Preserving Positivity in Discontinuous Galerkin Methods Using Truncation and Mass Aware Rescaling

Devin K. Light\textsuperscript{a,*}, Dale R. Durran\textsuperscript{b}

\textsuperscript{a}Department of Applied Mathematics, University of Washington, Seattle, Washington
\textsuperscript{b}Department of Atmospheric Sciences, University of Washington, Seattle, Washington

Abstract

In this paper we describe a uniformly high–order accurate positivity preserving limiter for a discontinuous Galerkin (DG) approximation to scalar advection. The positivity of an unknown tracer is preserved through a local and conservative limiter which utilizes a truncation and mass aware rescaling (TMAR) of the local approximating polynomial. The TMAR limiting maintains the high–order accuracy of the underlying DG scheme and is computationally inexpensive to implement. Additionally, in comparison to some previously described limiters, it is particularly suited to higher order polynomial truncations. We illustrate the performance of the proposed method on several numerical tests, including a two-dimensional time dependent deformation flow.

Keywords: Tracer Transport, Discontinuous Galerkin Method, High–Order Accuracy, Positivity Preserving Method

\textsuperscript{*}Corresponding Author

Email addresses: lightd@uw.edu (Devin K. Light), drdee@uw.edu (Dale R. Durran)

Preprint submitted to Journal of Computational Physics May 12, 2015
1. Introduction

Discontinuous Galerkin (DG) methods are a popular means of producing numerical approximations to systems of hyperbolic conservation laws. They are high-order, geometrically flexible, $h$-$p$ adaptive, compact, and scale well on distributed memory systems [2]. In this paper, we will consider DG approximations to the one- or two-dimensional transport of an inert scalar tracer $\psi(x,t)$ which is advected by a flow with velocity $u(x,t)$:

$$\frac{\partial}{\partial t} \psi(x,t) + \nabla \cdot (u(x,t) \psi(x,t)) = 0, \quad (x,t) \in \Omega \times \mathbb{R}^+$$  \hspace{1cm} (1)

$$\psi(x,t=0) = \psi_0(x)$$

where $\Omega$ is the spatial domain with suitable boundary conditions.

If the velocity field is non-divergent (i.e. $\nabla \cdot u = 0$) then analytic solutions to (1) satisfy a boundedness relationship determined by the initial data. For example, if $m \leq \psi_0 \leq M$ for all $x \in \Omega$ then $\psi(x,t)$ will also satisfy $m \leq \psi(x,t) \leq M$ for all $t \geq 0$ and $x \in \Omega$. We will focus on enforcing the lower bound in the case where $m = 0$, which can be of great practical importance when (1) is integrated as part of a more complicated system involving nonlinear source terms. One example is reactive chemical transport, where $\psi$ represents the mixing ratio of a chemical species which should remain non-negative at each stage of the integration. If spurious negative undershoots are generated in the numerical solution by the advective transport of poorly resolved gradients, the negative species concentrations can destabilize the method by inducing otherwise impossible reactions [3]. For such systems it is vital that the numerical solution remains positive-definite given positive-definite initial conditions. However, in general a DG scheme
is not guaranteed to maintain an initially positive–definite solution, so it is
necessary to augment standard DG methods with some positivity preserving
limiting technique.

One common method for generating a positive-definite DG solution for
conservation laws is to adapt the bounds preserving limiter proposed in [4],
hereafter the ZS limiter, for use as a positivity preserving limiter (see [5, 6, 7]).
This approach controls the positivity of the solution within each element by
linearly rescaling the polynomial approximation around its element aver-
age. The benefits of implementing the ZS limiter include its local definition,
straightforward implementation, and high-order accuracy [4]. In this paper
we propose an alternative limiter which is based on a conservative trunca-
tion of the approximating polynomial on a set of nodal points. Our proposed
limiter enjoys the same benefits as the ZS limiter but can perform better for
higher degree polynomial approximations with equal or less computational
effort.

