**Saturation analysis of ChIP-seq data**

1. For the statistical analysis of peak saturation, the authors make an assumption that each fragment position can be latched onto by the protein with equal probability. This is what gives them their ‘n2 qfrags’ in a region spanned by n forward and n reverse reads, giving their inferences greater power. However, is the assumption really true?
2. It is not clear how the method works single-end read data. Would its performance be concordant with the other methods compared to in this paper, if a single-end read dataset was used instead of a paired-end one?
3. Is it justified to assume that each fragment end is sequenced with equal probability from the forward or reverse strand? There are tests in place (Mann-Whitney U Test) to establish where there is a phase shift between the forward and reverse reads, or a shuffled distribution of the two reads. It seems that this assumption currently completely overlooks PCR biases and how those might confound the data.

**BayMeth**

1. The authors model the corrected coverage using two separate variable distributions, the region specific read density at full methylation and the copy number in the interval being considered. The authors do comment on adjusting for the ‘linear relationship between CN state and MBD-seq read density” by adding in the multiplicative offset. But it is still not clear to me how the multiplicative offset will ‘correct’ against CN state. It seems to me that, say for example in a CN gain region, the multiplicative offset will end up giving an inflated read density distribution where the read density is already higher due to the CN event.
2. In the Bock study, the authors masked high-valued prior parameters so as to improve numerical optimization. Is this a justified approach? I wonder if this masking of high priors is what subsequently resulted in underestimation of high methylation levels in the stem cell line, in this analysis?

**swDMR**

1. The explanation that the authors give for ComMet giving a high potential false positive seems very odd. If the tool identified the most regions in high/low methylation levels at low methylation differences, how does that act as a proxy for false positives? Perhaps the ground truth in this case is based on a narrow distribution of methylation between the high and low methylation zones?
2. Apart from enrichment analysis for processes in the set of genes that show high methylation, what are some other methods to evaluate the functional role of DMRs detected by either methods?