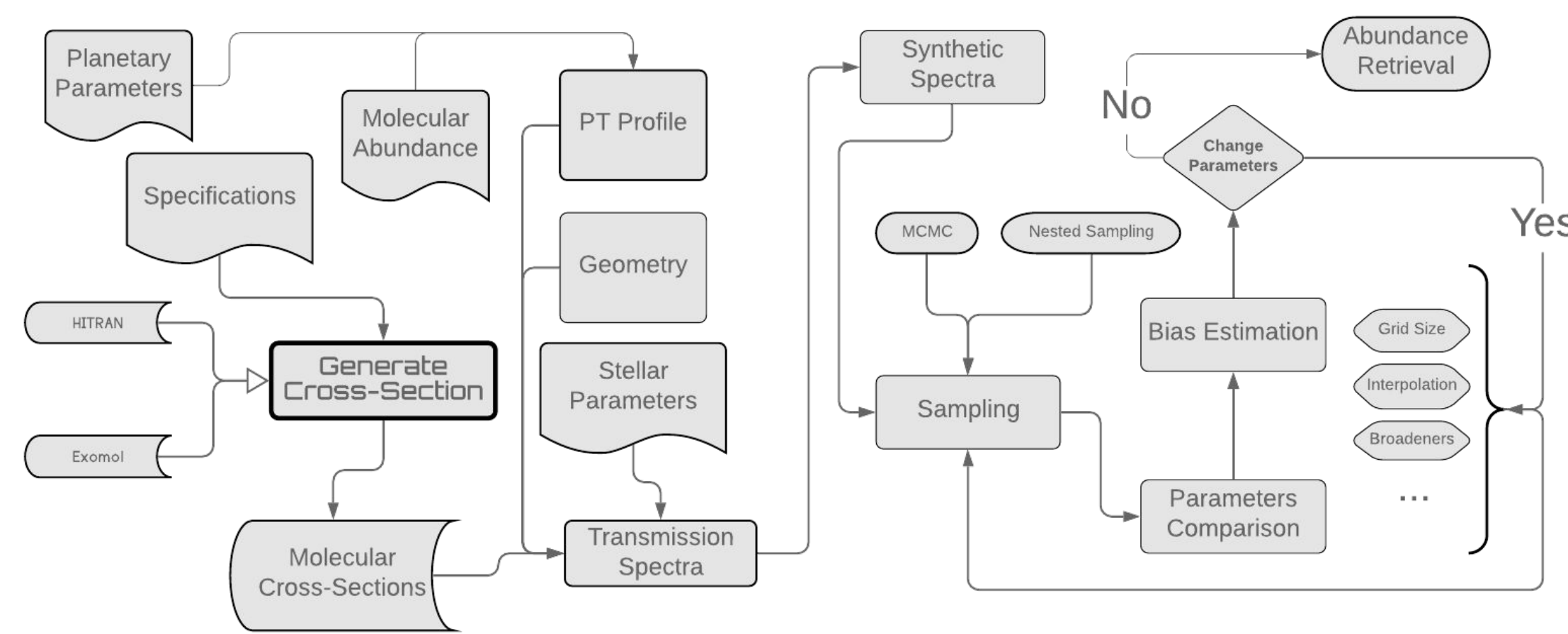


Abstract

Exoplanetary atmospheric retrieval techniques currently employ line-by-line generated opacities across a grid of temperature and pressure for relevant molecular species. These cross-sections are computed under assumptions of certain pressure broadening and isotopic fractions, which have inherent uncertainties associated with them. If not properly considered, these uncertainties will non-linearly propagate into the atmospheric retrieval process and may appreciably bias the results. Understanding these uncertainties will be increasingly important as we look forward to obtaining higher resolution spectroscopic data with the next generation of telescopes, and discerning small bio-signature signals in the atmospheres of temperate worlds such as TRAPPIST-1 planets. Different databases such as HITRAN [1], and ExoMol [2] have in recent years taken steps into providing new parameters such as pressure broadening coefficients and collision induced absorption in the anticipation of their utility for exoplanetary atmospheric studies. We are currently in the process of leveraging these databases to understand the potential biases present that current atmospheric retrieval techniques are vulnerable to.



Flowchart of our current framework for estimating biases.