The paper is structured as follows. In Section 2 we present the proposed
positivity preserving DG scheme for the one-dimensional problem and ana-
lyze its impact on convergence. In Section 3 we extend this approach to two-
dimensional problems. Section 4 examines the empirical performance of the
proposed limiter on a suite of standard one-dimensional and two-dimensional
test problems. Section 5 contains our conclusions.

2. Positivity Preservation in 1D

The proposed method is based on a Runge-Kutta DG (RKDG) formula-
tion using Lagrange interpolating polynomials [3, 8, 9]. Let $S^h$ be a Cartesian
discretization of $\Omega$ into $h$ elements with width $\Delta x$ and define $V_N^h$ as the vector space formally given by $V_N^h = \{ p : p|_{s_i} \in \mathbb{P}_N(s_i) \forall s_i \in S^h \}$ where $\mathbb{P}_N(s_i)$ is the space of polynomials within $s_i$ up to degree $N$. Let $\phi(x, t) \in V_N^h$ be the DG approximation to the solution of (1). We can express $\phi(x, t)$ inside element $s_i$ in terms of $N$th degree Lagrange interpolating polynomials $\{ \varphi_k(x) \}_{k=0}^N$ as

$$\phi_{s_i}(x, t) = \sum_{k=0}^N a_{i,k}(t) \varphi_k(x) \quad \text{for} \quad x \in s_i. \quad (2)$$

There are many possible choices for the set of points the Lagrange polynomials interpolate; for this paper we will use the $N + 1$ Gauss-Legendre-Lobatto (GLL) nodes which have been mapped to $s_i$ and are denoted by $\{ x_0, x_1, \ldots, x_N \}$. We also define the local solution vector at time level $n$ to be to be $\phi_{s_i}$ evaluated at the GLL nodes: $\{ \phi^n_{s_i}(x_0), \phi^n_{s_i}(x_1), \ldots, \phi^n_{s_i}(x_N) \}$. By the definition of the Lagrange interpolating polynomials, these nodal values agree exactly with the coefficients $a_{i,k}(t_n)$ in (2). Enforcing the Galerkin criteria and using quadrature rules defined at the GLL nodes produces a diagonal system of semi-discrete ODEs for the expansion coefficients. For the numerical simulations in this paper, each of these ODEs is integrated using the three stage, third-order strong stability preserving Runge–Kutta (SSPRK3) method described in [10].

Next we address the positivity of the DG solution. The ZS limiter is a bounds preserving limiter that can be easily simplified to only preserve positivity. Assuming that the mean value $\overline{\phi}_{s_i}$ of the numerical solution within $s_i$ is non-negative, the ZS limiter preserves positivity by replacing the original approximating polynomial with a modified polynomial $\phi^*_{s_i}(x)$. The new
polynomial is determined by linearly rescaling $\phi^n_{s_i}(x)$ about $\bar{\phi}_{s_i}$ so that all spurious negatives are removed. The rescaling factor $\theta$ is set by the minimum nodal value of $\phi^n_{s_i}(x)$, such that

$$\theta = \min \left\{ \frac{\bar{\phi}_{s_i}}{m_i - \bar{\phi}_{s_i}}, 1 \right\}, \quad m_i = \min_k \phi_{s_i}(x_k).$$

(3)

The modified polynomial is given by

$$\phi^*_n(x) = \theta \left( \phi^n_{s_i}(x) - \bar{\phi}_{s_i} \right) + \bar{\phi}_{s_i}. \quad (4)$$

In [4] it was shown that as long as $\bar{\phi}_{s_i} \geq 0$ the limiter (4) is not only conservative, but for a fixed polynomial order it uniformly maintains the asymptotic convergence rate of the unmodified DG method as the element size is reduced ($h$–refinement). Furthermore, it was shown that for RKDG methods non-negative element means can be preserved at every step using a sufficiently small time step in conjunction with the limiter.

