Interpolation of Relative Permeability across Rock Type Sets

This feature is needed in the following setting; two different components are injected such that concentration of the components in one of the phases changes dependent on both components.

In this example we will use the following example setup:
In a sample initially containing oil and standard saltwater (typically 4% salt), we first inject the same kind of saltwater (denoted high salinity brine, or just HiSal), followed by low salinity brine (LoSal), and finally surfactant. Salt and surfactant will dilute in the water, hence water properties will be altered, dependent on both salt and surfactant concentration present at any given time or position.

Moreover, relative permeability is dependent on both salinity and surfactant concentration, or stated in more detail:

1. Defining a Single Relative Permeability Interpolation set

In this example the relative permeability depends on *salinity*, such that the set is defined by two bounding curves, one valid for minimum occurring salinity (LoSal), and one for maximum (HiSal). At any position, time (x, t) the relevant relative permeability curve is defined as the interpolated curve

$$k_r(x, t, c_{salt}) = c_{salt} \cdot k_r^{Hi} + (1 - c_{salt}) \cdot k_r^{Lo}$$

where c_{salt} is the *normalized* grid cell salinity (or salt concentration) in cell at x, at time t, i.e. $c_{salt} = 0$ at LoSal and $c_{salt} = 1$ at HiSal. (For simplicity we have assumed linear interpolation, but STARS allows for more general interpolation schemes as needed and defined by the user.)
(Note, by the term *relative permeability curve*, we actually mean the set of two or three curves, water, oil (and gas). This notation is used to avoid confusion regarding several levels of curve sets.)

In STARS, the bounding curves and interpolation request is defined by keywords `RPT` (to define the curve set), `INTCOMP` (for relevant component and phase), and `DTRAPW` (for concentration bounds).

So the syntax to define curve set #1 for this example would be:

```
RPT 1                  ** Rel-perm set #1
INTCOMP 'Salt' WATER   ** Component 'Salt' diluted in phase WATER
KRINTRP 1              ** Curve number 1
DTRAPW 0.004           ** Concentration value relevant for this curve

SWT

… Rel-perm-table       ** Define standard relative permeability valid for LoSal conditions

…


KRINTRP 2              ** Curve number 2
DTRAPW 0.04            ** Concentration value relevant for this curve

SWT

… Rel-perm-table       ** Define standard relative permeability valid for HiSal conditions

…
```

> In this example we define two curves, the bounding curves LoSal and HiSal. But STARS permits any number of curves / DTRAPW-values. If DTRAPW values and corresponding curves are defined for $DT_0, DT_1, \ldots, DT_n$, then the interpolation will be carried through as:
> Curve 0 will be used for concentration less than DT_0; for concentrations between DT_0 and DT_1 curves will be interpolated between curve 0 and curve 1, etc.

Note also that in general the bounds can be defined separately for the wetting and non-wetting phase, by using DTRAPW and DTRAPN. For simplicity we assume these are equal.

Defining a relative permeability set for surfactant concentration is done in exactly the same fashion.

2. Double Interpolation – Interpolation between Different Rel Perm Sets

When two different components are injected, composition of the water phase will depend on two different concentrations, and hence the relevant relative permeability curve will also depend on two different concentrations:

$k_r = k_r(x, t, c_{salt}, c_{surf})$, where we assume that the two components in question are salt and surfactant.

This "double interpolation" would be performed as,

1. Define a "salt" rel perm curve valid for the salinity in question $c_{salt}(x, t)$, k_r^{Salt}
2. Define a "surfactant" rel perm curve valid for the surfactant concentration in question $c_{surf}(x, t)$, k_r^{Surf}
3. Calculate the final rel perm curve as an interpolation between k_r^{Salt} and k_r^{Surf}

How to define the final interpolation step is however not obvious.

A linear interpolation could be based on normalized values of the two concentrations in question, but some weight factor could or should be imposed, an issue which does not have any straightforward solution.

