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Fruit Senescence and Decay Simulation

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Abstract

Aging and imperfections provide important visual cues for realism. We present a novel physically-based approach for simulating the biological aging and decay process in fruits. This method simulates interactions between multiple processes. Our biologically-derived, reaction-diffusion model generates growth patterns for areas of fungal and bacterial infection. Fungal colony spread and propagation is affected by both bacterial growth and nutrient depletion. This process changes the physical properties of the surface of the fruit as well as its internal volume substrate. The fruit is physically simulated with parameters such as skin thickness and porosity, water content, flesh rigidity, ambient temperature, humidity, and proximity to other surfaces. Our model produces a simulation that closely mirrors the progression of decay in real fruits under similar parameterized conditions. Additionally, we provide a tool that allows artists to customize the input of the program to produce generalized fruit simulations.

Categories and Subject Descriptors (according to ACM CCS): I.3.7 [Computer Graphics]: Three-Dimensional Graphics and Realism—

Keywords: *Appearance Modeling, Natural Phenomena, Physical Simulation, Senescence*

1. Introduction

As objects age, their appearance changes over time. These shifts in appearance give important visual age cues that can enhance the realism of a synthetic scene. We attempt to address the rather unexplored area of organic decomposition, a fundamental step in a fruit's life-cycle. The visual simulation of the fruit aging process requires attention not only to aesthetic changes, but also to the underlying biology of senescence and decay. While artists can add visual imperfections to their models and environments through traditional texture mapping and physics-based modeling methods, these may be based on observation, intuition, and artistic skill. Parameterized procedural decay methods built on scientific principles could be useful to make artistic rendering more precise. Several surveys [DRS07, MG08] summarize aging and weathering phenomena in computer graphics. However, these methods neither directly include, nor can they be readily extended to, the complex biological processes associated with decomposition.

While there has been some significant work in the animation industry revolving around the creation of realistic computer generated food, there has been little emphasis on the reproduction of natural decay processes. Traditional surface

texture imperfection and aging techniques are visually satisfying, but they do not take into account the effect of mold and other microorganisms on environments in a way that is biologically accurate.

Figure 1: *An illustration of a simulated tomato decaying. Here multiple mold and rot processes affect the fruit.*

We present a novel, parameterized method to simulate fruit senescence and decay that is grounded in scientific research. As real fruits age, their physical structures become compromised and vulnerable to attack by infectious agents. Our model replicates these interactions between multiple biological processes. We generate growth patterns for areas

of fungal and bacterial infection with a reaction-diffusion model. As nutrients deplete, the fungal colony spread decreases. Additionally, the internal fruit substrate is affected by soft bacterial rot and the volume decreases over time to reflect water loss due to transpiration. Our work is one of the first simulations to link rot growth and transpiration in one model.

Our model changes both the overall shape and the appearance properties of the fruit's anatomy. First, the fungus and bacteria are grown on the fruit's exocarp, or outer skin. This process is directly affected by moisture, temperature, and nutrient concentration at each point on the surface. Second, we address the gradual collapse and shrinking of the internal structure. Because water accounts for a large percentage of a fruit's mesocarp (interior), water transpiration is a primary factor in the way a fruit decays and loses internal mass. Additionally, rot makes areas of the substrate soft and more prone to collapse.

The simulation is based on user-defined parameters for skin thickness and porosity, water content, flesh rigidity, ambient temperature, humidity, and proximity to other surfaces. These parameters allow direct control of the simulation and a broad range of results. We demonstrate visually accurate simulations on three fruits: a tomato, apple and orange. We provide a variety of fruit presets and parameters to automatically produce proper fungal growth and rot for the selected fruit. Additionally, we provide a tool that allows an artist to direct the simulation. This generalizes our simulation to a variety of fruits, real or imaginary, and even other geometry, allowing artists to produce decay simulations based on their production requirements. To the best of our knowledge, this is the first paper to describe a visual simulation of fruit decay.