Our proposed limiter replaces the linear rescaling in (4) by a truncation and mass aware rescaling (TMAR). Any spurious negative nodal values are first truncated to zero. Then the remaining non-negative values are multiplicatively rescaled to maintain mass conservation. The rescaling factor required for the TMAR positivity preserving limiter, denoted by $r$, is given by the ratio of the total mass to the non-negative mass within the element:

$$r = \frac{\bar{\phi}_{s_i}}{\sum_{k=0}^N w_k(\phi^n_{s_i}(x_k) + |\phi^n_{s_i}(x_k)|)/2}$$

(5)

where the $w_k$ are the weights for an $N+1$ point GLL quadrature. From the assumption $\bar{\phi}_{s_i} \geq 0$ it follows that $0 \leq r \leq 1$. For each $k$ the nodal value
\( \phi_{s_i}(x_k) \) is replaced by

\[
\phi^*_i(x_k) = \begin{cases} 
0 & \text{if } \phi_{s_i}(x_k) \leq 0 \\
 r^i_{s_i}(x_k) & \text{if } \phi_{s_i}(x_k) > 0 
\end{cases}
\]  

(6)

Since the \( \phi^*_i(x_k) \) are all non-negative

\[
\bar{\phi}_{s_i} = \sum_{k=0}^{N} w_k \phi^*_i(x_k) = \sum_{k=0}^{N} w_k (\phi^*_i(x_k) + |\phi^*_i(x_k)|)/2
\]

(7)

\[
= r \sum_{k=0}^{N} w_k (\phi_{s_i}(x_k) + |\phi_{s_i}(x_k)|)/2,
\]

(8)

which by (5) implies \( \bar{\phi}^*_i = \bar{\phi}_{s_i} \), so that TMAR limiting maintains mass conservation.

We conclude this section by showing that the TMAR limiter does not alter the uniform high–order accuracy as the element spacing is refined.

**Theorem 1.** Let \( \phi_{s_i}(x) \) be the unmodified \( M \)th order DG approximation to \( \psi(x) \) in \( s_i \) and assume that \( \phi_{s_i} \geq 0 \). Then the TMAR limited solution (6) is also an \( M \)th order approximation to \( \psi(x) \).

**Proof.** Because \( \phi_{s_i}(x) \) is an \( M \)th order approximation to \( \psi(x) \)

\[
\max_{x \in s_i} |\psi(x) - \phi_{s_i}(x)| = \mathcal{O}(\Delta x^M).
\]

(9)

it suffices to show that

\[
\max_{x \in s_i} |\phi^*_i(x) - \phi_{s_i}(x)| = \mathcal{O}(\Delta x^M).
\]

(10)
Since the coefficients in the Legendre polynomial representation of \( \phi_{s_i}(x) \) are given by the modified nodal values in (6),

\[
\max_{x \in s_i} |\phi_{s_i}^*(x) - \phi_{s_i}(x)| = \max_{x \in s_i} \left| \sum_{k=0}^{N} (\phi_{s_i}^*(x_k) - \phi_{s_i}(x_k)) \varphi_{k}(x) \right| \leq C_N \sum_{k=0}^{N} |\phi_{s_i}^*(x_k) - \phi_{s_i}(x_k)|
\]

where \( C_N \) is a constant which depends only on \( N \). Thus we need to show that \( \sum_{k=0}^{N} |\phi_{s_i}^*(x_k) - \phi_{s_i}(x_k)| = \mathcal{O}(\Delta x^{M}) \).