The double interpolation issue has raised some questions based on results from simulation run tests where different options and manners to define the relative permeability sets have been tried out. Aided by CMG support and the arguments below, we have now established a recommended "Modus operandi" for doing the double interpolation:

According to CMG documentation, the interpolation between two rel-perm sets k_{r1} and k_{r2} is done by the procedure (some parameters defaulted for simplicity):

1) First an interpolation weighting function G^{interp} is calculated:

$$G^{interp} = \left[\frac{\dfrac{1}{x - x_1 + \varepsilon} - \dfrac{1}{\varepsilon}}{\dfrac{1}{x_2 - x_1 + \varepsilon} - \dfrac{1}{\varepsilon}}\right]$$

2) Then the interpolated curve k_r^{interp} is calculated as

$$k_r^{interp} = k_{r1} + G^{interp}(k_{r2} - k_{r1})$$

The formula for the weighting function may appear complex, but works well in practice. For large values of the curvature parameter ε the weighting function is close to a straight line, and preference for the lower or upper bound can be set by using small positive or negative values of ε. See Figure 1, where the weighting function is shown in the relevant example interval for salinity, 0.004 – 0.04.

The key to understanding the double interpolation procedure is the definition of the weighting function, where x_1 and x_2 are the lower and upper bounds for the interpolation parameter x. Intuitively one would assume that the two different relative permeability curve sets in question would be e.g. salt and surfactant curves, but then the "interpolation parameter" would have to depend on lower and upper bounds for both salt and surfactant, in some sense of normalized concentration intervals. But as defined, the lower and upper bounds for the interpolation parameter *must belong to the same relative permeability family*; else the formula does not make sense. This was a key observation, and severely restricts the way the relative permeability sets can be defined. (Note that the STARS user guide can appear a bit confusing on the interpretation of lower and upper bounds.)

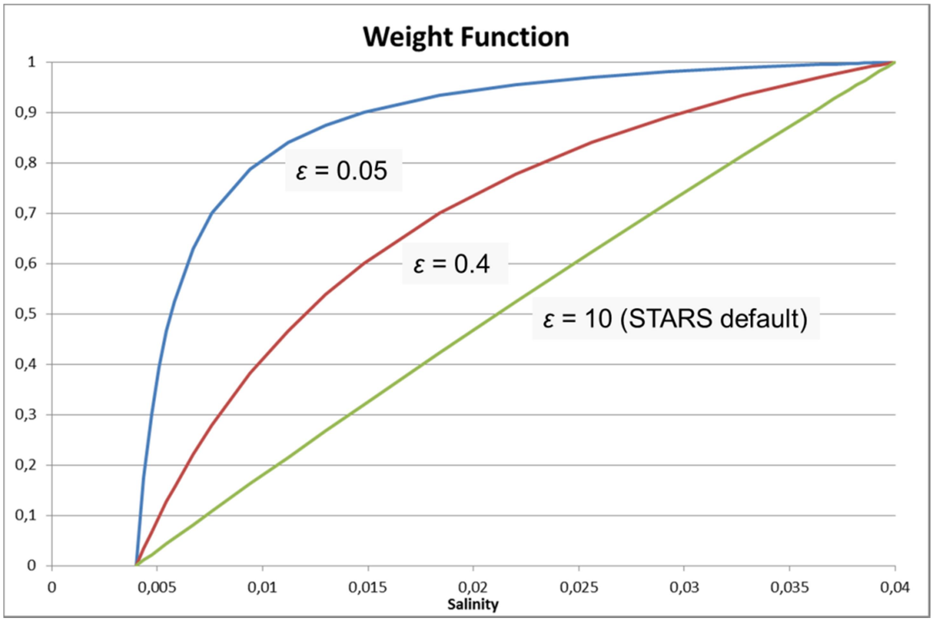

Figure 1. STARS interpolation weighting function for different values of the curvature parameter ε

For our salt – surfactant example, in order to restrict the interpolation parameter to the same family, the relative permeability sets must be defined as,

Alternative 1:

Curves are defined for min and max salinity. Interpolation on salinity is done by direct interpolation of curves, as in section 1. Interpolation on surfactant concentration is done by interpolating across sets.

```
RPT 1                      ** Rel-perm set #1; no surfactant
INTCOMP 'Salt' WATER       ** Component 'Salt' diluted in phase WATER
KRINTRP 1                  ** Curve number 1
DTRAPW 0.004               ** Concentration value relevant for this curve

SWT

… Rel-perm-table           ** Define rel perm for LoSal, no surfactant

…


KRINTRP 2                  ** Curve number 2
DTRAPW 0.04                ** Concentration value relevant for this curve

SWT

… Rel-perm-table           ** Define rel perm for HiSal, no surfcatant

…


RPT 2                      ** Rel-perm set #2; max surfactant concentration
INTCOMP 'Salt' WATER       ** Component 'Salt' diluted in phase WATER
KRINTRP 1                  ** Curve number 1
DTRAPW 0.004               ** Concentration value relevant for this curve

SWT

… Rel-perm-table           ** Define rel perm for LoSal, max surfactant concentration
```

```
…


KRINTRP 2              ** Curve number 2
DTRAPW 0.04            ** Concentration value relevant for this curve

SWT

… Rel-perm-table       ** Define rel perm for HiSal, max surfactant concentration

…
```

