

# Fracture Healing

The aim of this lab is to complete an implementation of a simplified version of [Simon et al. 2011](#). We will assume a perfect blood perfusion in the full domain such that the revascularization process can be neglected. Furthermore, the different tissue types are represented by their relative concentrations  $c(x, t)_i$ .

The description of the simulation is given in the template file "concChange.H".

## Tasks

1. Download the template implementation from the course site.
2. Edit the "concChange.H"-file such that the tissue type composition of the elements changes according to the mechanoregulated differentiation hypotheses of Claes & Heigele.
3. Use the makefile to compile the code and run it via:  

```
./labFracHealing 50 < materials
```

## Suggestions

- The executable needs an integer argument that defines the number of iterations following from an input stream that defines the initial material distribution
- The concentrations are saved in the dat-folder after each iteration with the formatation:  
*Column Row Concentration*      <- separated by one tab

