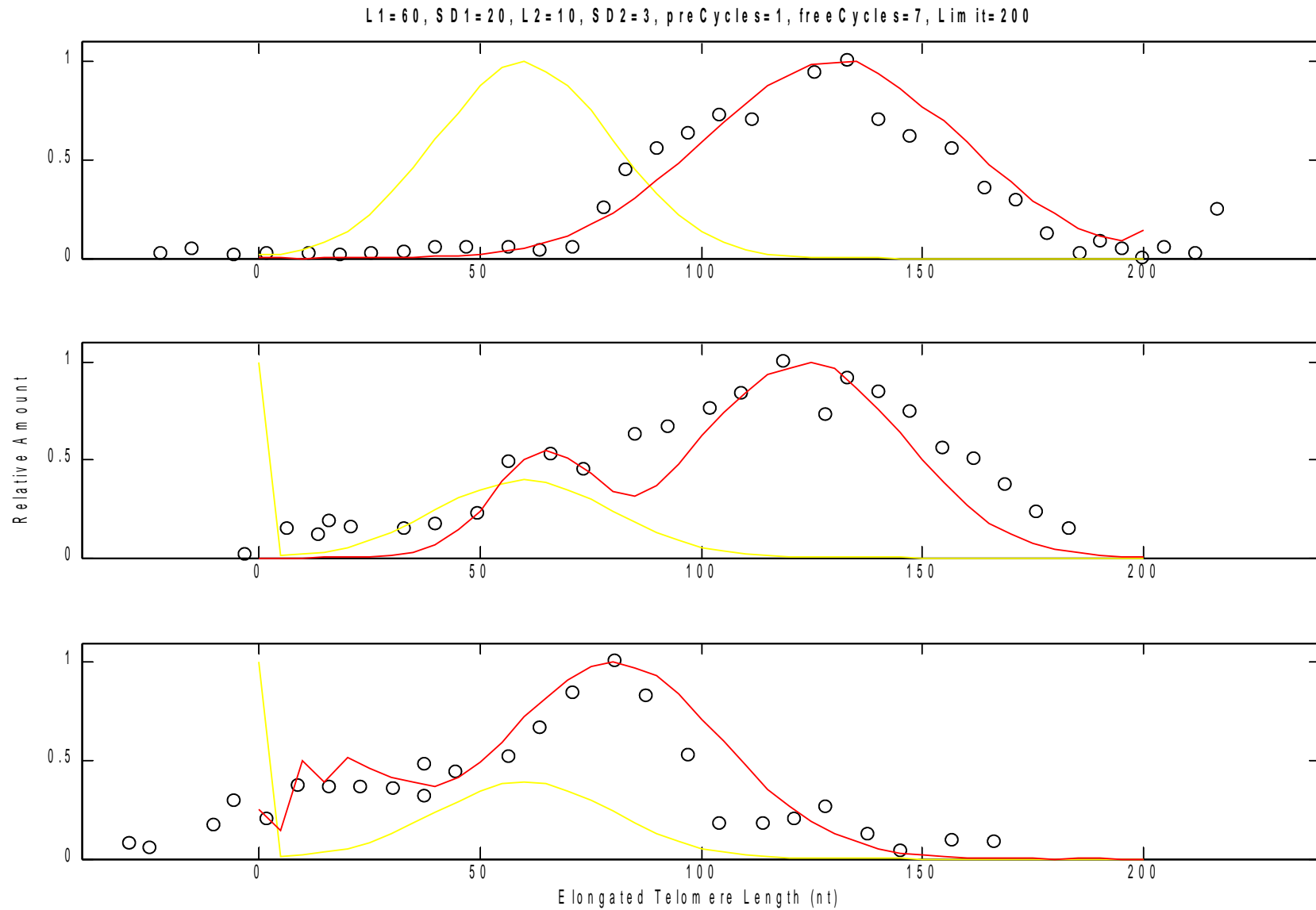
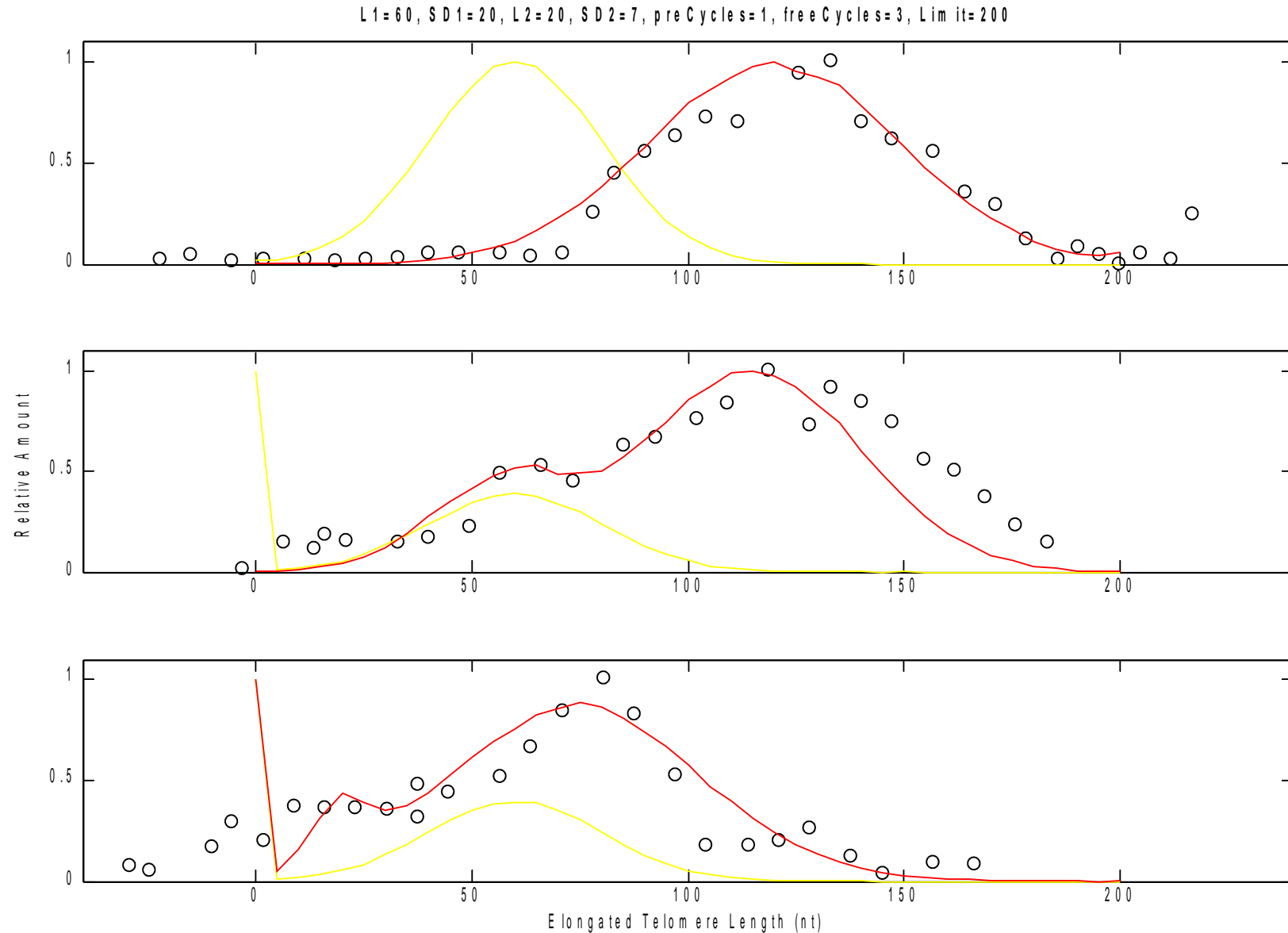


