

# An introduction to the personal methylome

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The era of personal genomics has arrived, and with it the opportunity to sequence one's own DNA for clues about disease, drug response and other traits. The challenge of personal genomics is that the discovery of genotype-phenotype relationships is difficult, and the interpretation of variants is currently limited to (weak) statistical association. Part of the reason for this may lie in the fact that factors external to the DNA may influence phenotype. One example of such an epigenetic phenomenon is methylation, which involves the chemical modification of cytosines adjacent to guanine nucleotides (CpGs). I will explain methylation, and then begin with a novel statistical argument that definitively demonstrates the existence of regions with excessive CpGs (CpG islands), even inside genes. Such regions affect gene regulation, and I will then discuss novel experimental techniques based on high-throughput sequencing for determining the methylation state in such islands. Finally, I will describe some applications of these techniques, and will conclude by discussing a personal experiment to measure my own "methylome". This is joint work with Meromit Singer, Dario Boffelli, David Martin, Alex Schoenhuth, Alex Engstrom, and Frazer Meacham.