides by the distribution law of branches. The growth node is defined as follows:

```

Struct growPoint
{
Int x; //x-axis in 3D
Int y; //y-axis in 3D
Int z; //z-axis in 3D
growPoint *parentPoint; //Point to Parent
growPoint *childPoint; //Point to Child
float flexibility; //Flexuous degree of B-spline curve
float R1; //the Angle of deflection around x-axis
float R2; //the Angle of deflection around y-axis
int branchLabel; //the Identification of branch around main axis
}
    
```

Williams 82 is taken for example to complete the visualization of soybeans morphology. The podding number is not quantified strictly but can be simulated simply. The corresponding L-system is shown as follows.

L-System: Soybeans:

$$\begin{aligned}
 w &: H(0, 0) \\
 p1 &: H(t, i): x < h \rightarrow F[B]H(t+1, i+1) \\
 p2 &: H(t, i): x < h \rightarrow [+(\alpha)/(\beta)]R[B]H(t+1, i+1): \pi \\
 p3 &:: H(t, i): i = m \quad \text{or} \quad t = T \rightarrow \phi
 \end{aligned}$$

Here, $H(0, 0)$ is the initial state. B is the pod, F is the internode, R stands for the branch and the sub-L-system is named as B-spline. t is the growing time of soybeans and T stands for growth cycle. H is the plant height and h stands for stem length. m is the number

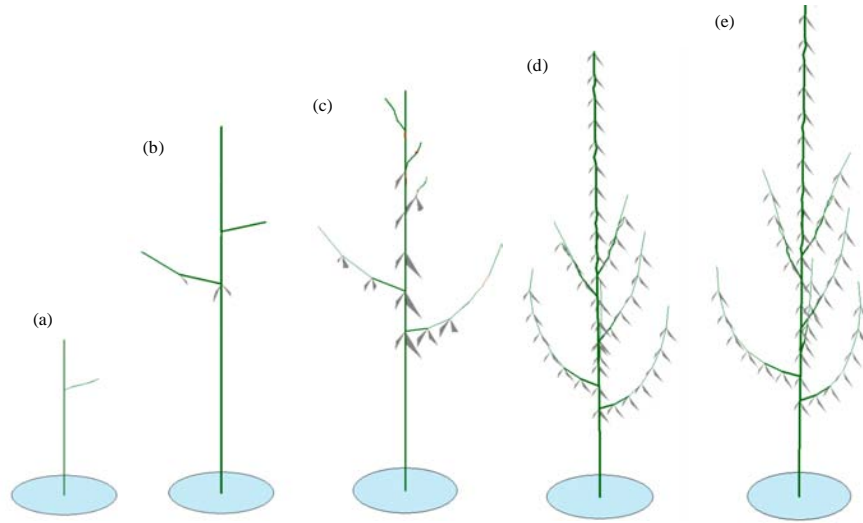


Fig. 4(a-e): Various branching form in days = 28, 42, 56, 70, 84---williams 82 (a) Days 28, (b) Days 42, (c) Days 56, (d) Days 70 and (e) Days 84

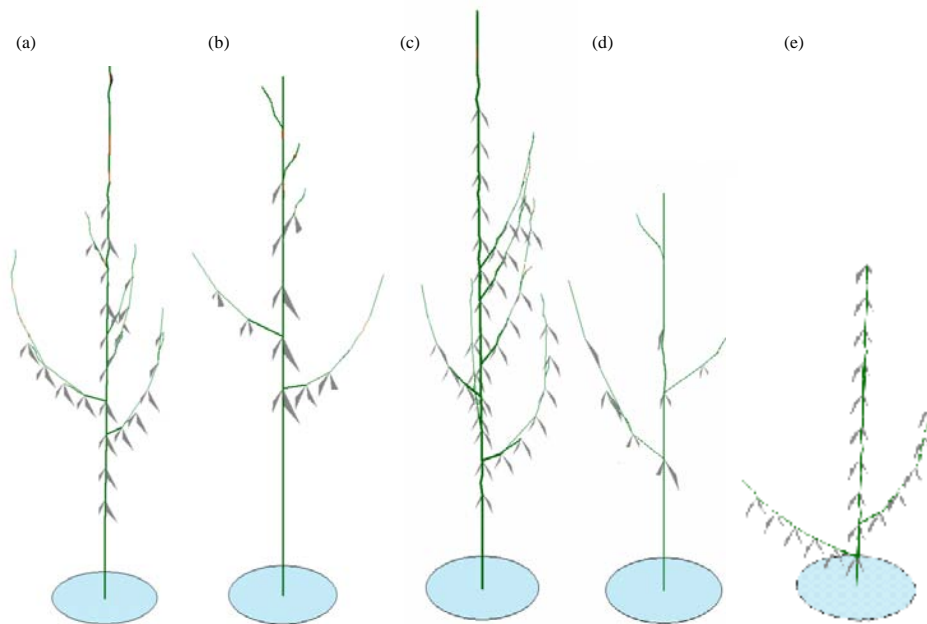


Fig. 5(a-e): Branching forms of five varieties of soybeans in the 56th day (a) 0754, (b) Williams 82, (c) Hedou 12, (d) Jilin 35 and (e) Zhonghuang 42

of internodes on the main stem. Production p1 means no branch to develop and p2 means a branch to develop on the main stem. p2 will be applied when it conforms to the distribution probability p of soybeans branching.

Applying the above L-system of soybeans, the branching form of Williams 82 in days 28, 42, 56, 70 and 84, respectively was obtained, as shown in Fig. 4.

The growth status of the five varieties of soybeans planted in the 56th day is shown in Fig. 5.

CONCLUSION AND PERSPECTIVE

The present study of the quantitative methods and visualization of soybeans branching morphology has not only injected new vitality into the application of computer

science, but also offered approaches and methods to quantify and formulate the design of the best soybeans plant type based on the measured data. In the long run, the present study has laid the foundation for plants form and environment, morphology and genetic biology and so on. Meanwhile, the study has also provided a new computing thinking and model for their practical application in many respects, such as gene analysis, bio-breeding and yield forecast, etc.

On the basis of the quantitative model of the branching morphology of soybeans, the future researches will focus on the accurate quantification and prediction of the yield of soybeans by measuring and analyzing the number of flowering, podding and hundred-seed weight per plant. Meanwhile, we will also strive to develop the innovative work for the multidisciplinary research and application in information science. First, we will make it more realistic in the visualization of plant morphology. Second, the strong support will be provided for biological research and teaching.

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