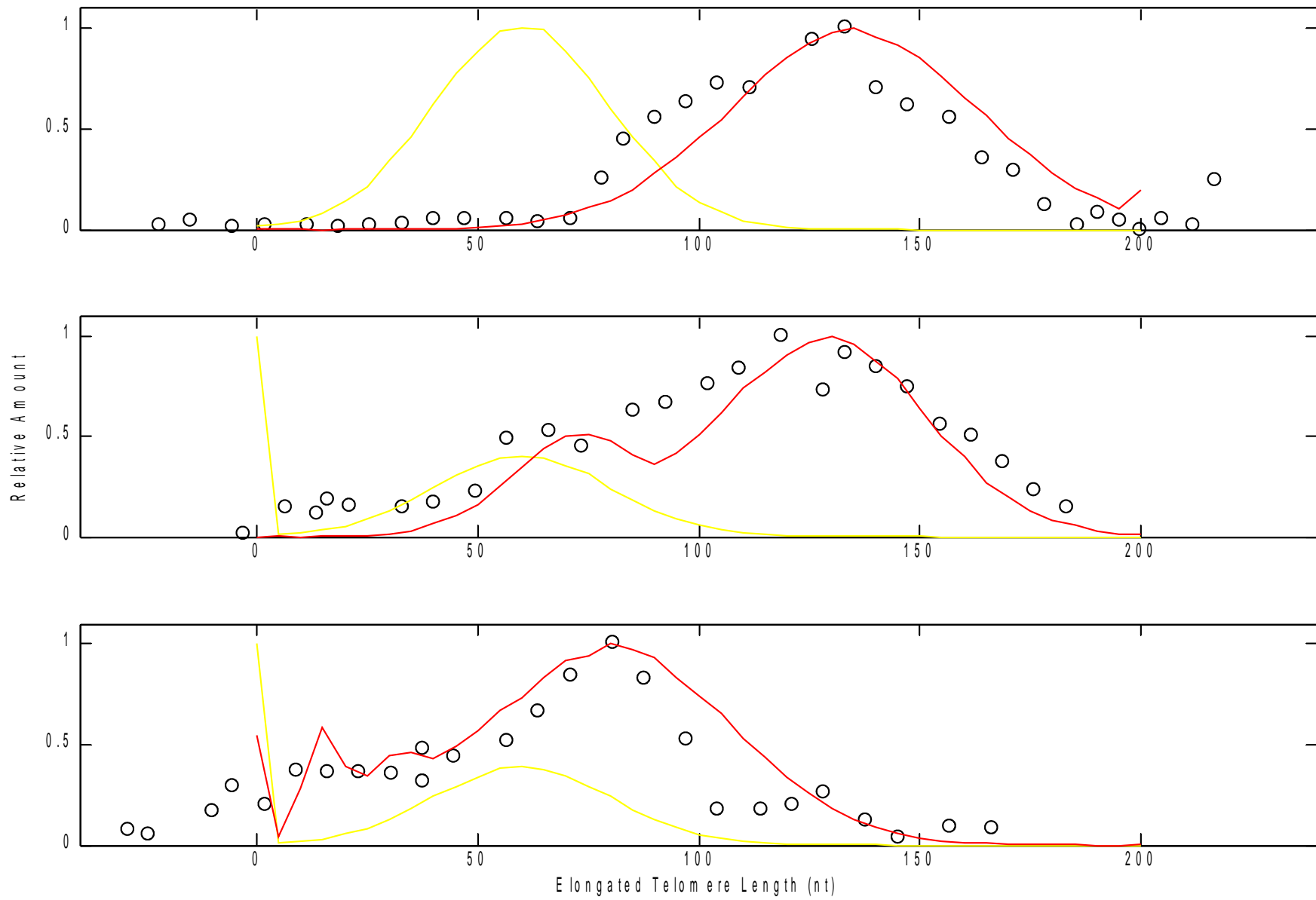
Best model (7 free cycles)



