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

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.

Design concepts

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The iDynoMiCS 2 structure inherits many concepts from previous packages [3,4], but also builds on these.

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Emergence

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Modularity Aids customisability

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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.*

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Initialization

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Input

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Native protocol file layout, but (hopefully!) able to read in other formats such as Hucka2003 [8] and Cuellar2003 [9].

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Submodels

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Results

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Discussion

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Supporting Information

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Acknowledgments

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