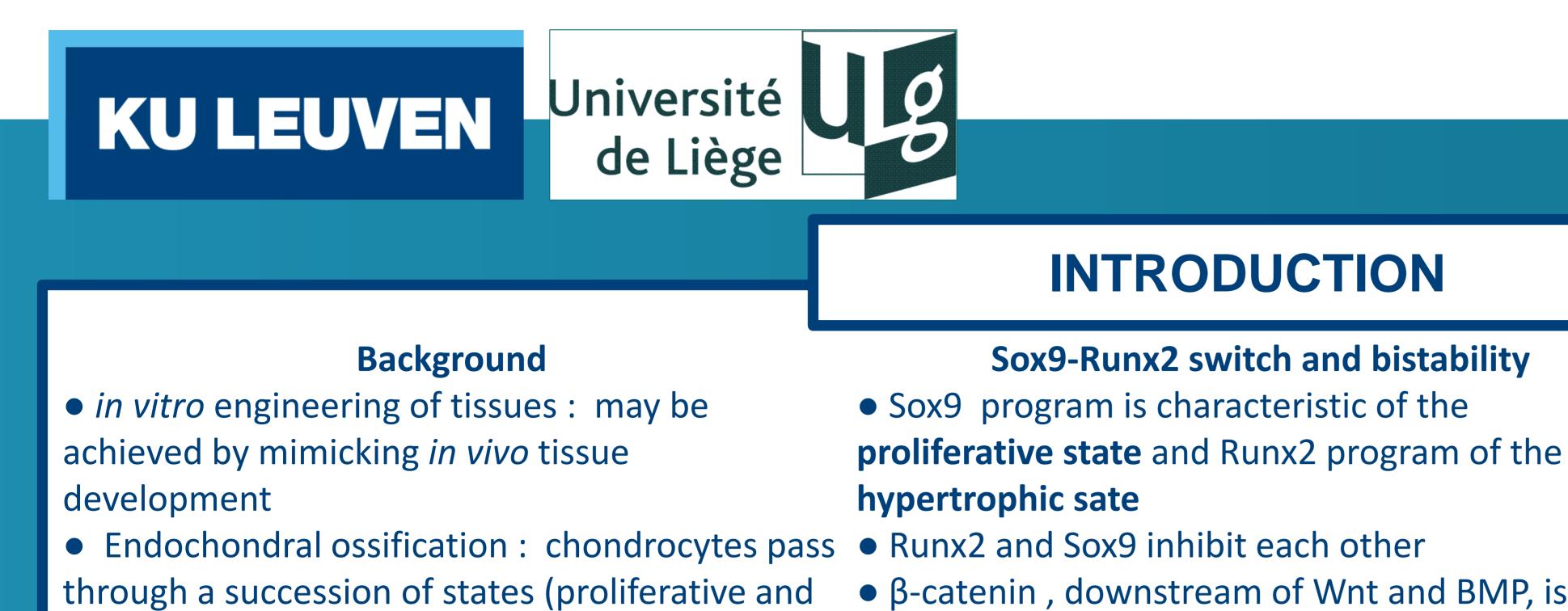
Mutual inhibition and bistability: two key elements of the endochondral ossification process

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Aim of this study

 model the switch between Sox9 (proliferative) program and Runx2 (hypertrophic) program • experimental validation

hypertrophic state)

• β -catenin , downstream of Wnt and BMP, is a key factor in this mechanism

MODEL 1

- a literature-based mathematical **model** descibing BMP and Wnt pathways and various cross-talks [1] • mutual inhibition between BMP and Wnt
- regulation of the amount of β -catenin in the nucleus
- parameter values derived from previous models [1] and experiments reported in literature [3]
- 19 variables, 49 parameters