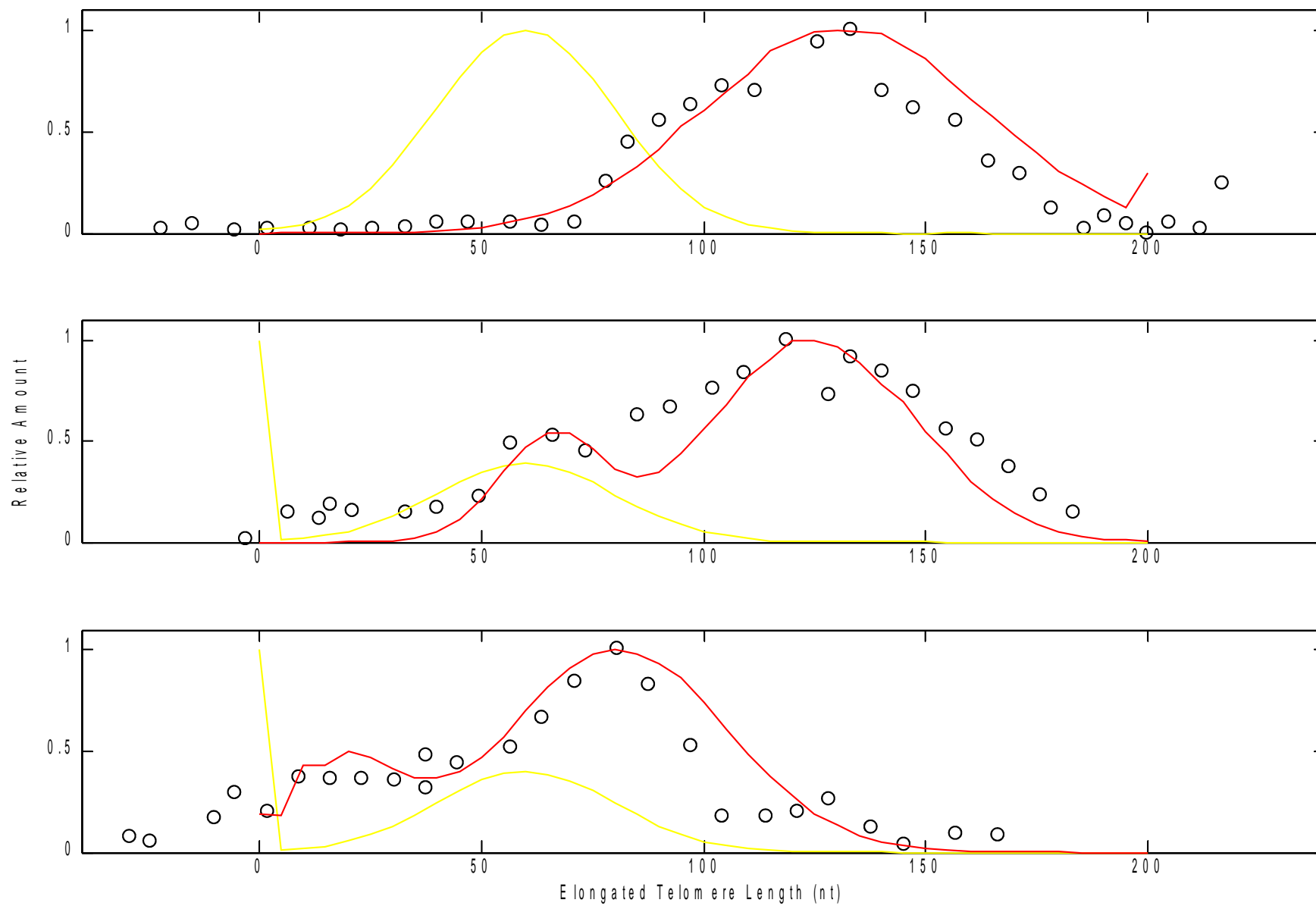
Other models (w. different free cycles)



