Figure W1: **percentage of configurations in which segregation into subpopulations increases sampling efficiency under Model** 1**: the species in the initial population are equiprobable.**
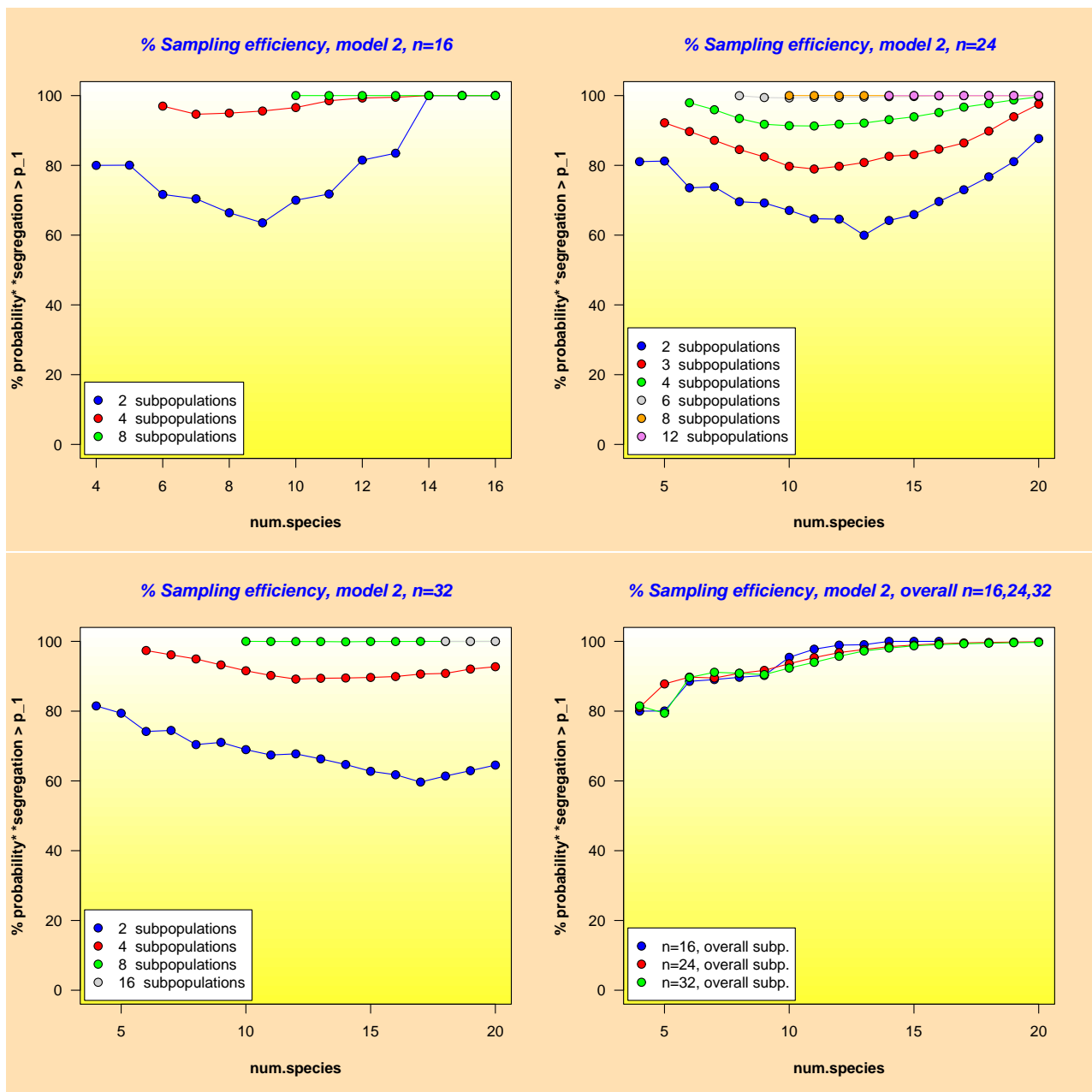
Figure W2: **percentage of simulations (summed over all possible configurations) in which segregation into subpopulations increases sampling efficiency under Model** 2**: no assumption is made on the probabilities of