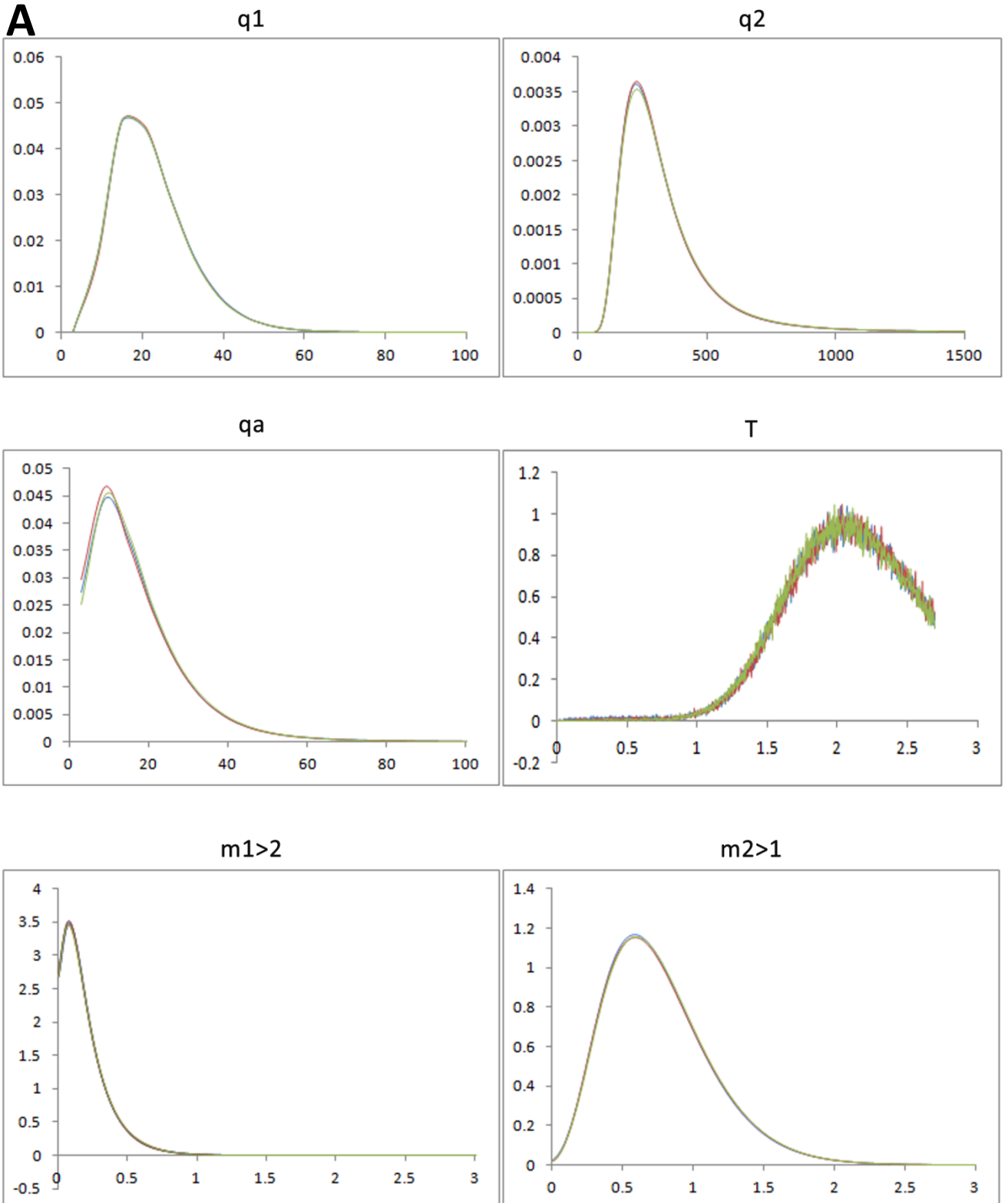


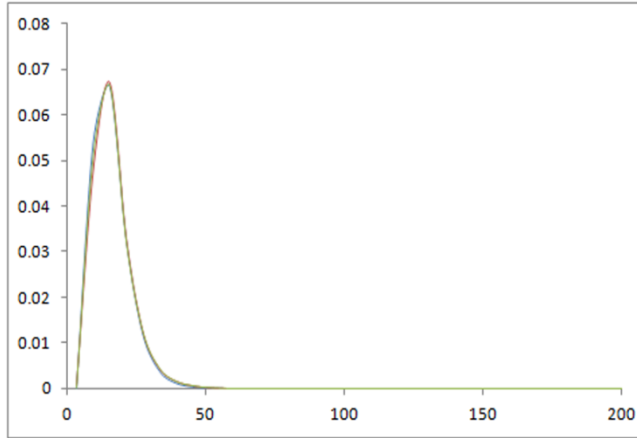
**Supplementary Figure S1.** Posterior distributions of parameter estimates of **q1**, **q2** and **qa** (effective population size of populations 1,2 and ancestral), **T** (splitting time), **m1>2** (gene flow rate per haplotype from populations 2 to 1) and **m2>1** (gene flow rate per haplotype from populations 1 to 2).

A) Sappada vs Cadore; B) Sappada vs Central-Western Europe; C) Sauris vs Udine; D) Sauris vs Central-Western Europe; E) Timau vs Udine; F) Timau vs Central-Western Europe.