There are two cases to consider. First suppose that \( \phi_{s_i}(x_k) \leq 0 \), then \( \phi_{s_i}^*(x_k) = 0 \), so \( \phi_{s_i}(x_k) \leq \phi_{s_i}^*(x_k) \leq \psi(x_k) \). Since \( \phi_{s_i}(x) \) is an approximation to \( \psi \) with error \( \mathcal{O}(\Delta x^{M}) \), it follows that

\[
|\phi_{s_i}^*(x_k) - \phi_{s_i}(x_k)| \leq |\psi(x_k) - \phi_{s_i}(x_k)| = \mathcal{O}(\Delta x^{M}).
\]

On the other hand suppose that \( \phi_{s_i}(x_k) > 0 \), then \( \phi_{s_i}^*(x_k) = r \phi_{s_i}(x_k) \) where \( r \) is given in (5). Then noting that \( r \leq 1 \),

\[
|\phi_{s_i}^*(x_k) - \phi_{s_i}(x_k)| = (1 - r) \phi_{s_i}(x_k).
\]

Defining

\[
\phi_{s_i}^+(x_l) = \begin{cases} 
\phi_{s_i}(x_l) & \text{if } \phi_{s_i}(x_l) \geq 0 \\
0 & \text{if } \phi_{s_i}(x_l) < 0
\end{cases}
\quad \text{and} \quad
\phi_{s_i}^-(x_l) = \begin{cases} 
0 & \text{if } \phi_{s_i}(x_l) \geq 0 \\
\phi_{s_i}(x_l) & \text{if } \phi_{s_i}(x_l) < 0
\end{cases},
\]

the coefficient \( (1 - r) \) may be rewritten as

\[
1 - r = \frac{\sum_{l=0}^{N} w_l |\phi_{s_i}^-(x_l)|}{\sum_{l=0}^{N} w_l |\phi_{s_i}^+(x_l)|}.
\]
Substituting (16) into (14) and using the inequality \( \sum_{l=0}^{N} w_l |\phi^+_s(x_l)| \geq w_k \phi_s(x_k) \) to bound the denominator in (16) from below gives

\[
|\phi^*_s(x_k) - \phi_s(x_k)| \leq \frac{1}{w_k} \sum_{l=0}^{N} w_l |\phi^-_s(x_l)|.
\] (17)

From (13) it follows that \( |\phi^-_s(x_l)| = O(\Delta x^M) \) for all \( l = 0, \ldots, N \). Thus

\[
|\phi^*_s(x_k) - \phi_s(x_k)| \leq D_N \Delta x^M = O(\Delta x^M),
\] (18)

where \( D_N \) is a constant which depends only on \( N \). Therefore \( |\phi^*_s(x_k) - \phi_s(x_k)| = O(\Delta x^M) \) for all \( k \), and the TMAR limiter maintains \( M \)th order accuracy relative to \( h \)-refinement.

3. Positivity Preservation in 2D

The TMAR limiter described in Section 2 may be easily extended to two-dimensional (and higher) problems. As in [9], we expand \( \phi_s(x, y, t) \) by taking the tensor-product of the one-dimensional Lagrange interpolating polynomials with roots at the \( N + 1 \) GLL nodes:

\[
\phi_s(x, y, t) = \sum_{k,l=0}^{N} a_{i,k,l}(t) \varphi_k(x) \varphi_l(y).
\] (19)

Assuming the element mean \( \overline{\phi}_s \) is non-negative and truncating any negative nodal values to zero, the 2D rescaling factor becomes

\[
r = \frac{\overline{\phi}_s}{\sum_{k,l=0}^{N} w_k w_l (\phi_s(x_k, y_l) + |\phi_s(x_k, y_l)|)/2}.
\] (20)
The limited nodal values for \( k, l = 0, \ldots, N \) are given by

\[
\hat{\phi}_{s_i}(x_k, y_l) = \begin{cases} 
0 & \text{if } \phi_{s_i}(x_k, y_l) < 0 \\
r\phi_{s_i}(x_k, y_l) & \text{if } \phi_{s_i}(x_k, y_l) > 0
\end{cases}.
\]  
(21)

A proof similar to the one outlined in Theorem 1 shows that this limiting does not reduce the asymptotic convergence rate of the underlying DG approximation.

