

Utah State University

DigitalCommons@USU

Fall Student Research Symposium 2021

Fall Student Research Symposium

12-9-2021

A Computational Model of Angiogenesis in Wet Age-Related Macular Degeneration

Brandon Pace

Utah State University, a01818577@usu.edu

Follow this and additional works at: <https://digitalcommons.usu.edu/fsrs2021>



Part of the [Engineering Commons](#)

Recommended Citation

Pace, Brandon, "A Computational Model of Angiogenesis in Wet Age-Related Macular Degeneration" (2021). *Fall Student Research Symposium 2021*. 41.

<https://digitalcommons.usu.edu/fsrs2021/41>

This Book is brought to you for free and open access by the Fall Student Research Symposium at DigitalCommons@USU. It has been accepted for inclusion in Fall Student Research Symposium 2021 by an authorized administrator of DigitalCommons@USU. For more information, please contact digitalcommons@usu.edu.



Computer models can help us learn more about progressive eye diseases



Brandon Pace
Utah State University
Kelsey Bradshaw
Utah State University
Dr. Zhen Zhang
Utah State University
Dr. Elizabeth Vargis
Utah State University

Introduction

By age 80, 1 in every 4 Americans will suffer partial blindness because of age-related macular degeneration (AMD). There is no cure, and treatments to halt the progression consist of biweekly eye injections.

Little is known about AMD due to limitations in lab models on long-term diseases. Simulating proteins and progression with computers can help us learn and test ideas effectively.

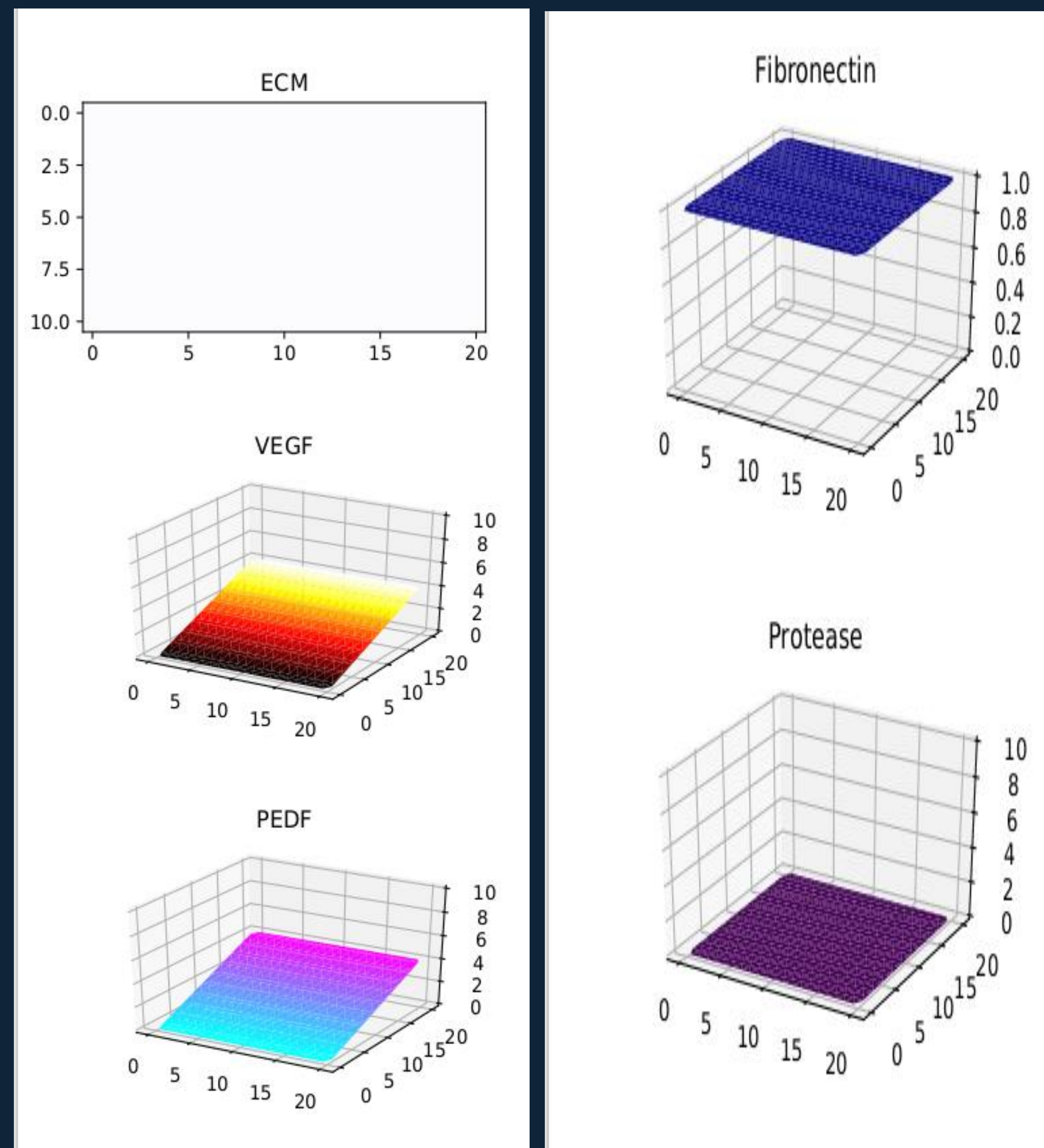
Methods

Wet AMD is enhanced by capillary growth in the back of the eye.

This computer model tests various protein expressions which can be from healthy or diseased cells.