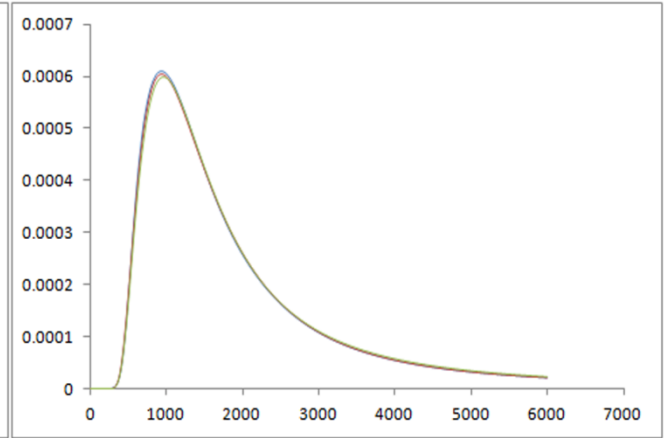


**B**

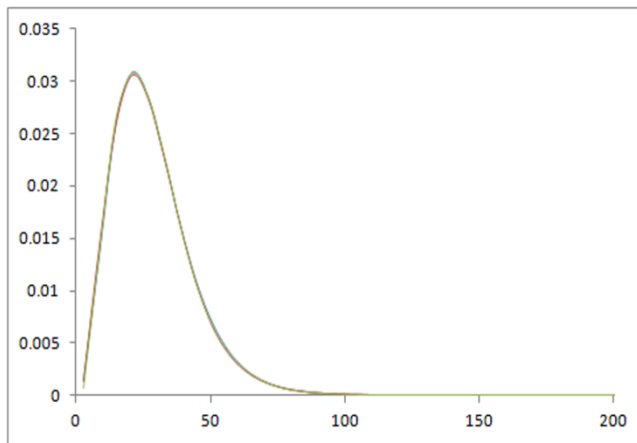
q1



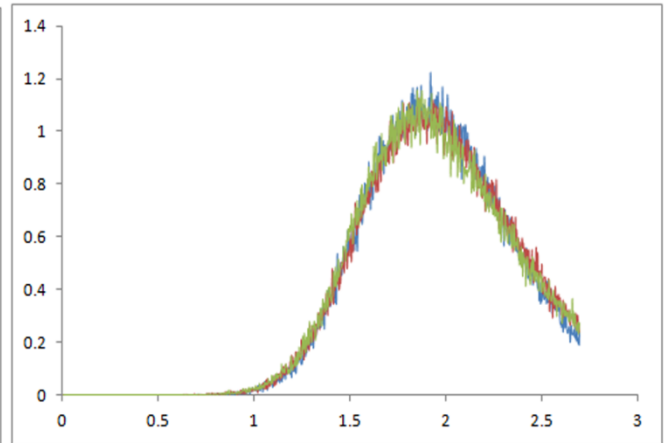
q2



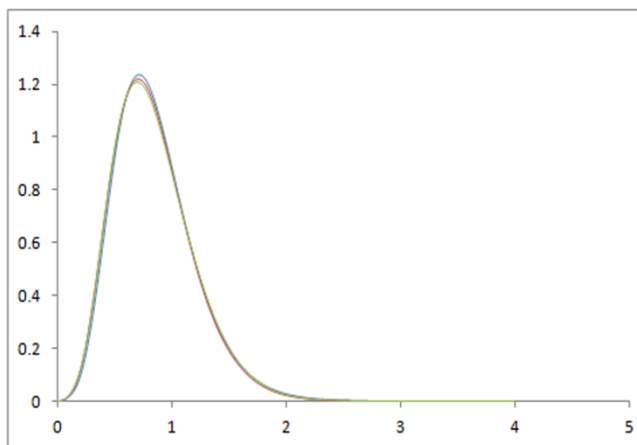
qa