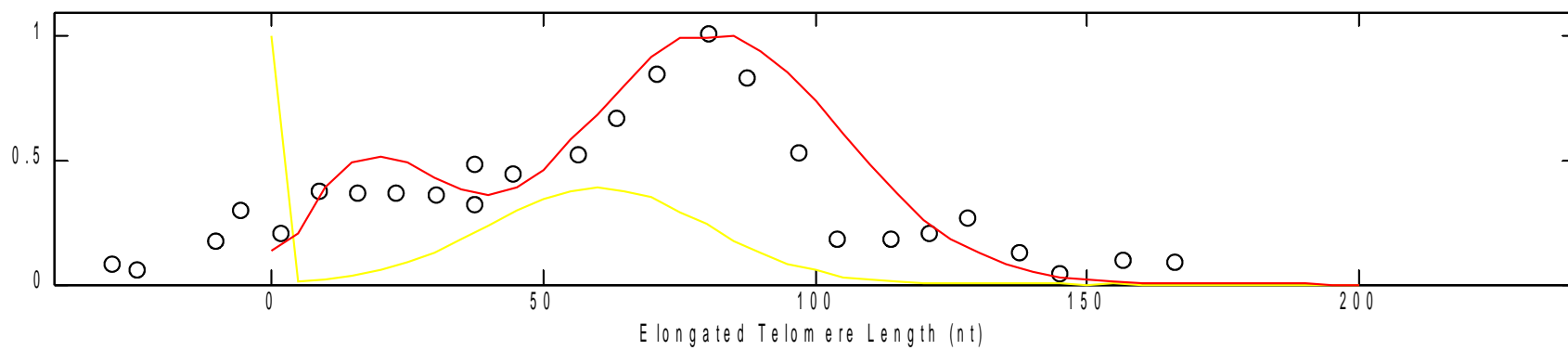
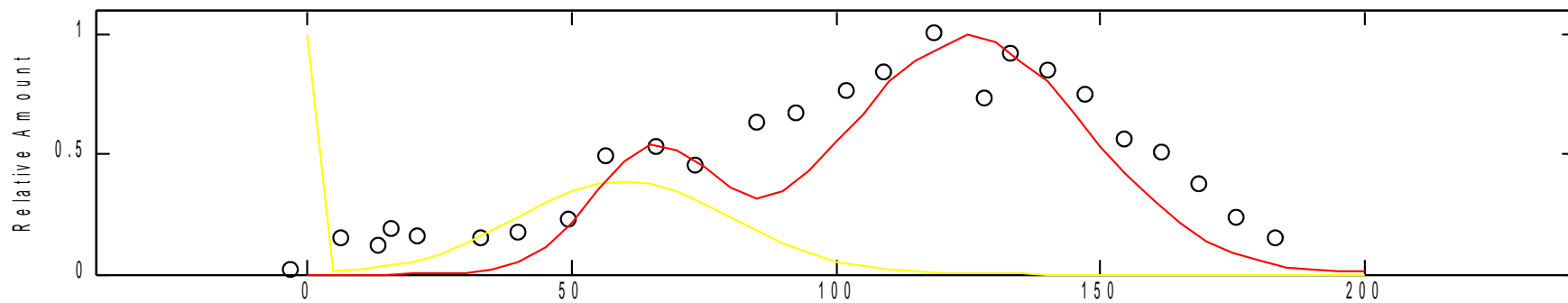
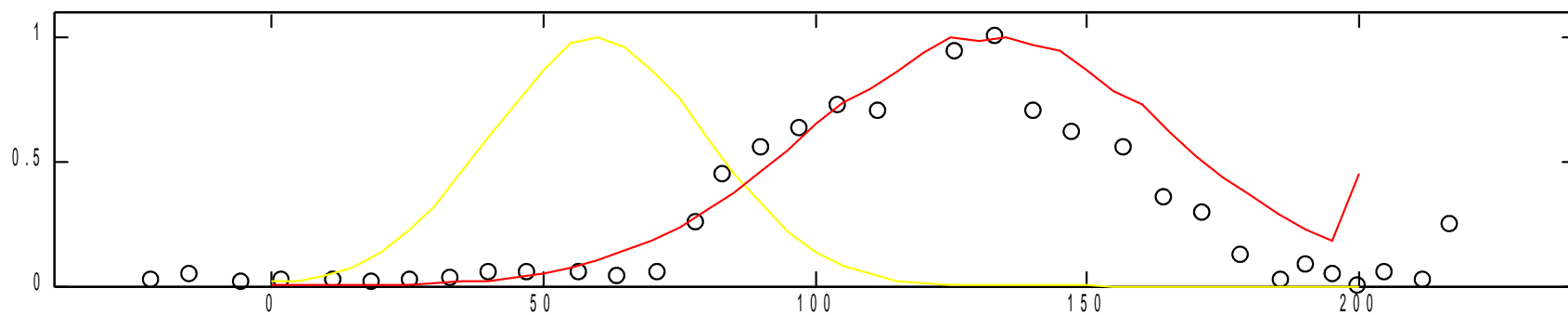
L1=60, SD1=20, L2=15, SD2=4, preCycles=1, freeCycles=5, Limit=200



