Spatial Reduction Algorithm for Atmospheric Chemical Transport Models

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Numerical modeling of global atmospheric chemical dynamics presents an enormous challenge, associated with simulating hundreds of chemical species with time scales varying from milliseconds to years. Here we present an algorithm which provides a significant reduction in computational cost. Since most of the fast reactants and their quickly decomposing reaction products are localized near emission sources, we use a series of reduced chemical models of decreasing complexity with increasing distance from the source. The algorithm diagnoses the chemical dynamics on-line, locally and separately for every species according to its characteristic reaction time. Unlike conventional time-scale separation methods, the spatial reduction algorithm speeds up not only the chemical solver but also advection-diffusion. Through several examples we demonstrate that the algorithm can reduce computational cost by at least an order of magnitude for typical atmospheric chemical kinetic mechanisms.

Introduction

The modeling of tropospheric oxidants (ozone and the hydroxyl radical $OH$) is of central importance for addressing issues of air quality, aerosol formation and evolution, acid formation, and global budgets of greenhouse gases such as methane [1]. Although the chemical factors controlling tropospheric ozone and $OH$ are fairly well established, the computational challenge of modeling concentrations in relation to changes in emissions or climate is enormous. Current photochemical mechanisms describing oxidant chemistry include hundreds of coupled chemical species reacting on time scales ranging from milliseconds to many years [2].

Typical chemical transport models (CTM) combine chemical reactions with advection by a meteorologically predicted flow velocity. The resulting system of equations is extremely stiff, nonlinear and involves a large number of chemically interacting species. The difficulty of solving these equations imposes severe limitations in the spatial resolution of the CTMs, as well as the timescales that can be simulated. This difficulty represents a major obstacle for progress in atmospheric chemistry research. Even with a simplified chemical mechanism of $\sim 100$ species, present computational resources limit the number of CTM grid points to $\sim 10^5$, corresponding to a horizontal resolution $\sim 100$ km and a vertical resolution $\sim 1$ km [3]. This is not adequate for resolving the vertical stratification of the troposphere [4], the dynamics of the planetary boundary layer [5], convective processes [6], or sharp horizontal gradients across fronts and coastlines [7]. The push for fast, high-resolution CTMs will be exacerbated over the next decade by the need to interpret satellite observations of tropospheric ozone and related species [8].

In this paper, we present a numerical algorithm that addresses two major aspects of this problem: the large number of interacting chemical species and extremely large stiffness of the chemical model. Our algorithm is inspired by the observation that atmospheric emissions have most of their fast reactants and their quickly decomposing reaction products localized near the emitter, typically near the ground. Far from the emitter, the fast reactants do not play a significant role. There is thus the opportunity to spatially reduce the chemical mechanism, where a full chemical mechanism is used near emission sources and reduced mechanisms are used far from sources.

To give an idea of the scale of the computational savings that could result from such an algorithm, consider the chemical mechanism of the GEOS-Chem CTM [9], extensively used for tropospheric chemistry applications [10]: about 65 of the 120 species describe nonmethane hydrocarbons (NMHC) and their oxidation products. These NMHCs are emitted by anthropogenic and natural processes at the surface of continents. Most have short lifetimes. The most important NMHC is biogenic isoprene, which has a lifetime of less than one hour against oxidation and whose oxidation products account for 25 species in the mechanism. Although proper simulation of isoprene and other NMHC chemistry is critical near the ground [11], in the remote troposphere concentrations of NMHCs and their reactive oxidation products are in general very low and a simpler chemical mechanism including 15 species can be sufficient [12].

The idea of reducing chemical mechanisms is quite old. Traditional methods address spatially uniform situations, and exploit the large range of timescales between different chemical reactions, by splitting the species ensemble into subsets that evolve over similar time scales [13, 14, 15, 16, 17, 18, 19]. This splitting speeds up computation by reducing the size and the stiffness of the individual Jacobian matrices to be inverted.