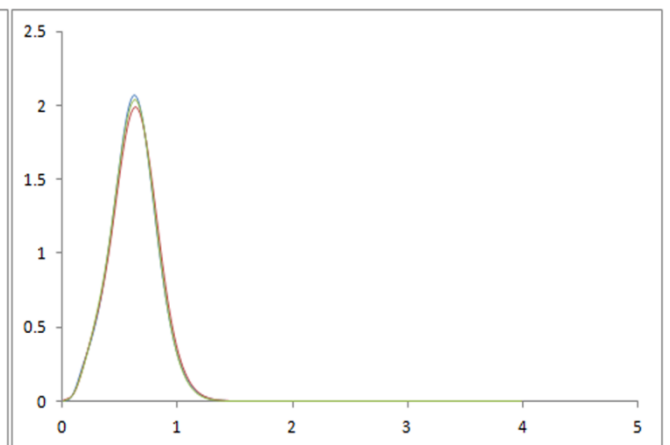
T



m1&gt;2

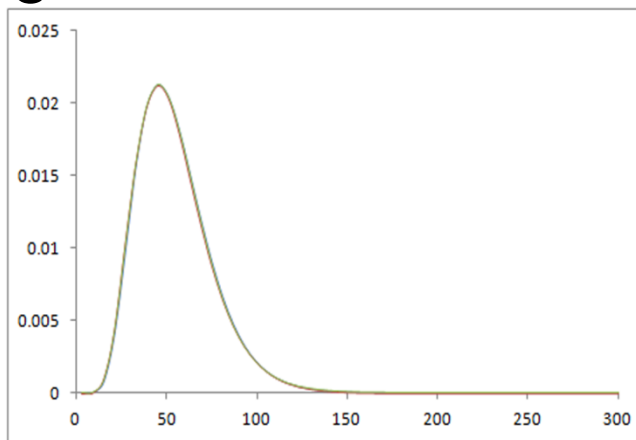


m2&gt;1

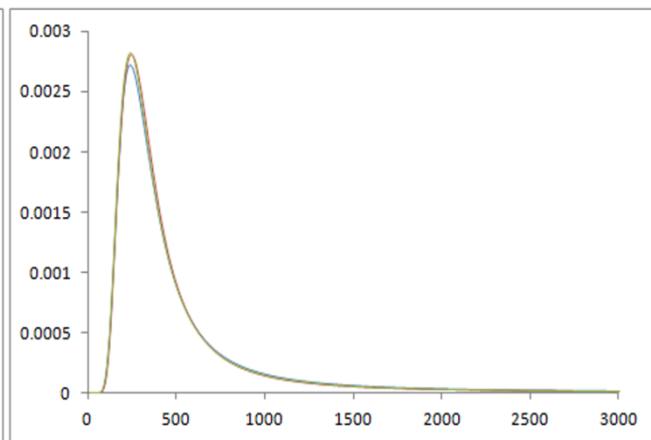


**C**

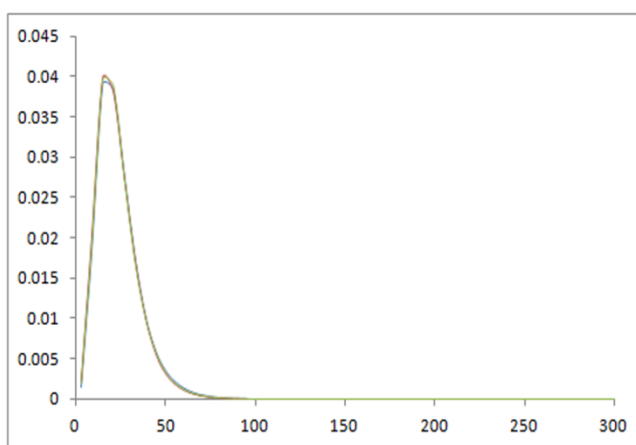
q1



