(Jaffe & Irizarray, (Teschenforff & Zheng, 2017)

Definition of epigenetics refers to the patterns of gene transcription changes that occur without alterations in the DNA sequence (check Grealy). What is interesting is that epigenetic is a dynamic process and epigenetic modiﬁcations are reversible as opposed to genetic changes (Föcking et al., 2019; Wróblewski et al., 2019). DNAm is the first described and most studied epigenetic mechanism.

We will be focusing on DNA methylation at cytosine positions – these are positions where a methyl group is covalently bound to a cytosine located immediately adjacent to a guanine. Methylation of cytosines is one area of epigenetics that has been actively studied for several reasons:

DNAm is a highly dynamic process and it is thought that disruption of the methylation-demethylation balance is what contributes to pathogenesis of many neurological and psychiatric disorders (Greenberg and Bourc’his, 2019; Ovenden et al., 2018).

Common and Specific effects of antipsychotics on DNA methylation in Psychosis

Why we chose psychosis as a phenotype rather than diagnostic categories. Something about “trouble at the borders”. In this case, it is not about the treatment effect on the disorder, but the fact that the drug was prescribed for the symptoms of psychosis. And you can argue that there can be differences in the expression of the psychotic state, where individuals with scz may experience negative and frightful voices while individuals with psychosis in bipolar mania may experience voices of grandiosity. Tragically, in bipolar depression, voices in a psychotic state may seem clear and rational, and this is the danger in terms of suicide risk. In MDD, psychosis is …

CpG dinucleotides in which the methyl group is transferred, are not randomly distributed in the human genome and are predominantly concentrated in "CpG islands" located at gene promoters. Hypermethylation of CpG islands which are normally hypo or unmethylated leads to transcriptional inactivation of associated gene. The second type of DNA methylation (cytosine methylation; 5mC) is observed at the gene body and gene-body DNA methylation is associated with the activation of genes in contrast to the methylation observed in CpG islands (Greenberg and Bourc’his, 2019). In the past, DNA methylation was believed to be an irreversible and static epigenetic event related to gene repression, which could only be alleviated by DNA replication (Rasmussen and Helin, 2016). Today, however, it is known that DNA methylation is a highly dynamic process. Indeed, studies have shown that ten eleven translocation (TET) proteins (TET1, TET2, TET3) can modify 5mC and potentially erase DNA methylation.