1. **Import & visualize data.**
   1. DataImport.m. This imports the tabularized data regarding the live-tracking of each filopodium at P60 for the different genotypes and saves it to ./AllData.mat. It also generates a number of plots to visualize the live-tracking data. The data is imported into a Data structure of the form Output.<mutant>.<time>.<type>

mutant: 'Atg6' or 'Atg7' or 'Atg6rescue' or ‘Control'

time: 'P60'

type: 'F' or 'sF' (fast filopodia- and slow [long-lived] filopodia)

Example: Output.Control.P60.F contains all data of fast (short-lived) filopodia at P60 for the Control (wildtype).

The following data was stored: 'LTimes' -Lifetimes; 'StartTimes' -when the filopodium emerged; 'EndTimes' -when it disappeared; 'GC' - which growth cone it belongs to.

* 1. DataImportBulbous.m. This imports the tabularized data regarding the live-tracking of each bulbous tip at P60 for the different genotypes and appends it to ./AllData.mat. It also generates a number of plots to visualize the live-tracking data. The data is imported into a Data structure of the form Output.<mutant>.<time>.<type>

mutant: 'Atg6' or 'Atg7' or 'Atg6rescue' or ‘Control'

time: 'P60'

type: ‘Bulb' (Bulbous tip)

Example: Output.Control.P60.Bulb contains all data of fast (short-lived) filopodia at P60 for the Control (wildtype).

The following data was stored: 'LTimes' -Lifetimes; 'StartTimes' -when the bulbous tip emerged; 'EndTimes' -when it disappeared; 'GC' - which growth cone it belongs to. ‘Censored’ – logical value. A true means that the bulbous tip existed before the imaging started, or after it ended (i.e. its actual lifetime could be longer than the imaging time horizon of 60 min) .

1. **Parameter estimation** 
   1. Parameters **c2\_sF, c2\_ellF**: Computed as the inverse of the average life time of short- and long-lived filopodia (which is computed in ‘PrintLifeTimeData.m’).
   2. Parameter **c1\_sF, c1\_ellF**: Can be computed using ‘PlotFiloNumbers.m’: Plots the number distribution of short- and long-lived filopodia and prints them into a LaTeX table (using the accessory function latexTable.m). Parameter c1 (birth rate parameter) is the mean number of (short- or long-) filopodia multiplied by its death rate (c2, above).
   3. Parameters **c4 & c6**: see supplementary methods.
   4. Parameters **B50**, **c5** and **r3(t):** We fitted the auto-inhibition model and its three parameters in the routine `FitFeedbackParameters.m’. The routine fits parameters for both a model without feedback (linear model) and a model with feedback by minimizing the Kullback-Leibler distance between the experimental- and model predicted probability densities of bulbous numbers at P60. Note, that the accessory routine 'PlotBulbousData.m' can be used to print the experimental number distribution of bulbous tips that is used in in this parameter estimation routine. The routine `FitFeedbackParameters.m’ also computes all parameters of Table S2
2. **Model Simulation**
   1. `SimulateGrowthCone.m’ excecutes stochastic simulations of the data-driven Markov Model. Input: mutant specification with possible entries 'Control';'Atg6\_mutant'; 'Atg7\_mutant'; 'Atg6\_rescue'. Saves the simulations into the File './EnsembleData/Simulation\_<mutant>.mat'.
   2. `PlotSimulation.m’ plots the average behavior from the Markov Model simulation, as depicted in Fig. 6d-f.
   3. Parameters of the model are loaded from the File 'AllParameters.mat', which can be generated by calling `writeAllParameters.m’.
3. **Mechanistic Model**
   1. **`**MechanisticModel.m’ simulated the mechanistic model for a given authophagy mutant and stores the results in AllSimulations.mat
   2. **`**PlotMechanisticModel.m’ Loads the simulations results from ‘AllSimulations.mat’ and plots the experimental vs the model-predicted numbers of bulbous tips per growth cone as in Figure 6h