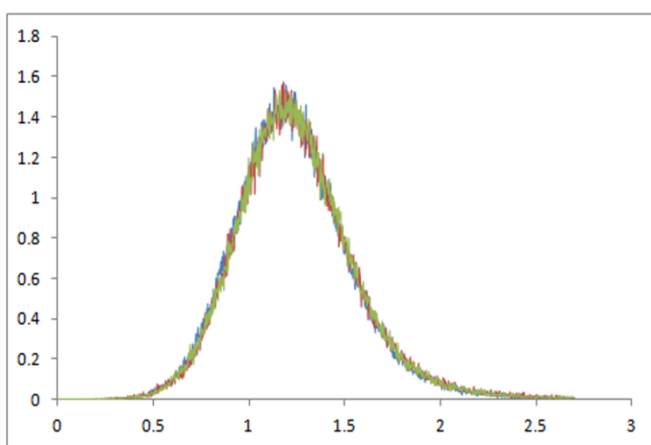
q2



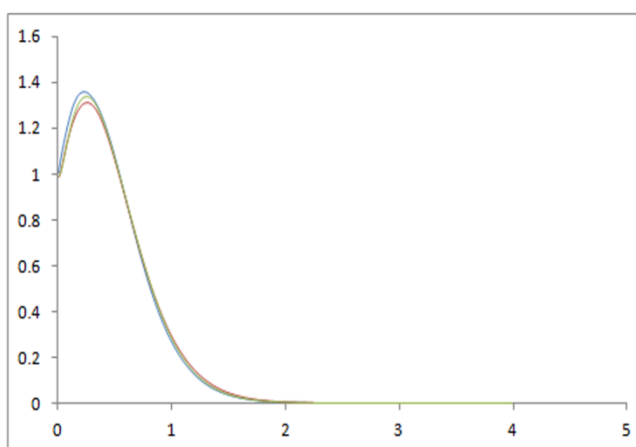
qa



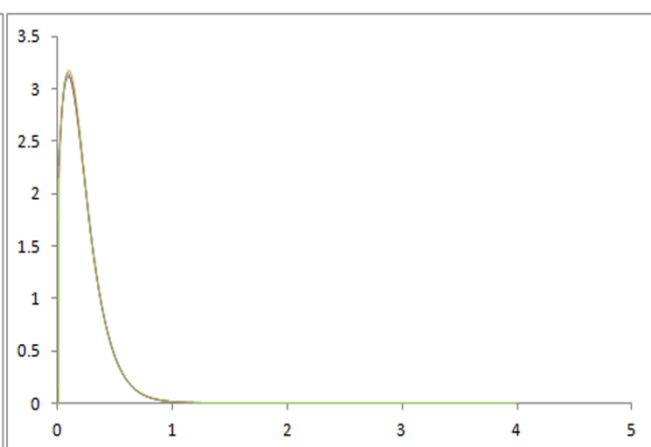
T



m1&gt;2

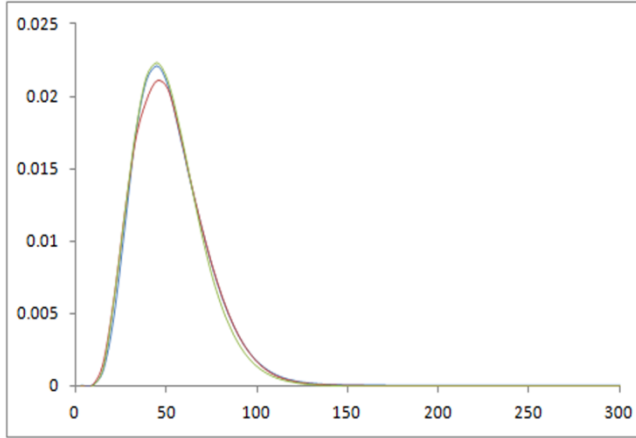


m2&gt;1

