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Myself

Master's

University of Arkansas at Pine Bluff

Thesis title: N-doped Rice Husk Biochar to Activate Persulfate and Sulfamethoxazole degradation

Advisor: Dr. Hao Chen

Ph.D. (3rd year)

Cornell University

Thesis title: Model Evaluation and development to understand below-ground processes

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Microbial Models for Simulating Soil Carbon Dynamics: A Review

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Friedlingstein et al., 2022







Friedlingstein et al., 2022









Figure 1: Historical Development of Microbial models

Figure 2: Microbial processes present in Microbial models



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Figure 3: Consideration of microbial processes



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Microbial process 1: Microbial-mediated decomposition of SOC

1. Zero-Order Microbial Model (ZO)

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2. First-Order Microbial Model





3. Forward Michaelis-Menten Kinetics (FMM)



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4. Reverse Michaelis-Menten Kinetics (RMM)





Microbial process 1: Microbial-mediated decomposition of SOC



Figure 4: Number of Microbial models adopted decomposition mechanisms

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Conventional model (CENTURY)

Microbial Process 2: Mineral Interaction

SOC Input



Millennial v2.0

F AВ OF DR. YIQI LUO

¹³C

C_{N-MAOM}

 p_aF_a

(1-p_a) F_a

 F_a

MIND

Breakdown

Aggregate C

Breakdown

Aggregation

Aggregation

 F_{pa}

CNF

Decomposition

Mortality

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Microbial Process 3: Microbial necromass recycling



Millennial model

GENDEC model

Microbial Process 4: Active and Dormant Microbial Physiological States







Challenges and Recommendations

1. Experimental evidence for rate-limitation in Microbial Models

2. Lack of observational data to estimate model parameters

3. Model complexity





Summary

- Four microbial processes were mostly incorporated into models with different mathematical equations
 - Microbial-mediated decomposition
 - Mineral interaction
 - Microbial necromass recycling
 - Active and Dormant Physiological states
- Diversity in model structures and parameters indicates uncertainty in translating current knowledge of microbial processes into models.
- Data-driven model development and parameterization are highly recommended to improve the prediction of microbial models.



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Thanks Any question?