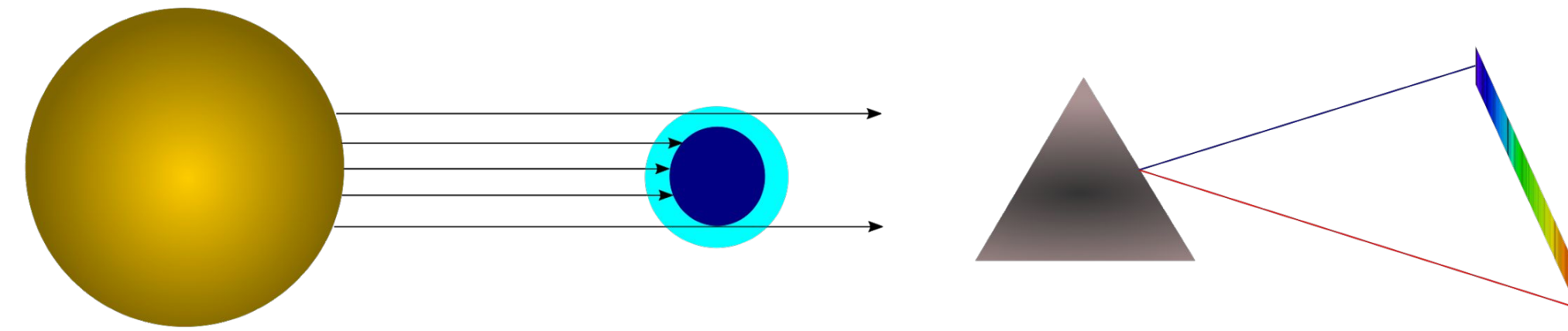


Fig 1. Schematic representation of Transmission Spectroscopy of an exoplanet.

Parameters under Consideration

1. Broadeners
2. Collision-Induced Absorption
3. Isotopic composition
4. Line Wings
5. Resolution of Line-by-Line Generated Cross-Section
6. Interpolation and gridsize
7. Binning of data