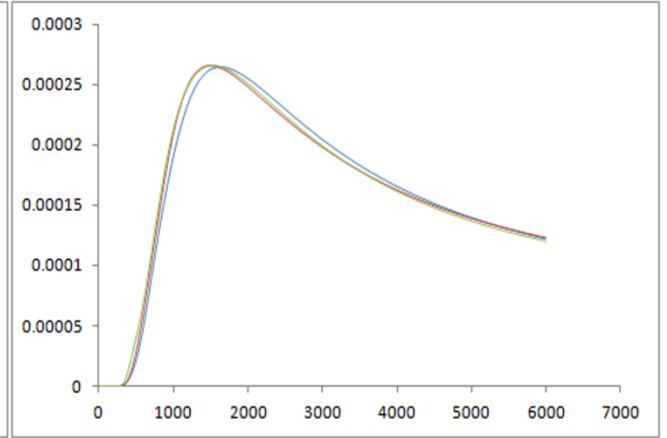


**D**

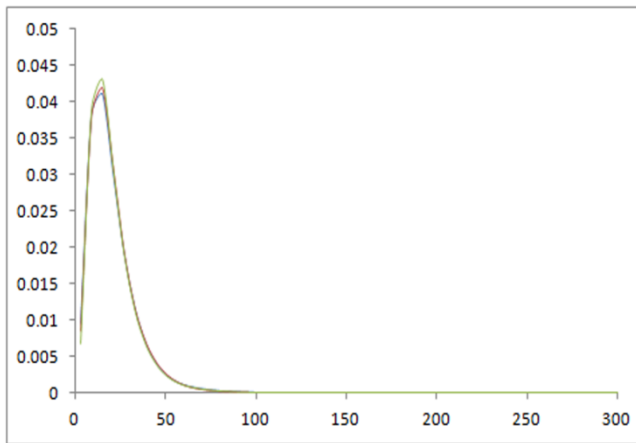
q1



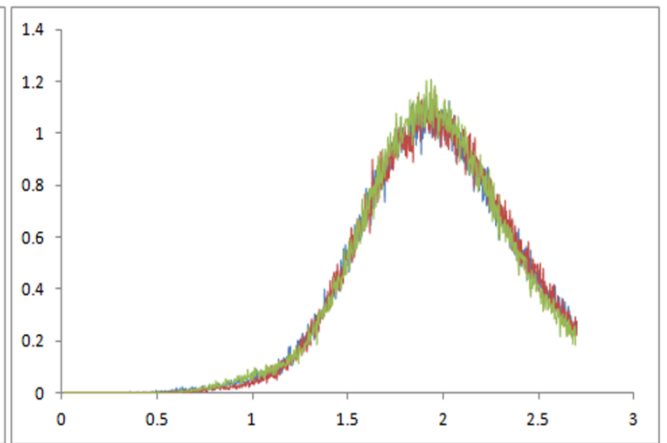
q2



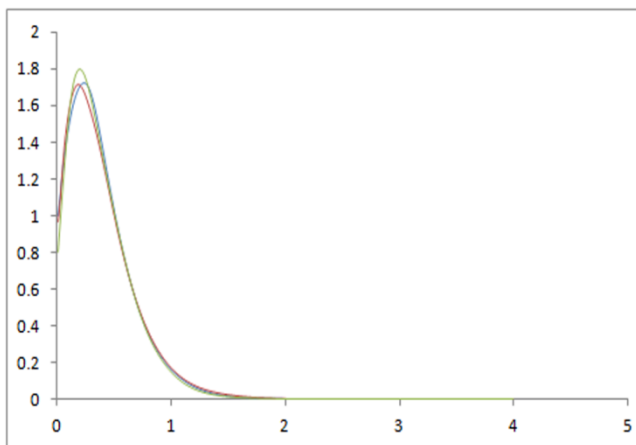
qa



