Master Internship Proposal:
Replaying the Tape of Rodent Molar Diversification

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Host team The internship will take place in the Cigogne team, which is part of the LBMC (Laboratory of Biology and Modeling of the Cell) at ENS Lyon. Cigogne is an interdisciplinary team that bridges experimental evo-devo, omics, and modeling. The team is led by Sophie Pantalacci (DR CNRS) and Marie Sémon (Full Prof. ENS). The internship will be supervised by Théotime Grohens, a postdoc in the team, who has a dual background in computer science and evolutionary biology.

Background In the team, we study molar development in rodents as a model system for the interplay between development, genome, and evolution. We use both wet-lab (tooth imaging) and dry-lab (genomics and transcriptomics, evolutionary simulations) approaches to understand the processes underlying tooth development in different rodent species. In particular, one of our aims is to understand how the house mouse evolved additional cusps (peaks) in their upper molars – contrary to the ancestral rodent trait – while retaining good tooth *occlusion*: the ability to chew food properly.

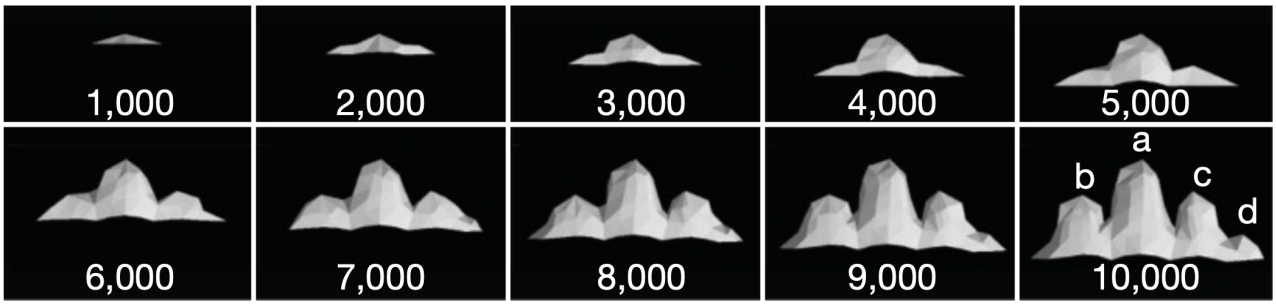

Figure 1: Simulated 3D development of an example tooth, taken from [2]. The epithelial tissue gradually invades the mesenchyme upwards, and differentiates into enamel knots that each give rise to a tooth cusp.

In order to study the evolution of 3D tooth shapes, our base tool is ToothMaker [2], a cell-based simulation that models tooth development using a reaction-diffusion system coupled with biophysical forces between cells. Around this model, we use an *in silico* artificial evolution approach: generation after generation, we simulate the evolution of a population of individual rodents, each defined by the set of developmental parameters that give rise to its upper and lower molars. For each individual, we compute a fitness value based on tooth occlusion, allowing us to select reproducers, and to create a new generation by mutating the genome of the reproducers [1].

Goals Right now, we use a 2D projection of the teeth of an individual to compute their occlusion, but we have a prototype to do this with the 3D models directly. The internship will start with an efficient reimplementation (in Python) of this 3D occlusion computation. Then, we will use our evolutionary simulation to study the diversity of tooth shapes that we observe when selecting for good occlusion. Depending on the intern's interest, we can also tweak ToothMaker itself to change the morphogenesis model and see how this impacts evolution, for example by making the model make a more biologically accurate rodent molar.

Expected skills We are looking for someone with an interest for interdisciplinary approaches, at the boundary between developmental and evolutionary biology, biophysics, and computer science. As the internship will be fully computational, we would like the intern to already have good programming and command-line experience.

References

[1] Hagolani, P. F., Sémon, M., Beslon, G., and Pantalacci, S. Pleiotropy accelerates tooth phenotypic and genomic evolution — an in silico study under the lens of development. *bioRxiv* (2025).

[2] Salazar-Ciudad, I., and Jernvall, J. A computational model of teeth and the developmental origins of morphological variation. *Nature 464*, 7288 (Mar. 2010), 583–586.