

Review of: "Enhancement of Network Architecture Alignment in Comparative Single-Cell Studies"

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Potential competing interests: No potential competing interests to declare.

This paper presents a new machine learning tool to identify similarities between cells from their respective genome content. This is interesting for automatically identifying cells from similar niches or from similar diseases in different species, which may help in translating preclinical results based on animal models to human clinics.

The ML tool proposed uses an encoder-decoder topology with some weights in the encoder part fixed from a pretraining process using transfer learning. This approach is chosen since the identification of similarities in single-cell RNA sequencing is made using nearest neighbor search in the latent space after encoding.

The paper is well-written and clear in introducing the reasons for this work, its main goals, methodology, and results. It also makes clear the possibilities of the ML tool and the improvements obtained against other alternatives.

My only concern is the small number of samples used for testing and the lack of sufficient external validation. This makes the conclusions not well supported by the results.

However, as a first proof of concept of this new possibility, it is a useful work with important potential applications.