

Response to Reviewer #1 Comments

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We sincerely appreciate the time and effort that you dedicated to reviewing our manuscript and are grateful for your insightful comments and suggested improvements. Thank you!

Point 1 — The gridded simplex framework proposed in the manuscript is utilized to replace the rectangular framework in GTM. However, both frameworks are grounded on the assumption that the data is uniformly sampled from the embedded manifold in the data space. This assumption may not hold true in real-world scenarios. How do the authors address this potential issue?

Response — Thank you for your comment. We agree that the assumption of uniform sampling in the latent space is a key limitation of the original GTM formulation. For the GSM we are introducing here, we have addressed this by introducing adaptive mixing coefficients π_k which are updated during the fitting procedure. As a consequence, the prior probability distribution is no longer uniform across nodes in the GSM latent space. Previously, we wrote “The second change is to replace equal prior probabilities with adaptive mixing coefficients π_k to allow the GSM to model HSI with nonuniform mixing distributions”. To further clarify this point, we have revised the text to now read:

The second change is to augment the equal prior probabilities of the GTM latent space with adaptive mixing coefficients π_k to allow for nonuniform sampling across the abundance simplex. This addition allows the GSM flexibly address many possible mixing scenarios without an *a priori* assumption for a specific mixing distribution.

Point 2 — The adaptive mixing coefficient is used instead of the equal prior probability of GTM to achieve the explanation of the endmember variation phenomenon. However, the adaptive update of the accuracy parameter β actually leads to the endmember variability estimated by the model being a range related to β in each band. How does the author determine the final endmember spectrum with variability?

Response — Thank you for your comment. The adaptive mixing coefficients π_k are utilized to account for nonuniform sampling of possible mixtures, not for estimating spectral variability. As you correctly point out, we use the precision parameter β for this corresponding to a normal distribution with a standard deviation of $\sqrt{\beta^{-1}}$ for all wavelengths. In future work we plan to extend the model to allow for wavelength-dependent spectral variability.

Point 3 — In the experimental section of the manuscript, the proposed method was compared with three early NMF methods. However, the reviewer believes that the experimental evaluation was not comprehensive and sufficient. Therefore, it is recommended that the authors compare their work with some of the latest and most advanced methods, such as nonlinear unmixing and spectral variability methods, as this, would enhance the contribution of the work in this paper.

Response — Thank you for your comment. The goal of our first experiment was to demonstrate that the GSM can model *linearly mixed* data without introducing unnecessary complexity, or in other words, the GSM should not incorporate non-linear effects for linearly mixed data. Our intention was not to suggest that the GSM is superior to other linear mixing models but rather provide a fair, apples-to-apples comparison to an established approach. To clarify this point, we have revised the text introducing the experiment to now read as follows:

To illustrate the effectiveness of the GSM, we first demonstrate its ability to model linear mixing. This serves as an important limiting case since linearly mixed spectra should not lead to the spurious introduction of non-linear contributions by the GSM. The goal of this first test is therefore to demonstrate that the GSM drives non-linear weights to zero for linearly mixed data while providing a fair test to compare the GSM to a well-established linear mixing model. This ability clearly distinguishes the GSM from other non-linear unmixing approaches such as autoencoders, which by their design, include non-linear mixing even when it is not present in the underlying data.

Additionally, we have included the following line after describing the varieties of NMF we chose to use:

We note that the goal of this test is not to prove the GSM is superior to other models for linear mixing, but rather to demonstrate that the GSM can model linearly mixed data without introducing unnecessary complexity.