

Convergence report for Biliary AdenoCA signatures 20000ROO RData

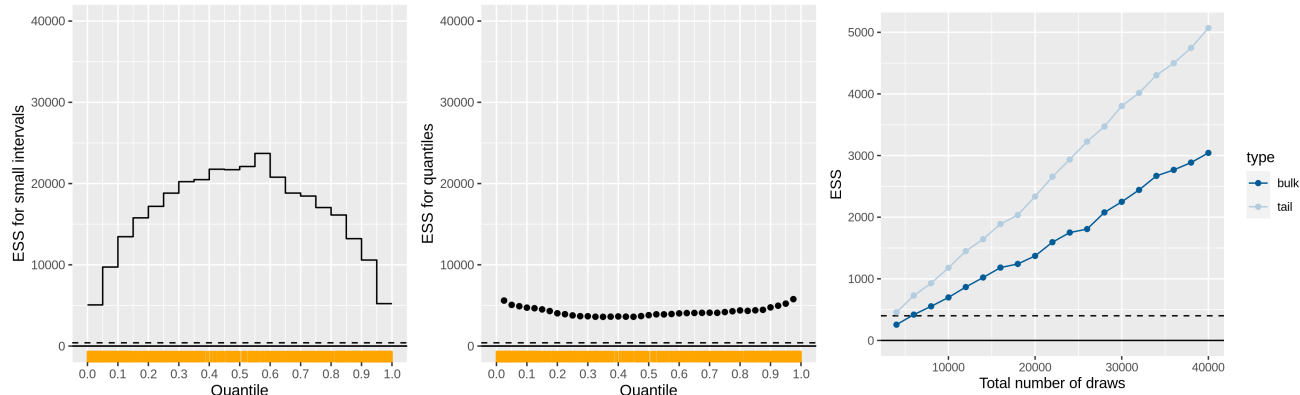
Date of inference: 2020-06-13

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: 1.00040233605695
- ess bulk: 1182.52380121004
- ess tail: 1232.21208596088



In the plots below ESS should have high values



Local ESS for β