the species in the initial population, but the species within each segregated subpopulation are equiprobable.**
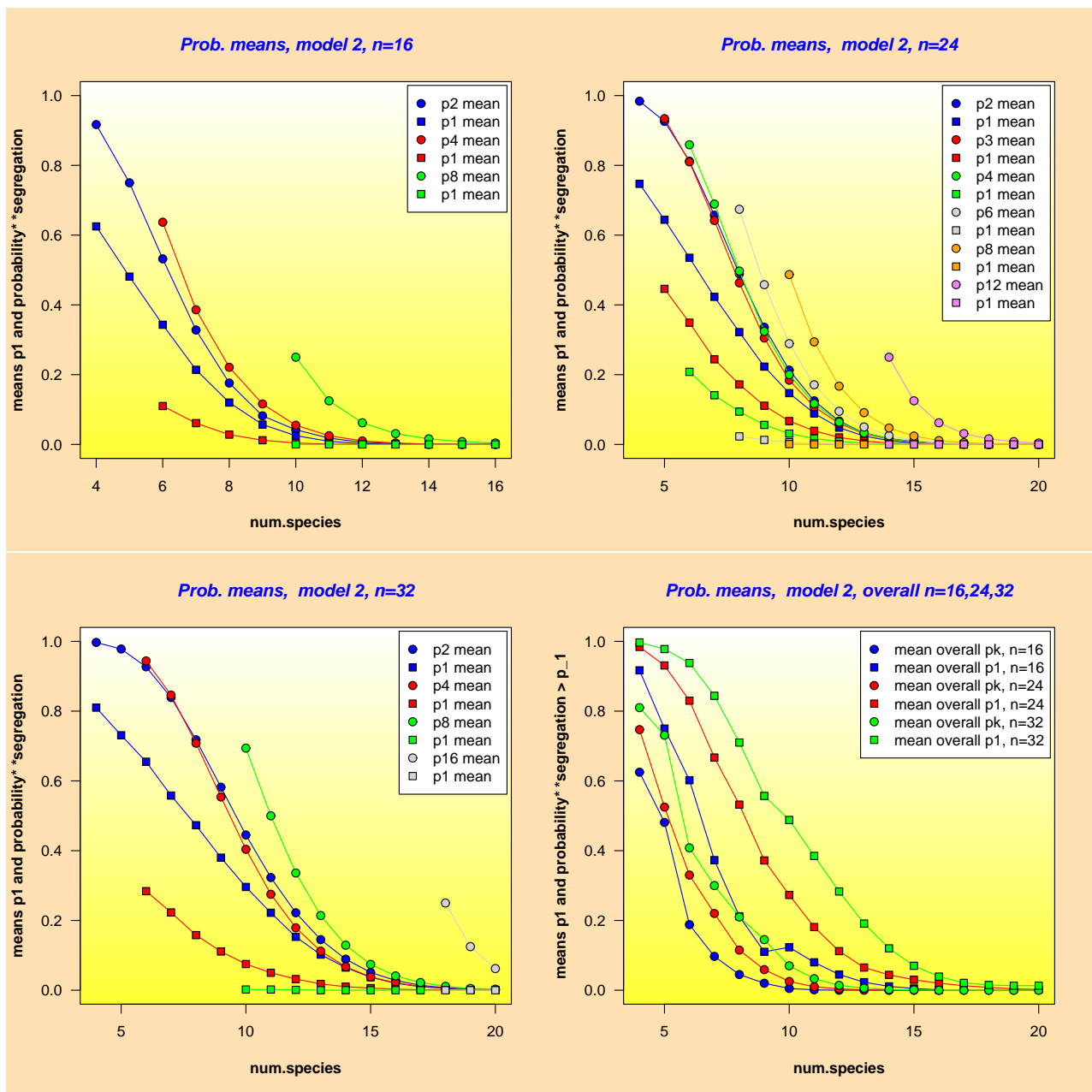
2

Figure W3: **means of the probabilities** p_k **and** p_1 **under Model** 2. As it is possible to see, the average of p_k, that is of the probability of sampling one clone from each novel transcript species after segregation, is larger than p_1, which is the probability before segregation.
