



RIME: River Meta-Ecosystem Model. Metabolic regimes in Alpine stream networks

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Streams and rivers have been recognized only recently as key components of the global carbon cycle. However, lacking are the studies that nowadays provide a mechanistic understanding of the major drivers and controls of the ecosystem metabolism, sum of gross primary production and ecosystem respiration. These two components must be investigated in order to forecast temporal and spatial metabolic dynamics, to estimate carbon budgets and to test mitigation measures.

Several methods have been developed to characterize riverine ecosystems and depending on the research question, two are the main types of models generally adopted in freshwater ecology: *ecosystem models* and the *metabolism models*. The former aims at simulating biomass dynamics coupled with the external environmental constraints, adopting a bottom-up approach with a clear focus on the biological processes occurring at the cellular level. They rely on biomass measurements for calibration and they do not focus on carbon fluxes estimations. Metabolism models instead explicitly aim at estimating the river metabolism integrating the ecosystem features with top-down techniques, using diel fluctuations of dissolved oxygen concentration to estimate gross primary production (GPP) and ecosystem respiration (ER), without considering biomass dynamics as well as hydrological fluctuations and are thus feasible for steady-state, low-flow conditions and reach scale simulations.

Here we propose a novel approach for modelling ecosystem metabolism at the reach scale, unifying the two frameworks by keeping the advantages of both (e.g. accounting for biomass dynamics and hydrological disturbance, the possibility of using high frequency dissolved oxygen measurements DO for calibration), while possibly avoiding their drawbacks (e.g. unnecessarily complexity and overparameterization). Such a model, named RIVER Meta-Ecosystem model (RIME) is a four-state variable, 0-dimensional, dynamic, continuous and spatially implicit model which simulates the reach scale benthic biomass dynamics, basic building block of the trophic chain, as well as high resolution, DO variations, using as forcings discharge, streamwater temperature, barometric pressure and photosynthetic active radiation (PAR).

The model has been tested using datasets coming from four study reaches of the 254 km² subalpine Ybbs River Network (YRN), Austria. High frequency dissolved oxygen measurements have been used for the calibration purpose as metabolic carbon dynamics are stoichiometrically correlated with oxygen fluctuations within the water column.

Finally, possible future scenarios have been tested in order to derive shifts in local metabolic regimes. The processing of organic carbon in the river network depends mainly on the interplay between the temperature regime which regulates the benthic biomass amount and its metabolic rates and the flow regimes which controls the hydraulic retention of carbon. Results of ecosystem metabolism under increasing average temperature and more erratic flowrate dynamics have been compared with the present situation predicted by the local RIME model.

This model has the potential to be upscaled at the entire river network by coupling local models in a spatially distributed way and in the view of the meta-ecosystem theory. It will allow to fully appreciate the metabolic regime at the entire river network scale and to provide new estimations of carbon fluxes from land to ocean.