

Convergence report for Myeloid AML signatures 20000 DMROO RData

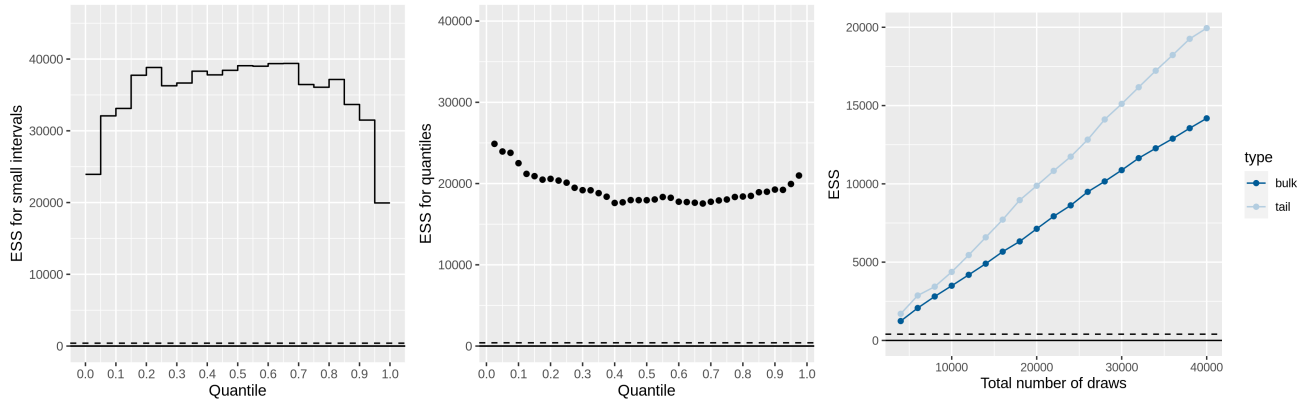
Date of inference: 2020-06-14

Explanation of parameters Rhat indicates the ratio of variance within a chain over variance pooling all chains. We recommend running at least four chains by default and only using the sample if R-hat is less than 1.05. ESS bulk/tail indicate the bulk/tail effective sample size estimate, i.e. show the sampling efficiency of mean and median estimates. We recommend running at least four chains by default and only using the sample if R-hat is less than 1.05. Both bulk-ESS and tail-ESS should be at least 100 (approximately) per Markov Chain in order to be reliable and indicate that estimates of respective posterior quantiles are reliable.

- Max Rhat: NA
- ess bulk: 210.465650663952
- ess tail: 200.975500699192



In the plots below ESS should have high values



Local ESS for β

