Withering Fruits: Vegetable Matter Decay and Fungus Growth

Bianca Cirdei
The National Centre for Computer Animation
Bournemouth University
cirdei.bianca@gmail.com

Eike Falk Anderson
The National Centre for Computer Animation
Bournemouth University
eikea@siggraph.org

Figure 1: Rendered results of the simulation, showing an apple decaying over time (*without fungus spores*).

ABSTRACT

We propose a parametrised method for recreating drying and decaying vegetable matter from the fruits category, taking into account the biological characteristics of the decaying fruit. The simulation addresses three main phenomena: mould propagation, volume shrinking and fungus growth on the fruit's surface. The spread of decay is achieved using a *Reaction-Diffusion* method, a *Finite Element Method* is used for shrinking and wrinkling of the fruit shell, while the spread of the fruit's fungal infection is described by a *Diffusion Limited Aggregation* algorithm. We extend existing fruit decay approaches, improving the shrinking behaviour of decaying fruits and adding independent fungal growth. Our approach integrates a user interface for artist directability and fine control of the simulation parameters.

CCS CONCEPTS

• **Computing methodologies → Physical simulation**; **Point-based models**; *Simulation tools*;

KEYWORDS

Decay, Mould, Simulation, Natural Phenomena

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1 INTRODUCTION

Withering of fruits involves a series of physical, chemical and biological changes that occur due to dehydration. During this process, transpiration causes the core of the fruit to lose water, causing the volume of the fruit to shrink and the fruit shell to wrinkle. As the fruit's nutrient levels deplete, mould spreads on its shell. Fungus growth develops, feeding from the fruit's transpiration. There exist a number of different approaches to simulating vegetable matter decay, each focussing on different aspects of this complex phenomenon. Kider et al. [2011] present a physically-based approach to recreating decay that simulates volume and shell shrinking with mould and fungus spread on the fruit's surface. Liu et al. [2012] apply a Finite Element Method (FEM) taking into account moisture content to calculate decay spread, volume shrinkage and skin deformation. Here we propose methods that combine and extend existing approaches to achieve more realistic and convincing results.

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2 OUR APPROACH

2.1 Overview

Our simulation uses an apple (Fig. 1) in a home environment (post-harvest), visualising its biological changes as it decays. The simulation's parameters are derived from the biological and physical properties of real apples.

The most common type of post-harvest apple moulds are *Penicillium expansum* (*Blue Mould*) and *Botrytis cinerea* (*Gray Mould*), which are simulated by our implementation. In terms of morphology, mould is a fungus which survives by decomposing and absorbing the organic matter on which it develops [Parrott 2009]. High relative humidity (70%-90%) causes mould germination and assures survival of mould colonies, recognisable by colour changes of the fruit's shell. The next most important factor for mould growth is temperature (30^{o}C being optimal). Internal structure changes are caused by transpiration, which is influenced over time by changing (increasing) porosity. Mould developing on the fruit feeds from its nutrients and water, causing volume shrinking. Fungus starts developing on the shell. Its growth is nutrient dependent and as the nutrient levels drop over time, its expansion ceases.

Our decay pipeline is split in three main categories, each customisable with an artist-friendly UI (Fig. 2): surface mould with

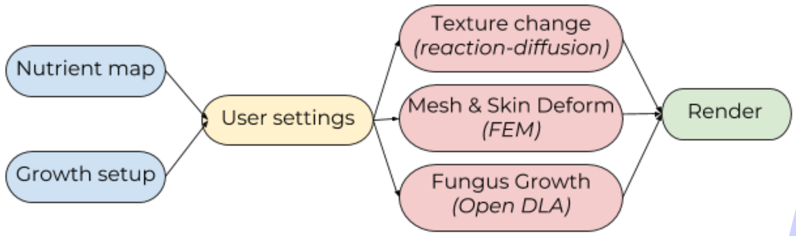

Figure 2: Decay pipeline structure, showing the correlation of different components of the simulation.

colour change, internal volume deformation with skin wrinkling and fungus growth.

2.2 Mould Development

Perlin Noise is used to determine the nutrient spread on the fruit's shell, which is controlled by the user. Mould spread is computed using the reaction-diffusion model described in equations 1 and 2 below. The computation results in a nutrient (alpha) map that changes the colour of the surface texture. The mould feeds on the nutrient, and according to the resulting values, fungus growth develops on the surface (until the nutrient values drop to ≈ 0).

$$\frac{\delta u}{\delta t} = \nabla \cdot (D_c \nabla u) + \theta f(u,n) - a(u.n)u \tag{1}$$

$$\frac{\delta v}{\delta t} = a(u,n)u \tag{2}$$

Equation (1) shows the diffusion equation, while (2) is the reaction equation. The sum $u + v$ represents the total mould quantity at each point of the fruit mesh, and n is the corresponding nutrient level. D_c is a diffusion coefficient, a(u,n) describes the reaction kinetics of enzymes resulting from the Michaelis-Menten kinetic function [Hegyi G. 2013] and f(u,n) is the nutrient depletion after every timestep.

2.3 Volume Shrinking

Shrinking forces are applied to a lower resolution proxy model according to the nutrient map resulting from the above reaction-diffusion calculations. Each point holds the physical parameters of the mould growth that are fed to the shrinking solver which evaluates the forces. Shrinking speed and behaviour are determined by the nutrient values, the biological parameters and the user defined timestep. In order to obtain high resolution detail of the wrinkling shell, instead of the more commonly used cloth solver a FEM simulation is developed to replicate thin organic tissue. The FEM solver uses the point deformation from the shrinking volume, adding wrinkle detail between the points. Fig. 3 shows some of the results obtained.

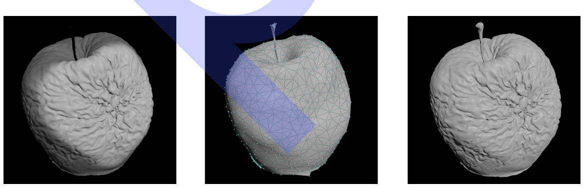

Figure 3: (Left to right) Nutrient alpha, low and high resolution deformed mesh.

2.4 Fungus Creation – *Work in Progress*

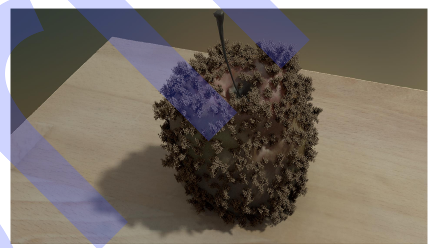

Figure 4: Fungus render – early result.

The most appropriate method for *Gray* and *Blue Mould* growth simulation is the Open Diffusion Limited Aggregation (Open DLA) Lichen growth algorithm proposed by Desbenoit et al. [2004], which was adapted to take mould seed points and create long branching filaments of multicellular aggregates (Fig. 4) emulating mould growth. This aggregation is based on nutrient levels of the fruit mesh and continues until nutrient levels deplete to ≈ 0.

3 CONCLUSIONS

This work combines and expands current techniques of decay simulation by integrating new interior volume forces to a decay model based on biological parameters (reaction diffusion and FEM), adding a point growth method for fungus expansion (Open DLA) with an extended dependency on decay state and shrinking forces. We have presented improvements to existing visual/artistic and technical methods, our approach creating high fidelity believable results.

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