1.1. Related Work

Early work on creating imperfections focused on procedural texture synthesis [BB90, WNH97]. This work manipulated surface features to simulate blemishes. These methods used simple distribution models. γ -ton tracing [CXW*05] is a recent rule-based approach to simulate weathering. Rather than a probabilistic approach, we use a reaction-diffusion system to produce decay phenomena on multiple texture and mesh layers. As nutrients diminish, mold growth stops. This would be difficult to recreate with γ -ton tracing. Turk [Tur91] and Witkin and Kass [WK91] proposed using reaction-diffusion for texture synthesis. Reaction-diffusion textures come from a biochemically inspired set of partial differential equations. This non-linear interaction process creates natural patterns, such as stripes and spots. In our approach, we also use a reaction-diffusion model, but apply this mathematical approach to complex biological processes, such as growth of fungus and bacteria, colony formation, and soft rot. Fungal colonies diffuse radially, interacting with each other and the nutrients on the fruit surface. The decay

affects both the surface and internal substrate of the fruit. Our model parameters for decaying fruit are biologically-derived and present a novel visual simulation method that has not been covered in previous approaches.

Several researchers have attempted physically-based simulation methods to automate the creation of realistic aging and imperfections. Dorsey and Hanrahan [DH96] modeled and rendered a metallic patina. This work showed the patination process heavily depends on environmental factors. They integrated these parameters into their phenomenological model to produce a variety of results. Several other corrosion models have been proposed that extend this work to more general conditions [CS00, MDG01]. Hsu and Wong [HW95] integrated surface properties such as inclination and stickiness to simulate dust accumulation. Paquette and Dretakis [PPD02] simulated paint cracking and peeling and surface aging by impacts [PPD01]. Bosch and his colleagues [BPMG04] simulated the formation of scratches and rendered their visual behavior. Cracks and fractures play an important role in aging solid structures [DGA05, GC01]. Other researchers proposed methods to simulate appearance-changing flows [DPH96], to weathered stone [DEJ*99], and to perform multiple weathering effects on fur [JW09].

Data-driven simulation techniques rely on carefully captured images and measurements to produce time-varying surface imperfections. Wang et al. [WTL*06] use a single image to construct an appearance manifold and Xue et al. [XWT*08] improve the transfer of weathering from the manifold between images. Our work differs from the appearance manifold approach since fruit decays in complex stages. One image will not capture the dynamics of the entire decay. Our technique models multiple types of appearance change on the surface and alters the underlying geometry. Lu et al. [LGG*07] captured and transferred weathering effects from real to synthetic shapes using a context aware texturing approach. Gu et al. [GTR*06] acquired a database of time-varying images using a multi-camera/light device. Their work looked at apples and banana skin captures. However, their approach simulates only the visual effect of the fruits' aging over time and not the biological factors behind the process. In addition, a data-driven approach for simulating decay is not practical given the numerous significant parameters (including the geometric context), and the challenges and time investment in acquiring the data. Fruit decays over the course of multiple weeks.

Biologically-inspired techniques attempt to simulate natural scenery. Yin and his colleagues [YFCT08] proposed a model for wood aging based on biological deterioration. Boissieux et al. [BKMTK00] simulated skin aging and wrinkles based on insight from cosmetics. Also, lichen [DGA04] and moss [OMC03] growth create realistic outdoor worlds.

Figure 2: Photographs of real fruit decay. (a) *Penicillium digitatum* formation on an orange. (b) *Neofabraea* formation on an apple. (c) *Rhizopus* formation on a tomato. (d)-(f) Time lapse of fungal growth on the bottom point of contact between a tomato and a glass platform.

1.2. Overview

The remainder of the paper is organized as follows: First, we describe the biological basis of fruit senescence and decay. Second, we describe our fruit decay pipeline and provide details for the mathematical model for our simulation. Finally, we present our results and describe how our method can be generalized by our user interface.