The spatial reduction mechanism proposed here gradually and continuously discards the equations for fast reacting species with distance from a pollution source. We track a series of chemical boundary layers (CBL) which separate regions where the concentration of a given species is computed with its equation of motion from those where the concentration is determined by extrapolation from the source. The number of domains (multiconnected in general) can be as large as the number of chemical species. The variable CBLs represent the region of the atmosphere affected by fresh emissions; they...
include not only the meteorological boundary layer but also possibly pollution plumes injected to high altitudes.

The Chemical Mechanism

Emissions of NMHCs and NOx are the principal drivers of complexity in tropospheric oxidant chemistry. The former are emitted by vegetation, combustion and industrial processes whereas the latter are emitted by combustion, soils and lighting. Since the oxidation schemes of all NMHCs follow similar schematics [20], we use propene \((C_3H_6)\) as representative NMHC for a simplified representation of the chemistry, and include only the most important reactions in its oxidation sequence. This greatly decreases the number of species in the chemical mechanism while retaining the essence of the mechanism complexity.

Figure 1 illustrates the major features of the reaction scheme. Oxidation of propene by \(OH\) produces a suite of carbon compounds leading eventually to \(CO_2\). The timescales of the reactions vary from seconds (lifetime of \(OH\)) to minutes (lifetimes of \(PO_2\), \(MCO_3\), \(MO_2\)) to weeks (lifetimes of other propene intermediates) to greater (\(CO\)).

The evolution of \(n_i(x,t)\), the number density of the \(i^{th}\) chemical species, couples chemical reactions with advection and diffusion through the continuity equation

\[
\frac{\partial n_i}{\partial t} + \nabla \cdot (\mathbf{u} n_i - \kappa \nabla n_i) = \omega_i + s_i(x,t) \quad i = 1 \ldots N \tag{1}
\]

where \(\mathbf{u}\) is the wind velocity, \(\kappa\) is the turbulent diffusivity, \(\omega_i\) is the production rate of the \(i^{th}\) chemical species, and \(s_i\) describes local emissions and non-chemical sinks. The local net production rate \(R(i) \equiv \omega_i + s_i(x,t)\) of ith species can be separated into the local gross production rate \(R^+ (i)\) and the local loss \(R^- (i)\) terms, i.e., \(R(i) = R^+ (i) - R^- (i)\). Emissions are in general near the ground but can extend to all altitudes (aircraft, lightning, volcanic emissions, etc.).

Spatial reduction algorithm

Introduction. The spatial reduction algorithm partitions the computational domain for every chemical species into a ‘fast region’ where we calculate the species concentration by solving the full system of equations, and a ‘slow region’ where we calculate the species concentration by extrapolating from the ‘fast region’. Since the analysis is done on a species-by-species basis, the spatial reduction is gradual with fast equations being eliminated closer to the source.

We explain our algorithm in the context of a very simple example. Consider a three species reaction system, comprised of chemicals \(A\), \(B\) and \(C\). The reactant \(B\) decays quickly through \(A + B \rightarrow C\). The concentration of \(B\) is assumed fixed, and there is a (slowly changing) flux \(f(t)\) of \(A\) at the ground. We assume that \(A\) is the fastest reactant, so that \(\tau_C \gg \tau_A\), \(\tau_B \gg \tau_C\) and \(\tau_A\) are the characteristic decay times for the elements \(B\), \(C\) and \(A\) respectively. Additionally, we assume that the only transport mechanism is \(1 \rightarrow D\) diffusion.

Under these conditions, the concentration of \(A\) is localized near the ground. The dynamics of \(A\) and \(C\) are described by

\[
\frac{\partial n_A}{\partial t} = -\frac{n_A}{\tau_A} + \kappa \frac{\partial^2 n_A}{\partial x^2} \tag{2}
\]

\[
\frac{\partial n_C}{\partial t} = -\frac{n_C}{\tau_C} + kn_B n_A + \kappa \frac{\partial^2 n_C}{\partial x^2} \tag{3}
\]

where \(\kappa\) is the diffusion coefficient, and the boundary conditions are \(-\kappa \partial_x n_A |_{x=0} = f(t)\). As long as \(f(t)\) varies more slowly in time than \(\tau_A\), the solution to equation (2) is approximately

\[
n_A(x,t) = f(t) \sqrt{\frac{\tau_A}{\kappa}} \exp (-x/\sqrt{\kappa \tau_A}). \tag{4}
\]