Note that both RPT 1 and RPT 2 are defined as functions of salinity, RPT 1 for minimum (no) surfactant, and RPT 2 for maximum surfactant concentration.

The interpolated surfactant relative permeability curves don’t exist as by direct interpolation, as in section 1, but only as interpolation between RPT 1 and RPT 2. This interpolation is defined in STARS by the keyword RPT_INTRP:

```
      RPT_INTRP

      COMP 'Surf' WATER      ** Define "interpolation component"
      LOWER_BOUND 0.0        ** Minimum surfactant concentration (x1)
      UPPER_BOUND 0.005      ** Maximum surfactant concentration (x2)
      UPPERB_RPT 2           ** RPT 2 is the High Surf-concentration, (UPPER_BOUND)
```

Alternative 2:

Curves are defined for min and max surfactant concentration. Interpolation on surfactant concentration is done by direct interpolation of curves, as in section 1. Interpolation on salinity is done by interpolating across sets.

```
RPT 1                  ** Rel-perm set #1; low salinity
INTCOMP 'Surf' WATER   ** Component 'Surf' diluted in phase WATER
KRINTRP 1              ** Curve number 1
DTRAPW 0.0             ** Concentration value relevant for this curve

SWT

… Rel-perm-table       ** Define rel perm for no surfactant, LoSal

…


KRINTRP 2              ** Curve number 2
DTRAPW 0.005           ** Concentration value relevant for this curve

SWT

… Rel-perm-table       ** Define rel perm for max surfactant concentration, LoSal

…


RPT 2                  ** Rel-perm set #2; high salinity
INTCOMP 'Surf' WATER   ** Component 'Surf' diluted in phase WATER
KRINTRP 1              ** Curve number 1
DTRAPW 0.0             ** Concentration value relevant for this curve

SWT
```

```
… Rel-perm-table             ** Define rel perm for no surfactant, HiSal
…


KRINTRP 2                    ** Curve number 2
DTRAPW 0.005                 ** Concentration value relevant for this curve
SWT
… Rel-perm-table             ** Define rel perm for max surfactant concentration, HiSal
…
```

Both RPT 1 and RPT 2 are defined as functions of surfactant, RPT 1 for minimum salinity, and RPT 2 for maximum salinity.

The interpolated salinity relative permeability curves don't exist as by direct interpolation, as in section 1, but only as interpolation between RPT 1 and RPT 2:

```
RPT_INTRP

COMP 'Salt' WATER       ** Define "interpolation component"
LOWER_BOUND 0.004       ** Minimum salinity (x1)
UPPER_BOUND 0.04        ** Maximum salinity (x2)
UPPERB_RPT 2            ** RPT 2 is the High Salinity, (UPPER_BOUND)
```

The two alternatives appear quite different, as:

1. Salinity: Direct interpolation. Surfactant: Interpolation across sets
2. Surfactant: Direct interpolation. Salinity: Interpolation across sets

But still, the formulations should be symmetric and equivalent.
Indeed, this has been tested by simulating a model of core flow, intentionally designed to challenge the interpolation routines:

1. Injection of High salinity brine (concentration 0.04)
2. Injection of gradually decreasing salinity brine (ending at concentration 0.004)
3. Injection of surfactant, gradually increasing concentration from 0.0 to 0.005
   This to test "all" values of the interpolation parameter

Results from this numerical experiment are shown in Figures 2 – 4.

