Interactive comment on "Technical Note: Monte-Carlo genetic algorithm (MCGA) for model analysis of multiphase chemical kinetics to determine transport and reaction rate coefficients using multiple experimental data sets" *by* Thomas Berkemeier et al.

Anonymous Referee #1

This technical note explains a method for inference of chemical and physical parameters relevant to atmospheric processes. As explained in the note, it could be of use to multiple types of atmospherically-relevant experiments investigating different parameters. It is therefore relevant to the journal and of importance to the research community.

I recommend publication pending minor revisions. Below are a description of these revisions (numbered). On the whole the note is very well written and presented, and I think goes into sufficient depth without being overbearing (as would be possible due to

the relatively complicated nature of the method in question).

1) The sentence spanning lines 103-106 is both complicated and elongated. Could it be made more readable?

2) In sect. 3 (around the genetic algorithm explanation) I am left unsure how homogenisation of the population is achieved. My interpretation of the text and Fig. 1 is that some set of the population with a satisfactorily high correlation survives and is not further changed. The remaining population of parameter sets (children) changes through recombination and mutation of extant children or through replacement of these children with new ones. How does this child population homogenise to a population with high correlation? Are their parameter values informed by the parent population (as the family names suggest)? If so, this needs to be made clearer I think. An alternative process that comes to mind is that the size of the parent population increases as more children meet the correlation criteria (i.e. a satisfactorily high correlation). They achieve this through the random process of parameter change (recombination etc) rather than through any inheritance from parents. Again, if this (or any other) process causes homogenisation then it needs to be explained more clearly in the text (and possibly in Fig. 1).

3) On lines 144-150 can some additional information be provided as to the relative pros and cons (if any) of the reseeding and migration approach vs. repetition of the MCGA approach? Furthermore, can statistical bounds be determined using the former approach as it is stated they can be for the latter?

4) In Fig. 1, I suggest making the distinction between the Monte-Carlo step and the genetic algorithm step clearer. From reading of the main text the difference is clear, however, the names of the two steps are combined in Fig. 1, and they could be separate and placed distinctly above their respective schematic representation. I only suggest this because it may make the concept of the approach easier to appreciate (I got confused with when the Monte-Carlo usage stopped due to the random nature of

mutations and introductions of new parameter sets in new generations of the genetic-algorithm step).

5) I ask the authors to consider expanding on their description of model development in the introduction to further emphasise the importance of the MCGA method. The increased model complexity they describe does allow for inference of parameter values from increasingly complex measurement setups. However, this is only possible through methods like MCGA. As atmospheric science tries to bridge the divide between laboratory measurements and the real atmosphere and simplified models and global ones, it seems that methods like the MCGA will be very important.

6) Typos: Should "similar model output" on line 27 be "similar model input"? Should "breath" on line 92 be "breadth"? Should "as heuristic" on line 110 read "as a heuristic"?