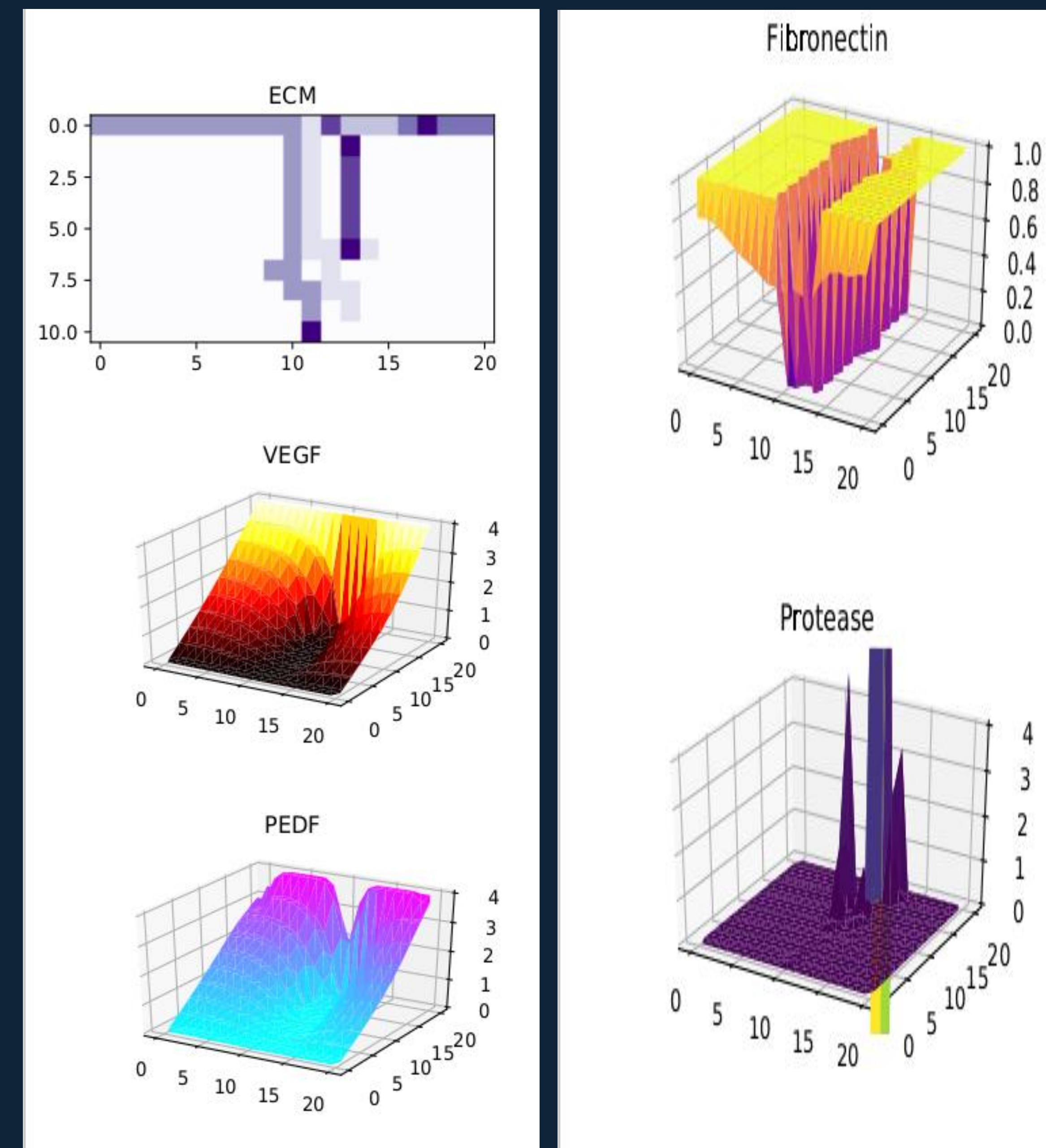
Observing the blood vessel growth that occurs over time can give us insight into how differences in protein expression affects AMD.

A computational model of angiogenesis in wet age-related macular degeneration



ECM: Extracellular matrix, your eye
VEGF: A protein that causes capillary growth
PEDF: A protein that is believed to inhibit capillary growth
Fibronectin: The main protein in the ECM
Protease: An enzyme that destroys fibronectin

This model compares a healthy simulation, where **PEDF** and **VEGF** are expressed in equal amounts, to a diseased simulation, when **PEDF** decays over the course of 48 hours.



Results

Simulations show that when PEDF and VEGF expression remain equal, no capillary growth is present.

As PEDF expression decays over time, capillaries grow from the parent vessel towards the source.

Important outputs such as velocities, direction, and time can be examined to greater understand disease progression over time

```
Data_Outputs - Notepad
File Edit Format View Help
Cell Number: 0
Directness: 0.48534065928536785
Accumulated Distance (um): 15.0
Accumulated Velocity (um/min): 0.05421686746987951
Euclidian Distance (um): 7.280109889280518
Euclidian Velocity (um/min): 0.02631365020221874
Time (min): 276.6666666666667

Cell Number: 2
Directness: 0.7546154281781181
Accumulated Distance (um): 12.000000000000002
Accumulated Velocity (um/min): 0.04164738546968996
Euclidian Distance (um): 9.055385138137417
Euclidian Velocity (um/min): 0.03142775961870922
Time (min): 288.1333333333333

Cell Number: 4
Directness: 1.0
Accumulated Distance (um): 4.0
Accumulated Velocity (um/min): 0.013850415512465374
Euclidian Distance (um): 4.0
Euclidian Velocity (um/min): 0.013850415512465374
Time (min): 288.8
```

The above image shows important outputs, such as velocities, for blood vessel growth

Stochastic Simulation

An important part of this simulation is that it is a probabilistic model. Equations are used to generate probabilities in movement to help represent the randomness found in biology

Extra results

Advancements in this model will include treatments to test effectiveness in preventing AMD