This equation for \(n_A(x,t)\) can then be used in equation (3), so that we now have a single equation for \(n_C(x,t)\) which is valid far from the source. This represents a (simple) spatial reduction since we now need to solve only one equation far from the ground. This equation is

\[
\frac{\partial n_C}{\partial t} = -\frac{n_C}{\tau_C} + kn_B n_A(x,t) + \kappa \frac{\partial^2 n_C}{\partial x^2} \tag{5}
\]

Equation (5) uses \(\gamma\) and \(\alpha\) as free constants, not necessarily given by \(\gamma = f(t) \sqrt{\tau_A/\kappa}\) and \(\alpha = 1/\sqrt{\kappa \tau_A}\) implied by equation (4). This is to emphasize that in more general situations, it is not possible to analytically solve for the fast reactant profiles. However, \(\gamma\) and \(\alpha\) can always be determined using matching conditions, by requiring that both concentrations and fluxes are continuous at the boundary between the fast and slow region. Thus, if \(n_{A_J}\) is the concentration of species \(A\) as computed by the full solver in the fast region, and the boundary between fast and slow occurs at \(x = x_0\), we require that \(\gamma = n_{A_J}(x_0)\), and \(\alpha = -\partial_x n_{A_J}(x_0)/n_{A_J}(x_0)\). This method for choosing \(\gamma\) and \(\alpha\) ensures that the spatially reduction conserves mass exactly.

This one-dimensional example illustrates the basic principles of spatial reduction: in the fast region, we solve the full chemical mechanism, whereas in the slow region we extrapolate concentrations of the fast reactants from the fast region. In the present example the full reaction system is comprised of two coupled partial differential equations (PDE), whereas the reduced system involves solving only one PDE. The computational cost of solving a PDE using an implicit solver increases with the number of dependent variables. In the present simple example, the CPU time reduction will thus be a factor of four. We note that in practice the CPU savings should be greater because by eliminating the fast variables we are eliminating the primary source of stiffness.
**Domain Partitioning.** How do we choose the borderline between the fast and slow region? Let us denote the fast and slow regions as $D_f$ and $D_s$, respectively, with the regions separated by a moving boundary $\Gamma$. In the above example, $\Gamma$ corresponds to the point $x_0$. It is intuitively clear that in the fast region $D_f$, the species density $n$ should either be sufficiently large, or have the potential to become large in a short period of time since its production rate is large. Our domain partitioning criterion thus relies on the local magnitudes of $n$ and the local net $R(i)$ or gross production $R^+(i)$ rates. Since $R(i) \leq R^+(i)$, the criteria based on the local gross production rate $R^+(i)$ is more conservative than the one based on the local net production $R(i)$. One definition of $D_f$ uses an absolute threshold for $n(i)$ and $R(i)$: for each chemical species $n(i)$, we require that the chemical concentration $n(i) > n(i)_0$, where $n(i)_0$ and $R(i)_0$ are prescribed thresholds. Alternatively, we can define $D_f$ by requiring that $n(i)$ and $R(i)$ are larger than some fraction $\delta$ of their values at the local maximum. The computations presented below use a relative threshold.

**Matching conditions and extrapolation algorithm.** We discussed above how we match the solution between the fast domain and the slow domain by imposing continuity of chemical concentrations and fluxes. In the one dimensional example these conditions fixed the parameters $\alpha$ and $\gamma$, which allowed extrapolation of the fast species into the slow region through exponential decay.

The situation is more complicated in multidimensions. Here, the matching conditions must be satisfied on the surface separating the fast region and the slow region. We need to find a method for extrapolating information on this surface into the slow region through the expected exponential decay. Stated mathematically, given a chemical species denoted by $g$ defined on $\Gamma$, we need to extrapolate $g$ so that it decays exponentially with distance from $\Gamma$, with the decay rate

$$\alpha_n = \frac{1}{g} \frac{\partial g}{\partial n}|_\Gamma,$$

[6]
determined by the rate of change of the $g$ normal to the interface. Note that $\alpha_n$ is constant, but varies over the interface $\Gamma$.

