

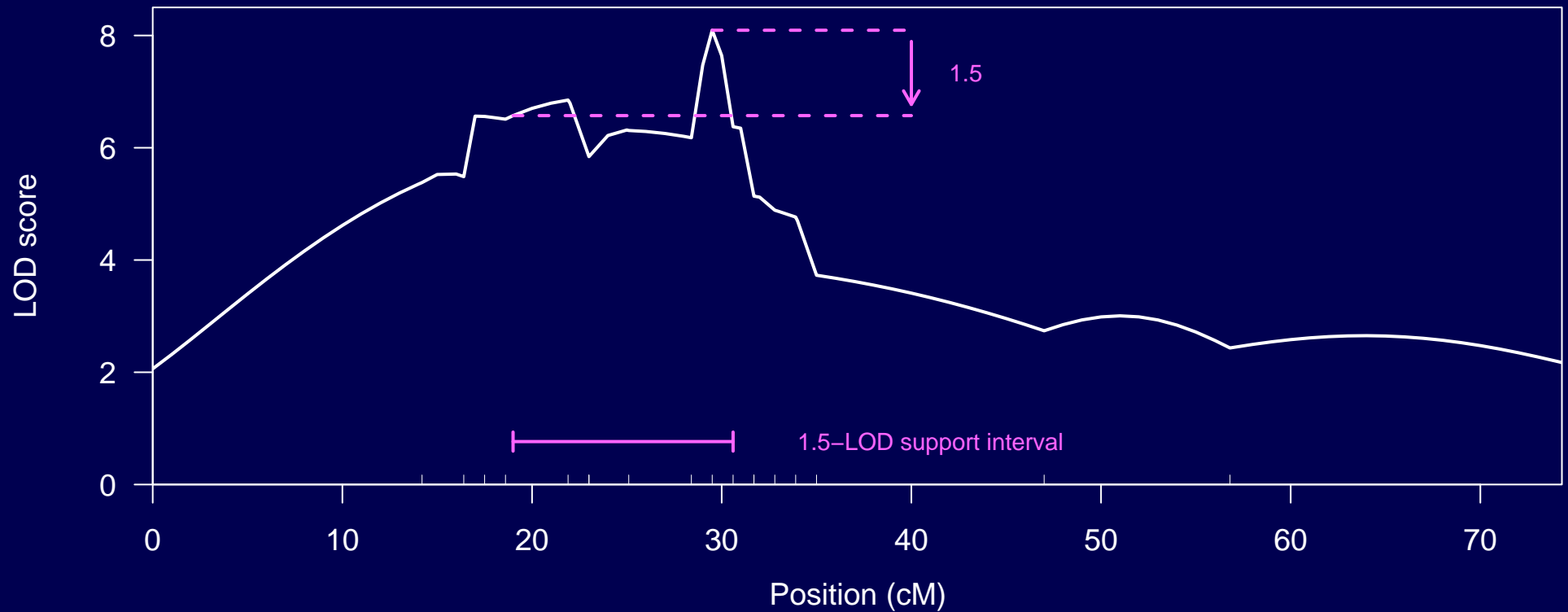
Poor performance of bootstrap confidence intervals for QTL location