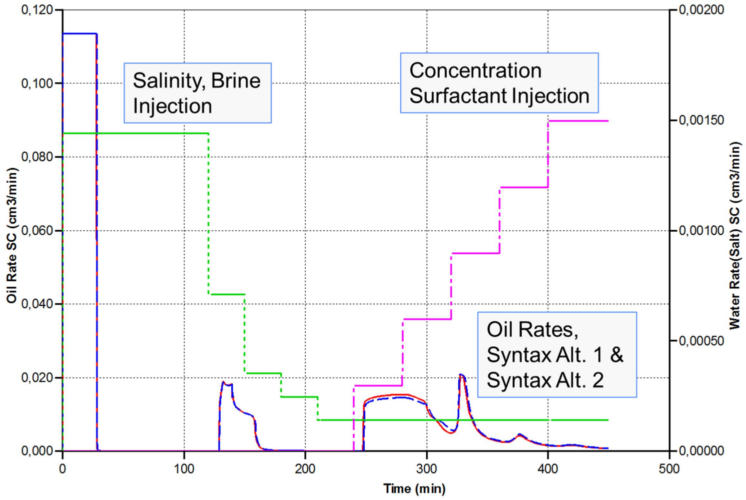

Figure 2. Comparison Interpolation Set Order: Injection and Production Rates

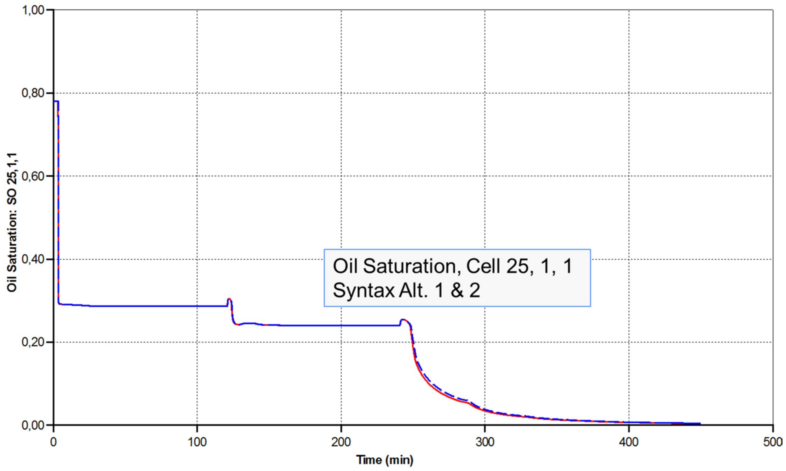

Figure 3. Comparison Interpolation Set Order: Saturations

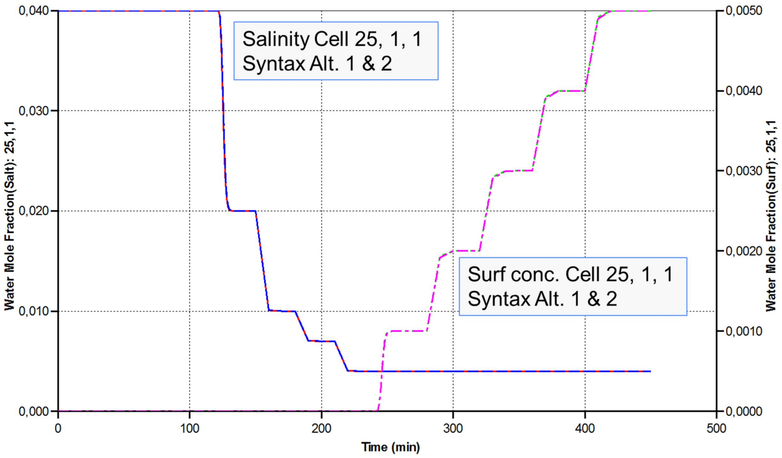

Figure 4. Comparison Interpolation Set Order: Salt and Surfactant Concentrations

As seen in the figures, results are (as good as) identical, confirming that the order of defining the two different relative permeability sets is immaterial – as it should be.

3. Capillary Number and Interfacial Tension

STARS uses the convention that if no interfacial tension data are defined, interpolation is based on the concentration values, as demonstrated in section 2 above.

However, in many situations it is believed that more realistic results are achieved by basing the interpolation on a Capillary Desaturation Curve (CDC) in lieu of directly on concentrations. In STARS this is implemented as; if a table of Interfacial Tension (IFT) vs. concentrations is defined for a relative permeability set (i.e. within the range of an RPT keyword), then the interpolation will be based on $\log_{10}(N_c)$, where the capillary number N_c is taken from the IFT table, IFTTAB in STARS.

