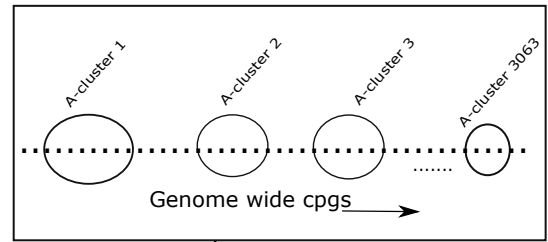


14 samples of DNA methylation Data (GSE41169)

random division into two groups

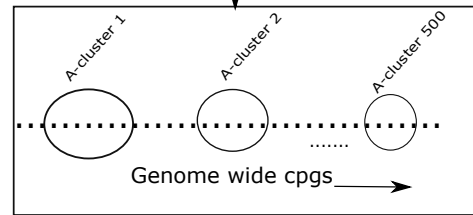
A-clustering

	group A	group A	...	group B	group B	...
cg00000029	0.46748	0.40972	...	0.390672	0.417321	...
cg00000108	0.935984	0.937811	...	0.939675	0.949266	...
...
cg27666123	0.858164	0.839337	...	0.825079	0.796012	...



repetition $r=1$

random selection of 500 A-clusters



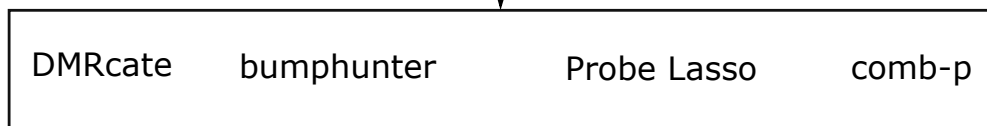
Addition of a specific $\mu \in \{0, 0.025, 0.05, 0.1, 0.15, 0.2, 0.3, 0.4\}$ to the group with higher mean beta value in 500 A-clusters

	group A	group A	...	group B	group B	...
cg00000029	0.46748+ μ	0.40972+ μ	...	0.390672	0.417321	...
cg00000236	0.742642+ μ	0.668882+ μ	...	0.640866	0.651623	...
...
cg2103060	0.849234+ μ	0.828295+ μ	...	0.790859	0.805921	...
cg00000108	0.935984	0.937811	...	0.939675	0.949266	...
cg00000109	0.895536	0.88019	...	0.903584	0.874905	...
...
cg27666123	0.858164	0.839337	...	0.825079	0.796012	...

CpGs belonging to the selected 500 A-clusters

Remaining CpGs in the genome

DMR identification



Comparison

Type of comparison

Power	Precision	DMRsize	DMR co-methylation	Overlap	Time
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repeat $r=5$ times