

Mathematical Descriptions of Bone Remodeling Dynamics in Myeloma Bone Disease

Bruce P. Ayati

Department of Mathematics and Program in Applied and
Computational Mathematics
University of Iowa

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Conflicts of Interest

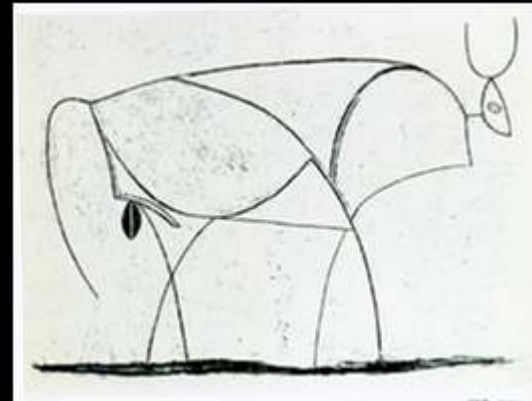
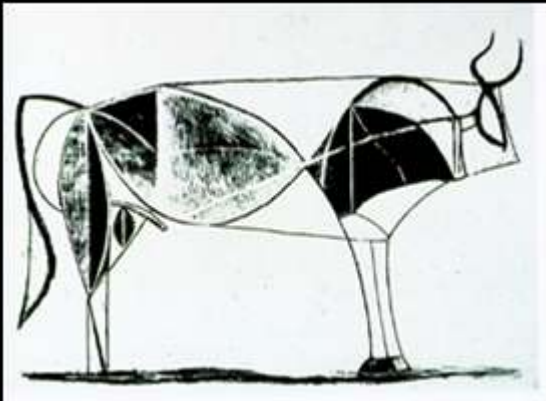
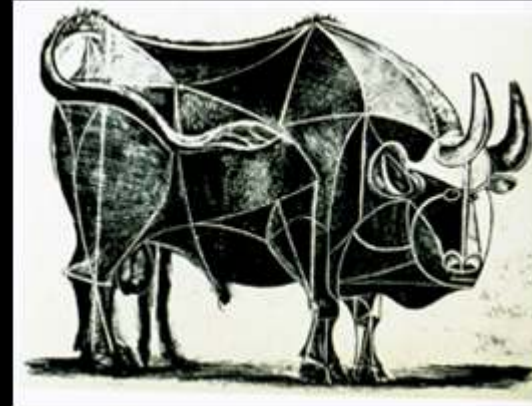
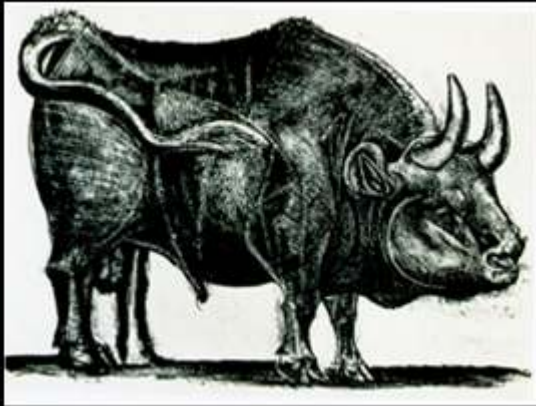
I have no conflicts of interest.

Value of a Mathematical Model

- Basic science:
 - ✧ Link mechanisms to phenomena
 - ✧ Generate hypotheses
- Rapid initial screening of drugs and therapies
- Predictive models facilitate patient specific medicine