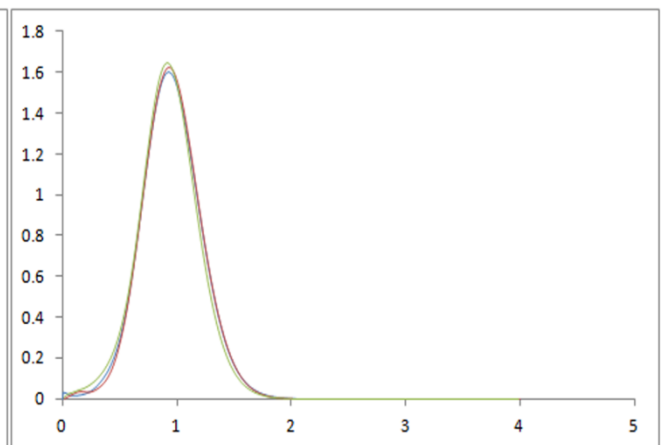
T



m1&gt;2

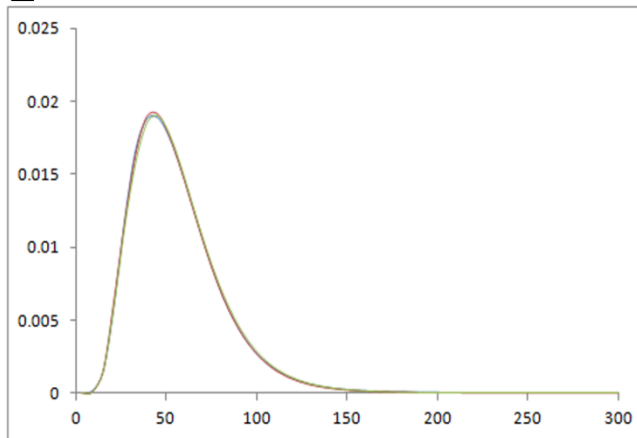


m2&gt;1

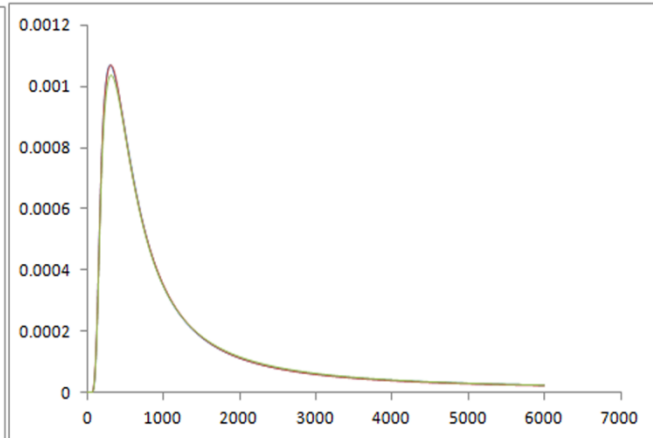


**E**

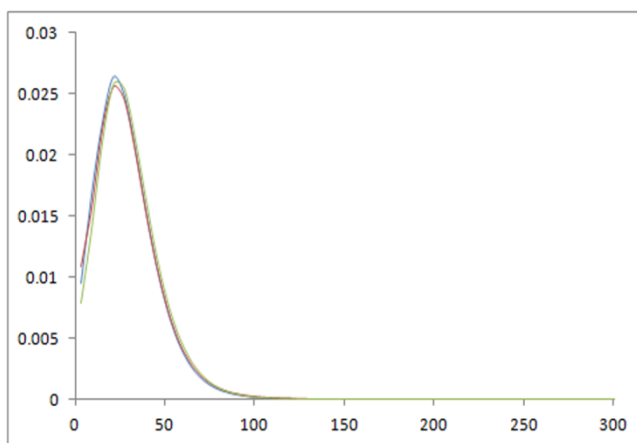
q1