The problem of efficiently extrapolating information defined at an interface to a full domain has been previously addressed extensively in the context of the level set method [21]. We first define a function $d$ which measures distance from $\Gamma$ in the region we wish to extrapolate. As a distance metric, we require that $|\nabla d| = 1$; additionally it must vanish on the interface $(d|_{\Gamma} = 0)$. Then we define the set of curves $\Gamma$ which includes the boundary interface $\Gamma$ as well as other equally-distanced from $\Gamma$ curves i.e. $\{\Gamma [d = \text{const}]\}$ as well as the set $\Gamma^\perp$, which are locally perpendicular to $\Gamma$ (See Figure 2).

To extrapolate $\alpha_n$ from $\Gamma$ to the entire region, we require that $\alpha_n$ is constant along each curve of $\Gamma^\perp$, and hence that on these curves $g$ decays exponentially. Since the normal vector $n = \nabla d$ to $\Gamma$ is tangent to $\Gamma^\perp$, these requirements are equivalent to the equations

$$\nabla d \cdot \nabla \alpha_n = 0$$

[7]

$$\nabla d \cdot \nabla g + \alpha_n g = 0.$$  

[8]

Equation (7) states that the gradient of the local exponential decay rate is orthogonal to the local normal vector $n$, so that $\alpha_n$ is constant along each curve of $\Gamma^\perp$. Equation (8) requires that $g$ exponentially decays with rate $\alpha_n$ along $\Gamma^\perp$. Equations (7,8) can be solved simultaneously and explicitly by marching outwards from the separating interface $\Gamma$ into the domain $D_s$ using the Fast Marching Method [22].

**Computational Savings.** How much will the spatial reduction algorithm reduce computation time in the full problem? To estimate the savings, let us assume that there are $N$ reacting species with $N_s$ slow-reacting species, that the volume of the computational domain is $V$ and that of the fast reacting domain is $V_f$. An implicit solver needs matrix inversion, which causes computational cost increase quadratically or even faster with the number of species. Assuming a constant mesh spacing, the reduced system has a fraction

$$\phi = V_f/V + \left(\frac{N_s}{N}\right)^2 (1 - V_f/V)$$

[9]
of the number of equations of the original full system. For the GEOS-Chem mechanism, we expect both $V_f/V$ and $N_s/N$ to be of order one twentieth, hence implying an order of magnitude expected speedup in the computation time. In making this estimate we have assumed that the spatial reduction does not substantially increase the CPU time i.e. the computational cost of (7) and (8) integration with described above explicit method is negligible (which is indeed true), and have also neglected additional benefits related to stiffness reduction.

**Summary of Algorithm.** To summarize, the numerical algorithm consists of three stages to implemented at each timestep. First, we construct a domain partitioning of every individual species based on the current species density $n(x)$ and source $S(x)$ distributions. This domain partitioning implies that there are different numbers of equations (and variables) to be integrated at each grid point. In the second stage we integrate the fast equations at each grid point to advance the solution to the next timestep. Finally in the third stage, we extrapolate the fast species concentration into the slow domains. Note that the domain partitioning is recomputed at every timestep, so that the distribution of fast and slow species changes dynamically throughout the simulation.

In the test simulations that follow, we advance equation (1) using second order Strang operator splitting for the time.
We now proceed to demonstrate the implementation of the algorithm in both one and two spatial dimensions.

**One-dimensional.** We first consider the perfor-mance of the algorithm in an example with one spatial dimension. To demonstrate the algorithm’s ability to locate and adapt to pollution sources, we choose an example where the location of the pollution source changes in time. The challenge here is that the source-sink pair simulates a simulation of the full chemical kinetics and the solid lines denote the spatially reduced model, with the relative tolerance parameter $\delta = 10^{-2}$. The gray regions in the figure denote the automatically generated domain partitioning. The test results demonstrate that the algorithm detects the changes in the source distribution, properly rearranges the domain splitting and maintains accuracy throughout the simulation.