2. Biological Background of Fruit Decay

Decay is an essential step in the reproductive process of fruiting plants - the decomposition of flesh frees and feeds the seeds of the fruit to grow into a new plant. While disease can strike a fruit at any stage of life, fruit naturally becomes more vulnerable to disease over time. We exclusively investigate post-harvest rot in a typical home environment. Food scientists and biologists recognize fruit decay as a serious problem in the shipping and storage of produce. The short ripening and post-harvest life-cycle of fruit influences their value.

Prasanna et al. [PPT07] and Pech et al. [PBL08] studied factors in the fruit ripening process. Numerical approaches were developed to predict morphological patterns of bacterial colonies [MM93, OMM92]. Post-harvest disease is typically initiated when a point on the fruit's surface is compromised, either due to injury or structural vulnerabilities. One major wound is the stem puncture where the fruit was picked. Once an initial infectious agent like bacteria has attacked, it further weakens the surface and leaves it susceptible to infection by other organisms. This is the reason that mold often forms in areas already infiltrated by bacteria. The soft rot serves as an entry point for fungal spores.

Fungal Growth. Various reaction-diffusion processes have been proposed to better predict fungal growth based on a variety of parameters [MGL93, ESRA10, IM09]. Bacteria and fungi thrive on the nutrient-rich surface of a ripened fruit. However, nutrient levels deplete over time as colonies use up resources, slowing down the growth process. Environmental factors such as temperature and humidity greatly affect mold and bacterial growth [Blo53]. Warmer temperatures lead to more rapid proliferation, while colder temperatures retard growth. Our model incorporates the interaction between these different factors to determine the concentration of bacteria and fungi at each point on the fruit surface.

Mold. Various types of mold affect fruit. Andersen and Frisvad [AF04] showed *Penicillium* and *Rhizopus* were two species present in moldy tomatoes. *Rhizopus* is a white thread-like *Mucoralean* mold that infects tomatoes. *Erwinia carotovora* is a type of soft rot that affects the internal substrate, making the fruit collapse in the infected regions. The species of mold that most commonly attacks apples is *Penicillium expansum*. Apples are also often infected by the organism *Neofabraea*, which causes a soft spot. This infected region appears as a growing and darkening brown spot on the surface. *Penicillium digitatum* primarily affects oranges. These colonies have a gray-blue center and are white along the edges.

Figure 2 provides three photographed examples of *Penicillium digitatum*, *Penicillium expansum*, and *Rhizopus* mold on an orange, apple and tomato. Additionally, Figure 2 shows three time lapse images of a tomato photographed from the bottom through a piece of glass. Mold starts to form at the points of contact with the glass. This occurs because the flesh weakens under the pressure of the weight of the fruit, providing entry points for pathological agents.

Fruit	Food Weight (g)	Water Weight (g)	% Water	K
Apple	138	116	84	0.17
Orange	140	122	87	8.48
Peach	87	76	88	14.1
Pear	166	139	84	0.68
Tomato	123	115	94	0.9

Table 1: This table provides the weight, water content, and the transpiration coefficient rates (K) for several fruits. [BH94, CRBG88].

Transpiration. Fruits have high water content in proportion to their weight [BH94, HD97, PUTV04]. Table 1 relates the weight of the fruit to the water content. Moisture loss due to transpiration is a major factor in fruit decay and is one of the main factors that drive changes in the internal structure [CG85, SB83, CRBG88, LBG00]. As water continuously transpires from a fruit, it loses mass and shrinks. The rate of this process largely depends on the structure and the properties of the fruit skin. Certain fruit skins are porous, while others are less permeable. A fruit exhibits a hydrostatic pres-

Figure 3: The system framework highlighting the important steps in our fruit decay pipeline. The user provides the input mesh and parameters to the system. Our model calculates the growth and decay and then renders the final image.

sure as it sits. Transpiration also depends on the physical environment. Temperature and water vapor pressure, as well as the size and shape of the fruit, are accounted for when calculating transpiration rate. Our model utilizes transpiration as the main factor for internal volume loss.