Karl W Broman

Department of Biostatistics
Johns Hopkins Bloomberg School of Public Health

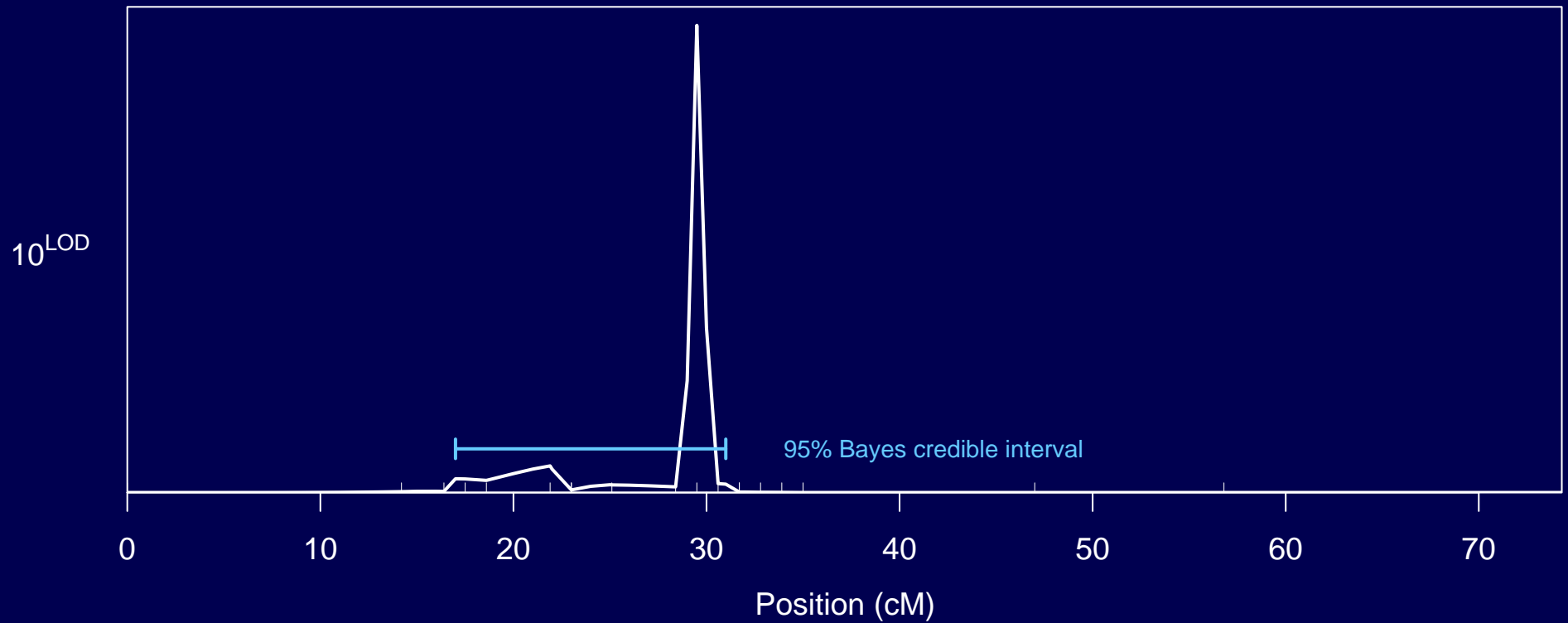
www.biostat.jhsph.edu/~kbroman

LOD support interval



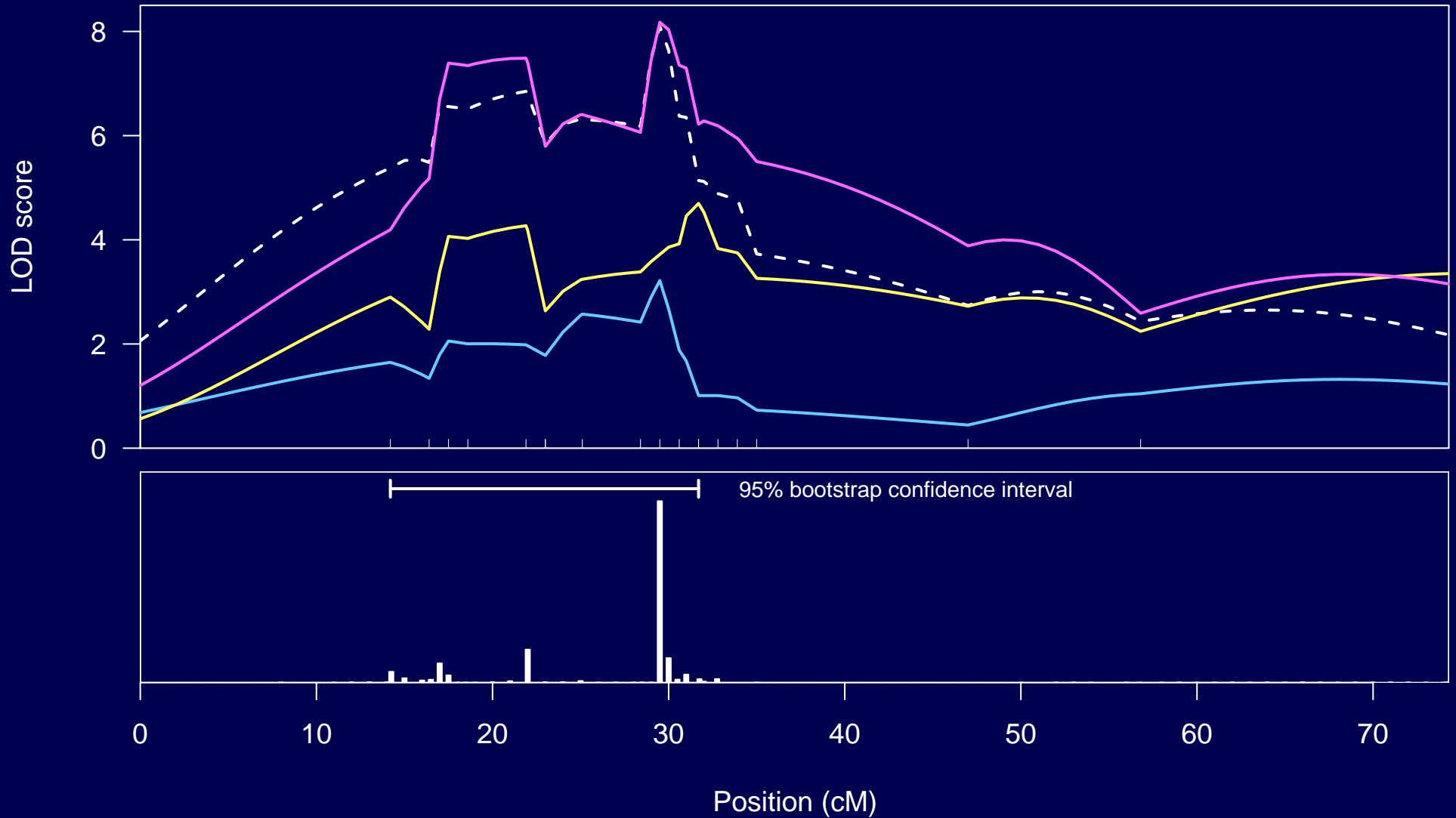
Data from Sugiyama et al. (2001) Genomics 71:70–77

