CS172 Requirements Specification

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As mentioned in the proposal, we will be developing a computational model of prion pathogenesis in a neural cell population. This model will be comprised of a collection of cells (each a separate object) into which some initial prion content will be input. Using a combination of statistical mechanical movement of vesicles (prion-filled “bubbles” excreted by cells) and a series of nonlinear ordinary differential equations (which describe the transport of prions between adjacent cells via tubules running between them, along with the spread of prions within an individual cell), this model will compute the spread of prions to what is hopefully a high degree of accuracy.

The software will take in a file containing initial prion counts for each cell, compute the resultant spread using the above described model, and output a file containing the final prion count for each cell.

While the parameters of both the random-walk motion and the differential equations are unknown, later updates to the model will include a system for adjusting these parameters to fit experimental data. This is a relatively minor step, but not worth implementing for this final project as we have no actual experimental data for such parameterization.

UML Diagrams