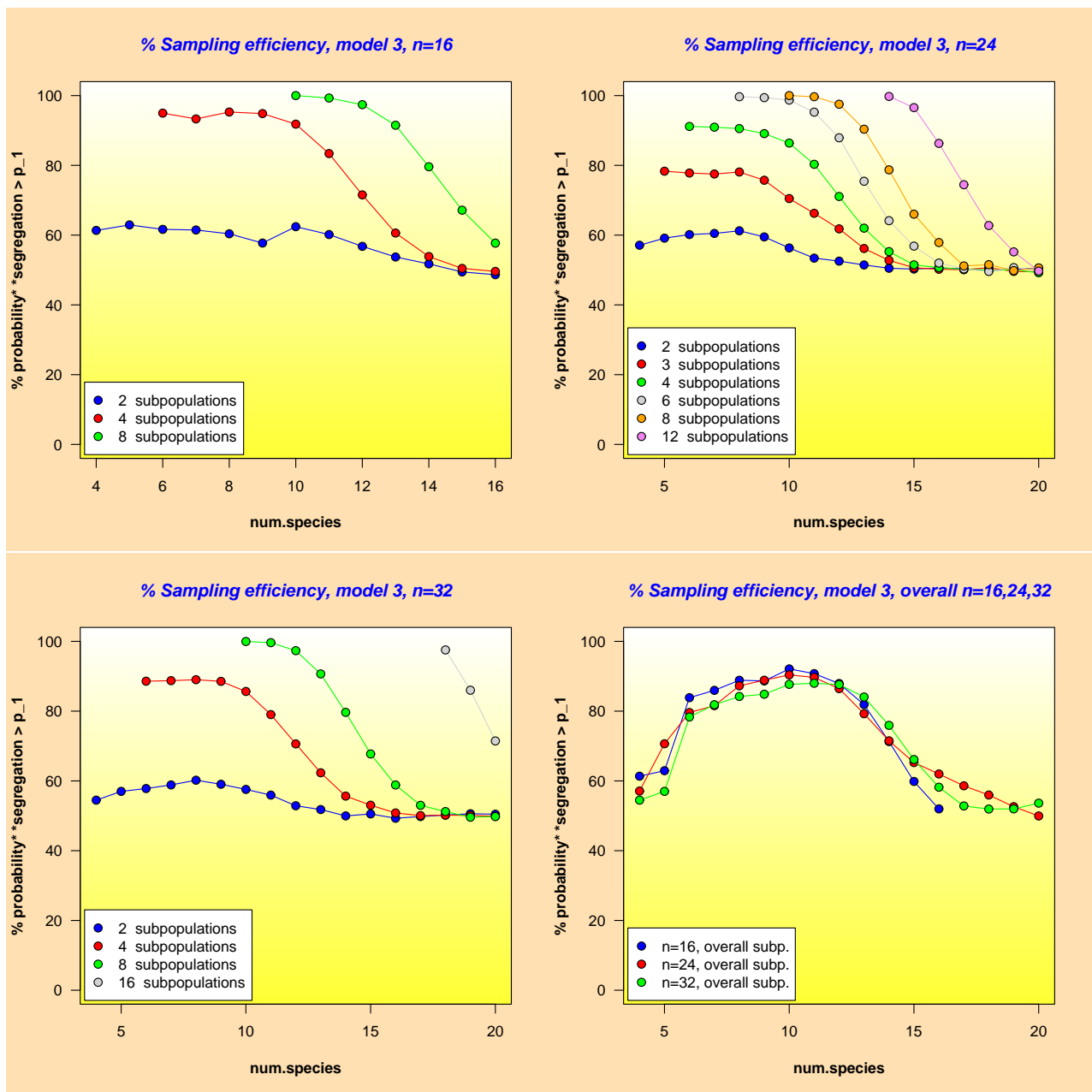
Figure W4: **percentage of simulations (summed over all possible configurations) in which segregation into subpopulations increases sampling efficiency under Model 3: no assumption is made on the probabilities of the species in the initial population, nor on the probabilites of the species in the segregated subpopulations.