It is worth noting that in the simulation all of the chemical concentrations are nonzero at every point in space, even in the slow regions where their governing reaction-diffusion-advection equations are not calculated explicitly. This is a

$$n_{O_3} = 10^{12} \text{molecules/cm}^3.$$ We impose zero flux at the edges of the domain for all species except the pollutants $C_3H_6$ and NO, where the fluxes at the ground are $J_{C_3H_6} = 10^{13} \text{molecules/s cm}^2$ and $J_{NO} = 10^{13} \text{molecules/s cm}^2$. We take the turbulent diffusion coefficient $\kappa = 3 \times 10^7 \text{cm}^2/s$.

In addition to the stationary source, we also implement a simple model of a thunderstorm partway through the simulation. Our thunderstorm rapidly transports pollutants from the lower to the upper troposphere. We assume that the thunderstorm starts at the time $t_0 = 3 \times 10^4$ s and ends at time $t_1 = 5 \times 10^4$ s. The thunderstorm is modeled by a pollutant sink which scavenges chemicals in the lower troposphere (defined to be $0 \leq x \leq x_0 = 1.5 \text{ km}$) and instantaneously transports them in a “chimney” upwards by a distance $x_1 = 9 \text{ km}$. The pollutant sink of the $i^{th}$ species is taken to be $s_i(x,t) = a_n(x,t)$ for $0 \leq x \leq x_0$, and the pollutant source is $s_i^+(x,t) = s_i^-(x-x_1,t)$. The source-sink pair simulates rapid transport upward by $x_1$. We choose $a_0 = 2.5 \times 10^{-5} \text{ sec}^{-1}$ so that during the thunderstorm half of the density of the original plume is transported upward.

Figure 3 shows the test results for this model at a time $t = 4 \times 10^4$ s, when approximately 25% of pollutants are transferred from the lower to the upper plume. The solid lines represent a simulation of the full chemical kinetics and the solid dots denote the spatially reduced model, with the relative tolerance parameter $\delta = 10^{-2}$. The gray regions in the figure denote the automatically generated domain partitioning. The test results demonstrate that the algorithm detects the changes in the source distribution, properly rearranges the domain splitting and maintains accuracy throughout the simulation.

It is worth noting that in the simulation all of the chemical concentrations are nonzero at every point in space, even in the slow regions where their governing reaction-diffusion-advection equations are not calculated explicitly. This is a

**Fig. 3.** (a) concentrations of three selected species $C_3H_6$, MAP and $O_3$ vs. $(x,y)$, (b) moving boundary $\Gamma$ which separates the computational domain into two sub-domains $\Omega_1$ and $\Omega_2$ where full and reduced models are employed accordingly, and (c) comparison of these species distribution obtained by the spatial reduction algorithm (spheres ans cubes) and conventional method (solid line) depicted in blue and red colors at $x = 750$ km and at $y = 0.5625$ km correspondingly, at time $t = 4 \times 10^4$ for the atmosphere with linearly distributed horizontal shear layer type flow. Vertical and horizontal spatial scales are $y = 0 - 15 \text{ km}$ and $x = 0 - 1500 \text{ km}$ (not shown in the figure) correspondingly. The computation is carried out in $1500 \text{ km} \times 15 \text{ km}$ physical domain uniformly resolved by $80 \times 80$ points.

**Numerical experiments**

We proceed to demonstrate the implementation of the algorithm in both one and two spatial dimensions.
The spatial reduction algorithm described herein allows great
slice at conventional technique (solid lines) and the spatial reduction
separating the fast and slow regions for these three species are
are shown in Figure 4(a) at time \( t \). Numerical experiments demonstrate that
this error increases by a factor of five if the extrapolation al-
gorithm in the slow region is not used, and the fast reactants are
required to vanish in slow regions. Additionally, numerical
experiments demonstrate that the error depends linearly on the
thresholds \( \delta \).

Two-dimensional. Now we turn to a two dimensional simula-
tion, where the extrapolation between fast and slow regions is
not so simple. Our test case assumes that the horizontal and ver-
tical components of the velocity field \((u(x, y, t), v(x, y, t))\)
form a shear layer, \( u(x, y) = u_0 + (u_1 - u_0)y / \gamma_{\text{max}} \) and
\( v(x, y) = 0 \), where \( x \) and \( y \) are the horizontal and vertical
coordinates and \( u_0 = 10 \text{ m/s}, u_1 = 30 \text{ m/s} \). The simulation
is carried out in a domain of dimensions \( 1500 \text{ km} \times 15 \text{ km} \),
with the computational domain uniformly resolved by \( 80 \times 80 \)
points.

