Instructions.

1. Clone the Surrogates repository to your desktop. It will create a two folders with data sets and rosters, and a collection of Mathematica files. This must be done on a Windows desktop, and all of the pointers in the Mathematica files assume $HomeDirectory is the desktop. Otherwise, replace, the homeDir assignment (currently homeDir=$HomeDirectory) with homeDir=*folder containing surrogates*.
2. Create a folder SVM on your desktop and download svm-light from http://svmlight.joachims.org/
3. The two folders in SmallHemorrhage are the data used for Sensitivity analysis and primers, respectively. Run1 refers to the SA, and Run2 refers to the primers. Each folder contains the outputs of 2000 models that are imported and processed by the Mathematica files.
4. Data in Denervation is located a single file, as is the collection of parameter vectors.
5. The mathematica files are structure as cells, and the cells are labelled with Figure number it encodes. Not all cells code figures, the background work of the SA, culling, etc. are included for transparency.
6. For questions, email wpruett at umc dot edu