Factors not discussed. Fruit decay is a complex natural phenomenon that is driven by innumerable conditions in addition to those we have discussed. We do not consider elements such as nutrient deficiency or poor fertilization while growing. Our mathematical model can be generalized to different types of fruits and infectious agents based on the input parameterization.

3. Fruit Senescence and Decay Pipeline

In this section, we provide details about our model structure and a set of parameters to generalize the decay process. Figure 3 shows the pipeline of our simulation using the plug-in tool we created. First, the user sets both the skin and internal substrate meshes. Next, the user either selects fruit, mold, and environmental presets, or sets custom values for each parameter. These input parameters drive the reaction-diffusion and transpiration mathematical models described in detail below. We use a cloth-like simulation as the external skin model. Then, the user selects contact points, which will serve as initial seed points for the bacterial *soft rot map*. Finally, the user runs the simulation. The program output includes a series of maps representing distributions of *fungus*, *bacteria*, and *nutrients* for each frame of the simulation. It also includes a vertex cache which is automatically applied to the internal substrate mesh. The alpha maps shade the different layers of the fruit-fresh surface, bacterial soft rot, and mold. We will describe our particular rendering approach later.

3.1. Maps

The results of the reaction diffusion processes that drive the surface component of our simulation are visualized as a sequence of time-varying *maps*. Our maps range X between $[0 \dots 1]$, with white representing a maximum density of 1, and black representing a density of 0. We use three different map sequences: the *nutrient map*, the *fungus map*, and the *soft rot map*. The *nutrient map* represents the distribution of nutrients over the surface of the fruit, and serves as a distribution map for fungal growth. We show in Figure 4 (a) how the nutrients deplete over time as the active fungus grows. Next,

the *fungus maps* track the areas of fungal colony formation. These grow over time based on our reaction-diffusion model. The *soft rot map* represents the areas of bacterial growth that form on fruit. This map serves as a probability map for the propagation of new fungal colonies. Mold grows primarily on areas that have already been infected by the bacteria. A new set of maps is generated and stored at each frame. For our implementation, the maps were sized at 512×512 pixels.

3.2. Internal Volume

The volume of the fruit is modeled as a deformable object. The shape and volume of this mesocarp changes based on the forces of rot and transpiration derived from our mathematical model. We use a mass-spring system that utilizes a set of point masses connected by elastic links. Each mass node corresponds to a specific vertex of the object. Initial spring constants are determined by the user-defined firmness parameter ($K_s = \text{firmness}$), which varies across different fruits. For example, tomatoes have high water content and are softer than apples. The spring constants and resting lengths ($rLen$) are governed by a *pressure map*, which may change at every time-step.

As the *soft rot map* changes the outer appearance from the reaction-diffusion growth, springs at the same locations in the *pressure map* decrease in stiffness and length, affecting the internal volume. This represents areas of soft bacterial rot where the fruit is softer. Therefore certain areas may collapse faster based on the level of infection. At each time step of the simulation, spring constants and resting lengths are decreased at a rate proportional to water content and the calculated transpiration rate.

Transpiration coefficients for various common fruit types, including those that we used in our simulation, are given in Table 1. The volume is proportional to the cube of the spring resting lengths. Since we know the proportion of the fruit's volume, which is water (*waterContent*), and the rate at which water volume is lost (*tRate*), the percent total volume we would want the fruit to lose at each time-step is: $tRate \cdot \text{waterContent} \cdot \text{volume}$. Therefore, change in resting length at each time step is given in equation 1:

$$\Delta rLen = -c \cdot rLen \cdot \sqrt[3]{tRate \cdot \text{waterContent}} \quad (1)$$

Where c is a weighting factor. In addition, we wanted the springs to lose tightness over time to reflect the softening that

Figure 4: Results of the final maps: Values range between $\{0 \dots 1\}$ for the phenomenon concentration values. These processes change the physical properties of the surface and internal volume substrate. (a) Shows nutrient depletion, (b) Fungal colony growth, (c) Soft rot spread, (d) Final rendered frames.

occurs due to water loss and decrease in structural integrity of the internal fibers. The change in K_s at each time-step is given by: $\Delta_{ks} = c \cdot \text{waterContent} \cdot tRate \cdot K_s$, where c is a weighting factor.