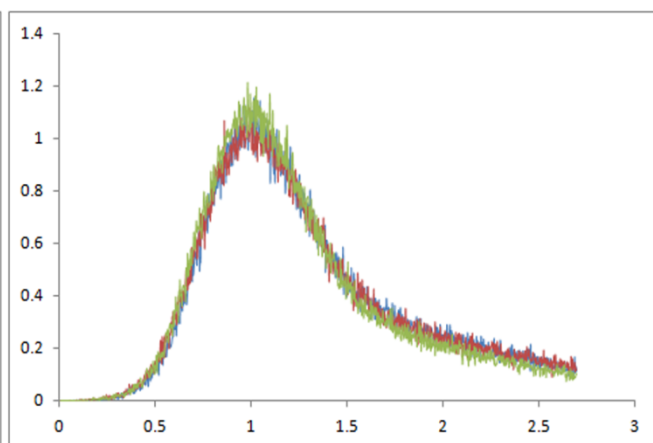
q2



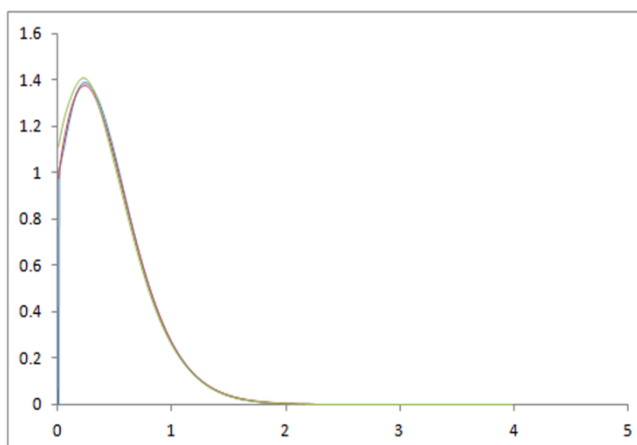
qa



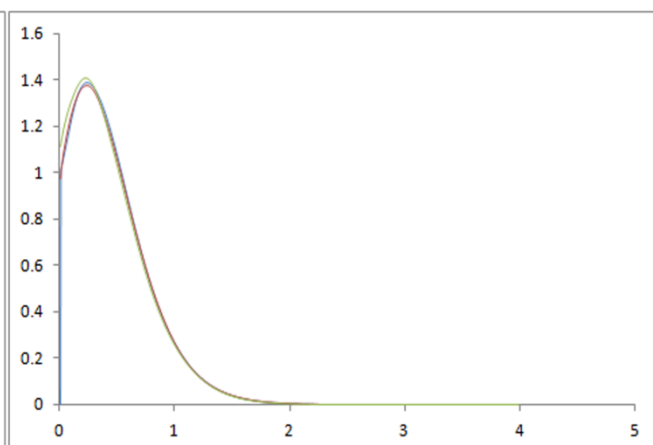
T



m1&gt;2

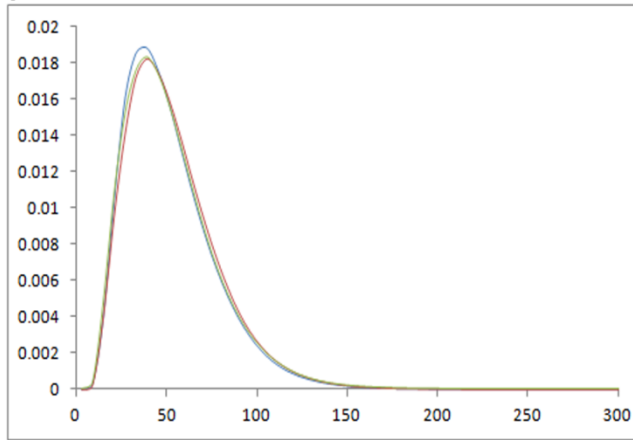


m2&gt;1

