

I want to make sure that the work-loop model I am running is doing what I expect it to do. in the figure above the black trace correspond to Kenneth’s Matlab version and the colored traces are my model. For the blue trace Passive force = F\_titin and for the green trace, Passive\_force = F\_titin+F\_collagen

\*\*\* At the moment 6-6-2017 time: 2:27pm… TmpC in python protocol = 22.5, passive = F\_titin + F\_collagen, ca2+ parameters are set to the original parameters Kenneth sent me (the same ones he uses for his simulations)

Changed SL in RiceTran\_workloop\_cycling\_fixedCai.cellml. it was 2.0 for some reason (?) so I changed it to 2.3



Changing the SL in the RiceTran XB code did not do anything (the red trace in the above image is the same as the green trace in the previous image)

\*\*\* In addition to the previous changes I want to make a note of, I also want to know why the Matlab model ca2+ and My model’s ca2+ do not match up?\*\*\* see image below:



The offset does not seem to be due to tstart value?? So maybe the question should be “Why does the tstart value not work??”

NEXT thing to try: Go back to the model version from the end of February… See what these work-loops look like compared to Kenneth’s matlab version🡪 actually theres no need for this, I have found the problem! (when Kenneth runs his isometric contractions the temperature is 22.5 and when he runs his work-loop contractions the temperature is 23… I was just running my work-loops at 22.5 instead of 23… so when I change the temperature to 23, my work-loops and keeneth’s work-loop match very closely! (see image below)



blue is where I started, red is me changing the passive force in the meganmodel, and green is changing the temperature from 22.5 to 23!