Approximate Bayes interval



Data from Sugiyama et al. (2001) Genomics 71:70–77

Bootstrap CI

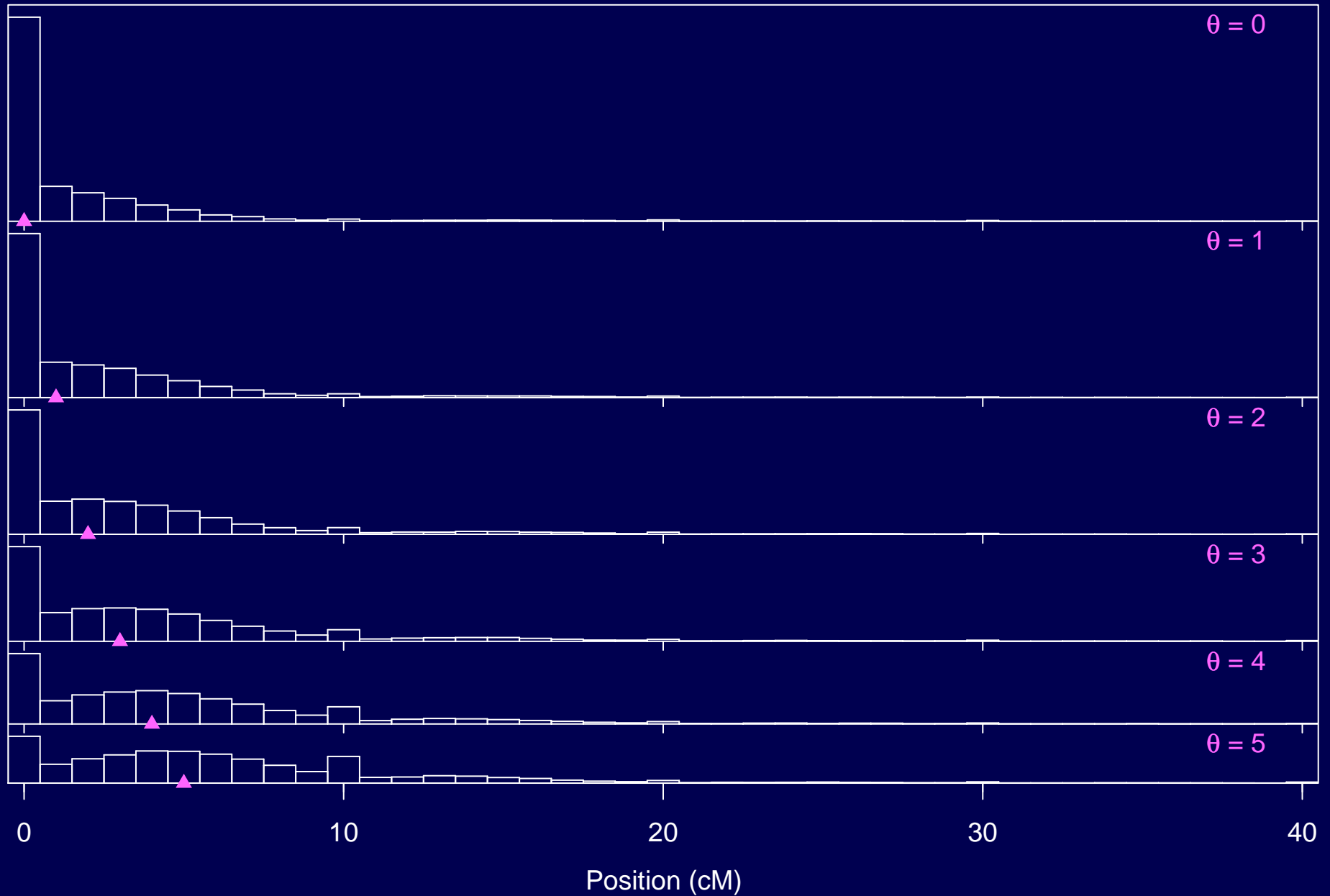


Data from Sugiyama et al. (2001) *Genomics* 71:70–77

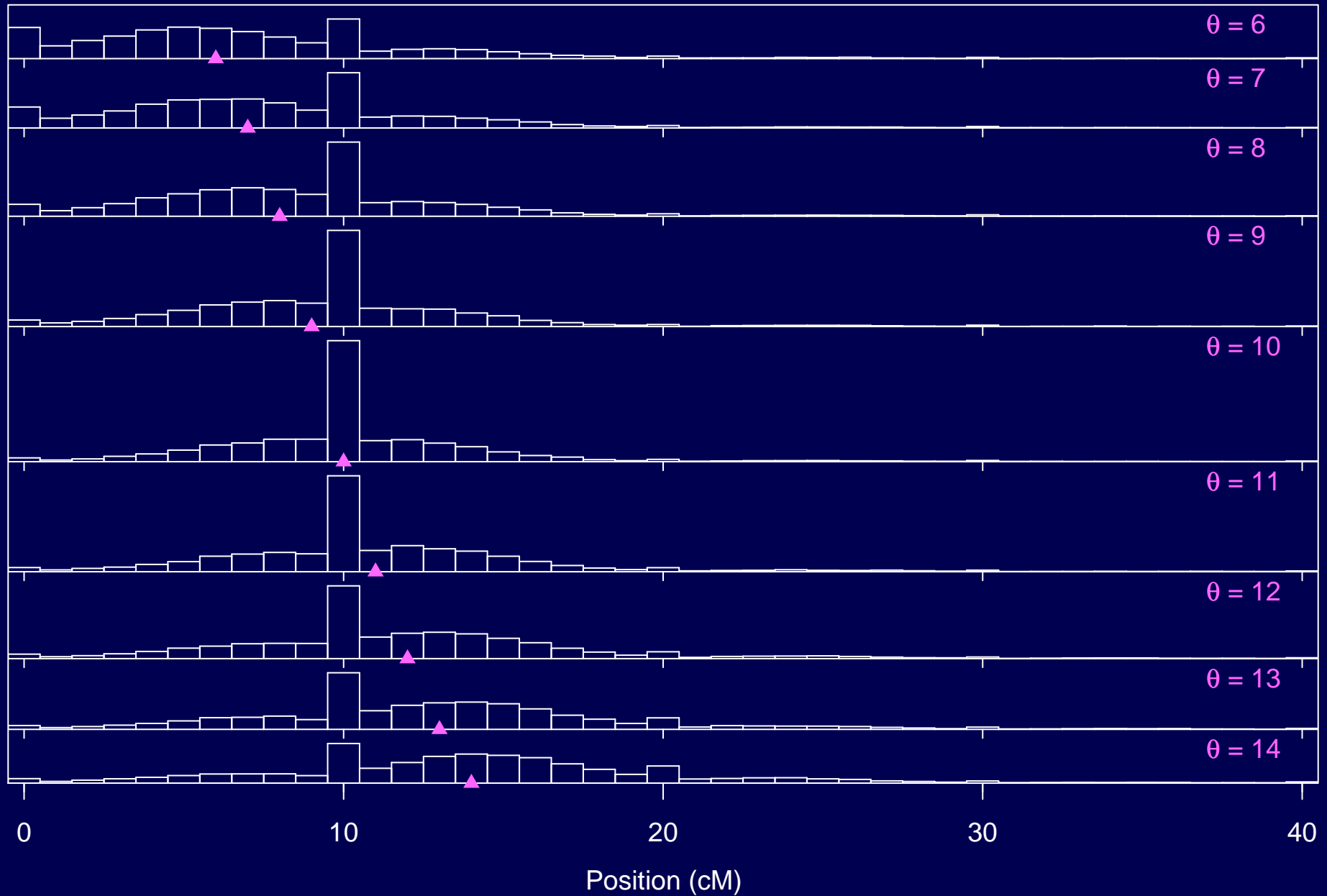
Simulation study

- Backcross, 200 individuals
- One chromosome of length 100 cM
- Markers at 10 cM spacing
- Single QTL responsible for 10% of phenotypic variance
- Normally distributed residual variation
- Varied location of QTL, at positions 0, 1, ..., 100 cM
- Analysis by standard interval mapping; calculations every 1 cM
- 10,000 simulations for each QTL position
- Bootstrap used 1000 replicates

