Empirical examples of how DNA methylation data can be used to ask ecological or evolutionary questions

1. Banovich\_2014\_PG.PDF – effects of local sequence variation on DNA methylation levels in humans
2. Dubin\_2015\_eLife.pdf – effects of both cis and trans variants on DNA methylation levels in Arabidopsis
3. Lea\_2016\_ME.pdf – effects of differences in diet on DNA methylation levels in wild baboons (note, we will use data from this paper during the workshop)
4. Hernando-Herraez\_2015\_PG.PDF – a review of what DNA methylation can teach us about the evolution of species differences (and how DNA methylation itself is shaped by evolutionary change)
5. Tobi\_2014\_NC.pdf – effects of exposure to famine during early gestation on DNA methylation levels in humans
6. VERHOEVEN\_2016\_ME.pdf – recent review from a special issue, summarizing what we currently know about the role of DNA methylation in ecological and evolutionary processes

Reviews and methods papers about analyzing DNA methylation data

1. Bock\_2010\_NB.pdf
2. Bock\_2012\_NRG.pdf
3. Liu\_2012\_BisSNP.pdf
4. Lea\_2015\_PG.pdf – we will use this program during the workshop

Materials (scripts, programs, and input files) that we will use to perform analyses

1. beta\_binomial\_model.R
2. macau (executable)
3. sites\_analyzed\_counts\_chr1\_n61.txt
4. sites\_analyzed\_mcounts\_chr1\_n61.txt