Level of Abstraction

Picasso's Bulls



Nature of Abstraction



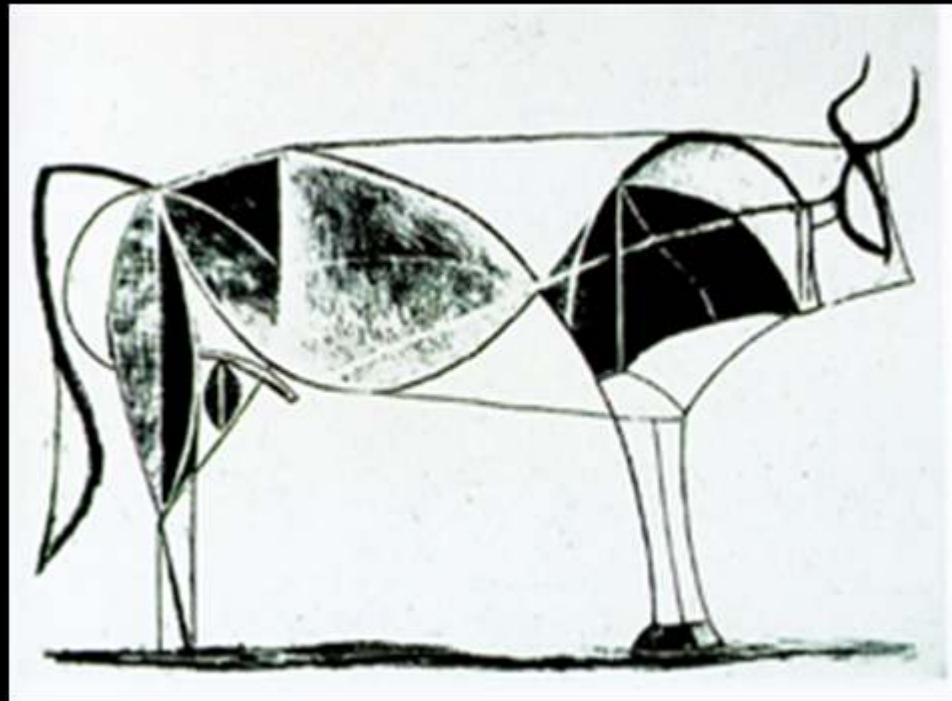
Georges Braque, Woman with a Guitar, 1913. Musée National d'Art Moderne

Abstraction in a mathematical model:

- Emphasize important relationships
- Represent things by what they do more than what they are

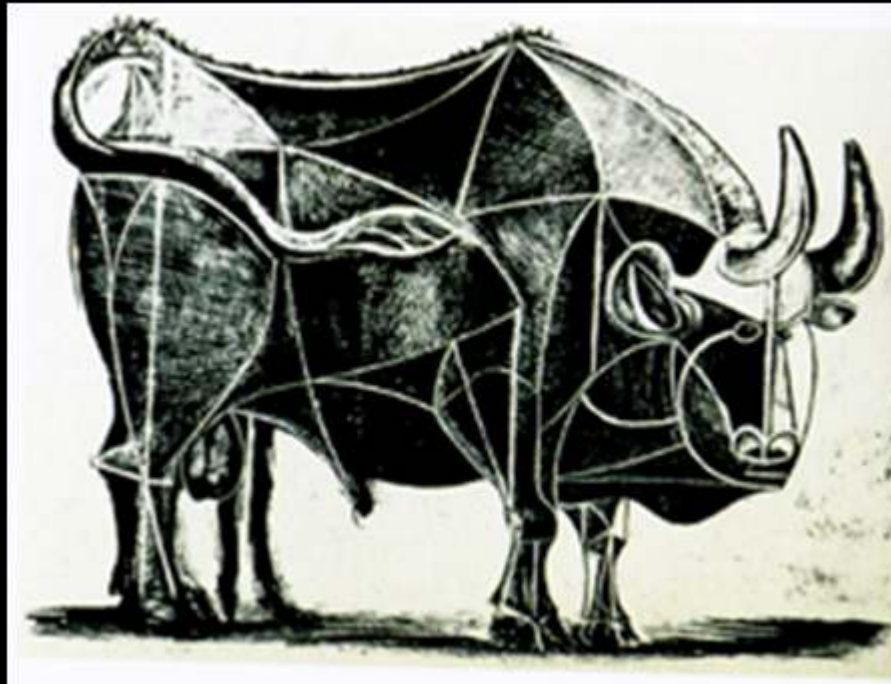
Non-Spatial Model

- Our representation of normal bone remodeling dynamics is taken from Komarova et al. 2003
- Power laws in the equations for cell types implicitly capture the cell signaling.

