

**Denitrification-driven transcription and enzyme production at the river-groundwater interface: Insights from reactive-transport modeling**

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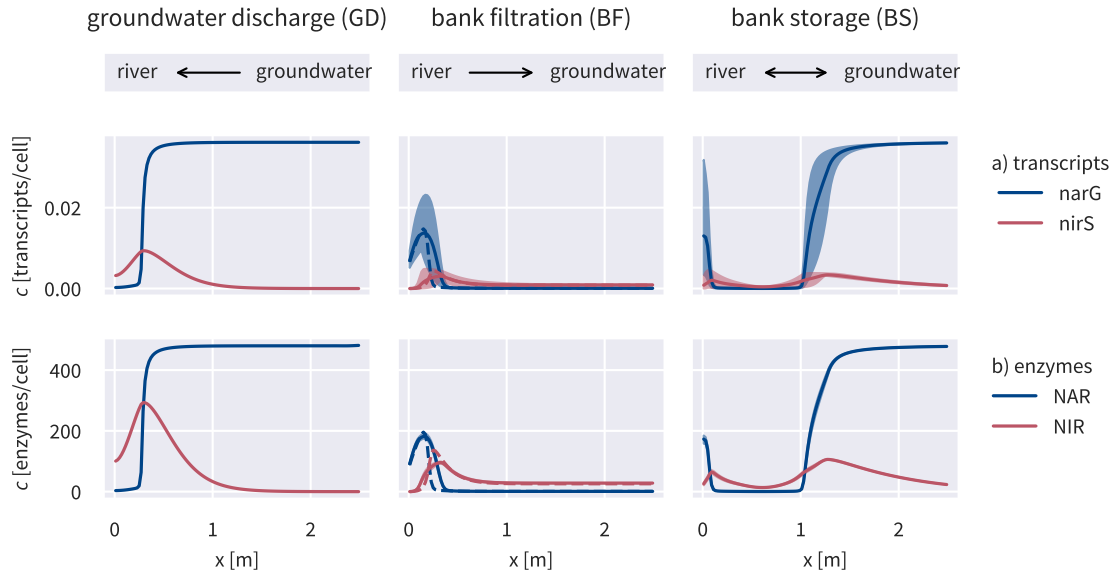
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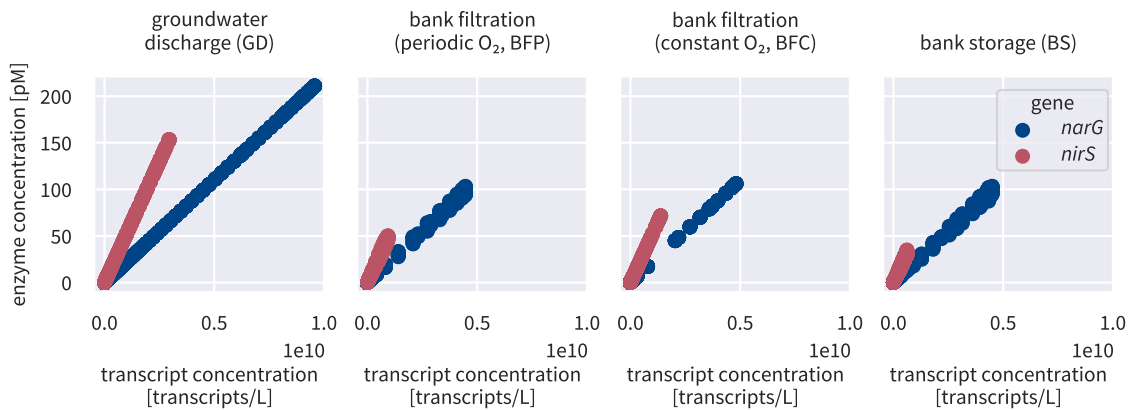
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**Introduction**

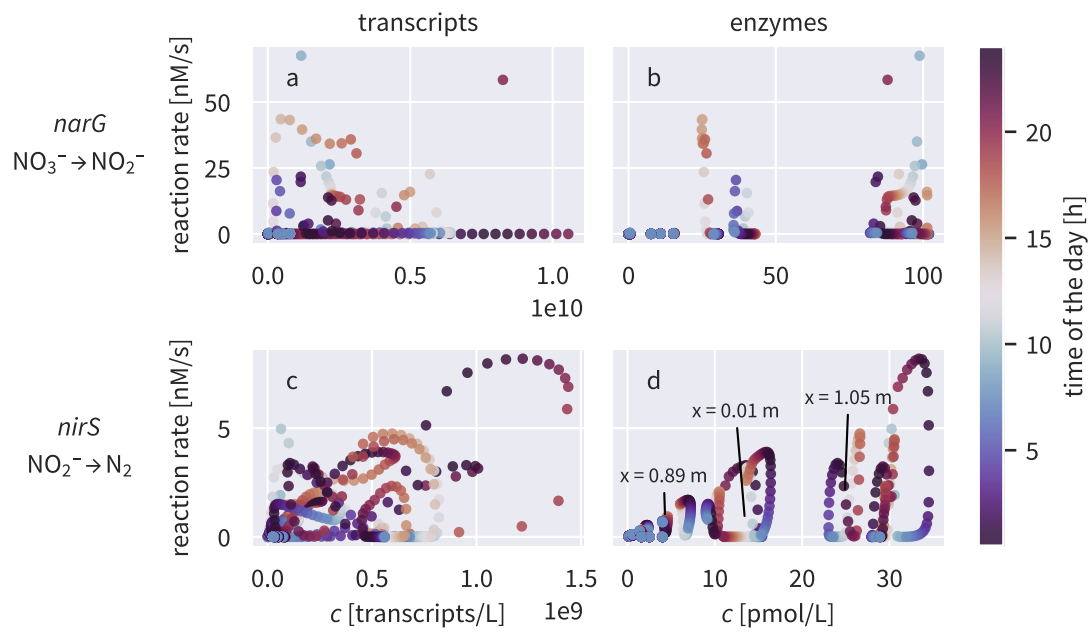
The supporting information includes additional figures created from the model outputs.



