# Article information:

SMURF: embedding single-cell RNA-seq data with matrix factorization preserving self-consistency | Briefings in Bioinformatics | Oxford Academic  
<https://academic.oup.com/bib/advance-article/doi/10.1093/bib/bbad026/7008800?login=true>

# Article summary:

1. SMURF is a tool that extracts low-dimensional embeddings from cells and genes using matrix factorization with a mixture of Poisson-Gamma divergent as objective while preserving self-consistency.

2. SMURF can reduce the cell embedding to a 1D-oval space to recover the time course of cell cycle, and can also serve as an imputation tool with robust gene expression recovery power.

3. SMURF has been tested on replicated in silico and eight web lab scRNA datasets with ground truth cell types, and successfully recovered the genes’ distribution from WM989 Drop-seq data.

# Article rating:

May be slightly imbalanced: The article presents the information in a generally reliable way, but there are minor points of consideration that could be explored further or claims that are not fully backed by appropriate evidence. Some perspectives may also be omitted, and you are encouraged to use the research topics section to explore the topic further.

# Article analysis:

The article provides an overview of SMURF, a tool for extracting low-dimensional embeddings from cells and genes utilizing matrix factorization with a mixture of Poisson-Gamma divergent as objective while preserving self-consistency. The article claims that SMURF exhibits feasible cell subpopulation discovery efficacy with obtained cell embeddings on replicated in silico and eight web lab scRNA datasets with ground truth cell types, and can reduce the cell embedding to a 1D-oval space to recover the time course of cell cycle. It also states that SMURF can serve as an imputation tool; the in silico data assessment shows that SMURF parades the most robust gene expression recovery power with low root mean square error and high Pearson correlation, and recovers the gene distribution for the WM989 Drop-seq data.

The article appears to be reliable overall, providing evidence for its claims through testing on multiple datasets. However, it does not explore any potential risks associated with using this tool or discuss any possible counterarguments or alternative approaches to solving this problem. Additionally, there is no mention of any potential biases or one-sided reporting in the article which could be addressed by exploring other perspectives or approaches to this issue. Furthermore, there is no discussion of any promotional content or partiality present in the article which could be addressed by presenting both sides equally or exploring other points of view on this topic.

# Topics for further research:

* Alternative approaches to matrix factorization
* Potential risks of using SMURF
* Counterarguments to SMURF
* Biases in scRNA datasets
* Promotional content in scRNA datasets
* Partiality in scRNA datasets

# Report location:

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