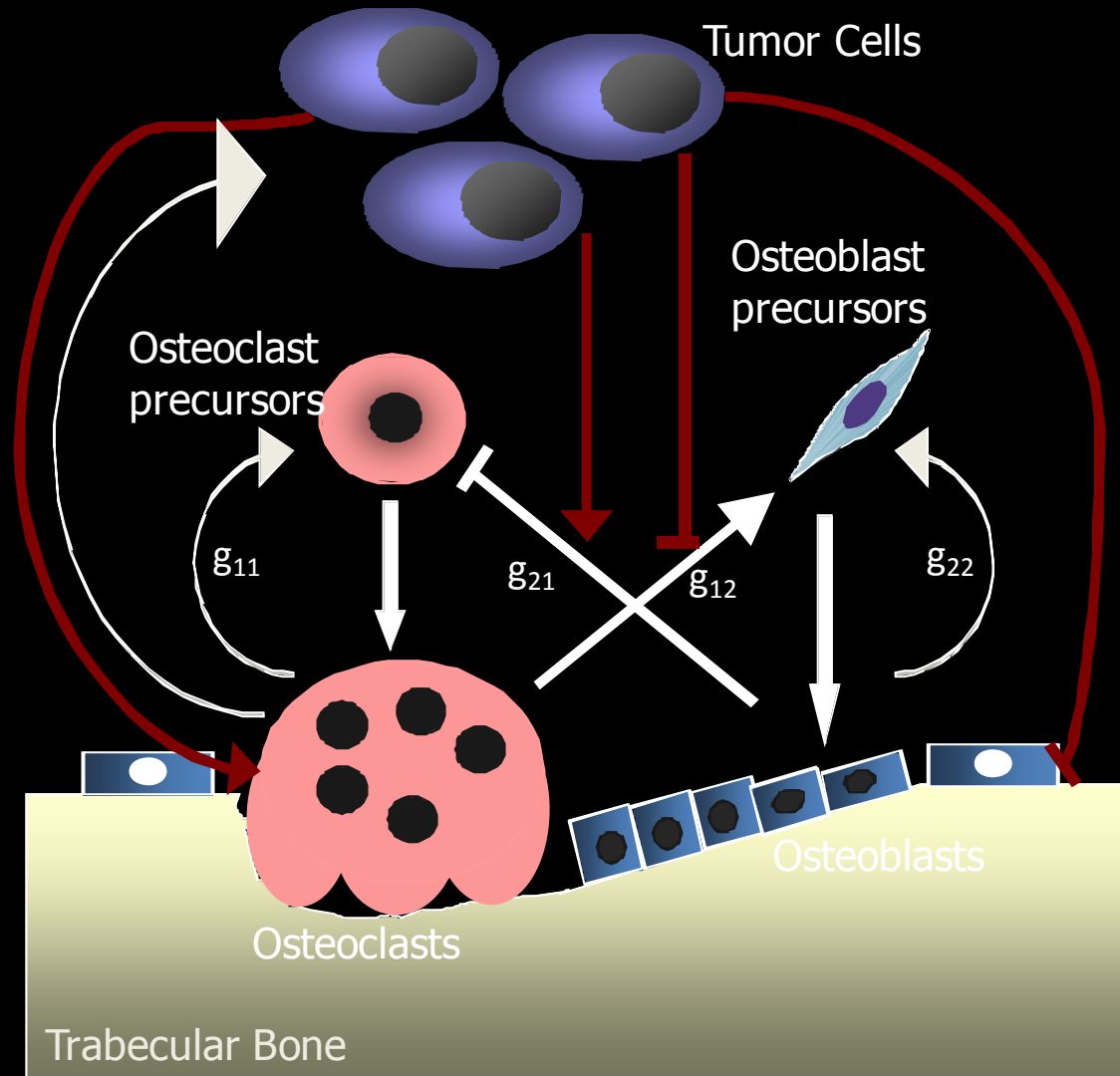


Non-Spatial Model

- A model with explicit compartments for the signaling molecules is given by Pivonka et al. 2008
- An approach of this type could form the basis of a more mechanistic model



Non-Spatial Model



Model Equations

- We modify the Komarova power laws to incorporate the impact of myeloma cells on bone remodeling
- We add an equation for growth of myeloma cells which can include the **effects** of a proteasome inhibitor:
 - ✧ direct anti-myeloma effects and direct stimulation of osteoblast differentiation

Model Equations

$$\begin{aligned}\frac{d}{dt}C(t) &= \alpha_1 C(t)^{g^{11}(1+r_{11}\frac{T(t)}{L_T})} B(t)^{g^{21}(1+r_{21}\frac{T(t)}{L_T})} \\ &\quad - \beta_1 C(t),\end{aligned}$$

$$\begin{aligned}\frac{d}{dt}B(t) &= \alpha_2 C(t)^{g^{12}/(1+r_{12}\frac{T(t)}{L_T})} B(t)^{g^{22}-r_{22}\frac{T(t)}{L_T}} \\ &\quad - (\beta_2 - V_1(t))B(t),\end{aligned}$$

$$\frac{d}{dt}T(t) = (\gamma_T - V_2(t))T(t) \log \left(\frac{L_T}{T(t)} \right).$$