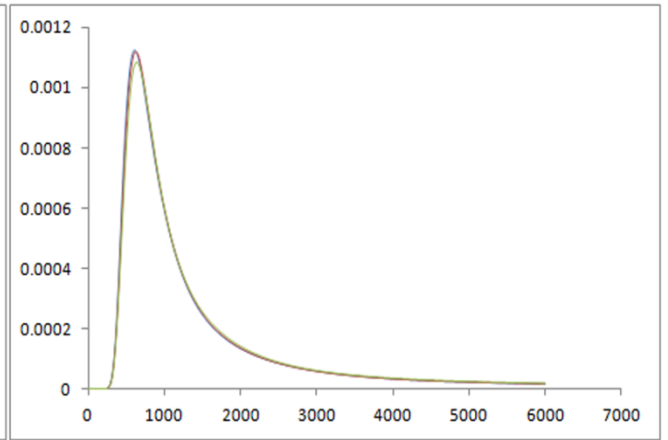


**F**

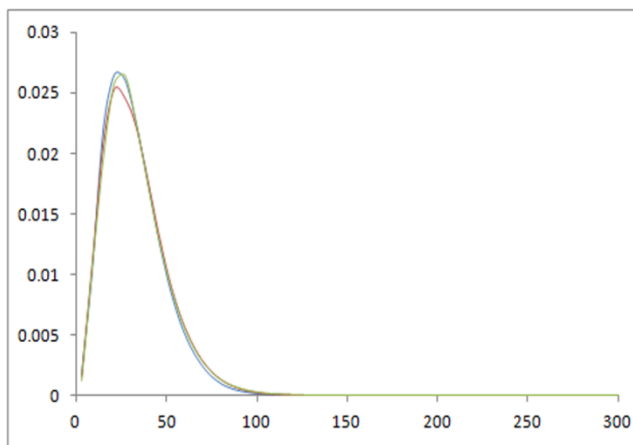
q1



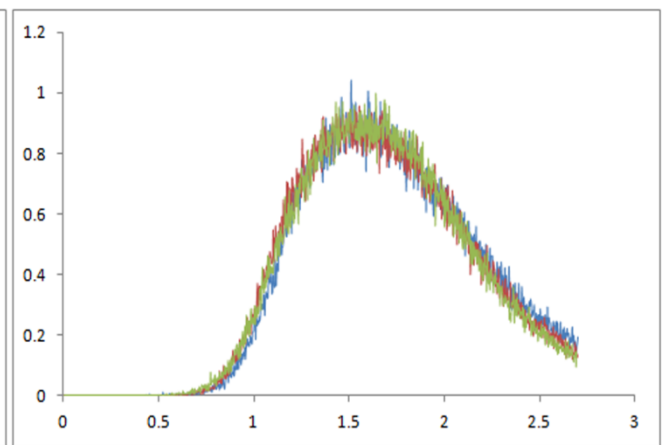
q2



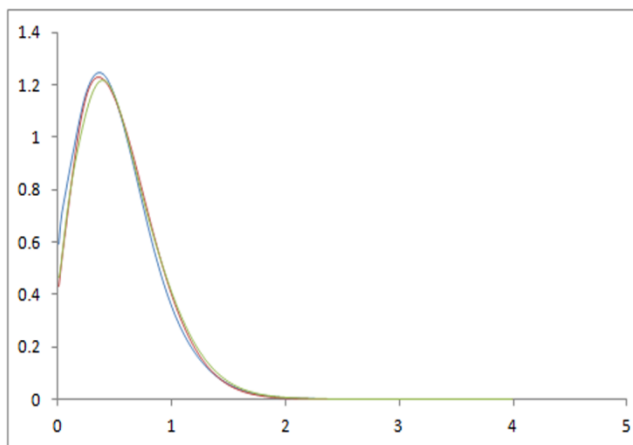
qa



T



m1&gt;2



m2&gt;1