3.3. External Skin

We found that the dynamic properties of fruit skin can be modeled in much the same way as cloth. First, we bound the skin to the internal volume mesh with point constraints. As the internal mesh started to collapse, it naturally produced the effects that occur during decay, such as wrinkling and shriveling. The simulation parameters of the cloth were determined by user-defined thickness (S_t). See Table 2 for our settings. The fruit skin layer was simulated using the *nCloth* cloth solver in Maya.

3.4. Presets and Parameters

We provide a set of fruit, mold, and environmental presets and parameters to effect the decay of fruit in our simulation. Fruit presets include tomato, orange and apple. Environment presets include tropical, cold desert, hot desert, and temperate climates.

To generalize the simulation, our custom parameters allow a variety of effects to be created. Surface parameters

	Apple	Orange	Tomato
Porosity	25	60	40
Thickness (S_t)	30	60	20
Firmness	80	40	50
Growth Rate	20	50	75
Propagation rate	5	3	1

Table 2: This table provides the input parameters for the different fruits in our results. The temperature was set to 72 degrees and humidity to 50%.

include the thickness and porosity of the exocarp. Internal parameters include water content, transpiration coefficient and firmness. Table 1 provided values for only fruit types found in our examples. Many researchers have conducted studies to accurately determine these values for other types of fruit [BH94, CRBG88]. Mold parameters, such as growth rate, propagation rate, and color allow for different mold growth patterns. Table 3 provides our preset parameters. Ito and Mizuno [IM09] specify other growth settings for more mold types. Environmental factors, such as temperature and humidity, also influence the simulation. Lastly, we allow the user to specify initial areas of rot by selecting vertices on the input mesh. By default, the simulation begins to rot at the points of contact with other surfaces and at the stem. How-

ever, a user can specify new wound points on the *pressure map* as desired, to get "directable" simulations.

Figure 5: A composite image of a cross-section view of our fruit's anatomy. (Right) shows a final rendered frame. (Left) shows the skin and deformable body of our substrate.

3.5. Rendering

In order to give our fruits a realistic look and feel, we modeled and rendered our results in Autodesk Maya 2010. The color and polygonal structure of each fruit were empirically derived by observing and photographing real fruit (Figure 2). However, a more complex capture process [GTR*06] can also be used. We used sub-surface scattering shaders to create the effect of translucency in the fruit flesh, and modified specularly and color to match the captured image data. We used a layered shading system, applying the map sequence acquired from our simulation as alpha maps for the decay layers. The fruit color changes based on the maps. We colored the soft rot layer brown and decreased specularly, and used the fungal map as a length and baldness map for *Maya Fur* to simulate hair-like mold fibers. Our results were rendered with Mental Ray for Maya.

4. Simulation Framework

We simulate both fungal colony and mold growth on the exocarp, and soft rot formation and transpiration on the mesocarp. We present mathematical models that tie together these time-varying biological processes on the multiple layers.

4.1. Implementation Overview

We utilize numerical reaction-diffusion equations to form fungal and bacterial colonies, and a transpiration model to drive the volume collapse. These calculations affect the underlying maps and substrate meshes as the fruit decays. Since the soft rot, nutrient, and fungal maps interact, we simulate all three processes, the internal deformable body, skin, and output the maps simultaneously.

The following actions are performed at each time step:

Step 1. We spawn new colonies in the *fungal* and *soft rot maps* to simulate the effect of individual cells spreading from the existing mold or bacterial colonies and taking root in nearby areas of the fruit's surface. For each existing colony, we create a seed point in a randomly selected

location within some radius r with a probability given by $1/(10 - \text{propagationRate})$, with *propagationRate*'s range between $[0 \dots 9]$.

