



**Fig. 9.** Approximated asymmetric generalized coherent state model of the yeast genome-scale mRNA lengths distribution data of Eq. (10). Line-joined graph of the arithmetic mean of the profiles of mRNA abundance levels of the  $P$  genes of Eq. (8). Graphs of the asymmetric Gaussian  $\exp[-a(x - p)^2]$  model the profiles of the genes, where the Gaussian amplitudes are determined by the arithmetic mean of the profiles, which models the relative abundance of each Gaussian peak among all genes.