L1=60, SD1=20, L2=9, SD2=3, preCycles=1, freeCycles=8, Limit=200



L1=60, SD1=20, L2=8, SD2=3, preCycles=1, freeCycles=9, Limit=200



Notes for above figures

- Black dots are the data points from Yong's data. To convert intensity(D) to length(L), I use a new linear formula $L = 2197 * D - 3836$ based on two data pairs([1.8034; 125.8] and [1.7469; 1.67]) calculated from Yong's formula $L = (69060 * D - 120480) / (2108 - 1151 * D)$.
- Yellow curve is the distribution after the first elongation step(by pre-positioning enzyme), and red curve is the final distribution after the elongation by the kinetic/free enzyme.
- The three panels(from top to bottom) in each figure are the samples with 0%, 60% and 90% enzyme suppression.

Simulation conclusion

- Pre-positioning enzyme elongation with Mean=60 & SD=20 for 1 cycle and kinetic elongation with Mean=10 & SD=3 for 7 cycles give good agreement to the experiment results as shown, may be the best model.
- For simulation purpose, the elongated length limit could be any number greater than 170~180.
- The enzyme activity suppression in the second and third samples are 60% and 90%. However, because the enzyme is much excessive than the substrate, the actual valid activity after suppression should be greater than 40% and 10%. Also consider the suppression difference for pre-positioning and free enzyme, so there are two adjustable parameters. In this simulation, 80% & 90% valid activity for the 60% suppression sample and 80% & 30% valid activity for the 90% suppression sample are used to give reasonable good fitting.