Study questions for “ebGSEA: an improved Gene Set Enrichment Analysis method for Epigenome-Wide-Association Studies” by Dong et al.

1. How does the number of probes mapping to a gene affect pathway enrichment analysis with traditional GSEA analysis?
2. Why is it a good thing to see a low correlation in figures 1f, h, and i?
3. What new problems does GSAmeth introduce?
4. What is being ranked in GSAmeth? What is being ranked in ebGSEA?
5. Once the ranking is determined using ebGSEA, how are enriched pathways determined?
6. What makes this method more sensitive than GSAmeth?