Model Results

The model was found to reflect accurately the basics of myeloma bone disease

- tumor burden is decreased and bone volume or markers of bone formation are increased in response to proteasome inhibitor

Spatial model

Current work: embedding the models for local interactions into a spatial model that reflects what are seen in sections of bone marrow biopsy

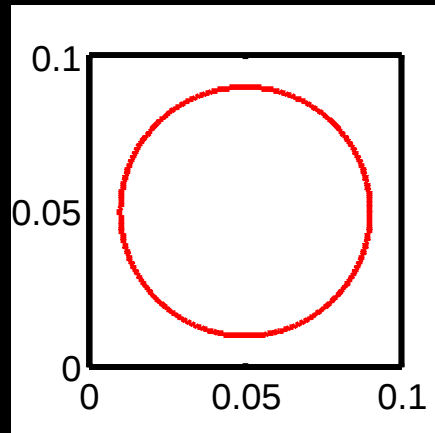
- 2D level-set formulation with normal bone remodeling is complete (Graham, Ayati, Ramakrishnan, Martin, submitted)
- Need refinement and parameterization of the local dynamics and extension to 3D

Spatial model

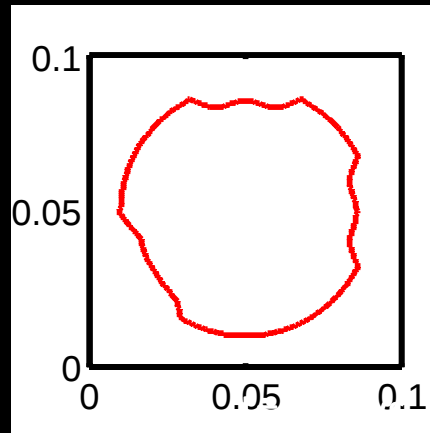
(proof of concept)

- We use a level set to define regions of bone and marrow.
- The interface moves according to the local dynamics of the interacting cell types (no-myeloma case), which are also simulated.
- A circular geometry is chosen for illustrative purposes and simplicity.

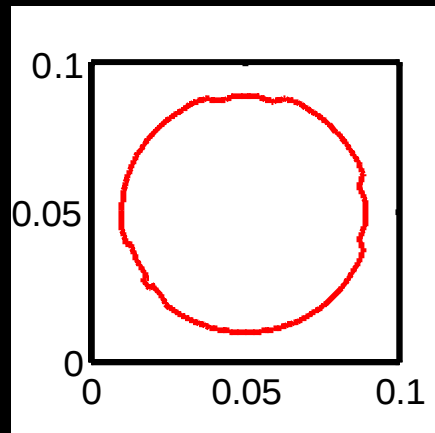
Spatial model (proof of concept)



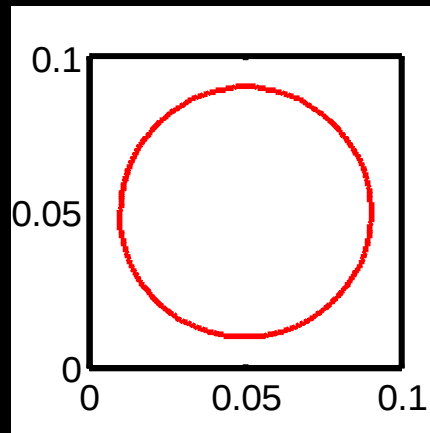
t=0 days



t=20 days



t=30 days



t=150 days

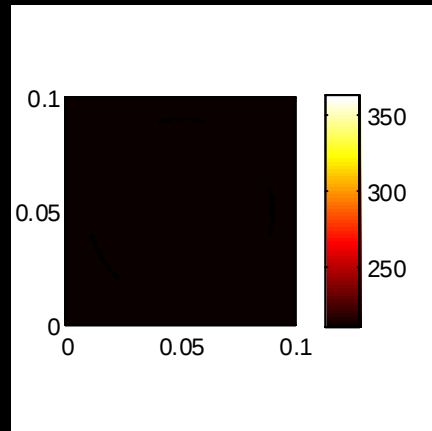
Snapshots during remodeling of a circular section of trabecular bone at three remodeling sites.