**
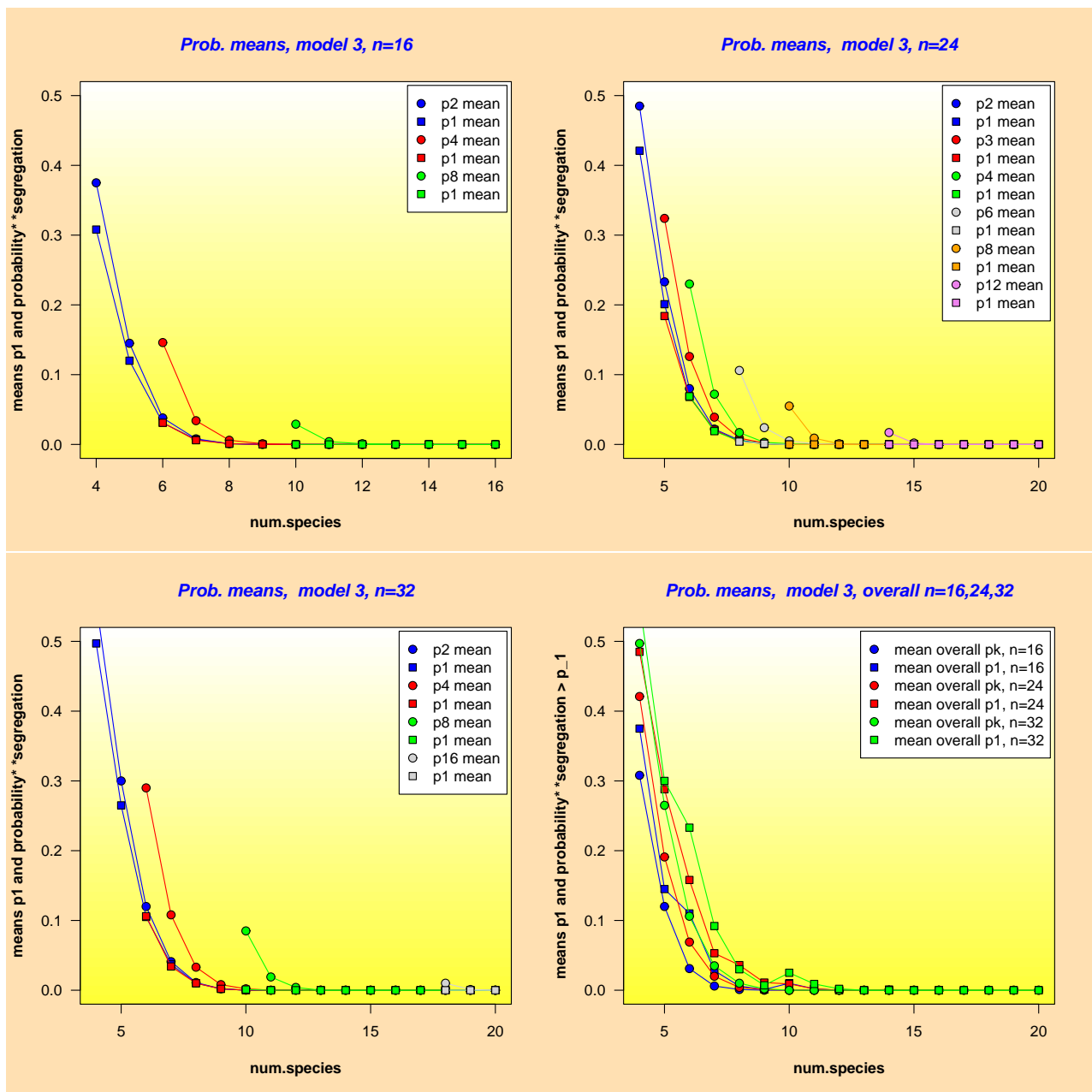
Figure W5: **means of the probabilities p_k and p_1 under Model** 3. As it was the case in figure W3, the average probabilities of sampling one clone from each novel transcript species is larger after than before segregation.