In the example used in section 2, salinity will typically be used as is, while surfactant concentration will be replaced by a desaturation curve, as this is seen as more realistic.

As the IFT table must be defined together with the relative permeability data for which it applies, the interpolation component must be “Surfactant” in this case – hence only the order used in Alternative 2 in section 2 is applicable. So introducing a desaturation curve restricts the correct or possible way to define relative permeability sets to a single option; the one defined in Alternative 2. The IFT table must then be given twice, once in each RPT set.

In order to test how STARS handles interpolation based on a desaturation curve compared to using concentrations directly, we constructed a rather artificial IFT table, namely an exponential variation, such that $\log_{10}(N_c)$ is linear and should be identical to the concentration variation. The CDC used was,

$$\sigma = 16e^{-1614.181}$$

where σ is the interfacial tension. This gave the following IFT table, used in STARS:

```
IFTTAB
**    Conc.       IFT(Conc)
      0           16
      0.0005      7.138468248
      0.0010      3.184858058
      0.0015      1.420938008
      0.0020      0.633957553
      0.0025      0.282842866
      0.0030      0.126191551
      0.0035      0.056300899
      0.0040      0.025118886
      0.0045      0.011206898
      0.0050      0.005000005
```

The curve passes through (0, 16) and (0.005, 0.005) as in the original data.

Figures 5 and 6 show that the simulated results from the two alternatives: concentration or CDC based interpolation are indeed (as good as) identical when the IFT data were suitably tuned.

