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Beyond ideal fractal models: A testable biophysical framework for aquatic floc as living microecosystem

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Suspended particulate matter (SPM) is often modeled as inert grains or self-similar fractal aggregates governed by shear and gravity. These useful approximations can fail when biological activity changes floc structure during transport. Three-dimensional imaging, microbial ecology, and transport studies reveal biologically active, hierarchical aggregates (Figures 1A-C). The question is when biological state improves prediction beyond physical-only descriptions.

We use "living microecosystem" operationally for aquatic flocs in which measurable biological activity is coupled to architecture and transport. Our testable framework links biological state (EPS, microbial biomass, and activity) to attachment and mechanical response; architecture to permeability, drag, settling, and reactions; and both to improved independent prediction against matched physical-only models. Neither universal metabolic activity nor the obsolescence of fractal models is implied.

BEYOND PHYSICAL-ONLY AGGREGATION MODELS

Smoluchowski aggregation equations and DLVO theory describe collisions and particle stability; fractal geometry approximates porosity, density, and settling. Their assumptions weaken when microbial growth and polymers change collision efficiency, binding, permeability, or density. Thus, equal hydrodynamic forcing may produce different flocs in biologically distinct waters, whereas physical-only models may suffice in low-organic systems.

The proposed advance is operational: test whether coupled physical, chemical, and biological state variables improve predictions.[1,2] Structural imaging, measurements of bio-induced drag, and observations of microplastic incorporation and benthic burial during bedform dynamics and biogeochemical cycling, such as carbon, make this feasible. We use the latter two processes to test the proposed biological-state, to flocs' architecture, and their transport pathway.

BIOLOGICAL MEDIATION: THE LIVING GLUE IN NATURAL WATER

Diatoms and bacteria can change particle surfaces, polymer bridging, permeability, and aggregate strength through growth and extracellular polymeric substances (EPS). Biology thereby affects attachment and mechanical response, while shear and gravity govern collision opportunities, breakup, and transport.

Reported multi-fold biological effects on collision efficiency or drag and changes in settling velocity are system-specific, not transferable constants. Mineralogy, salinity, temperature, nutrients, organic composition, concentration, shear history, and measurement definitions differ across studies. Strong microbial growth and EPS production may amplify effects under shear that promotes contact without persistent breakup; nutrient or temperature limitation, sparse coatings, and strong shear may diminish/reverse them. Settling can respond in either direction as biomass and minerals increase density while porosity and roughness increase drag. Accordingly, Figure 1 omits generalized multipliers; local calibration, uncertainty analysis are needed.

Biopolymers also impart elasticity and enable structural reconfirmation. Under shear, some bio-sediment flocs compact or become more spherical instead of fragmenting immediately, thereby changing drag and settling without proportional mass loss. These observations support biological state as a potentially important structural control while retaining the essential role of physical forcing. A useful framework must therefore predict not simply whether biology is present, but whether measurable biological state explains architecture and transport after hydrodynamic and mineral controls are accounted for.

3D IMAGING AND SCALE-DEPENDENT ARCHITECTURE

Focused ion beam nano-tomography, micro-CT, and related volumetric methods have fundamentally challenged, rather than eliminated, the assumption that natural flocs are uniformly self-similar across scales. High-resolution reconstructions reveal pronounced deviations from ideal fractal behavior and a scale-dependent, heterogeneous architecture. Fractal dimensions may still provide useful first-order descriptors within limited size ranges or environmental conditions, but a single dimension cannot capture the full hierarchy of biologically active aggregates.[1]

Reconstructions span primary minerals and dense, cell-associated flocculles (FG-1 and FG-2, Figure 1B) through microflocs, macroflocs, and porous megaflocs (FG-3 to FG-5). Clay may organize around cells; filaments and EPS bridge irregular domains and pore channels. Internal pore water may sustain diffusion and redox conditions distinct from ambient water (Figure 1C), making whole-floc function more than the sum of its components.

Evidence supports EPS-mediated capture, colonization, and altered drag or permeability. We propose a bounded competing-feedback hypothesis for organic-rich, active suspensions under low-to-moderate shear: EPS and capture promote growth, whereas compaction and reduced permeability may limit substrate supply and accretion. Persistent high shear may instead remove or alter polymers. No universal organic-matter threshold is defensible because polymer composition, surface area, salinity, and SPM vary. Tests should establish a measurable EPS-associated change in attachment or permeability against mineral controls at matched shear. Microbially generated fluid motions and any resulting size limit remain hypotheses requiring direct velocity, permeability, and mass-transfer measurements.

BOUNDARY TESTS OF THE FRAMEWORK: MICROPLASTIC INCORPORATION & BENTHIC CAPTURE AND BURIAL

Microplastics provide a tractable boundary test because incorporation directly links biological surface state and aggregate architecture to a measurable transport outcome. Recent synthesis identified a size-dependent boundary separating conditions in which microplastics are transported mainly as individual particles from those in which they are incorporated into flocs.[3] Their fate depends not only on plastic density and shape but also on EPS production, microbial colonization, aggregate size, and hydrodynamic history.

