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Publisher Correction: Learning interpretable cellular and gene signature embeddings from single-cell transcriptomic data

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Correction to: *Nature Communications* <https://doi.org/10.1038/s41467-021-25534-2>, published online 6 September 2021.

In the original PDF version of this Article, there was an error in the code within the 'Methods' subsection 'scETM software'. The original text read:

```
“from scETM import scETM,  
UnsupervisedTrainermodel = scETM(adata.n_  
vars, adata.obs.batch_indices.nunique())  
trainer = UnsupervisedTrainer(model, adata)  
trainer.train(save_model_ckpt = False)model.  
get_all_embeddings_and_nll(adata)”
```

The correct format is:

```
“from scETM import scETM, UnsupervisedTrainer  
model = scETM(adata.n_vars, adata.obs.batch_indices.nunique())  
trainer = UnsupervisedTrainer(model, adata)  
trainer.train(save_model_ckpt = False)  
model.get_all_embeddings_and_nll(adata)”
```

This has been corrected in the PDF version of the Article; the HTML version was correct at the time of publication.

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