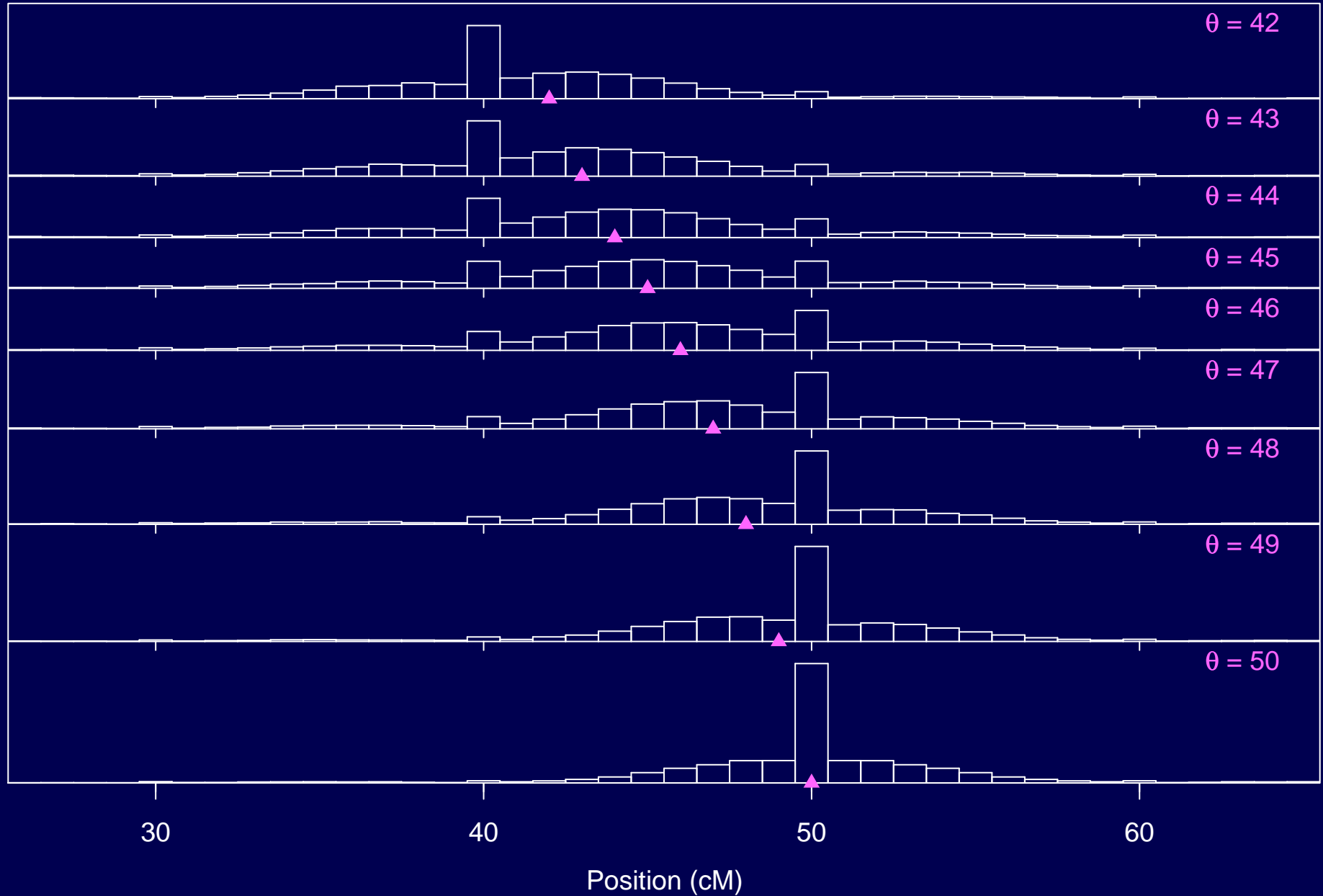
Distribution of estimated location



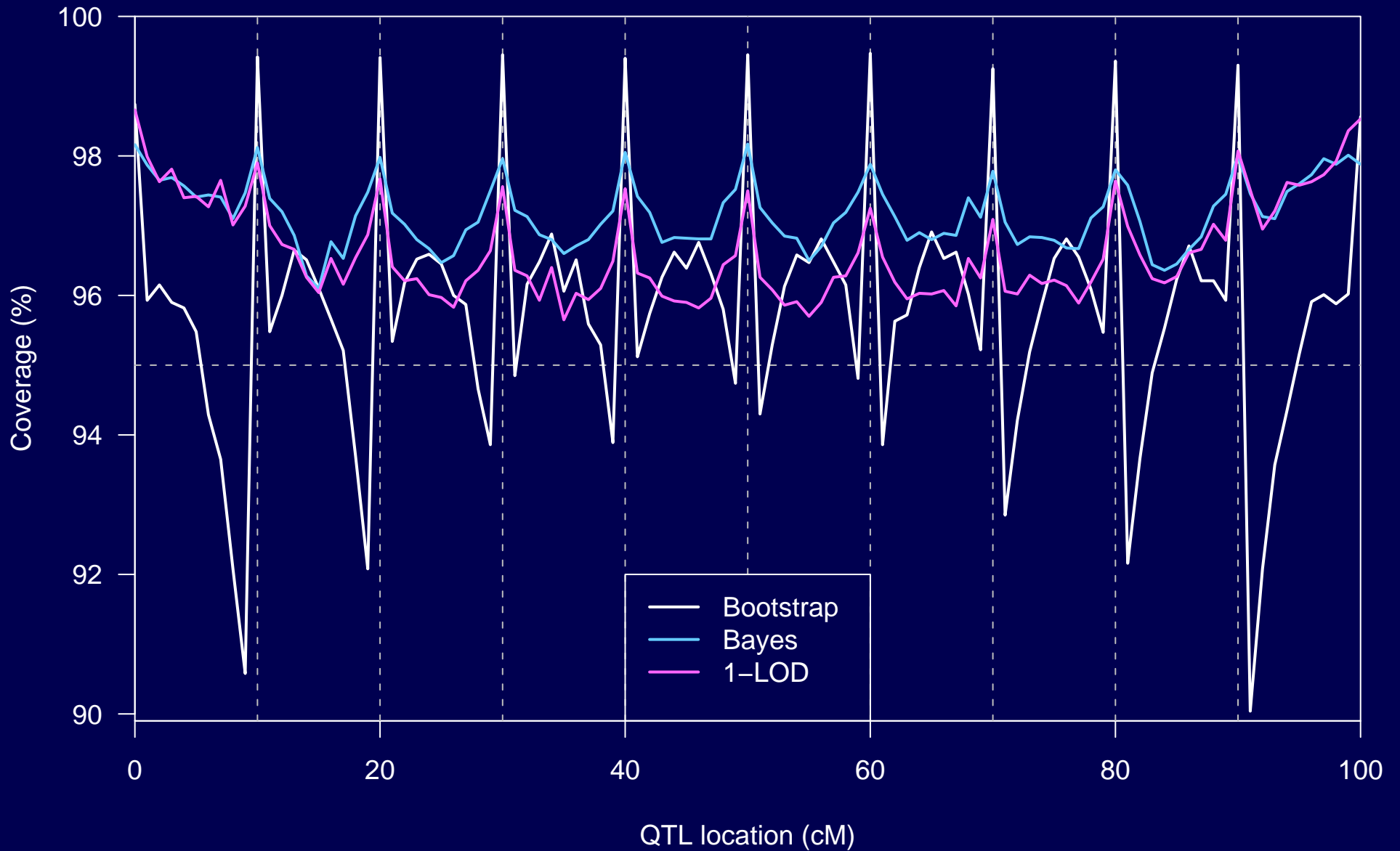
Distribution of estimated location



