Process-Structure Linkage during Static Recrystallization: an overview of recrystallization

Static recrystallization is defined as formation of new strain free grains from deformed matrix occurring after deformation during subsequent annealing. This phenomenon occurs by the formation and migration of high angle grain boundaries. Given into account that different parameters such as the strain rate, dislocation density, initial grain size, temperature of working and impurity will affect recrystallization process, the final recrystallized microstructure can be controlled to some extent.

There exists different models in literature regarding recrystallization process which are: – Phenomenological modeling of JMAK (Johnson, Mehl, Avrami and Kolmogorov model) – Vertex models – Discrete models (Monte Carlo ,MC, and Cellular automaton ,CA) – Phase field models – Coupled models with crystal plasticity finite element method (CPFEM)

The phenomenological modeling assumes spatially and temporally constant growth rate and homogeneous nucleation. Since these assumptions are not in agreement with real conditions, its results deviate from experiments. It is also unable to handle the spatial complexities of recrystallization due to the fact that the microstructure change during recrystallization needs to be described by more parameters. This necessitates the development of computer simulations.

In vertex models the grains are represented by their vertices Nj and each is assigned a crystallographic orientation Oj (Fig. 1). The positions of vertices, the identification of their neighbors, and the 3 orientations associated with each vertex is stored in the computer. Events are determined by the equations governing the motion of the boundaries and vertices.

This method reduces the amount of data needed to be held in the computer in 2-D therefore larger microstructures can be investigated. Its other advantage is that the only inputs are initial microstructure & the properties of the boundaries. Moreover, different mechanisms such as subgrain rotation and coalescence can be included. However due to geometrical complexities, the generation of 3-D models are difficult. The other downside is that this method requires small integration time step which will be computationally expensive. Thereby, this method is currently less common.

Discretizing the microstructure in space and time, discrete models can be of two approaches. Energetic approach which searches for a trajectory to the lowest energy state and kinematic approach which anticipates the trajectory utilizing kinetic relations. The MC and CA are energetic and kinematic approaches, respectively. In both cases for each discrete cell in space at any given time steps a transformation rule was applied to change the state of a cell from deformed to recrystallize or to leave it unchanged. The major advantage of these models is their ability to consider material heterogeneity. Since in MC models Monte Carlo steps are considered the measure of time, physical time is not available which makes drawing comparison between MC results and experimental results difficult. Moreover, MC is a probabilistic approach, i.e. there is no criterion to favor any recrystallization front evolution and since it is well suited for
isotropic dilatation/shrinking it is mostly used for grain growth than recrystallization. Thereby, MC modelling of recrystallization has now largely been replaced by the use of CA models. A cellular automaton consists of a grid of cells and is typically characterized by parameters such as: * Cell geometry * The number and type of states that a cell can have * The definition of the neighborhood of a cell (Fig. 2) * The rules of transition for a cell

CA is a deterministic approach, i.e. depending on the current state of the cell and comparing to its neighbors, the crystallization front evolution is anticipated. One advantage of this method is that the transformation can be dependent on stored energy, disorientation, local temperature and pressure etc.

Phase field models describe the microstructure by functions of phase field variables which are continuous in space. Describing grain boundaries as diffuse transition regions of the phase field variables, a distinction is made between conserved (measures of the local composition) and non-conserved (contain information on the local structure and could represent the crystallographic orientation) variables. While phase filed models can capture evolution kinetics of microstructural systems by considering the comprehensive action of thermodynamically driving force, they require enormous calculations in treating the rapidly changing fields across the diffuse interface. Moreover, it should be taken into account that the formulation of the energy densities, required for capturing physical microstructure features, is not trivial and nucleation of new grains are not easily handled. Therefore, although this method is currently attracting a lot of attention, it is time consuming.

In the case of facing insufficient knowledge about the external boundary conditions and internal starting conditions, which is limiting discrete models, further experiments or simulations are needed. This will lead to coupled models. As an instance, one may use CPFEM to obtain the deformed microstructure which is the input of the CA model.