4. Numerical Tests

4.1. One-dimensional tests

Each of the one-dimensional tests use constant windspeed \( u = 1 \) on a periodic domain \( \Omega = [0, 1] \). The exact solution for all \( x \) and \( t \) is given by the translation \( \psi(x, t) = \psi_0(x - t) \). We will consider several sets of initial conditions, all of which satisfy the positivity condition. The time step used for each test is chosen to satisfy the condition in [4] on the Courant–Friedrichs–Lewy (CFL) number which guarantees element–mean positivity

\[
\mu \equiv \frac{\max |u| \Delta t}{\Delta x} \leq \min_k \frac{\hat{w}_k}{2}.
\]  
(22)

Here the \( \hat{w}_k \) are the weights for an \( L \)-point GLL quadrature over the interval of \([-1, 1]\) and \( L \) is chosen to satisfy \( 2L - 3 \geq N \). Each of the following tests use \( \mu = 0.8 \). First consider the square profile

\[
\psi_0(x) = \begin{cases} 
1 & \text{if } x \in [0.4, 0.6] \\
0 & \text{otherwise}
\end{cases}.
\]  
(23)

Figure 1 displays the unlimited, TMAR, and ZS limiter numerical solutions at \( t = 5 \) (after five cycles around the periodic domain) using piecewise quartic
polynomials and sixteen elements. Each dot in Fig. 1 indicates the polynomial value at one of the 5 GLL nodes. The $L_2$ and $L_\infty$ norms, along with the maximum and minimum values are also listed in each panel. The spurious negatives present in the unlimited solution (Fig. 1a) are completely removed by both limiting methods (Fig. 1b and c) with only a slight increase in each of the error norms. Both limiters produce roughly equivalent $L_2$ and $L_\infty$ errors and similar visual improvements compared to the unlimited solution. The only noticeable difference between the limited solutions is on the upwind side of the square wave where a small overshoot is more pronounced in the ZS solution.

One of the most important benefits of implementing DG methods is that they allow the flexibility of refining the approximate solution by either adding additional elements ($h$-refinement), using a higher degree local polynomials ($p$-refinement), or a combination of the two. Consider, therefore, the influence of each limiter on the $h$- and $p$-convergence rates for smooth initial
data. Let $s(x) = 4|x - 1/4|$ and define a smooth initial tracer density by

$$
\psi_0(x) = \begin{cases} 
\left( \frac{1 + \cos(\pi s(x))}{2} \right)^p & \text{if } s(x) \leq 1 \\
0 & \text{otherwise}
\end{cases},
$$

(24)

where $p = 1, 2, \text{ or } 4$. By design $\psi_0(x)$ in (24) is $C^{2p-1}$ so larger $p$ values permit faster convergence rates depending on the degree of the DG polynomial truncation. No matter what $p$ is used, each initial profile still features steep gradients so that the unlimited solution will develop small negative densities which must be removed. Figure 2 illustrates the impact of each limiting method on $h$-convergence in the $L_2$ error. All three methods use fifth degree polynomials with a time step chosen for SSPRK3 integration so that $\Delta t \sim \mathcal{O}(\Delta x^{5/3})$ to guarantee that spatial convergence is observed. As expected, the effective order of accuracy (i.e. the slope) of both limited solutions closely match that of the unmodified method. Note, however, that for all three initial conditions the error generated by the TMAR limiter is

Figure 2: Convergence results under $h$–refinement: $L_2$ error as a function of the number of elements for a) $C^1$, b) $C^3$ and, c) $C^7$ cosine bell tests as defined by the initial conditions (24).
smaller in magnitude than that produced by the ZS limiter.