We assume the pollution source is two grid spacings wide,
occurring between \( 485 \text{ km} \leq x \leq 522 \text{ km} \). Like the one dimensional simulation above, the nonzero pollu-
tant fluxes are \( J_{C_l} \mu_a = 10^{11} \text{ molecules/s cm}^2 \) and \( J_{NO} =
10^{13} \text{ molecules/cm}^2 \).

The molar concentrations of three selected species \( PRPE, MAP \) and \( O_3 \) with very different characteristic reaction times are shown in Figure 4(a) at time \( t = 4 \times 10^4 \). The domains
separating the fast and slow regions for these three species are
shown in Figure 2a(b).

Figure 4(c) shows a quantitative comparison of the con-
tentional technique (solid lines) and the spatial reduction algo-
rithm (dots). The blue line shows a one dimensional slice at \( x = 750 \text{ km} \), while the red line depicts a slice at
\( y = 0.5625 \text{ km} \). When \( \delta = 10^{-2} \) the largest error is \( e_{PO_2} =
3.7 \times 10^{-2} \).

Conclusions

The spatial reduction algorithm described herein allows great
computational savings in the accurate simulation of chemical
dynamics in the atmosphere. The algorithm relies on the fact
the concentration of fast reacting species decays rapidly with
distance from the pollutant source. For each chemical species,
we therefore partition the computational domain into two re-
gions, where the full and reduced models are used accordingly.
We have demonstrated the versatility of the method by ap-
plying it to a reduced mechanism for tropospheric oxidant
chemistry. The algorithm works robustly and automatically
in one and two spatial dimensions, with time dependent or
time independent pollution sources.

Our current goal is to implement the algorithm into actual
atmospheric solvers, while keeping the details simple enough
that it can be easily implemented by the research community
as a whole. The most difficult part of our algorithm to imple-
ment is the extrapolation between the fast and the slow re-
regions: Although computationally efficient fast marching algo-
rithms have been constructed for two- and three-dimensional
problems [24, 25, 26, 27], the technical difficulties associated
with complex geometries shape of the moving separating inter-
face could provide prohibitive for widespread implementation.
For this reason we have instituted a major simplification of our
algorithm, in which we require that the domain boundaries
separating the fast and the slow regions have simple geo-
metries. In our discussion above, we required the shapes of the
domain boundaries to correspond to constant relative or ab-
solute thresholds; however, there is no fundamental reason to
do so. Increasing the size of the fast domain slightly can result
in enormous simplification of the domain shape with only a
slight increase in computational cost. The simplest possible
shapes are rectangular patches made to be coincident with the
existing grids used in current CTM’s. We have adopted the
fast marching algorithm for this geometry, and are currently
working on adapting and implementing the algorithm for
rectangular shapes in GEOS-Chem.

As an illustration, a three-dimensional domain splitting for
the chemical \( PRPE \) (based on the \( PRPE \) density distribu-
tion produced by GEOS-Chem) is shown in Figure 55. The
computational mesh covering the fast sub-domain is depicted
by sets of dots at different horizontal layers. In the code, the
earth’s troposphere is uniformly resolved by \( 91 \times 144 \) points in
horizontal \( x - y \) planes and by 20 layers of increasing thickness
in vertical \( z \) direction. Figure 55 depicts grid cross-sections
at \( z = 1, 14, 17 \), corresponding to the altitudes \( \delta = 0.17, 12.087, \) and 15.198 km. The multi-connected fast sub-domain
is well captured through the rectangular patches; for example,
Figure 55(a) shows that the fast region essentially coincides
with the locations of the continents, where the pollutant con-
centration is the highest.

