FlowSorted.DLPFC.450k User's Guide
A Public Illumina 450k Dataset

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1 Introduction

The FlowSorted.DLPFC.450k package contains publicly available Illumina HumanMethylation450 ("450k") DNA methylation microarray data from a recent publication by Guintivano et al. 2013 [1], consisting of 58 samples, formatted as an `RGChannelSet` object for easy integration and normalization using existing Bioconductor packages. For example, this dataset may be useful "example" data for other packages exploring, normalizing, or analyzing DNA methylation data.

Researchers may find this package useful as these samples represent two different cellular populations of brain tissue generated on the same 29 individuals using flow sorting, a experimental procedure that can separate heterogeneous biological samples like brain into more pure cellular populations, like neurons and non-neurons using NeuN labeling [2]. This data can be directly integrated with the minfi Bioconductor package to estimate cellular composition in users' frontal cortex Illumina 450k samples using a modified version of the algorithm described in Houseman et al. 2012 [3] and Guintivano et al 2013 [1].

References

[1] J. Guintivano, M. J. Aryee, and Z. A. Kaminsky. A cell epigenotype specific model for the correction of brain cellular heterogeneity bias and its application to age, brain region and major depression. *Epigenetics*, 8(3):290–302, 2013. `doi:10.4161/epi.23924`.

[2] A. Matevossian and S. Akbarian. Neuronal nuclei isolation from human postmortem brain tissue. *J Vis Exp*, (20):914, 2008. `doi:10.3791/914`.

[3] Eugene A Houseman, William P Accomando, Devin C Koestler, Brock C Christensen, Carmen J Marsit, Heather H Nelson, John K Wiencke, and Karl T Kelsey. Dna methylation arrays as surrogate measures of cell mixture distribution. *BMC Bioinformatics*, 13(1):86, 2012. `doi:10.1186/1471-2105-13-86`.