Step 2. We form additional new colonies in the *fungal map* in areas of the surface affected by bacterial soft rot. The *soft rot map* serves as a probability map, with more concentrated areas of bacteria containing higher probabilities of spawning a new colony.

Step 3. We calculate the reaction diffusion step. The *fungal* and *bacterial maps* follow similar reaction diffusion processes, with differences in equation parameters, while the nutrient map undergoes a separate nutrient diffusion process.

a) The fungal and bacterial concentrations at each cell (corresponding to a pixel on the map) are calculated from known concentrations at the previous time step and based on Equation 2, where u is the active fungal density at the cell in the previous time step.

b) The diffusion term is determined as an average of the immediate neighboring cells, each with a contribution given by Equation 4 and offset by a stochastic element determined by Equation 5 to represent random movement.

c) The reaction term is computed in Equation 7 based on density at the corresponding cell in the nutrient map during the previous time step.

d) We calculate the nutrient reaction-diffusion process, which is defined in Equation 9.

e) We update the maps by writing the new concentration values at each *fungal*, *rot*, and *nutrient* cells.

Step 4. We integrate the deformable body at each time step using the explicit fourth order Runge-Kutta scheme. A time step size of 6 milliseconds was found to be sufficiently small to guarantee numerical stability, although for more complex polygonal meshes, an implicit scheme may be preferred.

4.2. Algorithm Details

Fungal and Bacterial Growth. Multiple researchers have modeled fungal proliferation and morphological colony formation based on a non-linear reaction-diffusion process [MGL93, ESRA10, IM09]. In our model, the fungus is separated into two states, active and inactive. As active fungi grow and proliferate, they deplete the underlying nutrient concentration defined in our *nutrient map*. As values in the *nutrient map* approach 0, the fungi at that point become inactive and cease to spread. We calculate the concentration of both active and inactive fungi by the following reaction-diffusion equations describing the fungal movement:

$$\frac{\delta u}{\delta t} = \nabla \cdot (D_c \nabla u) + \theta f(u, n) - a(u, n)u \quad (2)$$

$$\frac{\delta v}{\delta t} = a(u, n)u \quad (3)$$

Equation 2 provides the diffusion term which governs the non-linear growth at time t . Equation 3 is the reaction term which depends on the nutrient concentration n , fungal density, and environment parameters. $(u + v)$ is the total density of the active u and inactive v fungus. The motility of active fungus is expressed by the diffusion coefficient D_c , which is defined by the logistic Equation 4. $d_1, d_2 > 0$ are model parameters and σ_1 is a scaling parameter. An additional scaling parameter $s = porosity + temp + humidity + waterContent$ produces the growth rate difference between the soft rot and fungal colonies, and between different species of fungus. This parameter is determined by the user through the interface tool. A stochastic element, σ'_1 , adds random movement to the diffusion coefficient in Equation 5.

$$D_c = s \cdot \sigma'_1 \cdot d_1 u \left(1 - \frac{u}{d_2}\right) \cdot n \quad (4)$$

$$\sigma'_1 = \sigma_1(1 + \delta), \quad -0.5 < \delta < 0.5 \quad (5)$$

Fungal growth depends heavily on the physical environment. Relative humidity ϕ and temperature T dampen $D_{damp} = norm(T + phi)$ the diffusion coefficient D_c expressed in Equation 6.

$$D_{c(u,n,T,\phi)} = D_c \cdot D_{damp} \quad (6)$$

We then use a Michaelis-Menten kinetic function (Equation 7) to model the reaction kinetics of enzymes. In Equation 2, $f(n, u)$ describes the consumption of nutrients by the active fungus u . Here θ is the constant rate in which fungal proliferation connects to nutrient consumption. f_1, f_2 are model parameters and σ_2 is a scaling parameter.

