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In class activity (Individual with group): Evaluate your model (due end of class 9/27)
Questions to discuss during group rotation meetings. For these meetings focus on HOW and WHY you solved and programmed the problem the way you did.
1. What are different assumptions that you made about the physical properties of the system? Did you use different data? How would these differences impact the model?
<p>Notes:</p> <p>First Group:</p> <ul style="list-style-type: none">• My group and I used the Choi-Okos equation to calculate the thermodynamic properties of our food item.• The non-team members looked up thermodynamic properties for their product in the literature and used them.• They feel that this may be better since the properties are found and not estimated.• Everyone assumed that we had an infinite cylinder, that is, that heat transfer only occurred in one direction – radially.• My group ended up not considering convection at the edge of the can during cooling since the equation was not behaving well in MATLAB• For reduction of bacteria, we used the “worst-case-scenario” values (high D250 and Low Ea). While for the vitamins, we used the average values. My other team member did not, wanted to also assume worst-case-scenario for the vitamins. <p>Second Group:</p> <ul style="list-style-type: none">• The other group assumed an average temperature in the can and used that to calculate the thermal properties using the Choi-Okos equation.• They used convection at the outside from Geankopolis.• The other team assumed an infinite cylinder, that is, no heat transfer in the z direction.• Assumed huge convection coefficients, both teams did (yoda).• The other team assumed best case scenario• Calvin was concerned with getting the bag and assumed best-case-scenario for vitamins.• They did, however, assume worst case-scenario for the bacteria.• The other group used the integral of $k \cdot dt$ method to calculate the sterilization.

2. Do a line-by-line comparison with the other individuals programming files. How did your programming strategies differ? What advantages do you see in how they did their model? What advantages do you see in your own?

Notes:

First Group:

- My team used Kelvin for the temperature profiles, while they used Fahrenheit
- Everyone used while loops, I was the only one who used a for loop.
- Calculation of vitamin destruction was identical for the microorganisms. We all did them the same way.
- We all assumed a long heating time, and found the time required to get the necessary log reduction of bacteria. We then started the cooling right at that time point and changed the matrices.

Second Group:

- Other group used the for-loop to iterate through the entire finite difference method.
- I should have done it where you can cut off the matrix at the point where the sterilization meets the requirements.
- The other group and I used the same method of re-calculating the heating given the new process time.
- The other group only examined the destruction of Vitamin B1. While my group examined all three vitamins.
- The cooling was calculated using the same process as the heating, rather the ambient temperature was changed for the cooling (the water temperature).
- The other group assumed that the other vitamins (other than B1) would experience a much lower level of degradation relative to the B1, so they did not examine them, and thought that the degradation would be negligible.