

# Simulation of stromatolite growth using diffusion-limited aggregation and discrete model of biogeochemical exchanges in microbial mat

Thèse de doctorat par

**Damien Chapatte**

## **Abstract**

Better understanding of stromatolites and microbial mats is an important topic in biogeosciences as it helps studying the early forms of life on Earth, provides clues regarding the ecology of microbial ecosystems and their contribution to biomineralization, and gives basis to a new science, exobiology. On the other hand, modelling is a powerful tool used in natural sciences for the theoretical approach of various phenomena. Models are usually built on a system of differential equations and results are obtained by solving that system. Available software to implement models includes mathematical solvers and general simulation software.

The main objective of this thesis is to develop models and software able to help to understand the functioning of stromatolites and microbial mats. Software was developed in C++ from scratch for maximum performance and flexibility. This allows to build models much more specific to a phenomenon rather than general software.

First, we studied stromatolite growth and morphology. We built a three-dimensional model based on diffusion-limited aggregation. The model was implemented in two C++ applications: a simulator engine, which can run a batch of simulations and produce result files, and a visualization tool, which allows results to be analysed in three dimensions. After verifying that our model can indeed reproduce the growth and morphology of several types of stromatolites, we introduced a sedimentation process as an external factor. This led to interesting results, and allowed to emit the hypothesis that stromatolites morphology may be the result of external factors as much as internal factors. This is important as stromatolite classification is usually based on their morphology, imposing that a stromatolite shape is dependant on internal factors only (i.e. the microbial mat). This statement is contradicted by our findings.

Seconds, we decided to investigate deeper the functioning of microbial mats. We built a two-dimensional reaction-diffusion model based on discrete simulation. The model was implemented in a C++ application that allows setting and running simulations. We could then compare simulation results with real world data and verify that our model can indeed mimic the behaviour of some microbial mats. Thus, we have proposed and verified hypotheses regarding microbial mats functioning in order to help to better understand them, e.g. the cycle of some elements such as oxygen or sulphur.

In conclusion, this PhD provides a simulation software, dealing with two different approaches. This software is free and available under a GPL licence.