

iDynoMiCS 2: Fully flexible computer modelling platform for microbial ecology

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Abstract

The source code is publicly available to download from https://github.com/roughhawkbit/iDynoMiCS-2.

Author Summary

Introduction

Individual-based modelling of microbial communities is becoming ever more widespread as software is developed and computational power increases [1]. Drive for more generic software: checked by more people, so more reliable [2]; easier to compare different model formulations, i.e. structural sensitivity [?]. Software based on [3,4].

Models

The model description follows the ODD (Overview, Design concepts, Details) protocol [5,6]. Further details are available in Supporting Information for some parts of the model description.

Purpose

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State variables and scales

Process overview and scheduling

Each compartment is self-contained. No interaction between compartments within a global time-step, all transfers are stored and happen instantly between timesteps.

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Design concepts
The iDynoMiCS 2 structure inherits many concepts from previous packages [3,4], but also builds on these.
Emergence
Modularity Aids customisability
Ease of comparison Since iDynoMiCs 2 already adopts the hybrid approach to modelling (discrete) cells in (continuous) concentration fields, it is straightforward from a design perspective to instead treat cells as a continuum. This "retrofit" allows easy comparison of the hybrid IbM approach with more traditional population-based approaches [7] for the same system. Such calibration is already used often, but implementing this feature is, to our knowledge, the first time it has been offered within a single software package.
Initialization
Input
Native protocol file layout, but (hopefully!) able to read in other formats such as Hucka2003 [8] and Cuellar2003 [9].
Submodels
?
Results

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Discussion

Supporting Information

Acknowledgments

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