Spatial model

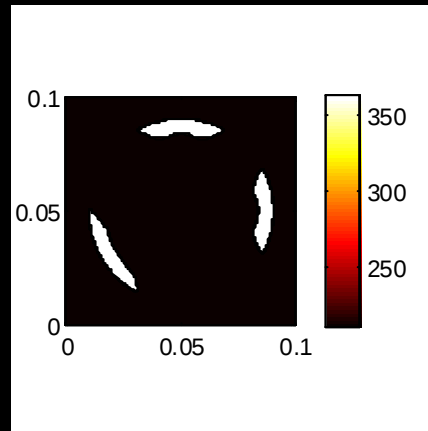
(proof of concept)

- In addition to the bone/marrow interface, we compute the densities of osteoclasts and osteoblasts (and in other simulations the explicit concentrations of RANKL and OPG concentrations).
- The local Ob/Oc interactions are what actually drive the bone/marrow interface dynamics in our simulation.

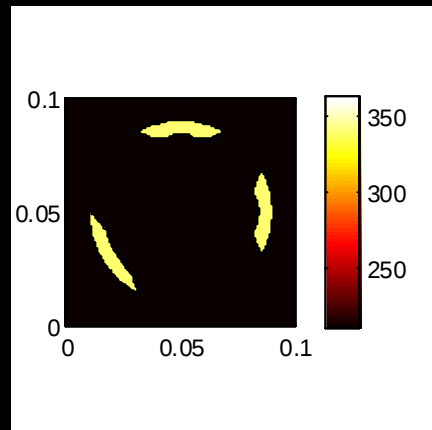
Spatial model (proof of concept)



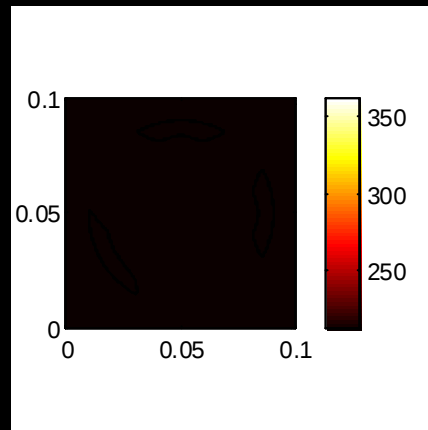
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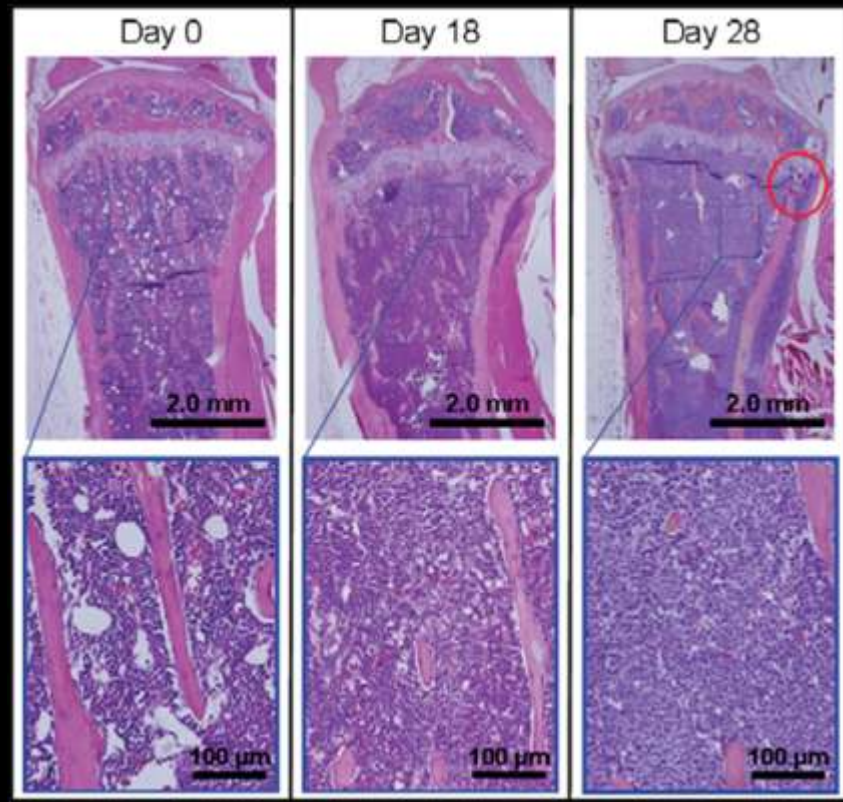
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Snapshots during remodeling of osteoblast densities at three remodeling sites.

Spatial Model (Extension)



The level set method is designed for much more complicated geometries.

Framework extends naturally to these geometries at a range of spatial scales

Figure courtesy of C. Edwards

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