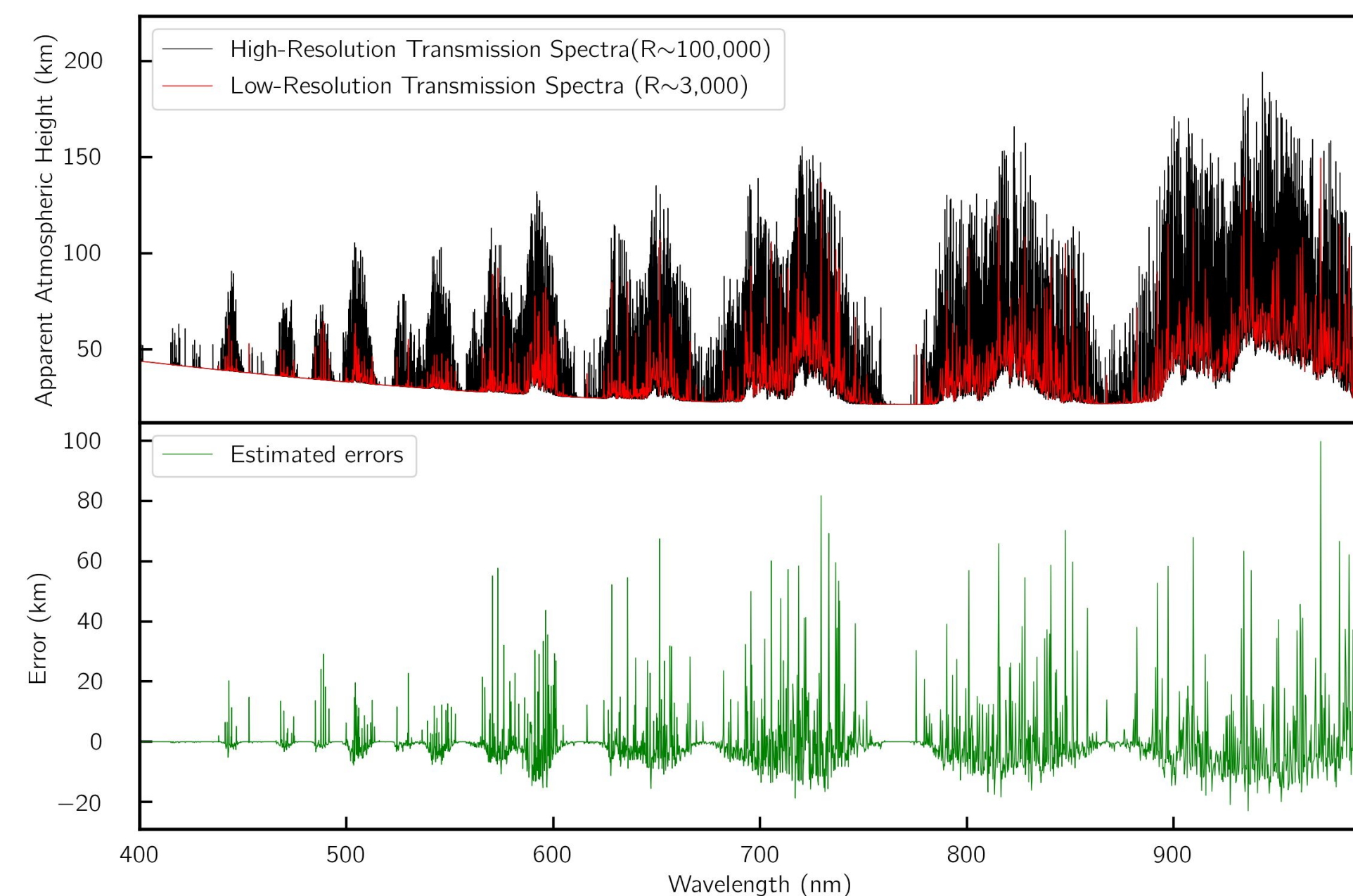


Fig 2. Estimated difference in the theoretical transmission spectra of a typical super-Earth dominated by water due to use of different resolution of cross-section.