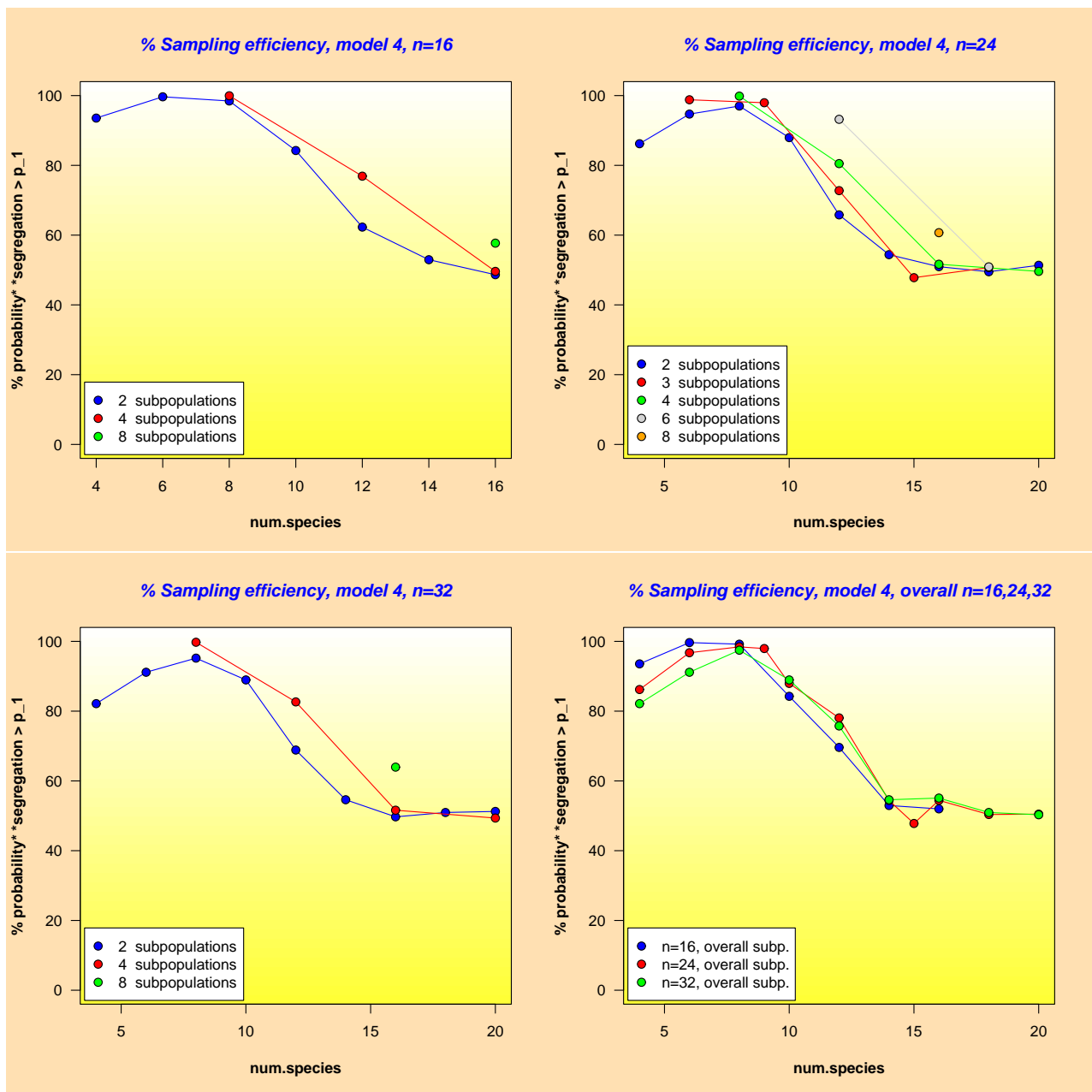
Figure W6: **percentage of simulations (summed over all possible configurations) in which segregation into subpopulations increases sampling efficiency under Model** 4**: no assumption is made on the probabilities of the species in