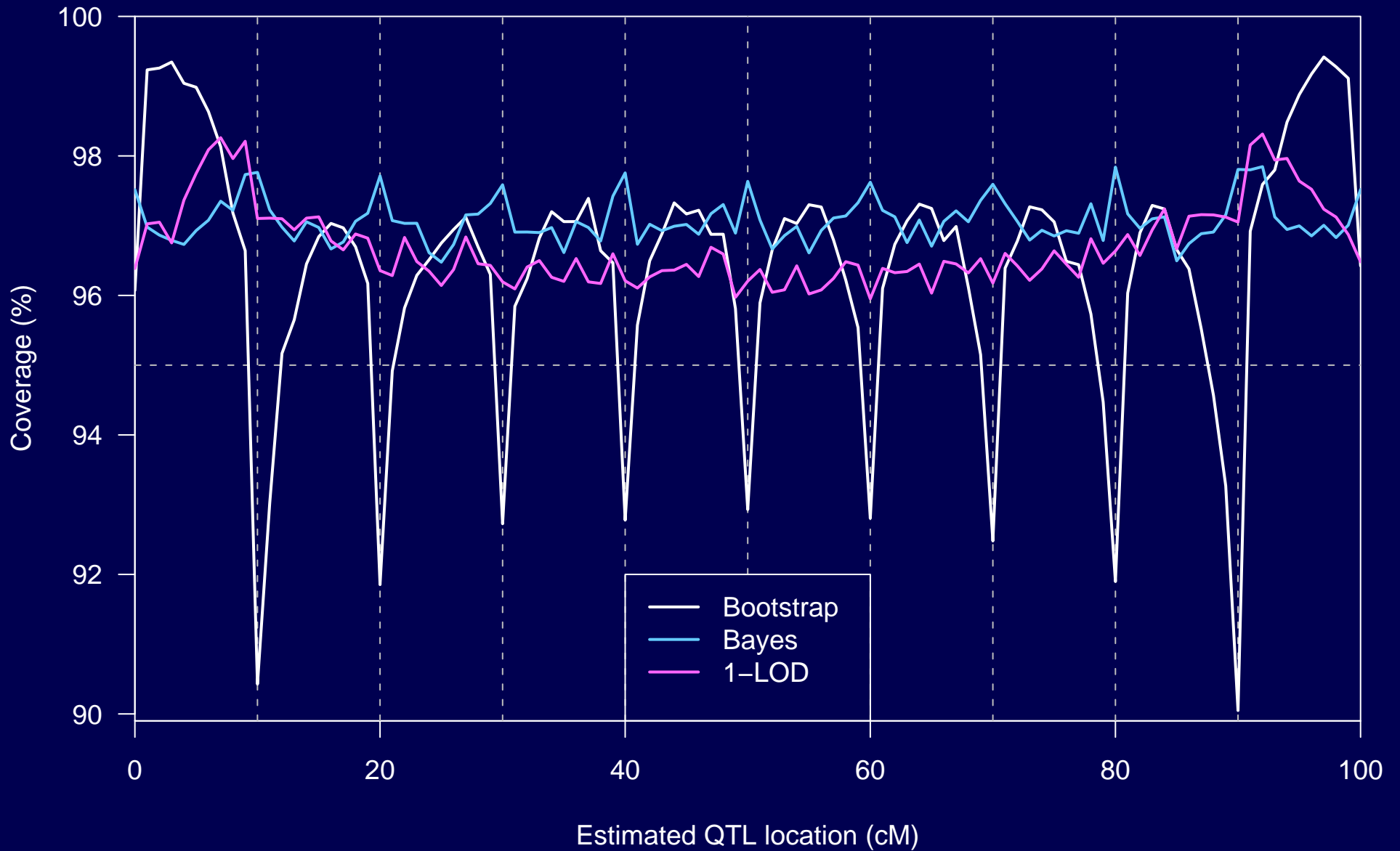
Distribution of estimated location



Coverage vs. true location



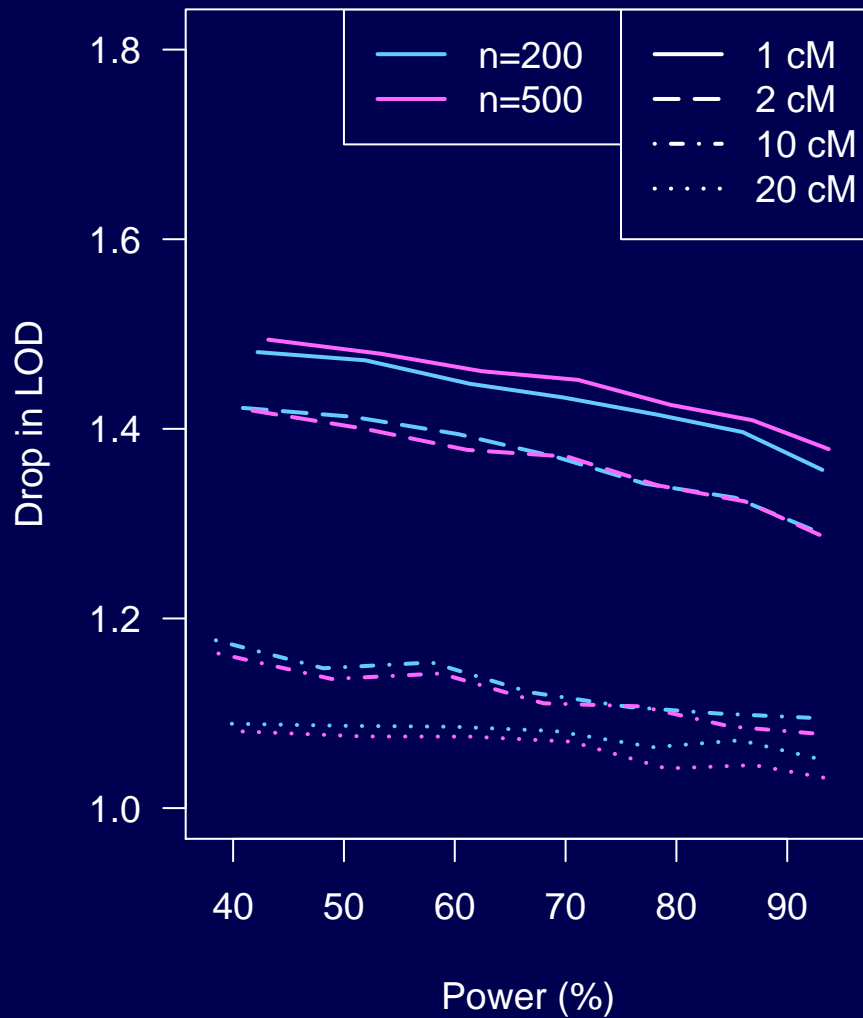
Coverage vs. estimated location