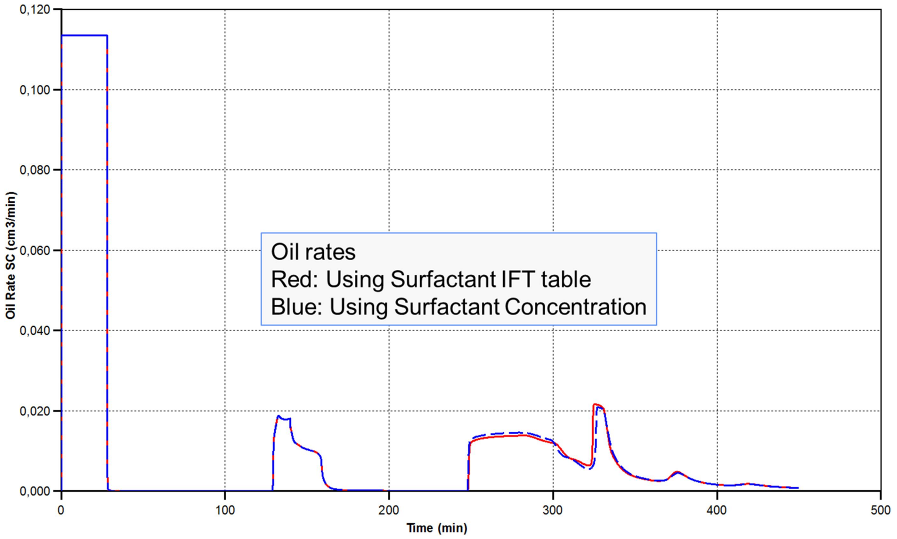

Figure 5. Comparison Interpolation based on CDC or concentration: Oil Rates

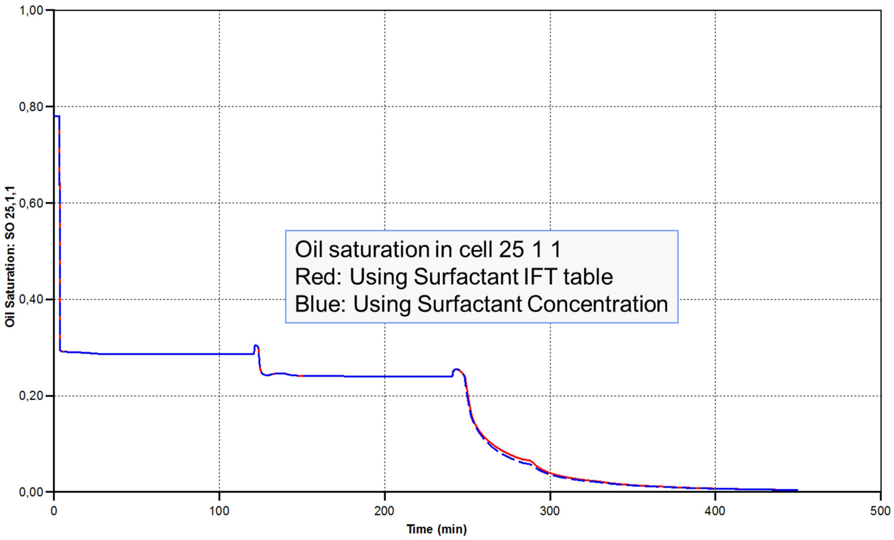

Figure 6. Comparison Interpolation based on CDC or concentration: Oil Saturation Cell Values

Lastly, Figure 7 confirms that the relative permeability interpolator is indeed identical to the surfactant concentration, respectively the $\log_{10}(N_c)$.

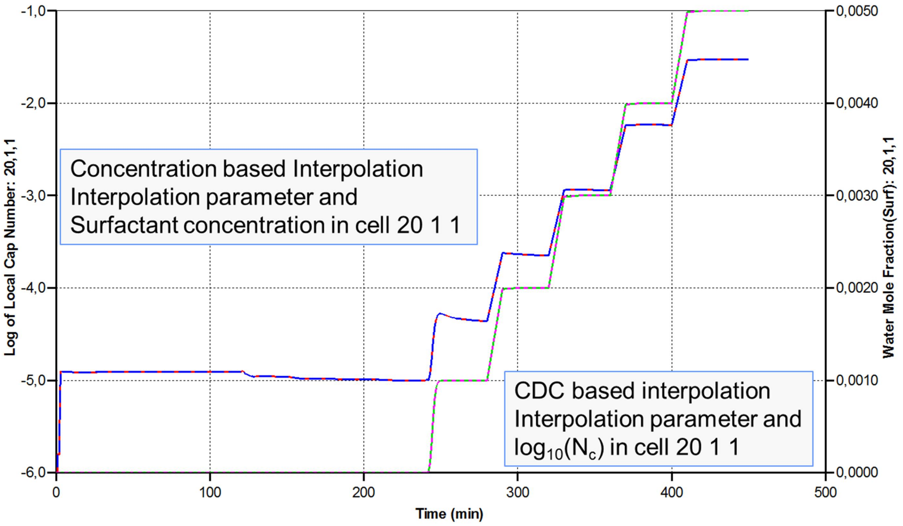

Figure 7. Comparison Interpolation based on CDC or concentration: Interpolator vs. Concentration or CDC

4. Conclusion

In the experiments / simulations performed at Uni Research / CIPR, the relevant EOR fluids are LoSal brine, surfactant, and polymer – the two latter injected in LoSal. For these fluids, the appropriate interpolation of relative permeability curves is as described above:

- Salinity curves determined by direct interpolation based on concentration
- Surfactant curves determined by direct interpolation based on Capillary Desaturation Curve
- Polymer: No relative permeability interpolation (see below, though)
- Interpolation across salinity – surfactant curves for any given combination of salinity and surfactant concentration

For this situation we have identified the syntax described in section 3 as the *only* recommended manner to define relative permeability sets in a STARS complex interpolation scheme.

Final Comments

As described in the STARS user guide, the interpolation formula given in section 1 is the one used by STARS. This equation describes direct interpolation between a pair of relative permeability curves. The user guide does not mention scaling of the mobile interval (water saturation between connate water and (1 - residual oil)), hence we must assume that such scaling is not included in the procedure. This appears to be a drawback in the formulation, as the consequence is that e.g. the residual oil value will never take "intermediate values", but immediately "jump" from e.g. HiSal value to LoSal once salinity decreases slightly below HiSal.

Hitherto, no relative permeability effects of polymer have been included in our simulations. This was partly due to a belief that polymers did not change the relative permeability curves, at least not significantly. Later studies have however shown that the relative permeability effects of polymer in many cases can be considerable, and should definitely be included in the simulations.

There has been, and is a strong desire that the interpolation algorithms in STARS (and GEM) could be extended to handle more than two interpolation sets. It is however clear from the formulation we identified as "the only valid one" in section 3, that this procedure *cannot be generalized*.

Hence, to develop generalized interpolation schemes for more than two interpolation sets, completely new algorithms and ways of thinking must be developed. We encourage CMG to start this process.