$$f(u, n) = \sigma_2 \left(\frac{f_1 n}{1 + f_2 n} \right) \cdot u \quad (7)$$

Equation 2 transforms active fungus u to inactive fungus v . Here we used Mimura's formula (Equation 8). Active fungus normally diffuses along the border while inactive fungus resides in the center. Once again, a_1, a_2 are model parameters and σ_3 is a scaling parameter.

$$a(u, n) = \sigma_3 \cdot \frac{1}{\left(1 + \frac{u}{a_1}\right) \cdot \left(1 + \frac{n}{a_2}\right)} \quad (8)$$

We model the spread of bacterial colonies using the same formula. The bacterial *soft rot map* guides the propagation of fungal colonies. The fungi cannot propagate into areas unaffected by bacteria, thus reflecting the notion that the growth of certain organisms on the surface depends on existing infection.

Nutrients exist in a non-uniform random distribution on the surface and substrate of the fruit. This is the main factor for fungal growth in our model. Nutrients deplete and do not allow fungus to remain active indefinitely. Nutrient transport is defined by Equation 9. The nutrients are diffused by the term $D_n \nabla^2 n$ and consumed by $f(u, n)$. D_n is the nutrient diffusion coefficient.

$$\frac{\delta n}{\delta t} = D_n \nabla^2 n - f(u, n) \quad (9)$$

Table 3 provides the initial model parameters of our simulation. These parameters change the growth rate and nutrient depletion. This process is further affected by water vapor pressure, humidity and temperature. Our system provides default parameters for the most popular types of mold growth. However, our simulation method below can generalize to different mold types by manipulating the input parameters.

Model Parameters		
$\sigma_1 = 0.01,$	$d_1 = d_2 = 0.01,$	$n_0 = 1.0$
$\sigma_2 = 5.0,$	$f_1 = f_2 = 1.0,$	$\theta = 0.05$
$\sigma_3 = 5.0,$	$a_1 = 1/2400,$	$a_2 = 1/120$
$u_0 = 1.0,$	$v_0 = 0.0,$	$D_n = 0.000001$

Table 3: This table provides the biologically inspired parameters [IM09] for our reaction-diffusion mathematical model.

Transpiration. The transpiration rate of fruit plays a considerable role in the water balance and weight during decay. Equation 10 expresses the typical transpiration rate m . Here K is the overall mass transfer coefficient. Table 1 provided values for the various fruit types found in our examples. (Depending on various characteristics of each individual fruit, this coefficient varies slightly sample by sample.) A is the surface area of the fruit. P_s is the water vapor pressure at the evaporating area surface. P_a is the water vapor pressure of the surrounding atmosphere.

$$m = KA(P_s - P_a) \quad (10)$$

The water vapor pressure P_s is calculated by $V_p \cdot P_{sat}(T_s)$ [CG85]. Here P_{sat} is the saturation vapor pressure of water, T_s is the surface temperature and V_p is the vapor pressure set as either 0.98 or 0.99. T is the atmospheric temperature. P_s is P_{sat} 's steam point pressure. A good estimate of the saturation of water vapor pressure at a given temperature can be acquired using the Goff-Gratch equation.

$$\begin{aligned} \log P_{sat} &= -7.90298 \cdot (T_s/T - 1) \\ &+ 5.03808 \cdot \log(T_s/T) \\ &- 1.3816 \cdot 10^{-7} \cdot (10^{11.344(1-T/T_s)} - 1) \\ &+ 0.0081328 \cdot (10^{-3.49(T_s/T-1)} - 1) \\ &+ \log P_s \end{aligned} \quad (11)$$

5. Results

We simulated our results on a 3.2GHz quad core Xeon processor with 4 GB of memory. The deformable body and fungal growth codes were written in C++. Each time-step averaged around 10 seconds to compute the reaction-diffusion, transpiration, and deformable collapse, and to write the texture maps. Applying the vertex cache data generated by the deformable body simulation to the user-defined mesh took

Figure 6: A comparison of real photographs (right), and our simulation results (left) of a tomato and orange.