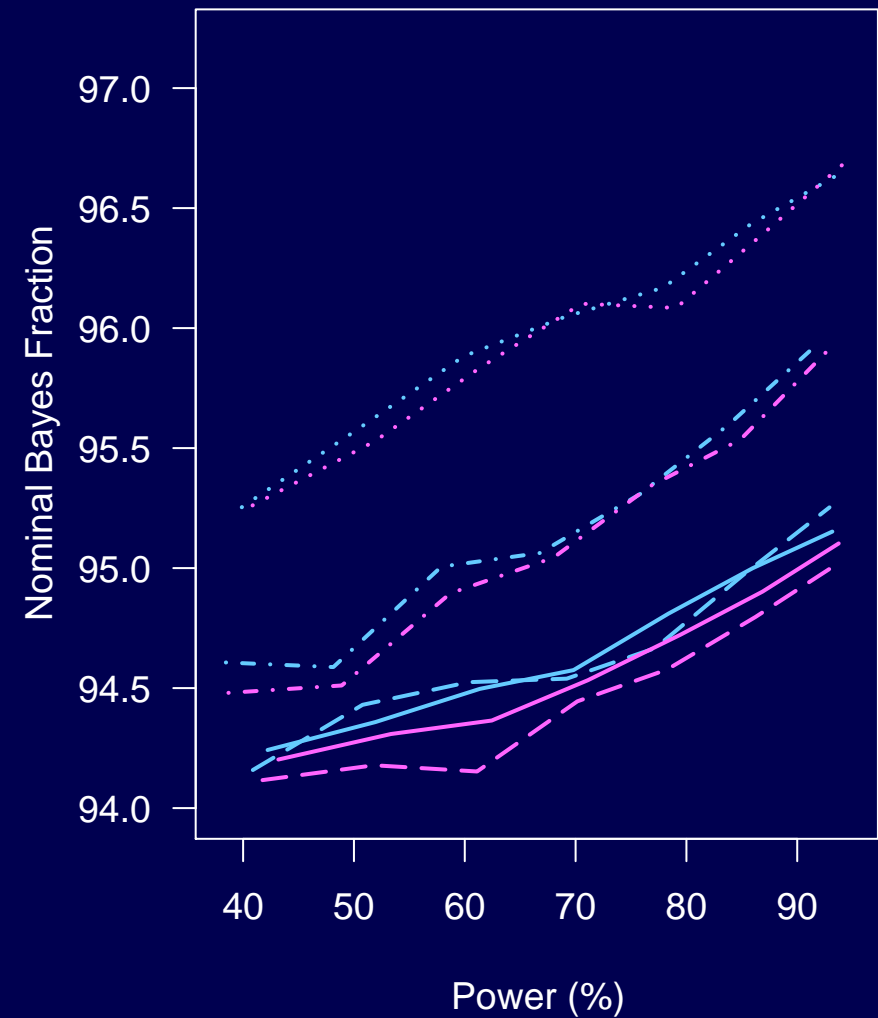
Optimal drop/fraction

Backcross

LOD support intervals



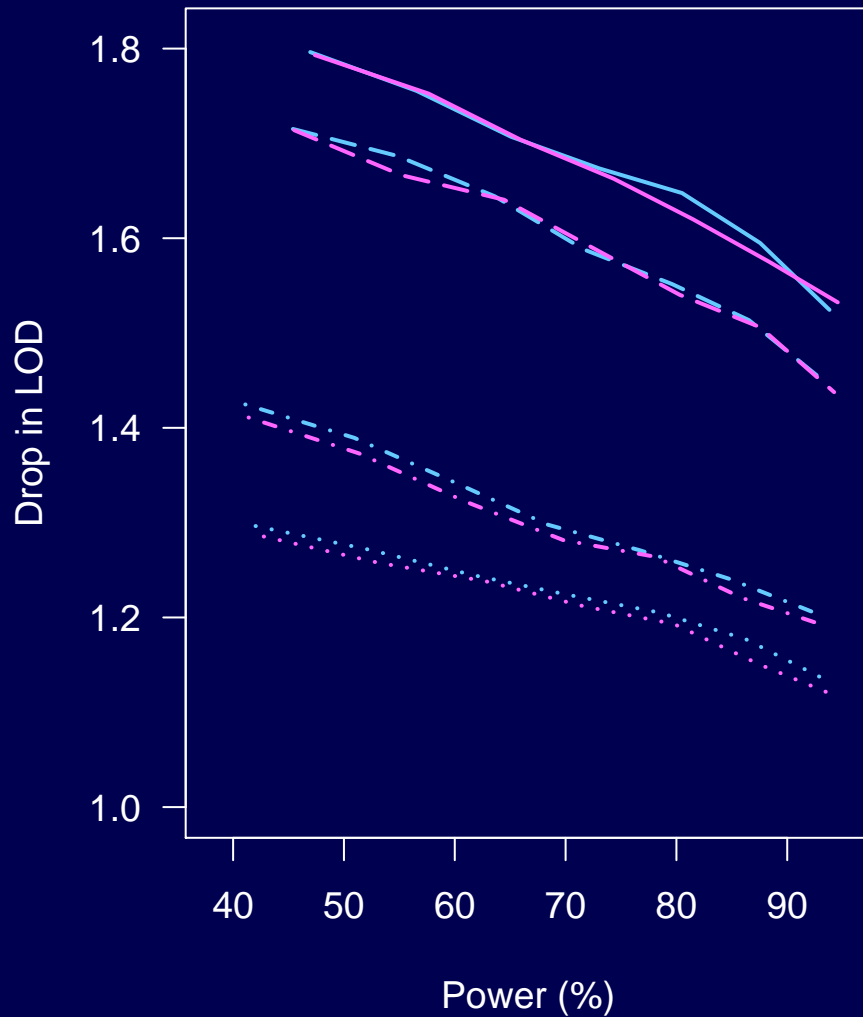
Bayes credible intervals



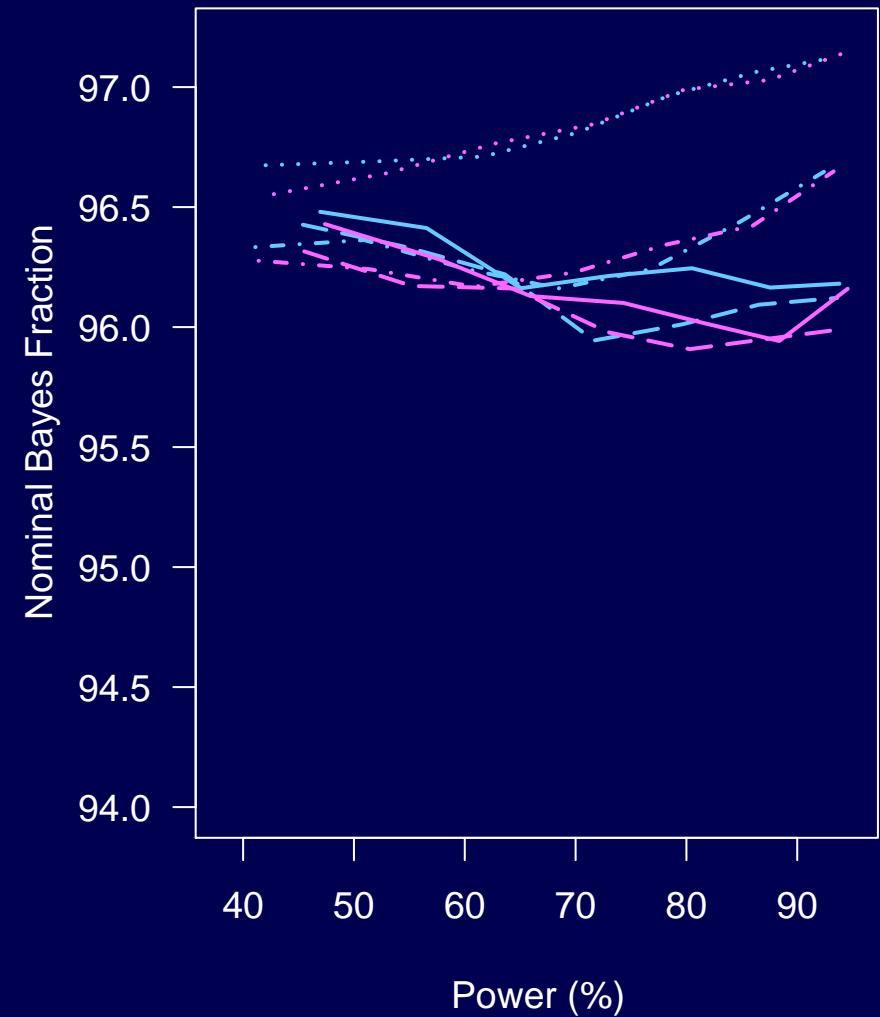
Optimal drop/fraction

Intercross

LOD support intervals



Bayes credible intervals



Acknowledgements

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