“Epiclomal: Probabilistic Clustering of Sparse Single-cell DNA Methylation Data”

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Objectives:

- Comprehensive clustering pipeline for single-cell DNA methylation data
- Epiclomal outperforms other methods on both synthetic and published datasets.
- Using in-house data, we show that Epiclomal discovers sub-clonal patterns of methylation in aneuploid tumour genomes, thus defining epiclones. We show that epiclones may transcend copy number determined clonal lineages, thus opening this important form of clonal analysis in cancer.

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