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**Table 1.** Reduced propene-NOx – HOx – O3 atmospheric chemistry mechanism.1

<table>
<thead>
<tr>
<th>Reaction*</th>
<th>Reaction rate6</th>
</tr>
</thead>
<tbody>
<tr>
<td>O3 + hν → 2OH</td>
<td>10−6</td>
</tr>
<tr>
<td>O3 + NO → NO2 + O2</td>
<td>2 × 10−14</td>
</tr>
<tr>
<td>O3 + OH → HO2 + O2</td>
<td>7.3 × 10−14</td>
</tr>
<tr>
<td>O3 + MO2 → HCHO + HO2 + 2O2</td>
<td>10−17</td>
</tr>
<tr>
<td>HO2 + NO → OH + NO2</td>
<td>8.1 × 10−12</td>
</tr>
<tr>
<td>HO2 + HO2 → H2O2 + O2</td>
<td>2.1 × 10−12</td>
</tr>
<tr>
<td>NO2 + hν → NO + O3</td>
<td>8.8 × 10−3</td>
</tr>
<tr>
<td>NO2 + OH → HNO2</td>
<td>2.5 × 10−11</td>
</tr>
<tr>
<td>HCOOH + O2 → CO + NO2 + H2O</td>
<td>9 × 10−12</td>
</tr>
<tr>
<td>CO + OH → HO2 + CO2</td>
<td>2.5 × 10−13</td>
</tr>
<tr>
<td>C3H6 + OH → O2 + PO2</td>
<td>3.1 × 10−11</td>
</tr>
<tr>
<td>PO2 + NO → NO2 + HO2 + HCHO + ALD2</td>
<td>8.7 × 10−12</td>
</tr>
<tr>
<td>ALD2 + OH → O2 + MCNO + H3O</td>
<td>1.4 × 10−11</td>
</tr>
<tr>
<td>MCNO + NO2 → PAN</td>
<td>1.1 × 10−11</td>
</tr>
<tr>
<td>PAN + MCNO + NO2</td>
<td>1.3 × 10−3</td>
</tr>
<tr>
<td>HO2 + MCNO → MAP + O2</td>
<td>1.3 × 10−11</td>
</tr>
<tr>
<td>OH + MAP → 0.5OH + 0.5HCHO + 0.5MCNO + H2O + 0.5CO2</td>
<td>7.4 × 10−12</td>
</tr>
<tr>
<td>MO2 + NO2 → HCHO + HO2 + NO2</td>
<td>7.7 × 10−12</td>
</tr>
<tr>
<td>MO2 + HO2 → MP + O2</td>
<td>4.6 × 10−12</td>
</tr>
<tr>
<td>MP + OH → MO2 + H2O</td>
<td>5.2 × 10−12</td>
</tr>
<tr>
<td>MCNO + NO2 → MCNO + NO2 + CO2</td>
<td>2 × 10−11</td>
</tr>
<tr>
<td>HCHO + hν → O2 + 2H2O + CO</td>
<td>1 × 10−4</td>
</tr>
<tr>
<td>MP + hν → HCHO + HO2 + OH</td>
<td>1 × 10−5</td>
</tr>
<tr>
<td>OH + HO2 → H2O2 + O2</td>
<td>1 × 10−10</td>
</tr>
</tbody>
</table>

*Reactions and rate constants are extracted from the GEMS-Chem mechanism documentation. Rate constant values are computed for a temperature of T = 298 K and a pressure of 1 atm. The following shorthand notation is used: P02 ≡ CH3CH(OH)CHO2, ALD2 ≡ CH2CHO, MCNO ≡ CH3C(0)O2, MO2 ≡ CH2O2, PAN = CH3C(0)(O)O2, MAP = CH3C(0)(O)OH, MP = CH2CHO.

1Reactions with species above the reaction bar are multi-step processes in which the species above the bar are not involved in rate limiting steps and thus do not contribute to the rate calculation. Letter “M” above the reaction bar indicates an inert molecule (in the atmosphere, mainly NO2 and O2) that stabilizes a reaction product (3-body reaction) or drives thermolysis.

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*Rate constants are applied to the species or products of species on the left side of the reaction bar, and are in units of s−1. In the first case and cm3 molecule−1 s−1 in the second case. Photolysis rate constants (hν) are in units of s−1.