

1. Epigenetic epidemiology has systematically underestimated measurement error on DNA methylation microarrays. [*This thesis*].
2. DNA methylation microarray probe exclusion lists can neither guarantee the complete exclusion of artifactual probes nor the utter inclusion of otherwise “healthy” probes. [*This thesis*].
3. Pooled whole-genome bisulfite sequencing experiments can simultaneously capture inter-haplotype, inter-cell and inter-individual variation in a cost-effective and privacy-preserving fashion. [*This thesis*].
4. Cmb-Im provides linear predictions and errors even at extreme missingness, ideal for applications such as age prediction in FFPE, cfDNA, single-cell or even forensic and paleoepigenetic samples. [*This thesis*].
5. Due to the tissue-specific nature of DNA methylation, convenient human proxy tissues (buccal cells, venous blood, cord blood) are often poor surrogates in EWAS and mQTL mapping studies. [*This thesis*].
6. “To call in the statistician after the experiment is done may be no more than asking him to perform a *post-mortem* examination: he may be able to say what the experiment died of”. [Sir R.A. Fisher].
7. “Statisticians, like artists, have the bad habit of falling in love with their models”. [George Box].
8. “Molecular biology is essentially the practice of biochemistry without a license”. [Erwin Chargaff].
9. “There are no facts, only interpretations”. [Friedrich Nietzsche].
10. Unidisciplinary scientists tend to judge interdisciplinary research the same way monolingual speakers react to minor deviations from the linguistic norm. [Benjamin Planterose Jiménez].
11. “Insert coin to continue”. [Arcade].