MATERIALS & METHODS

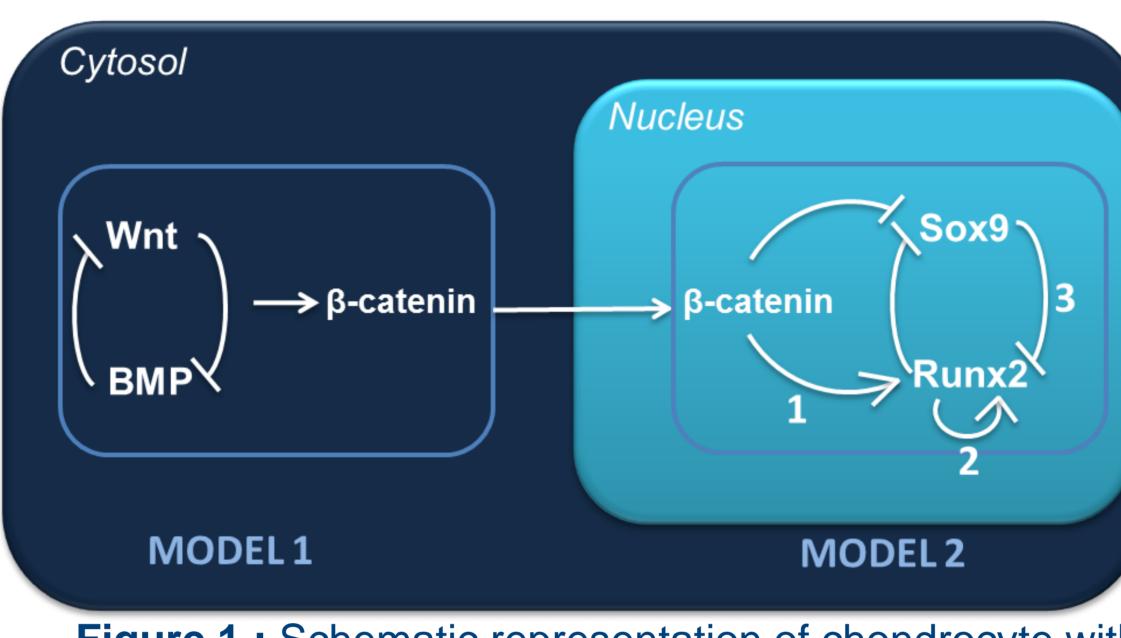


Figure 1 : Schematic representation of chondrocyte with indication of both models

MODEL 2

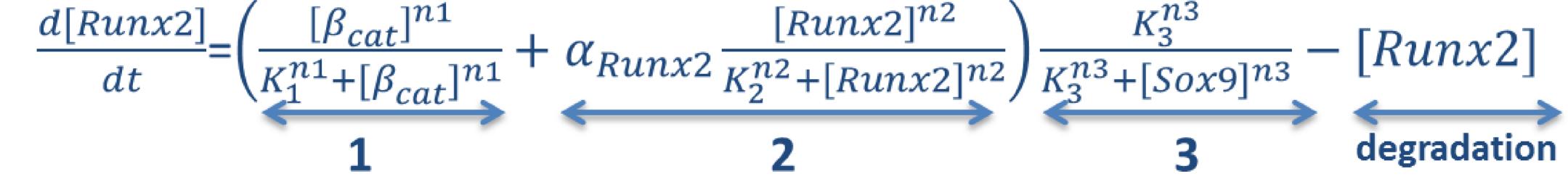
• a literature-based mathematical **model** describing the switch between Sox9 and Runx2

• mutual inhibition between Sox9 and Runx2

- **auto-activation** of Runx2
- parameter values by screening of parameter space to find parameter sets generating **bistable behavior** [2] • 3 variables, 16 parameters

