

## Experiment on UCUT data with the various number of mutation signatures

We analyzed the data using our new model, with increasing number of mutation signatures  $K = 2, 3, \dots$ . Results are shown in Figure 1. As expected, the likelihood increased with  $K$ . Bootstrap-errors started to increase at  $K = 5$  (Figure 2).

With  $K = 2$  (Figure 1(a)) we observed a mutation signature that appears to correspond to AA (T > A substitutions at CpTpG sites with strong transcription strand specificity). Increasing to  $K = 3$  introduced an additional mutation signature corresponding to the APOBEC enzyme (C > [AGT] at TpCpN sites) (Figure 1(b)). Increasing to  $K = 4$  introduced an additional signature (T > A at NpTpN sites with strong strand specificity) that is somewhat similar to the AA signature (Figure 1(c)). The membership in the AA signature and this “AA-like” signature were correlated ( $R = 0.77$ ; Figure 3). This additional signature may be just making up for the residual of the AA signature which the original AA signature could not explain due to a slight deviance of the probabilistic model.

The strong correlation among estimated membership parameters started to be shown at  $K = 4$ . Considering all these factors together,  $K = 3$  seems to be a reasonable choice in terms of the interpretability, and we adopted  $K = 3$ .

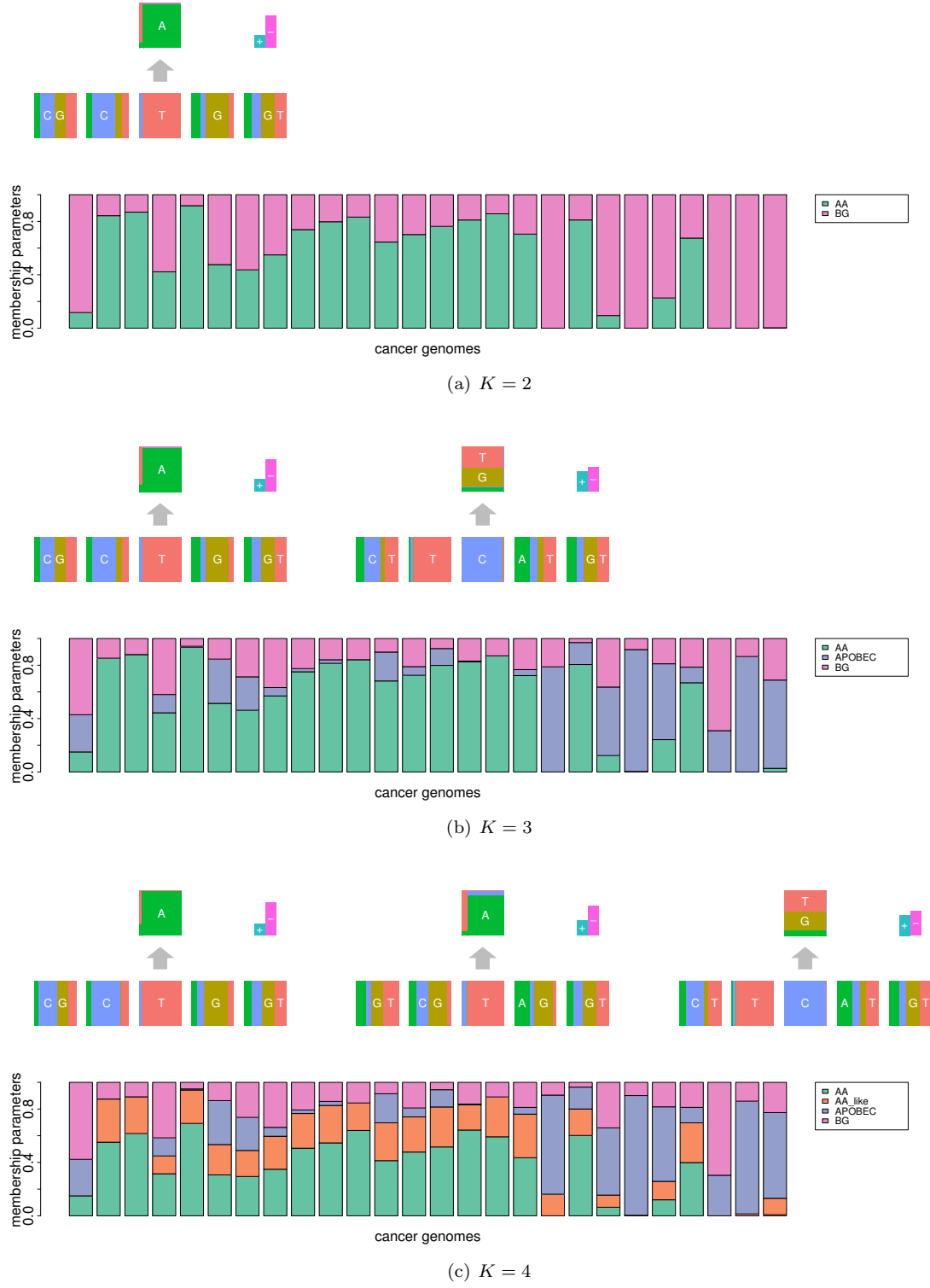


Figure 1: The result of estimated mutation signatures and membership parameters for UTUC data when changing the number of mutation signatures  $K$ .

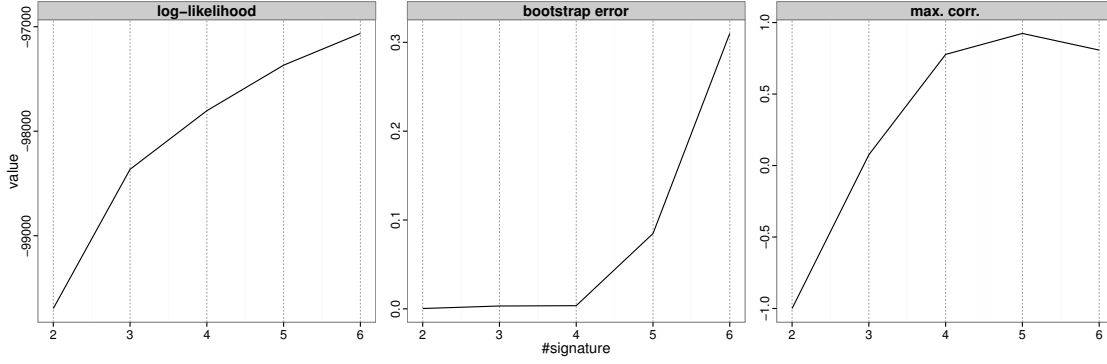


Figure 2: The log-likelihood, bootstrap-errors and maximum correlation values among estimated membership parameters for several numbers of signatures  $K$  in UTUC data.

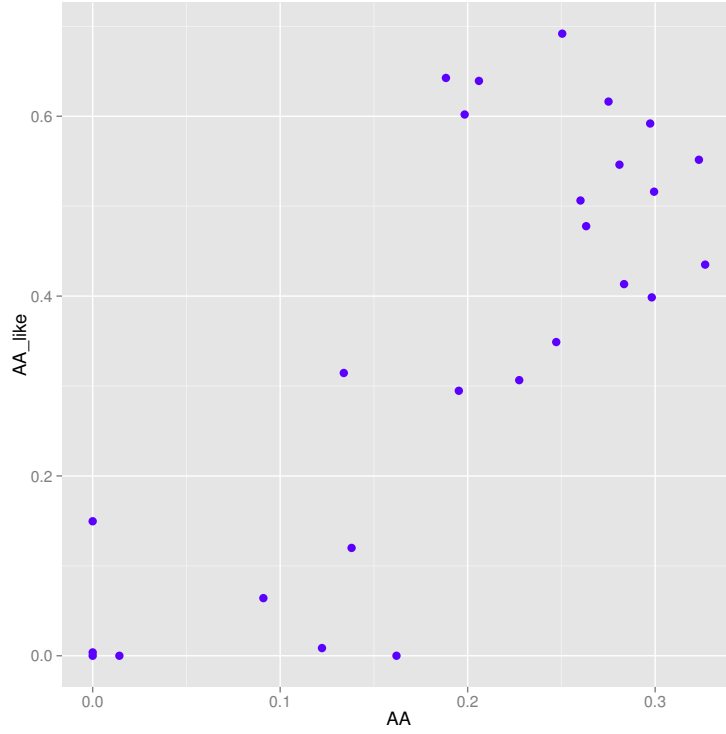


Figure 3: The relationships between the two membership parameters, AA (the first signature in the Figure 1(c)) and AA\_like (the second signature in the Figure 1(c)) signatures.