Type of methods	Examples	Purpose	Statistical tool	Suitability for lineage tracing data
One-by-one SNP selection methods	Monovar[10] SCAN-SNV[11] Conbase[12] Monopogen[13] mgatk[14] MQuad[15]	Identify a few SNPs that are non-randomly distributed and likely to be biologically functional or informative.	Ranking of p-value or other probability metric	Not suitable because the same SNP can appear in multiple close lineages in lineage tracing data.
Genotype-demultiplexing methods	SCG[16] BnpC[17] Cardelino[18] VireoSNP[19] Souporcell[20]	Demultiplex single cells from different genotypes in somatic mutation or donor-mixing experiments.	Factor analysis involving vectors of SNPs	Not suitable because optimal vectors of SNPs in lineage tracing data are highly correlated so convergence problems easily occur.
VAE-based cell-centric methods	SNPmanifold bmVAE[30]*	Cluster single cells to neighboring cells with similar genotypes in general SNV mutation data.	Learning a better cell-cell distance metric using VAE	Suitable because VAE does not suffer convergence problems and performs well even in high-covariance lineage tracing data.

*SNPmanifold is better than bmVAE[30] in terms of accuracy and silhouette score according to quantitative benchmarking (Supp. Fig. 1).