1.5 seconds per frame. Rendering time was approximately 10 minutes per frame with our scene lighting.

In this paper, we have provided final renders for three types of fruit: an apple, an orange, and a tomato. We demonstrate that we can simulate a variety of fruits and fungi. Figure 9 shows a final rendered sequence of an orange and tomato. Figure 4 displays the apple sequence.

Figure 7: A screen shot of our user interface tool in Autodesk's Maya. Our plug-in tool allows users to choose presets and parameterize the simulation to generalize output. The user imported her own geometry and is currently displaying the nutrient map on the object.

5.1. User Interface Tool

We have designed and developed an authoring tool that integrates our simulation into a plug-in to Autodesk Maya 2010. Our user-interface is scripted in MEL and uses the Maya plug-in API to develop features to allow the user to create and parameterize our simulation. Figure 7 shows the various features our tool provides the user. The designer selects meshes to use, and customizes the simulation. The user may also visualize the various *fungus*, *soft rot*, and *nutrient maps* on the mesh using the button on the top of the tool. Additionally, the user may select *pressure points* that allow new

fungus to begin to grow and the fruit to begin collapse on directed input.

5.2. True Life Comparison

In Figure 6 we compare our final rendered frames to real photographs. We demonstrate that our method produces similar effects. A key feature of our system is that the biologically derived models simulate perceptually equivalent and indistinguishable results. Every individual piece of fruit has its own unique decay since it will have some random variation and growth. However, our simulation produces similar decay patterns to the real data.

Figure 8: Here we simulate a group of fruit. Mold begins to form at the main contact areas where the oranges are grouped.

5.3. Multiple Fruit

We have demonstrated our simulation on a group of oranges. Figure 8 shows a final rendered result. In this example, there are more contact points between the multiple pieces of fruit. These contact points provide more pressure to the fruit skin causing wounds and locally high humidity. When a fruit becomes damaged, fungus begins to appear at these locations due to the increase in nutrient concentration. Since our simulation is parameterized on pressure points, it was straightforward to show the results of mutual contacts among the grouped fruits, demonstrating the full power of our method.

6. Conclusions

We describe a system for simulating fruit senescence and decay. Our approach is perceptually similar to real photographs and time-lapse videos. The system takes advantage of a biologically-derived reaction-diffusion model to create growth patterns for areas of fungal and bacterial infection. We simulate interactions between multiple phenomena acting on both the surface and internal substrate. Additionally, we provide presets and parameters that allow a user to simulate a variety of novel effects. We demonstrate our method on three fruits: an apple, orange, and tomato. To demonstrate our method's generalization to any user-defined object, we

imported a unique mesh into our user interface and simulated the decay processes based on user parameterization. Our model simulates a complex class of time-varying aging effects. In utilizing common production tools to render our images, we show that our final product has straightforward industry applications in movie and production pipelines that require images or animations of decomposing fruit.

Though our model attempts to create a wide range of effects, it still does not demonstrate every single process. We do not consider factors such as calcium deficiency, infection while on the vine, and poor fertilization. Nor do we consider if the fruit was sliced, and we also do not take into account any liquid phase losses from the fruit. Certain fruits, when wounded, tend to leak volume from a tear in the surface as they decay. Lastly, we do not consider the effects of macroscopic organisms such as worms or flies.

In the future, we wish to extend our model to other growth and decay time-varying phenomena. Adding even more complex wrinkling and color changes are easy extensions to our model. Additionally, we wish to look at ways to develop our simulation to cooking and roasting food. Another possible extension would be to use real input photographs and movies to seed the simulation.

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Figure 9: Simulation results of a tomato and an orange under three different parameter settings set by three users from our user interface. Simulation (a) and (b) set two different pressure points and produce different results. (c) changes parameters in the mold growth to simulate different growth rates.

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