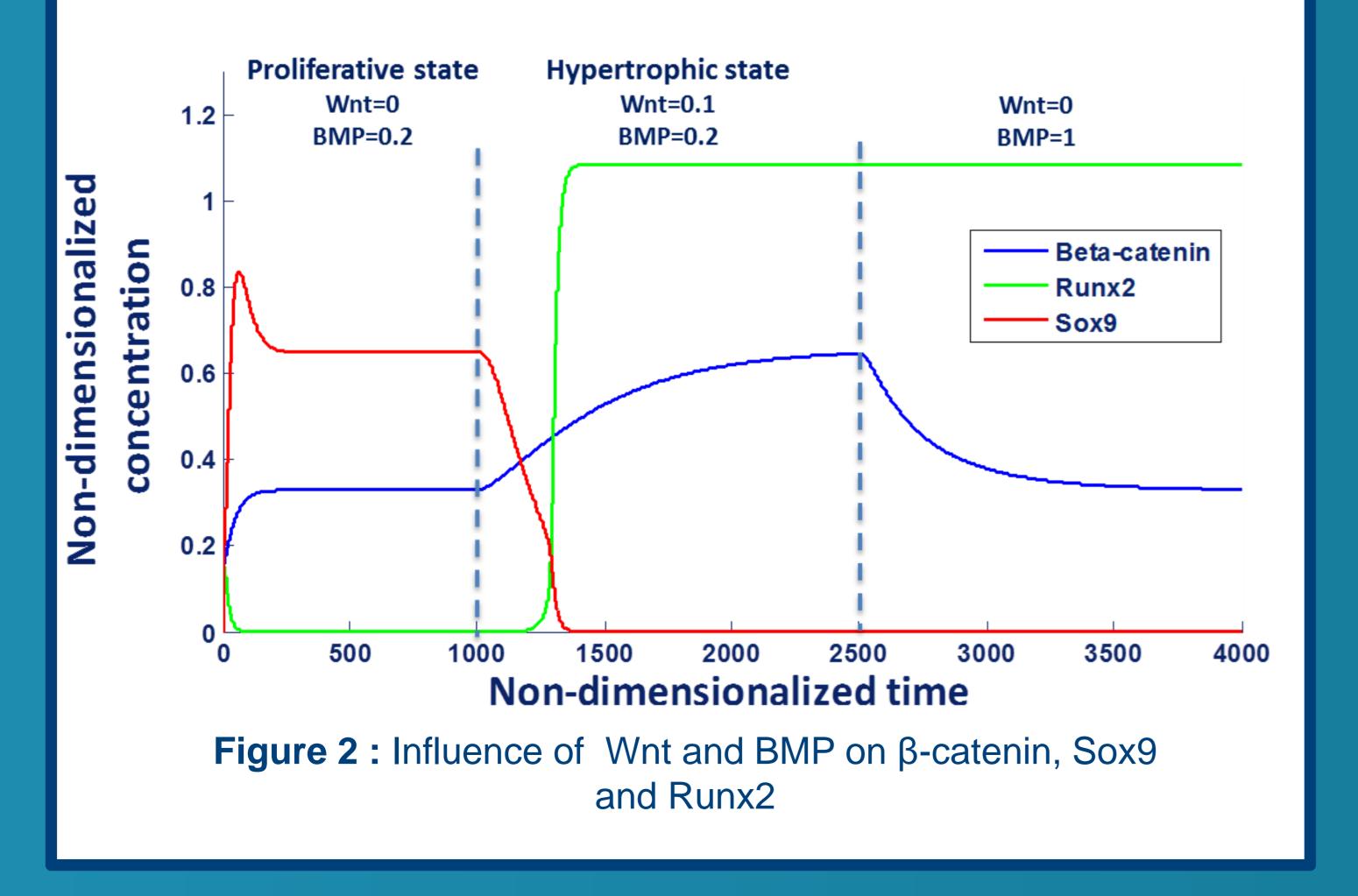
Ordinary Differential Equations (ODEs) describe the temporal evolution of the various model constituents (numbers refer to interactions in Figure 1)

 $[Runx2]^{n2}$



RESULTS

- the model predicts that :
 - \checkmark activation of Wnt upregulates β -catenin and provokes the switch between the Sox9 state and the Runx2 state
 - \checkmark activation of BMP inhibits the transition of β -catenin to the nucleus but cannot provoke a switch from the Runx2 state towards the Sox9 state
 - ✓ two stable states (bistability) are obtained for appropriate parameter sets



DISCUSSION

- in absence of quantitative parameter information, the ODE model presented here provides qualitative predictions on changes in the concentrations of all modelled components • the model is able to reproduce the switch between the Sox9 program and the Runx2 program for specific parameter sets • the model behavior is in concordance with experimental results present in the literature [4] • mathematical models can be used to enhance our understanding
- of signaling cascades and their interactions



REFERENCES

[1] Geris, Vandeput et al, 2010, Termis-EU Galway; [2] Yao, Tan et al, 2011, Molecular Systems Biology, 7:485; [3] Zou, Zou et al, 2006, Adv Exp Med Biol. 585:431-41; [4] Lui, Andrade et al, 2010, Bone, 46(5): 1380–1390

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