

Faculty member 1: *The proposal is to extend/refine Network-based stratification (Hofree) with gene expression.*

Thanks for your time reviewing my proposal. Since the feedback pointed out my proposed method only providing methodological difference/improvement, I decided to improve the method to make biological significance. After this revision, I not only refine clustering technique but also extend model for novel and meaningful data integration.

How is this distinct from Chang et al 2016?

Chang's paper is merely a direct use case of NBS package and standard NMF package. Revised proposal distinct from that paper in both clustering method and integrated data sources.

It is fine if the distinction is purely methodological, just describe more clearly.

I rewrite most of the description and introduction to clarify my goal.

Then include in your data analysis, a comparison between your method and the previously published ones.

Yes, I will generate test and use real dataset to make comparison. Since there is no NMF based method integrating both mutation and expression data, I will compare with other methods integrating those data types, such as iCluster. I will also compare to standard NMF and NBS to test the non-smooth network-regularized NMF I proposed.

Faculty member 2: *I see the scientific question and the big picture. However, after reading the abstract, I'm unclear about the difference of the proposed method with existing works. Also I don't see how the proposed method can improve over existing methods.*

Thanks for incisive comments, I agree that my previous description is unclear about what is existed already and what is my novelty, so I re-wrote most of the introduction and updated methods. Also, I decided to improve my previous method by adding biological significance. So I revised my proposal to integrate both mutation and expression data for comprehensive stratification. Also mutation and expression clusters can be discovered together for stratified patients.

Before using technical terms, the abstract should explain the limitations and drawbacks of existing works in layman terms first.

Introduction is mostly re-written, strength and limitations are explicitly pointed out in existing works section.

When using technical terms, the abstract should specifically point out which parts of the proposed method are novel and different from existing works.

The novelty section is updated. The proposed model is distinct from existing models in terms of data integration and a more compact clustering ability.