the initial population, nor on the probabilities of the species in the segregated subpopulations, but the number of species is homogeneous across them.**
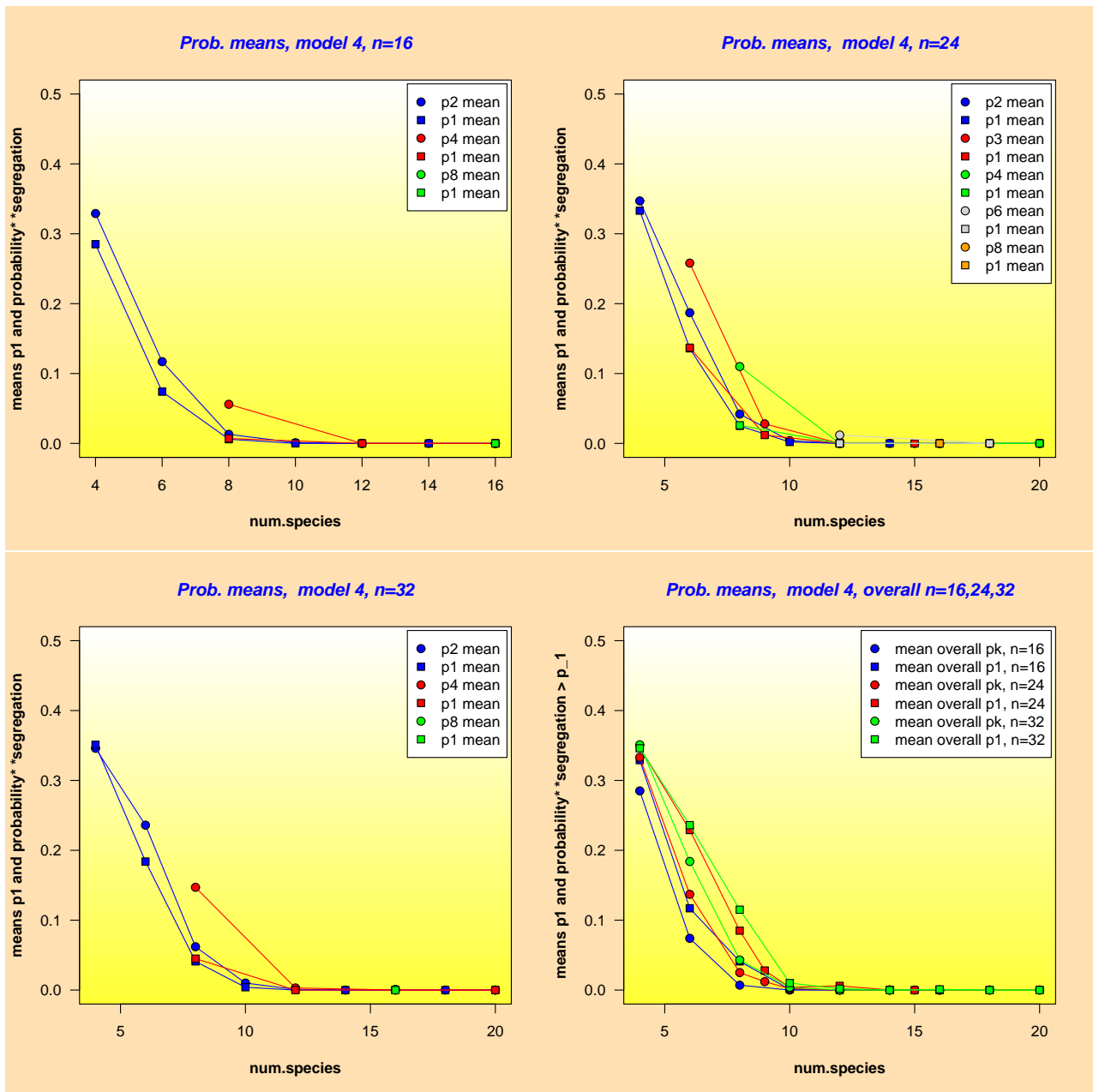
Figure W7: **means of the probabilities** p_k **and** p_1 **under Model** 4.