
Map / filter reads (*S. cer.* genome)
Count cut and uncut fragments at all genomic positions
Determine cut site positions with RE motif
Remove RE sites with close neighbour RE sites
Collect cut and uncut counts within window near cut sites to correct for resection
Calculate shearing probability for background correction
Recalibrate uncut correction factors or use provided factors
Estimate accessibility at each cut site using cut and uncut counts