Figure 3 examines the $p$–convergence for the same set of initial conditions as $N$ is refined from 4 to 9. Each method uses a fixed mesh of 32 elements and a time step $\Delta t = \Delta x^{N/3}/2$ which ensures that spatial convergence is observed. The unlimited solution generates the fastest convergence rate for the smoothest cosine bell which features errors that begin to approach machine precision at the highest degree truncations. This is expected since as the smoothness of the solution increases, $p$–refinement should begin to produce spectrally convergent results. The TMAR limited solution introduces slightly larger errors than the unlimited scheme, but nevertheless parallels the unlimited solution’s convergence for all three initial conditions. On the other hand, $p$–refinement produces little to no improvement in the ZS limited solution for the $C^1$ and $C^3$ cosine bells and only modest improvement for the smoothest example. Therefore, while both limiters maintain the original method’s convergence rate under $h$–refinement, only the TMAR limiter maintains the performance under $p$–refinement.
4.2. Two-dimensional tests

In multi-dimensional problems, complex velocity fields can stretch and deform smooth initial data into filaments with poorly resolved steep gradients regardless of how well the initial conditions are resolved. This behavior can be replicated by using a time-dependent velocity field to deform an initially circular tracer distribution into a narrow coil before reversing and returning the tracer to its original shape. We will use the unit square domain $\Omega = [0, 1] \times [0, 1]$. The non-divergent velocity field originally proposed in [1] is defined over a time interval $0 \leq t \leq T = 5$ by the streamfunction

$$\Psi(x, y, t) = \frac{1}{\pi} \sin(\pi x)^2 \sin(\pi y)^2 \cos\left(\frac{\pi t}{T}\right), \quad (25)$$

and the relations

$$u = \frac{\partial \Psi}{\partial y}, \quad v = -\frac{\partial \Psi}{\partial x}. \quad (26)$$

The initial condition $\psi_0(x, y)$ is specified by (24) with $p = 2$ and $s(x)$ replaced by the two–dimensional extension

$$s(x, y) = 4 \left( (x - \frac{1}{4})^2 + (y - \frac{1}{4})^2 \right)^{1/2}. \quad (27)$$

Tests using this same flow and the $C^3$ initial condition were also considered in [11]. Figure 4a shows the exact solution at $t = 0$ and $T$, while Fig. 4b shows a reference solution obtained using very high time and space resolution at the time of maximum deformation $t = T/2$.

Figure 5 shows the results of each method for the deformation flow test as the polynomial degree is increased while keeping the total degrees of freedom (DOF) constant. In each panel there are a total of 120 DOF along each
Figure 4: Tracer concentration field for the $C^3$ cosine bell in the reversing deformation flow (26) at times a) 0 and T, and b) $T/2$. Contours at intervals of 0.1.

coordinate. Panels a), b), and c) use a $30 \times 30$ element grid with $N = 3$ (4 DOF along each coordinate per element). Panels d), e), and f) use a $24 \times 24$ element grid with $N = 4$. Lastly, panels g), h), and i) use a $20 \times 20$ element grid with $N = 5$. The time steps taken for each method are chosen to remain near 90% of the maximum value that will maintain element–mean non-negativity.

For polynomial expansions truncated at the same degree $N$ (across each row), the spurious negatives in the unlimited approximations, shown with gray contours, are completely removed in the results using either limiter. The first column of Figure 5 illustrates the effects of $p$-refinement on the unlimited method. Despite having identical degrees of freedom, the results obtained using higher degree polynomials show an improvement in both error norms as well as in the magnitudes of undershoots. Additionally, the higher degree results maintain the circular symmetry and approximate the maximum value of the final solution better than the cubic case. The second column of Fig. 5
Figure 5: Comparison of tracer concentration fields at $t = T$. Each panel uses the same 120 total DOF along each coordinate. The limiting scheme and degree at which the polynomial expansions are truncated are given in each panel. Contours are every 0.1 and negative contours are highlighted in light gray. Exact solution contours at 0.05 and 0.75 shown in heavy solid lines.
Figure 6: Tracer concentration field for a slotted cylinder at $t = T$. Contours are every 0.1 and negative contours are highlighted in light gray. Exact solution is contoured at 1 by the heavy solid line.

shows that the TMAR limited solution similarly improves as $N$ is increased. In contrast, the ZS limited solutions in the third column of Fig. 5 are severely degraded as $N$ is refined.\(^1\) In addition to the pronounced visual distortion, there is a 45% reduction in the global maximum when $N = 5$.

