Response to Reviewer #2 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 — Please reorganize the contributions in Introduction part and highlight the differences with other jobs.

Response — Thank you for your comment. We have updated the introduction to explicitly include a list of the novel contributions made by our approach. The updated text now includes the following:

> In summary, the key innovations introduced by the GSM are:
>
> - the GSM can model linear and nonlinear spectral mixing
> - the GSM does not assume the presence of pure pixels in the dataset
> - the probabilistic formulation of the GSM accounts for spectral variability
> - the simplex used for the latent space structure of the GSM is directly interpretable and forces abundances to satisfy both the abundance sum-to-one and abundance non-negativity constraints
> - the fiting procedure introduced for the GSM maintains non-negativity of endmember spectra.

Point 2 — Give more explanations on the functions, variables, and the dimension of variables in equation. For example, what is in Equation (2)? What is the meaning of and in and in Equation (3)?

Response — Thank you your comment. We agree that explicitly mentioning the dimension of included variables will improve the text. Unfortunately, it appears that the symbols you've coppied into your comment are not appearing. With this in mind, we have made the following updates to the manuscript:

- "$\boldsymbol{x}$ (reflectance spectra)" now reads "$\boldsymbol{x}$ (reflectance spectra of length d)"
- The description of Equation (1) has been updated to now read

> where $\boldsymbol{z} = \left(z_1, z_2, ..., z_{N_v}\right)$ corresponding to N_v-many sources and $\boldsymbol{W}$ is a $D \times M$ matrix of model weights which parameterize the mapping ψ.

- Equation (2) now includes the following description:

> where $\delta(\cdot)$ is the Dirac delta function and $\boldsymbol{z}_k$ are the positions of each node within the simplex.

Point 3 — Authors model non-linear mixing by designing an activation function . What is the physical significance of this function?

Response — Thank you for your comment. Together with the model weights $\boldsymbol{W}$, the activation function defines the mixing model, i.e. $\psi(\boldsymbol{z}; \boldsymbol{W}) = \boldsymbol{W}\varphi(\boldsymbol{z})$. We have designed these activation functions to account for linear mixing with $\varphi_m(\boldsymbol{z_k}) = [\boldsymbol{z}_k]_m$ and non-linear mixing via the radial basis functions described in Equation (4). To further clairfy this choice, we have updated the text to include the following statement:

> Equation 4 is specifically chosen so that no non-linear contributions are possible for pure spectra at the vertices of the simplex.

Point 4 — Only Figure 5 is the result of compared experiments, it is suggested to increase the data set and do more comparative experiments.

Response — Thank you for your comment. The goal of the linear unmixing experiment presented in Figure 5 was to demonstrate the the GSM can successfully unmix *linearly* mixed spectra without introducing unnecessary complexity, that is, that the GSM can successfuly solve a linear unmixing task while driving all non-linear terms to 0. We therefore chose NMF specifically as a well-established method to perform this comparrison. To make this clear, we have updated the text 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 spurous 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 clealy distinguishes the GSM from

> other non-nonlinear unmixing approaches such as autoencoders, which by their design, include non-linear mixing even when it is not present in the underlying data.

Additionaly, 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.

Point 5 — The related works should be enhanced. Some recently proposed methods should be investigated, such as GMOGH and Rev-Net.

Response — Thank you for your comment. We have updated the introduction to refer to multi-objective optimization methods and have included a citation for GMOGH as suggested. Since this paper is explicitly concerned with non-linear unmixing methods, we have not cited the recent Rev-Net paper (https://doi.org/10.1109/TGRS.2024.3403926) which, while very interesting, appears to adopt a linear mixing model.