

Numerous advantages can be stated regarding the current macro/micro constitutive laws as compared to the other numerical micromechanical approaches in the literature, e.g. the finite element unit cell approach. One advantage is that any type of simple or combined loading (multiaxial state of stress) can be applied irrespective of whether symmetry exists or not, as well as without resorting to different boundary condition application strategies as in the case of the finite element unit cell procedure. Another, advantage concerns the availability of an analytical expression representing the macro elastic-thermo-inelastic constitutive law, thus ensuring a reduction in memory requirements when implementing this formulation into a structural finite element analysis code. Furthermore, this formulation has been shown to predict accurate macro behavior given only a few subcells, within the repeating cell (see references [2], and [4]). Whereas, if one employs the finite element unit cell procedure, a significant number of finite elements are required within a given repeating unit cell to obtain the same level of global accuracy as with the present formulation. Consequently, it is possible to utilize this formulation to efficiently analyze metal matrix composite structures subjected to complex thermomechanical load histories. This is particularly important when analyzing realistic structural components, since different loading conditions exist throughout the structure, thus necessitating the application of the macromechanical equations repeatedly at these locations.

The equations of **GMC-3D** (and consequently through appropriate specialization **GMC-2D**) have recently been reformulated [7] in a way that significantly increases the computational efficiency of the model. This new reformulation has now been implemented into **MAC/GMC** and is the default computational mode. By nature of the traction continuity conditions within the original generalized method, all six stress components are not unique in every subcell. Normal stress components are constant in certain rows of subcells, while shear stress components are constant in certain layers of subcells. The unique subcell stress components are denoted as,

$$T_{11}^{(\beta\gamma)}, T_{22}^{(\alpha\gamma)}, T_{33}^{(\alpha\beta)}, T_{23}^{(\alpha)}, T_{13}^{(\beta)}, T_{12}^{(\gamma)}. \quad (\text{EQ 13})$$

Consequently, a more efficient formulation of **GMC** can be obtained by applying traction continuity directly (i.e. recognizing that traction continuity conditions require no more and no less than the aforementioned reduction in subcell stress components) and using subcell stresses rather than strains as the basic unknown quantities. Accordingly, the continuity of displacement conditions are formed in terms of subcell stresses (through the use of the subcell constitutive and kinematic equations), and the *mixed concentration equations* for the unit cell are constructed,

$$\underline{T} = \underline{G}^{(\alpha\beta\gamma)} \underline{\varepsilon} + \underline{G}^{IT(\alpha\beta\gamma)} (\underline{\varepsilon}_s^I + \underline{\varepsilon}_s^T) \quad (\text{EQ 14})$$

Here, \underline{T} is the vector of all subcell stress components (listed in EQ 13), $\underline{G}^{(\alpha\beta\gamma)}$ is the subcell mixed concentration matrix, and $\underline{G}^{IT(\alpha\beta\gamma)}$ is the subcell inelastic-thermal mixed concentration matrix. The term *mixed* is used here because EQ 14 relates local (subcell) stresses to global strains. Clearly this equation contrasts with its original formulation counterpart, EQ 11, which relates local strains to global strains and is thus the unit cell strain concentration equation. As one could obtain EQ 1 from EQ. 12 in the original formulation, similar expressions for the global quantities (\underline{B}^* , $\underline{\varepsilon}^I$ and $\underline{\varepsilon}^T$) can be determined easily from EQ 14 (see [7] for details).

The increased efficiency of the reformulation of **GMC** emerges mainly due to the increased efficiency of forming EQ 14 versus forming EQ 11. The formation of EQ 14 requires solution (of linear equations) for the unknown independent subcell stress components listed in EQ 13, numbering $N_\beta N_\gamma + N_\alpha N_\gamma + N_\alpha N_\beta + N_\alpha + N_\beta + N_\gamma$. The formation of EQ 11 requires solution for 6 unknown strain components for each subcell, or a total of $6N_\alpha N_\beta N_\gamma$ unknowns. Solution of linear equations, in essence, amounts to the inversion of a matrix which has the rank of the number of unknown quantities. Since the computational effort associated with matrix inversion increases approximately as the **cube** of the matrix rank, reducing the number of unknown quantities has a major impact on computational efficiency. The reduction in unknowns due to the reformulation is shown in Figure 3 and can be quite significant. For example, a $10 \times 10 \times 10$ unit cell originally required solution for 6000 unknowns. In the reformulated version of **GMC-3D** the number of unknowns is reduced to 330. Consequently, the corresponding execution times are reduced as well. Table I gives sample CPU times for identical cases executed using the original and reformulated versions of **GMC** with continuous reinforcement. Clearly, as the number of subcells in the repeating unit cell increases, the increase in efficiency attributable to the reformulation becomes astronomical. It is important to note that:

- (1) The reformulation of **GMC** gives **identical results** as the original formulation of GMC **in every case**.
- (2) The significant increase in the computational efficiency of GMC due to the reformulation allows:
 - (a) **Analysis** of simple unit cells (i.e. few subcells) **in a fraction of the time**.
 - (b) **Analysis of refined unit cells** (i.e. many subcells) which was **previously impossible** (due to excessive execution times and memory requirements) can now be performed in times comparable to those previously required for analysis of simple unit cell, see Table I.

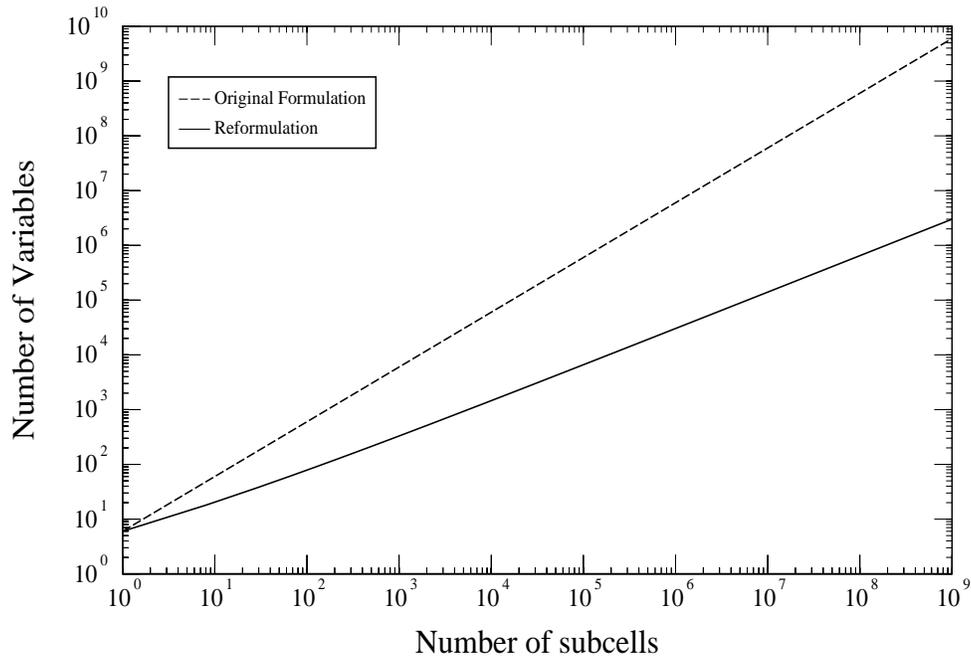


Figure 3. Number of subcells vs. number of unknown variables for the original and reformulated versions of GMC-3D for $N_\alpha = N_\beta = N_\gamma$

Table I: CPU Times (seconds) for Heat-Up of Unidirectional SiC/TiAl

GMC Version	Subcell Discretization							
	2x2	4x4	6x6	8x8	10x10	12x12	20x20	100x100
original	0.87	19	182	508	8,679	43,781	-	-
reformulated	0.18	0.25	0.5	0.9	1.5	2.3	8.3	796
speed-up ratio	4.8	76	364	564	5,786	19,035	-	-

👉 **Note:** These execution times are for a specialized version of **GMC-2D** and not **MAC/GMC**, therefore one should not expect to see the same execution times when running **MAC/GMC** due to increased overhead. However, speed-up ratios should be comparable.