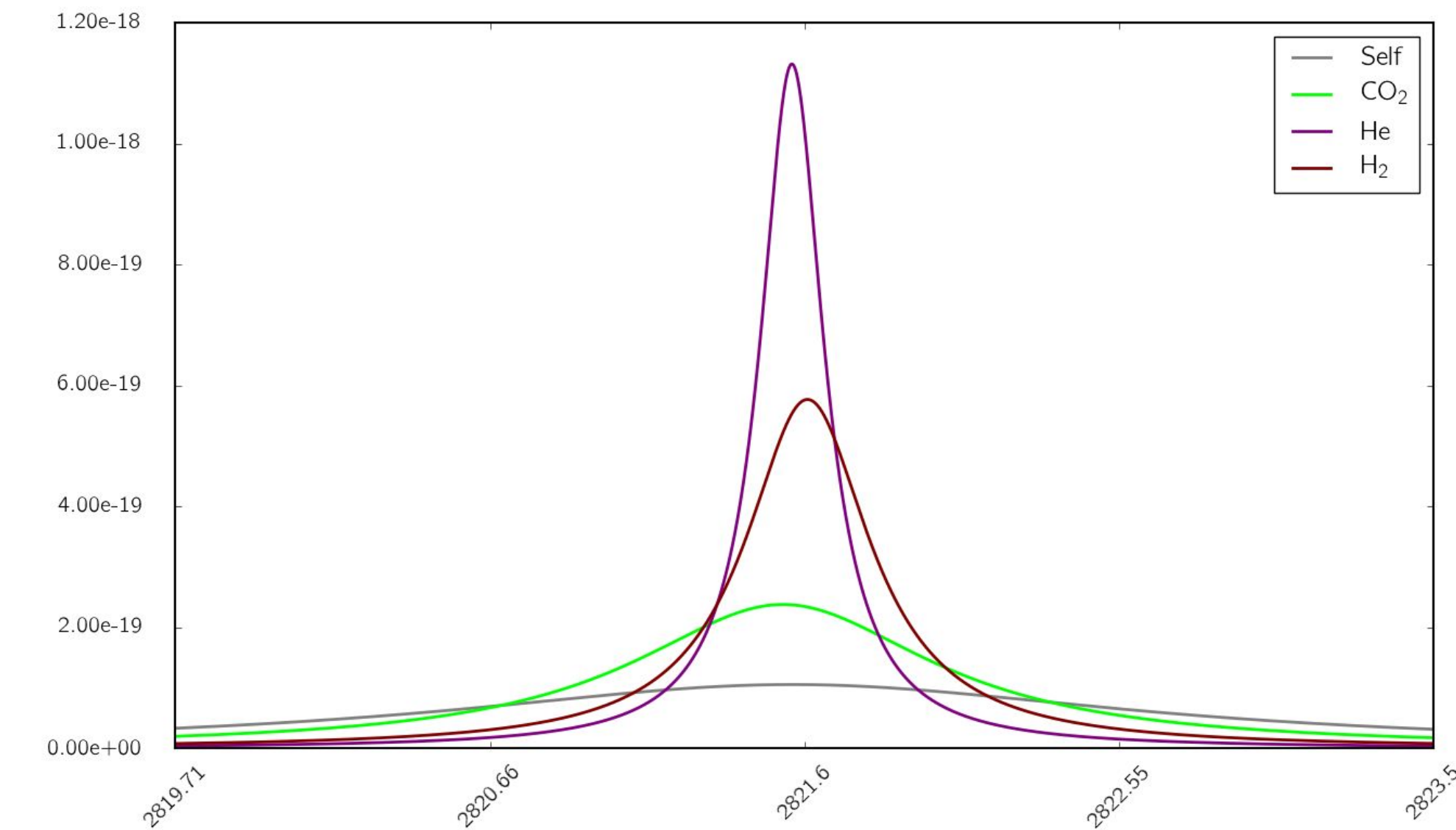


Fig 3. Theoretical cross-section of HCl molecule with different broadeners. We will be assessing biases introduced by such deviation in the cross-section during the retrieval process.

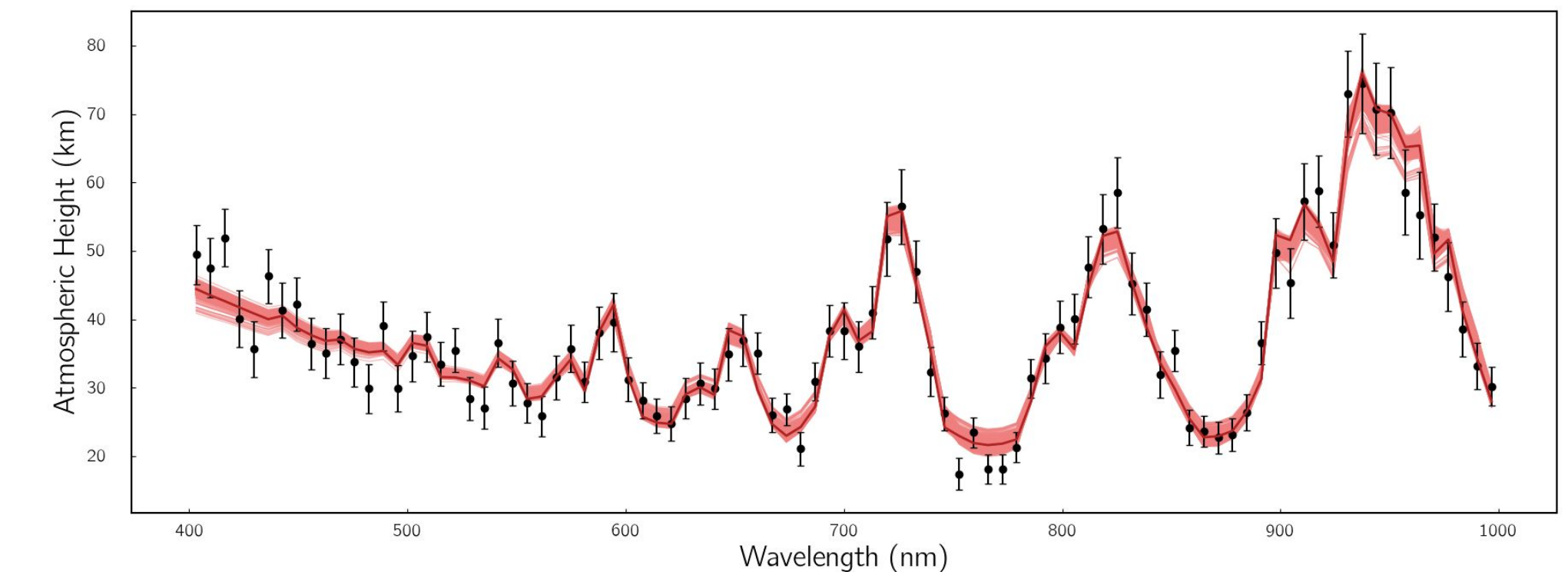


Fig 4. A sample of MCMC run for abundance retrieval of molecular species. We plan on estimating the biases propagation, and their effects on the retrieved abundances next.

Conclusion and Outlook

We are in the process of developing and refining our pipeline, creating cross-sections with different assumptions using hapi [3] and benchmarking speed and accuracy against other publicly available codes. Our preliminary work show parameters such as pressure, and interpolation are important for retrieving the injected parameters. We are in the process of putting these biases in a better theoretical framework to understand, and mitigate their effects on the retrieval.

References

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2. Tennyson, J., Yurchenko, S. N., Al-Refaie, A. F., et al. 2016, Journal of Molecular Spectroscopy, 327, 73
3. Kochanov, R. V., Gordon, I. E., Rothman, L. S., et al. 2016, JQSRT, 177, 15