## INDIVIDUAL-BASED COD SIMULATION WITH ML-RULES

Maria E. Pierce, Tom Warnke, Tobias Helms, Adelinde M. Uhrmacher

Institute of Computer Science University of Rostock Albert-Einstein-Straße 22 18059 Rostock, GERMANY

Uwe Krumme and Cornelius Hammer

Thünen Institute of Baltic Sea Fisheries Alter Hafen Süd 2 18069 Rostock, GERMANY

#### ABSTRACT

A dramatic increase in malnourished cod can presently be observed in the Eastern Baltic. Simulation studies help unraveling possible reasons behind this. Particularly, individual-based modeling approaches are promising as they facilitate taking into account the heterogeneity of the cod population, where size, temperature etc. determine behavior patterns. Thus, we develop an individual-based model of cod implemented in the rule-based multi-level modeling language ML-Rules that allows to specify dynamically nested entities with attributes and complex multi-level reaction rules. By using this language, we are able to deal with several challenges when modeling such complex systems, e.g., dynamic structures, complex interaction rates and interdependencies. Here, we discuss the current state of our model that already represents a near realistic cod metabolism and we discuss how ML-Rules helped to solve emerged challenges.

# **1 MOTIVATION**

The condition of the Eastern Baltic cod stock has decreased dramatically within the last years (?). Several causes may explain this development, e.g., stratification changes or the lack of experienced cod. Typically, simulation studies are used to help analyzing these causes. Individual-based modeling approaches are preferred to analytical approaches because they are able to take the heterogeneity of the cod population into account (?). To analyze the behavior of cod for different scenarios, we develop such an individual-based model in the rule-based multi-level modeling language ML-Rules (?, ?). A rule-based language is particularly useful in this setting, because it allows to describe the behavior and the dynamics of cod with few rules succinctly.

In ML-Rules, the basic entities are called species that may represent any objects of interest, e.g., cod, prey, oxygen, or stratified layers. Species can be equipped with attributes, e.g., to specify the length, weight and temperature of a cod. An essential feature of ML-Rules is that species can be dynamically nested, i.e., species can contain other species and the organizational structure of species can change during the simulation. This feature is especially useful to model the ecosystem of which cod are an essential part, because stratified layers can emerge and diminish over time and cod constantly move between these layers. In ML-Rules, the dynamics of a model are specified by rule schemes that are encoded during the simulation

into concrete rule instantiations. A rule scheme consists of reactants, products, and a reaction rate equation that determines the propensity of a rule instantiation. Reaction rate equations can include conditions and function calls and they can use attribute values of reactants to calculate the propensity. Further, functions on sets of species can be defined (?), e.g., the number of cod in a stratified layer that are bigger than a specific threshold can be calculated within a rule. Basically, the semantics of ML-Rules translates to continuous-time Markov chains, i.e., state transitions follow an exponentially distributed random waiting time (?).

### 2 RESULTS

The basic species of our developed model represents the cod (Cod). It consists of three attributes representing the length, weight, and temperature of a cod. Further, each cod contains oxygen (O) and energy (E) entities, and a stomach species used for its metabolism. Cod hunt prey, digest eaten prey and grow depending on the available energy. The cod's metabolism is specified with no more than ten rule schemes. Most of these rules use reactant attributes to calculate the propensities. For example, the following rule describes the growth of a cod:

$$Cod(l,w,t)[4 \ O+12 \ E+s?] \xrightarrow{prop(w,t)} Cod(l+f(w),w+gi,t)[s?].$$

The reactant of this rule scheme is a *Cod* species that must contain at least 4 *O* species and 12 *E* species. The variables *l*, *w*, and *t* represent the length, weight and temperature of the selected *Cod* species and the variable *s*? represents all other species that are enclosed by this cod. Further, the conditional function cond(w,l), that depends on the weight and length of the selected *Cod*, must hold so that an instantiated rule can be executed. The rate of an instantiated rule is computed by the function prop(w,t), that depends on the weight and temperature of the selected *Cod*. When executing an instantiation, 4 *O* and 12 *E* within the selected *Cod* are removed, the length is increased by the function f(w), and the weight is increased by the constant growth increment *gi*.

To include stratified layers, we added a layer species with different attributes to characterize the position and further properties like the temperature of each layer. Layers can change their properties, they can diminish and emerge and cod can move from a layer to a neighboring layer. Due to the powerful features of ML-Rules, these dynamics can easily be described with few rule schemes.

The current model already simulates the cod's metabolism in a near realistic way that has been cross-validated with empirical data. Further, we currently execute experiments with small swarms of cod to analyze the behavior for different stratification scenarios. In the future, we plan to add more interaction rules, e.g., experienced cod and cannibalism, and we plan to add more complex stratification systems.

### REFERENCES

- ICES Advisory Committee 2015. ICES WGBFAS Report 2015. Report of the Baltic Fisheries Assessment Working Group (WGBFAS). Copenhagen.
- Maus, C., S. Rybacki, and A. M. Uhrmacher. 2011. "Rule-based multi-level modeling of cell biological systems". *BMC Systems Biology* 5 (166).
- Uchmański, J., and V. Grimm. 1996. "Individual-based modelling in ecology: what makes the difference?". *Trends in Ecology & Evolution* 11 (10): 437–441.
- Warnke, T., T. Helms, and A. M. Uhrmacher. 2015. "Syntax and Semantics of a Multi-Level Modeling Language". In Proceedings of the 3rd ACM SIGSIM Conference on Principles of Advanced Discrete Simulation, 133–144.

Wilkinson, D. J. 2011. Stochastic Modelling for Systems Biology. 2nd ed. CRC Press.