

Interactive comment on “GenChem v1.0 – a chemical pre-processing and testing system for atmospheric modelling” by David Simpson et al.

Anonymous Referee #2

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General comments

This manuscript documents the software package GenChem used to generate the code for calculation of chemical reactions in atmospheric chemical transport models (CTMs). Although in principle being a standalone pre-processor, GenChem is in practice strongly tied to the EMEP CTM. The naming convention, structure etc are closely linked to that model and users without knowledge of the EMEP model could presumably have difficulties getting into the nomenclature. This is not meant as a negative comment. The EMEP CTM is a key model in atmospheric science and European abatement policies and the documentation of GenChem is an important issue in that respect.

Additionally, the possibility of using GenChem for testing and comparing various chem-

ical mechanisms in a box model setup is a very valuable facility.

The manuscript is a technical documentation that appears somewhat like an extended user manual and is somewhat hard to read without actually sitting down and trying out the various parts of the preprocessor. That said, the manuscript seems very well worked through without any major shortcomings and could be accepted with a few minor or technical corrections.

Specific comments

The authors use various names for the EMEP model. It would help the clarity if they stick to one name (e.g. EMEP CTM).

Line 70. It is probably true (as the authors believe) that the EMEP model is among the fastest CTMs, but it would be of to interest to know if there actually has been any comparison of the speed of some of today's main CTMs.

Table 1: The authors might consider to add the output files generated by boxChem either in this table or in a separate table. Now, Table 1 contains the files generated by the GenChem only and not the boxChem.

Technical corrections

Line 105. Replace “box-model code” with boxChem.

Line 150: Species M should be explained here (it is explained later in the doc).

Line 168: Should there be a “-v” in the command similarly to the command at Line 163?

Line 215. Missing chapter info (“?”)

Line 227: What does NPAS stand for?

Line 304: “OXN- indicates that this species that belong to a group”. Rephrase.

Table 4 (caption). Mentions EMEP's default 'PNAS' scheme. Presumably misspelling

of NPAS?

Suppl. Info (p S6): “Even with dt of 120 s RRMSk values don’t exceed 1%.R”. Remove the last “R”

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