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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?** |
| Notes:  Same:   * Convection on the surface, conduction outside * Finite difference * Equations in the Geankoplis, Okos-derived equation * Choi-Okos equations * High d250 and low Ea as discussed in class * Botulism as the target organism   Differences   * Mass-fraction from paper vs. USDA database * Iterating the Choi-Okos equation and using one temperature point * Integration: trapz vs midpoint functions * Deltat: 1 second, 25 seconds * Choosing deltat vs deltar and calculating the other from M * Calculating alpha using other k/rho\*cp * Defining N as a variable * Use d250 vs calculating d(temperature) |
| 1. **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:  For loops vs while loops  Big matrix of every temperature at every time vs. one array of one temperature point every time  Number of layers. 7 - 70  Sub-functions vs. no  Calculating the final time and reduction: for loops, array of sums, trapz, while loop  One vs all microorganisms/vitamins  Changing steam temperature for water temperature  Combined plot of heating and cooling  Number of nodes changes: they used each node, I only used center |