Initialization

* Now generates KTPts

Main file

* Adds F\_chr\_chrS(:,i)+F\_chr\_chrB

Into net force on chromosome

* Adds F\_cent\_chrS(:,i)+F\_cent\_chrB

Into net force on centrosome

KTCentMT\_Calc

* Attempted to have binding force if MT end inside kinetochore region, KT points
* Attempted to have binding force if closest point on MT is inside kinetochore region (a,b,slope)
* Now graphed in main file

ChrCentMT\_Calc

* Bind or slipping if in or near chromosome
* ChrCentMTInteractions=zeros(3,n\_MT)… 1st row has prime # factor to know which chromsomes and 2nd row has a 1 if binding, 3rd row has a 1 if slipping

ForceChrSlipCalculation

* F\_cent\_chrS Has overall + sign for slipping forces from chromosome that are added onto the centrosome
* F\_chr\_chrS Has overall – sign for slipping force from chromosome that are added on chromsome

To do list…

* Force file to account for KT forces… add to net force for centrosome and chromosome
* Force file should be similar to bound chr force.
* Might need f0\_chKT and v0\_chKT… set in parameters to be a generic value…