We thank the reviewer for their detailed and helpful comments and suggestions for the manuscript. All helped to clarify our presentation of the material, and we were especially appreciative of the comments pertaining to the split and merge tool and the PBC procedure. We understand that the initial discussion pertaining to these areas specifically was complex and challenging to follow in some places, so we welcomed the opportunity to expand upon our work.

Line 1-3: Could you please use a better title?

We appreciate the reviewer's interest in seeing an improved title. Under GMD submission guidelines, we are required to put the name and version number of the software tool before providing any other details in the title, so we cannot change this part of it. While we understand that our title is wordy, we believe this was the most succinct yet comprehensive way to address the improvements to *tobac* and their purpose covered in the manuscript.

Line 32: Delete "diffusive, advective"? Do you think diffusion and advection are neither dynamic nor thermodynamic processes?

Thank you for your comment, we have removed this from the text.

Lines 281-282: I don't understand the logic of this sentence. If there are just a few examples of splits and mergers in the atmosphere, why is there a clear need for splits and mergers processing within tobac?

We realize this statement was worded in a confusing way. It is not that there are few examples of splits and mergers in the atmosphere, it is that we only provide a few examples in the text. We have clarified this passage at lines (289-291) to read:

"These examples are just a few of the many processes involving splits and mergers in the atmosphere, and thus there is a clear need for splits and merger processing within *tobac*.[...]"

Line 292: What do you mean by minimizing the movement of the object centers?

This sentence was intended to summarize part of the approach used by Dixon and Weiner (1993) for tracking in TITAN. For each time step, Dixon and Weiner predict the possible motion of all detected feature centroids, resulting in many potential tracks. The first step in their determination of the actual path is the consideration that "the correct set will include paths that are shorter rather than longer". As such, we initially summarized this process by referring to it as "minimizing the movement of the object centers.", but have rephrased this to say "selecting the shortest, and thus most likely, path.", now on line (301).

Line 325-331: Is Figure 8 consistent with the descriptions here? T2 in cell 1 is neither the last nor the first feature. What do you mean by linking the last feature of a cell to the first feature of a nearby cell? I may misunderstand something, but I need more detailed clarification of the method. In addition, could you please provide two real examples: one for merging and one for splitting? The purpose is to ensure that tobac works as you expect.

Thank you for identifying this inconsistency between text and figure. Our initial text did not properly describe some of the details of the procedure, and we apologize for the ensuing confusion. For split/merger determination, we allow a user-set window (the default is 5 timesteps) with which to match the last feature of one cell to the start of a nearby cell. The end of one cell can occur after the start of the nearby cell, and as long as those fall within the 5 timesteps (or whatever the user decides) and the distance thresholds, they can match. Thus, in Figure 8, where the T1 of Cell 2 has a line drawn into the T2 of Cell 1, it would technically be 'more' correct to draw the line between T0 of Cell 2 to Cell 1. We have depicted this below in the revised Figure 8, which has also been updated in the manuscript.



Figure 8: An illustration of merging cells (Cells 1 and 2) and a standalone cell (Cell 3) as perceived by tobac. All three cells are comprised of features in radar data which exceeded a 15 dBZ threshold. Merging criteria (size and proximity) for the "tail" of Cell 1 and "tip" of Cell 2 are met at time t2, thus, these cells are judged to have merged over their lifetimes.

We have also changed the text to give a more accurate description of the process:

"works by linking the last feature of a cell to the first feature of a nearby cell. We take the last feature of all cells, and then find the distance between each last feature and each initial feature within a user-set number of timesteps (the default value is 5) for all timesteps. This distance is the weight of the branches in the MEDST. Before further processing these paired points (i.e., the location of the last feature in a cell and the additional feature in another cell) [...]" (335-338).

Additionally, we have produced a new Figure 9 in the manuscript as well as a Supplemental figure, Figure S1, in response to your comment and a similar comment from Reviewer 2 interested in seeing more timesteps of the split and merge processes. We hope these examples are sufficient to demonstrate that the split/merge tool works as intended.

Lines 347-355: Yes, it is hard to select an appropriate distance parameter since you used the distance between features. Did you consider using the distance between segmentations? I meant the minimum distance between two segmented regions. It might eliminate the issue in Figure 9.

Thank you for this great suggestion. We have not yet considered using the distance between segmentation regions for split and merge criteria in the present implementation within *tobac*. This is now being explored for future versions.

Lines 427-431: Why did you remap the brightness temperature dataset? According to the last paragraph, the segmentation could be conducted on the new (brightness temperature) grid. If so, plotting on the original GEOS-16 satellite grids would be more beneficial to introduce the new characteristic of tobac. In addition, in Line 430, I didn't find the top-right feature marked by the grey dot. Did you mean that in the top-left corner?