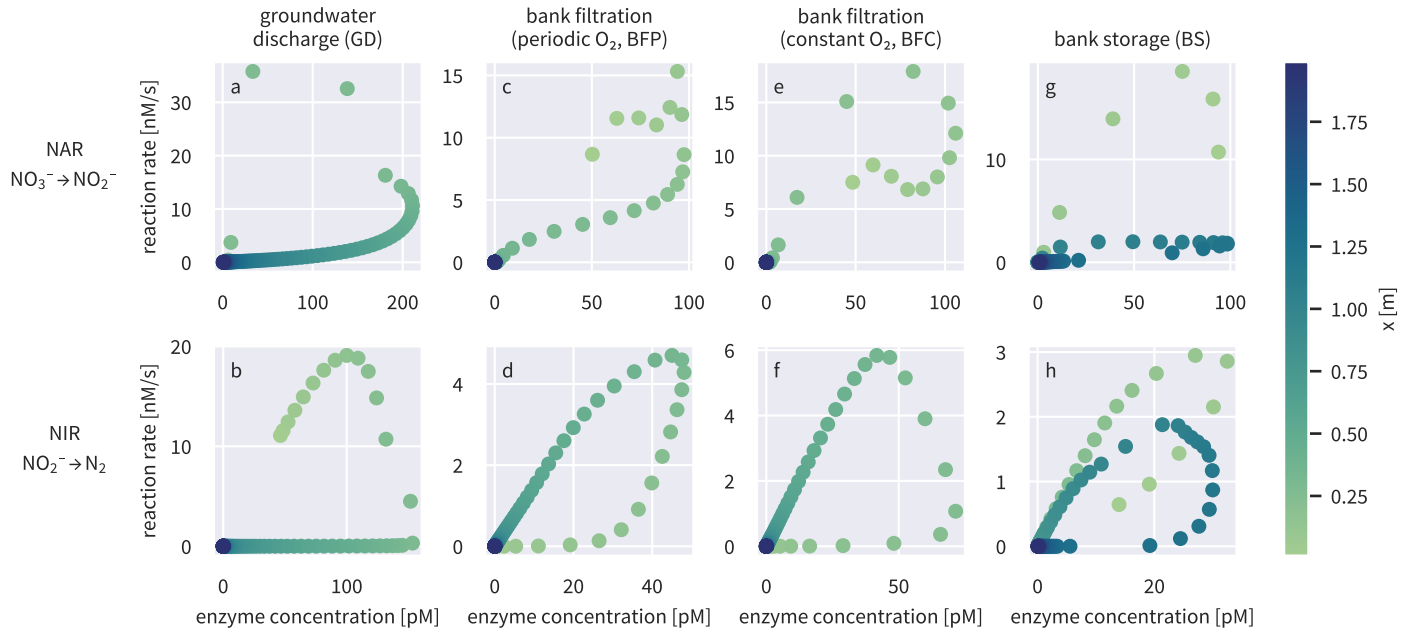
**Figure S1:** Spatial distributions of transcript and enzyme concentrations normalized by biomass. The steady-state solution in scenario BFC is indicated by a dashed line. For the periodic solution in scenarios BFP and BS, the minimum and maximum value over time are indicated by the shaded area, the mean value is plotted as a solid line. Concentrations between 2.5 m and the groundwater-side domain boundary at 4 m are omitted because they are almost constant.



**Figure S2:** Relationships between transcript concentrations and enzyme concentrations. In scenarios GD and BFC, concentrations are at steady state. In scenarios BFP and BS, transcript concentrations, but not enzyme concentrations, are averaged over time.



**Figure S3:** Relationships between transcript (left column) respectively enzyme (right column) concentrations and denitrification rates for the bank storage (BS) scenario. Colors indicate the time point within the diurnal cycle. Every location shows a distinct pattern (with one “loop” corresponding to one location), and many of them are non-linear and hysteretic in time.



**Figure S4:** Relationships between the concentrations of enzymes NAR (upper row) and NIR (lower row) with the denitrification rates in the different scenarios. In the scenarios where concentrations do not reach a steady state but stable diurnal cycles, daily averages of rates and concentrations are shown. The color indicates the spatial coordinate with dark blue corresponding to the groundwater inflow boundary and light green corresponding to the river boundary.