The poor performance of the ZS limiter under $p$-refinement can be explained by comparing its formulation with the TMAR limiter. For both limiters, non-negative nodal values are modified using a linear rescaling but with a different rescaling factor. When the ZS limiter is active, the local polynomial is modified so that the largest magnitude negative value is scaled to

\(^1\)Our implementation of the ZS algorithm was checked against a code developed independently by Frank Giraldo. Here we are enforcing positivity at both the set of nodes specified in (3.10) of [4] and the tensor product of the GLL nodes themselves. Including the tensor product of the GLL nodes ensures that none of the nodal values plotted in Fig. 5 are negative, but has almost no impact on the overall quality of the solution.
zero and other, more minor, undershoots are moved into positive values. In contrast, where the TMAR limiter is active, negative nodal values are truncated to zero, giving a smaller modification for all but the minimum nodal value. Additionally, if an undershoot is at a node with a small weighted contribution to the element–averaged density, with the TMAR limiter it has a correspondingly small effect on the value of $r$. Both of these factors allow the TMAR limiter to produce less damping than the ZS limiter when the positive nodal values are modified. As $N$ is refined, the differences in the results produced by the two approaches can be exacerbated by the non-uniformity of the GLL nodal spacing for higher degree polynomials.

To examine the behavior of these limiters on a 2D flow with actual discontinuities, the smooth initial tracer field used in the previous tests is replaced by a unit–amplitude slotted cylinder of radius 0.15 centered at $(x_0, y_0) = (0.25, 0.5)$. The slot, in which the tracer density is zero, includes all points within the cylinder for which $|x - x_0| < 0.025$ and $y > y_0 + 0.0625$. Figure 6 compares the solutions at time $T$ obtained using no limiting, TMAR limiting, and ZS limiting with $N = 5$ and 32 elements (for a total of 192 DOF) along each axis. With discontinuous initial data, the magnitude of the overshoots and undershoots in the unlimited solution are about 20% of the initial height of the cylinder. The overall structure of the TMAR solution is very similar to the non-negative portion of the unlimited solution. The ZS limiter does remove the negative undershoots, but simultaneously produces short-wavelength noise which distorts the solution and erroneously increases the amplitude of the solution within the slotted section of the cylinder.
5. Conclusion

In this paper we have introduced a positivity preserving limiter for nodal discontinuous Galerkin approximations to the scalar advection equation. The proposed limiter is appropriate to apply when the analytic solution to the PDE also satisfies a positive definite principle. Our approach truncates the negative nodal values and applies a mass aware rescaling (TMAR) to the remaining positive nodal values. The TMAR scheme can be easily implemented as an alternative to existing limiting techniques with similar computational effort. Like the ZS limiter, this approach preserves the order of accuracy of the unlimited scheme under $h$–refinement. Empirical tests also suggest that the TMAR limiter performs nearly as well as the unlimited scheme under $p$–refinement. In contrast to the ZS limiter, the TMAR limiter does not rescale any negatives into positive values. The advantages of the TMAR limiter relative to the ZS limiter are most apparent when using a relatively high degree polynomial truncation because spurious negative nodal values near element boundaries that contribute little to the total element mass also exert only a minor influence on the TMAR rescaling.

6. Acknowledgements

We greatly benefited from discussions with Frank Giraldo and Peter Blossey. This research was supported by National Science Foundation Grant DMS-1216576.
7. References


