# Article information:

Clustering of single-cell multi-omics data with a multimodal deep learning method | Nature Communications
<https://www.nature.com/articles/s41467-022-35031-9>

# Article summary:

1. Multimodal sequencing technologies have been developed to jointly profile multiple modalities of data in a single cell, such as mRNA expression, surface protein abundance, and chromatin accessibility.

2. Different modalities provide complementary biological information, and integrating them can lead to a higher resolution of cell typing.

3. Clustering analysis is an essential step in most single-cell studies, and numerous clustering methods have been designed for the analysis of scRNA-seq data.

# Article rating:

Appears moderately imbalanced: The article provides some useful information, but is missing several important points or pieces of evidence that would be required to present the discussed topics in a balanced and reliable way. You are encouraged to seek a more balanced perspective on the presented issues by exploring the provided research topics and looking at different information sources.

# Article analysis:

该文章介绍了单细胞多组学数据的聚类分析方法。然而，该文章存在一些潜在的偏见和不足之处。

首先，该文章没有充分考虑到不同模态数据之间的差异性和互补性。例如，ADT数据可以可靠地量化细胞活动，但只能测量几百种蛋白质。因此，在聚类分析中可能会忽略罕见或次要的细胞类型。相反，mRNA数据可以捕获全面的细胞类型，但由于其高维度和大量缺失值，可能会导致聚类结果不准确。因此，在整合多模态数据时需要更加谨慎地考虑这些问题。

其次，该文章没有提供足够的证据来支持所提出的主张。例如，在讨论ADT数据时，该文章声称“ADT数据似乎是表征细胞功能和类型的理想选择”，但并没有提供任何实验证据来支持这一观点。

此外，该文章也存在宣传内容和偏袒现象。例如，在讨论聚类方法时，该文章只介绍了作者所使用的方法，并未对其他方法进行公正客观地比较评价。

最后，该文章也没有充分考虑到可能存在的风险和限制。例如，多模态数据的整合可能会导致更高的计算复杂度和更多的噪声干扰，从而影响聚类结果的准确性。

综上所述，该文章需要更加客观、全面地考虑不同模态数据之间的差异性和互补性，并提供充分的实验证据来支持所提出的主张。同时，也需要公正客观地比较评价不同聚类方法，并充分考虑可能存在的风险和限制。

# Topics for further research:

* Differences and complementarity between different modalities of data
* Lack of evidence to support claims made in the article
* Promotion and bias in the article
* Need for objective comparison of clustering methods
* Risks and limitations of integrating multimodal data
* Importance of considering these issues in analysis of single-cell multi-omics data.

# Report location:

<https://www.fullpicture.app/item/996ae3740c14ae2a87af05db25b184c2>