

**Supplementary information**

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**Simultaneous dimensionality reduction  
and integration for single-cell ATAC-seq  
data using deep learning**

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In the format provided by the  
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Simultaneous dimensionality reduction and  
integration for single-cell ATAC-seq data using  
deep learning

Kopp *et al.*

Supplementary Table 1: **Runtime and memory comparison.** Runtime comparison on a dataset with 12000 cells and 80000 peaks. We fitted a BAVARIA, PeakVI, scVI and SCALE for 100 epochs utilizing a GPU. For BAVARIA, a single VAE model was fitted. cisTopic was fitted with 10 topics and otherwise default parameters on a CPU.

Method	Time [sec]	Memory [Gb]
BAVARIA	794	5.1
PeakVI	903	2.9
scVI	1176	2.9
SCALE	1819	2.9
cisTopic	5401	3.4

Supplementary Table 2: **Summary of hyperparameters for the experiments.** Number of replications refers to the number of re-trained models with random initial weights. \* denotes the dataset and setup on which the binary and multinomial noise models were evaluated.

Dataset	Epochs	Batch size	latent hidden dims.	dims / layer	Ensemble size
Buenrostro 2018*	100	64	10/16		10
Buenrostro 2018 bulkpeak	100	64	10/16		10
Cusanovich 2018 subset	120	256	10/16		10
Cusanovich 2018 full	100	256	30/16		3
10x 5k PBMC	100	64	10/16		10
Bonemarrow clean	100	128	3/16		10
Bonemarrow coverage 5000	100	128	3/16		10
Bonemarrow coverage 2500	100	128	3/16		10
Bonemarrow coverage 1000	100	256	3/16		10
Bonemarrow coverage 500	200	512	3/16		10
Bonemarrow coverage 250	150	512	3/16		10
Bonemarrow coverage 20% noise	100	256	3/16		10
Bonemarrow coverage 40% noise	200	512	3/16		10
Erythropoiesis clean	100	256	3/16		10
Erythropoiesis 20% noise	100	256	3/16		10
Erythropoiesis 40% noise	100	256	3/16		10
mouse brain cell integration	200	64	15/25		10