We disagree with the reviewer that performing segmentation on the brightness temperature grid would have better demonstrated this new aspect of *tobac*. As feature detection was initially performed on the radar data grid, we feel that remapping the brightness temperature dataset so we could perform segmentation on the same grid that feature detection was performed on is more appropriate for analysis purposes. Further, the GOES-16 grid is more spatially coarse than the NEXRAD data, so remapping the detected features and/or radar data to this grid would lose some numerical precision.

Additionally, we appreciate your identification that Figure 13 does not match the associated text in the manuscript, and we have adjusted the text to remove any mention of the absent feature:

"Ultimately, the segmentation outlines shown in Fig. 13b depict the anvils corresponding to each marked radar reflectivity feature." (440-441)

Section 4.3: Could you please provide more details about the PBC treatments? I can understand the improvements from Figures 14 and 15 but don't understand what you did to achieve them (I guess you just extended the x dimension to include the data from the next timestep in Figure 14). Is your method still valid if a feature crosses the boundary two times? In Figure 14c, the feature crosses only one boundary. If the feature is large enough, crossing another boundary on the right (or more), can tobac v1.5 get the correct result?

Thank you for your comment. This was actually a complex undertaking which required different approaches for each of feature detection, segmentation, and tracking. As such, we avoid spending too much time focusing on this treatment in the manuscript due to the number of other improvements in v1.5 which needed to be discussed. We have provided a more detailed explanation of our approach here in our response to you and have also prepared a short appendix, but are reluctant to add extensive additional text to the primary manuscript given the length of the existing text.

Once labeling of data fields is performed during the feature detection treatment, the PBC routine "looks" across one or both model boundaries to see if there are any labeled regions which are contiguous, but artificially separated by the model boundaries. Overwriting of labels in eligible data regions is performed continuously until all contiguous data regions have their own discrete label.

Tracking handles PBCs by implementing a custom distance function that removes the "wraparound" distances found across these boundaries.

The PBC treatment for segmentation is more complex. We provide an illustration of two particular use cases the treatment has been designed to address in Figure B1 below:



Figure B1: A depiction of two elements the PBC segmentation treatment. In Panel (a), we have two sets of regions (the red and blue shapes, and the magenta and white shapes) which are artificially separated by a model boundary. The white shape in Panel (a) is "eligible but unseeded", meaning it exceeds the segmentation magnitude threshold but did not have a marker placed within it to conduct watershedding. Since the magenta shape is in contact with this shape across the model boundary, we first seed all adjacent boundary points (as depicted in Panel (b) ) and then use these to watershed the relevant "eligible but unseeded points" as shown in Panel (c). The red and blue shapes shown in Panel (a) have both been watershed by different feature markers, but are artificially separated by the model boundary. This necessitates the selection of these two shapes into their own contiguous domain (the dashed orange "Buddy Box" depicted in Panels (c)-(f) ) so that watershedding can be performed again to obtain the correct segmentation boundaries. After transforming these grid points and their included data into the "Buddy Box" domain as shown in Panel (d), we place our feature markers (the red and blue boxes with black outlines) in the domain and perform watershedding again, as shown in Panel (e). Subsequent to the "Buddy Box" watershedding, the correct segmentation regions are transformed back into the original domain, as shown in Panel (f). Boxes with bright colors and black outlines depict the feature markers used for watershedding; the paler corresponding colors denote the regions segmented by these markers through watershedding; the white boxes denote "eligible but unseeded" regions

(i.e., above the segmentation magnitude threshold but not marked by a feature), and the gray boxes denote regions that are beneath the magnitude threshold and are not eligible to undergo watershedding.

The simplest case occurs when a segmentation field on one side of a boundary has been marked and watershed, but the same contiguous field on the other side of that boundary has not (the magenta and white shapes in Figure B1(a)). Here, we simply assign the same label to the unlabeled region as that which has already been watershed (Figure B1(b)-(c)).

For cases when two or more labeled segmentation regions meet at a model boundary (the blue and red shapes in Figure B1(a)), a new sub-domain (the dashed orange outline, which we refer to as a "Buddy Box" in this figure and our source code) is constructed of only the grid cells corresponding to these segmentation regions, but with all artificial boundaries removed so the fields are continuous. Then, markers are placed again (Panel (d)) and watershed segmentation is performed on this new sub-domain (Panel (e)). The segmentation boundaries ensuing from this procedure are then adapted back to the original segmentation field before PBC treatment, as shown in Panel (f).

Lines 493-496: Please rewrite it with shorter sentences.

Thank you for this comment, we have broken up this passage into shorter sentences as shown below:

"One key element planned for the next major release includes integration with the TiNT is not TITAN (TiNT; Raut et al., 2021) tracking package. We are also seeking to transition away from tobac's current memory-intensive data structures to data structures that allow for out-of-memory computation instead (e.g., Dask from Rocklin, 2015; xarray from Hoyer and Hamman, 2017)." (503-506)