Formal Analysis of Bone Clinical Pathologies

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Biological background



2 Computational modeling of bone pathologies



Outline



Biological background



Bone remodeling

- Bone remodeling (BR) is the process by which aged bone is continuously renewed in a balanced alternation of bone resorption and formation
- BR is driven by **osteoclasts** (the diggers) and **osteoblasts** (the fillers), forming *Basic Multi-cellular Units* (*BMUs*)
- Imbalances between resorption and formation lead to bone pathologies (e.g. in osteoporosis resorption > formation)





Key events in BR (1/2)



 $Osteocytes^{(1)}$ send signals to the fluid part, activating Preosteoblasts⁽²⁾ (Pb) and Pre-osteoclasts⁽³⁾ (Pc)

Key events in BR (1/2)



Pbs express $RANKL^{(4)}$. *Pcs* express $RANK^{(5)}$ receptor.

Key events in BR (1/2)



RANK/RANKL binding⁽⁶⁾ induces **Pcs' proliferation**⁽⁷⁾. *Pcs* enlarge and fuse, forming mature **Osteoclasts**⁽⁸⁾ which start bone **Resorption**⁽⁹⁾. Mature osteoblasts express the decoy receptor **OPG**⁽¹⁰⁾.

Biological background

Key events in BR (2/2)



Osteoblasts start the bone $Formation^{(11)}$ process. RANKL/OPG binding⁽¹²⁾ inhibits RANKL, protecting bone from excessive resorption.

Key events in BR (2/2)



During the $\mbox{Mineralization}^{(13)}$ process, osteoids secreted by osteoblasts calcify.

Key events in BR (2/2)



Resting⁽¹⁴⁾: the initial situation is re-established







2 Computational modeling of bone pathologies



$$\begin{aligned} \dot{x_1} &= \alpha_1 x_1^{g_{11}} x_2^{g_{21}} - \beta_1 x_1 \\ \dot{x_2} &= \alpha_2 x_1^{g_{12}} x_2^{g_{22}} - \beta_2 x_2 \\ \dot{z} &= -k_1 x_1 + k_2 x_2 \end{aligned}$$

- Osteoclasts
- Osteoblasts
- Bone mass



$$\dot{x_1} = \alpha_1 x_1^{g_{11}} x_2^{g_{21}} - \beta_1 x_1$$
$$\dot{x_2} = \alpha_2 x_1^{g_{12}} x_2^{g_{22}} - \beta_2 x_2$$
$$\dot{z} = -k_1 x_1 + k_2 x_2$$

- 1. Modeling a portion of BMU
 - Parameter sensitivity and identifiability
 - New parameters after model fitting operations



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2. RANKL and aging paramaters

- *RANKL* strongly affects the resorption phase
- Aging expressed as reduced cellular activity



$$\dot{x_1} = \alpha_1 x_1^{g_{11}} x_2^{g_{21}} - \beta_1 x_1$$
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$$\dot{z} = -k_1 x_1 + k_2 x_2$$

New model

$$\dot{\mathbf{x}}_1 = \alpha_1 x_1^{g_{11}} x_2^{g_{21}/\underline{\mathbf{rankl}}} - \beta_1 x_1$$
$$\dot{\mathbf{x}}_2 = \alpha_2 x_1^{g_{12}} x_2^{g_{22}} - \beta_2 x_2$$
$$\dot{\mathbf{z}} = -\underline{\mathbf{ag}} k_1 x_1 + \underline{\mathbf{ag}} k_2 x_2$$



Stochastic model

From the modified ODE, we derive a CTMC model for the PRISM model checker.

	Original	BMU portion	
States	21,021	5,616	(-73.28%)
Transitions	103,060	27,345	(-73.47%)

Stochastic model

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	Original	BMU portion	
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Modified ODE model

$$\dot{x}_1 = \alpha_1 x_1^{g_{11}} x_2^{g_{21}/rankl} - \beta_1 x_1$$

$$\dot{x}_2 = \alpha_2 x_1^{g_{12}} x_2^{g_{22}} - \beta_2 x_2$$

$$\dot{z} = -ag \cdot k_1 x_1 + ag \cdot k_2 x_2$$

Stochastic model

$$\begin{bmatrix} x_1 > 0 \to \beta_1 x_1 : x_1 = x_1 - 1 \\ x_1 < max_{x_1} \to \alpha_1 x_1^{g_{11}} x_2^{g_{21}/rankl} : x_1 = x_1 + 1 \\ [resorb] x_1 > 0 \to ag \cdot k_1 x_1 : true \end{bmatrix}$$

$$\begin{bmatrix} x_2 > 0 \to \beta_2 x_2 : x_2 = x_2 - 1 \\ x_2 < max_{x_2} \to \alpha_2 x_1^{g_{12}} x_2^{g_{22}} : x_2 = x_2 + 1 \\ [form] x_2 > 0 \to ag \cdot k_2 x_2 : true \end{bmatrix}$$

Model checking bone pathologies

Diagnostic estimators:

- Bone density monitor
- Papidity of density changes

Comparison of two configurations over a 4 years-time:

- healthy conf: rankl = 1 and ag = 1
- pathological conf: rankl = 1.2 and ag = 2





2 Computational modeling of bone pathologies



Bone mineral density

$$\begin{array}{l} f_{+}(t): \ R\{'' \textit{boneFormed}''\} =?[C \leq t], \\ f_{-}(t): \ R\{'' \textit{boneResorbed}''\} =?[C \leq t], \\ f_{BD}(t): \ f_{+}(t) - f_{-}(t), \quad t = 0, 10, \dots, 1460. \end{array}$$



Density change rate



- Statistical analysis of ODE model for reducing the state space and incorporating *RANKL* and *aging* parameters
- Derivation of a stochastic model in PRISM
- Comparison of healthy and pathological configurations
- Probabilistic verification of bone pathologies with clinical estimators

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