Integrating Artificial Intelligence and Modeling for investigation of permafrost disturbance in the Arctic

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ABSTRACT. As systems become increasingly complex and data more abundant, Artificial Intelligence (AI) in the form of machine learning is providing novel approaches for studying systems undergoing critical transitions. However, to exploit the full capabilities of machine learning in predicting unexpected change, algorithms need to move beyond data mining. In this research, we propose the approach how to study permafrost disturbance in Siberia. The AI sensors are analyzing remote sensing and field data and feeding the data to a stochastic ecosystem model. The model predicts critical transitions and sends the information back to AI to evaluate a risk of collapse in the complex soil system.

Overview: Permafrost ecosystems are warming six-times faster than the global mean[1], exposing huge stocks of organic carbon (C) and nutrients to microbial attack [2]. As permafrost thaws, organic matter will be decomposed by microorganisms, potentially emitting globally relevant amounts of greenhouse gases in a phenomenon termed the "permafrost climate feedback." Permafrost thaw is a phase transition involving complex interactions between surface collapse, hydrology, redox conditions, and microbial metabolism. Mechanistic ecosystem models fall short in capturing these multidimensional and stochastic phase changes, resulting in demonstrably unrealistic predictions and large uncertainties. For example, Earth system model (ESM) estimates of net C release from the permafrost zone do not agree in sign or magnitude for 2100 or 2300[3,4], and some models predict more than a doubling of Arctic and Boreal biomass due to uncoupled CO_2 fertilization effects and exclusion of disturbance such as wildfire and thermokarst[5,6]. Our proposed research develops a new approach to simulate phase changes in landscape geometry and subsequent response of soil microbial communities using stochastic, multiscale models validated with "meta-omics" molecular data. Building off recent advances in stochastic bifurcation theory in physics and technical breakthroughs in microbial ecology, our approach may provide a computationally-frugal predictive framework for simulating high-latitude ecosystem trace gas flux during and after permafrost degradation. Because of their uniquely simple and spatiotemporally explicit structure, the developed models will be the first to incorporate microbial succession with topographic restructuration, using interdepencies to resolve internal feedbacks in energy balance and greenhouse gas release. The novel approach will be validated with molecular data from active-layer soils, permafrost soils, and a chronosequence of landscapes in different stages of recovery from permafrost collapse in Arctic and Boreal Alaska. Stochastic approaches developed here may open avenues for addressing diverse spatiotemporal problems including pathogen evolution and transmission, risk of collapse in agroecosystems during nutrient loading, and exploring possible microbial activity in permafrost ecosystems on Mars.

Background: Many climate-change-driven feedbacks in complex Earth systems are not and may never be precisely and definitively modeled on a mechanistic basis. Even when extensive empirical evidence and relatively complete theoretical frameworks are available, compounding uncertainties and emergent interactions often reduce the power of both top-down and bottom-up simulations to predict ecosystem processes across space and time. The problem is magnified in systems where data are sparse and central physical and biological mechanisms are not constrained, as is the case with the permafrost climate feedback[2]. Current modeling frameworks still cannot account for internal and external complexities

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associated with warming in terrestrial systems, as evidenced by a lack of agreement in sign and magnitude of projected C balance, nutrient availability, and landscape evolution[3–6].

It is increasingly recognized that the fate of thawed permafrost C will depend on the reorganization of hydrology and associated redox conditions in permafrost landscapes[7]. The distribution of wet and dry surfaces affects the amount of permafrost C thawed, the redox conditions to which it is exposed, and the rate and type of microbial metabolism[8]. Stated otherwise, permafrost thaw causes rapid shifts in microbial community and activity, which interact with surface hydrology to determine greenhouse gas production and the availability of nutrients in terrestrial and aquatic environments[9,10]. Subsequently, nutrient availability controls the recovery trajectory of vegetation, altering the thermal properties of permafrost, albedo and rate of permafrost degradation[11,12]. These interdepencies illustrate why efforts to model the physics and ecology of permafrost thaw separately have been difficult, given that the types of modeling used to understand ecological and physical processes are typically quite different. Consequently, large-scale ESMs have almost universally overestimated plant C uptake during permafrost thaw due to overemphasis of CO_2 fertilization and an under emphasis of disturbance and nutrient limitation[2,3,6]. Integrating permafrost thaw and microbiology into Earth system models is a critical priority that could provide crucial pathways towards improving predictions of the permafrost climate feedback[13–15]. However, physically based models have had only limited success simulating current and future permafrost collapse and subsequent ecological dynamics even at small scales, and limitations in microbial data availability have thus far prevented development and testing of alternative modeling frameworks.

Proposed approach: Here, we propose a completely different modeling approach, using conceptual, multiscale models to simulate phase changes in surficial geomorphology and subsequent successional dynamics in microbial communities experiencing permafrost degradation. Taking advantage of newly available data streams from remote sensing and new methods in microbial ecology[16,17], we propose developing and testing stochastic models of microbial community, predicting diversity and function of microorganisms following transition across critical states. Specifically, we propose testing stochastic models with new techniques for characterizing the overall microbial capacity for different metabolic pathways (metagenomics, metatranscriptomics, and metaproteomics, together referred to as meta-omics) in active-layer, permafrost, and a chronosequence of soils recovering from permafrost collapse. We hypothesize that unlike many temperate and tropical ecosystems, microbial community will be strongly dispersal limited during active-layer deepening, due to limited connectivity within soils. Conversely, abrupt subsidence will homogenize initial microbial community, triggering a more metabolically diverse successional trajectory when soils transition from frozen to thawed or drained to saturated. While exceedingly complex on a process level, these linkages could allow scaling of site-level processes to landscape and regional levels if the geometry and extent of changes in permafrost lakes could be simulated.

To mathematically describe microbial community dynamics, we will test fundamental models such as Hopfield networks and genetic circuits, which can directly connect with the Ginzburg–Landau equation for phase transition in frozen ground that is already used to describe permafrost thaw during environmental temperature changes [18]. Using this approach we could construct a new conceptual model including representation of coupled interactions between micro-scale (microbial community), macro-scale (permafrost landscapes), and global-scale (climate forcing) systems.

To integrate microbial community dynamics into simulations of the permafrost climate feedback, we propose using concepts of the Freidlin-Wentzell stochastic theory for dynamical systems[19]. In this case, we can estimate probability of positive and negative competition effects leading to extinctions in

microbial population or rapid growth of microbial biomass that will dramatically change the level of greenhouse gas emissions. Incorporating the climate feedback parameter into this stochastic model[20] will provide an independent test separate from current modeling approaches to determining the strength of positive and negative climate feedbacks in the permafrost zone.

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