This is the main modeling folder, to be used for generating the final paper analyses

ABC\_rejection\_sampling\_mouse.R

* This is for the “comet” model dynamics
* The output is an array with N columns, where N is the number of samples from the prior. Here N=200,000
* Output is saved, for BT and no-BT dynamics as:
  + ABC\_results/TEB.BT.mix\_01.RData
  + ABC\_results/TEB.noBT.mix\_01.RData

ABC\_rejection\_sampling\_vanilla.R

* This is for the canonical cancer growth model with surface growth
* The output is an array with N columns, where N is the number of samples from the prior
* Here N=205,000
* Output is saved as
  + ABC\_results/ Branch.surface\_01.RData

ABC\_rejection\_sampling\_analysis.R

* Takes in the outputs from the mouse and vanilla rejection sampling scripts
* Calculates the distance between experimental and simulated data
* Output is saved as
  + ABC\_results/ABC\_OUT\_TEB.BT.mix\_01.RData
  + ABC\_results/ABC\_OUT\_TEB.noBT.mix\_01.RData
  + ABC\_results/ABC\_OUT\_Branch.surface\_01.RData

ABC\_rejection\_sampling\_model\_fit.R

* Visualize the model fit by comparing the 15 tumor results against the top percentile of model fits
* Output is a PDF figure <Figure\_4H.pdf>

ABC\_rejection\_sampling\_Model\_Selection.R

* Loads the different models (ABC\_OUT\_TEB.BT.mix\_01.RData etc)
* Calculates Bayes’ factors and visualizes their dependence on cut-offs