Eco-corona formation can increase surface stickiness and initiate attachment, while plastisphere development can subsequently change density, roughness, permeability, and biological activity. These changes may accelerate settling when added biomass and mineral matter increase effective density, but increased drag, shear-induced detachment, degradation, and resuspension can delay or reverse transfer to the bed. The relevant test of the framework is therefore whether measured biological state and architecture improve prediction of incorporation and settling beyond plastic properties and hydrodynamics alone.

The second boundary test follows flocs from the water column to the bed. Migrating subaqueous dunes can capture clay flocs in their lee and bury them as organized group deposits (Figure 1D).[4] As settling flocs approach the

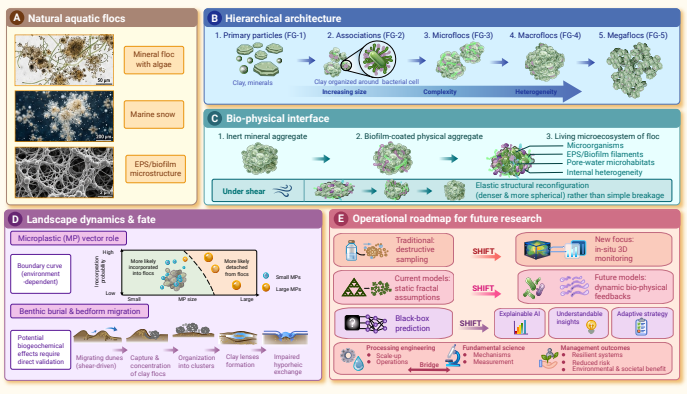

Figure 1. From idealized, scale-invariant physical representations to a testable bio-physical framework for aquatic flocs (A) Natural aquatic flocs and EPS-rich structures. (B) High-resolution 3D imaging reveals hierarchical assembly and departures from ideal fractal scaling; fractal descriptors may remain useful over restricted ranges. (C) Biological state can modify attachment, structural response, settling, and drag, but the magnitude and even sign of these effects are context dependent; generalized cross-system multipliers have therefore been removed. (D) Microplastic incorporation and benthic capture are presented as two boundary tests linking floc state and architecture to measurable fate. Potential downstream biogeochemical effects require direct validation. (E) The operational roadmap links standardized in situ imaging and metadata, dynamic state-variable parameterization, controlled validation, and interpretable or causal analysis before more ambitious digital-twin applications.

gel point, they form a volume-filling network that marks the transition from hindered settling toward a consolidated bed. Repeated capture can create clay-rich lenses that store particle-bound material, reduce sediment permeability, and impair hyporheic exchange; energetic disturbances may later remobilize this material. These observations provide a direct route for testing whether water-column floc architecture leaves a measurable imprint on bed structure and exchange.

Computational fluid-dynamic simulations further show that microbial colonization can materially alter drag on suspended sediment relative to uncolonized particles of equivalent size.[2] This result supports the need to represent biological surface state in transport models, but it does not by itself establish a universal effect on carbon export. Added biomass and mineral loading may accelerate export, whereas roughness, porosity, and drag may slow settling and increase water-column remineralization. The balance must therefore be resolved from coupled measurements of effective density, drag, settling, and organic-matter transformation rather than inferred from any single property.

Benthic biogeochemical consequences should likewise be treated as conditional downstream hypotheses. EPS-rich encapsulation may limit oxidant diffusion and enzyme access, while reduced permeability and oxygen penetration may create redox gradients that favor anaerobic metabolism. However, carbon preservation or methane production cannot be inferred from floc structure or burial alone; they require direct measurements of organic-matter lability, pore-water oxygen and redox state, gas production, burial depth, and disturbance frequency. We therefore use these processes as examples of testable consequences of altered exchange, not as established climate feedbacks of the living-microecosystem framework.

FROM MEASURABLE STATE VARIABLES TO TESTABLE PREDICTION

Test predictive value with the simplest adequate model. Machine learning (ML) has helped optimize coagulation and predict flocculation,[5] but requires defined measurements and validation. Complex models are warranted only if they outperform interpretable physical-only and simple bio-physical baselines on independent data.

A minimum core dataset should pair hydrodynamic forcing (mean shear and turbulence descriptors), salinity and temperature, SPM concentration and primary-particle properties, hydrated floc size and shape, and at least one quantitative biological-state measure such as EPS concentration, microbial biomass, or respiration. Extended datasets can add mineralogy, pH, three-dimensional pore architecture, biofilm development, and contaminant surface state. Prediction targets should be defined before model fitting and can include collision efficiency, breakup probability, floc-size distribution, permeability, effective density and drag, settling velocity, or contaminant incorporation. This prioritization keeps the framework centered on variables that can be measured repeatedly across laboratory and field settings.

TESTABLE HYPOTHESES AND AN IMPLEMENTABLE RESEARCH ROADMAP

Our central question is whether measurable biological state and scale-dependent architecture provide reproducible predictive information beyond physical-only floc descriptions. This question generates four hypotheses that can be rejected under controlled comparison rather than numerical performance targets chosen in advance. (H1) After controlling for hydrodynamic forcing, particle concentration, and mineral properties, biological-state variables such as EPS, microbial biomass, or metabolic activity will explain residual variability in attachment, permeability, drag, or settling. (H2) Under measurable EPS-rich, low-to-moderate-shear conditions, competing growth and permeability-limiting processes will produce saturation, truncation, or other departures from scale-free floc-size behavior; the signature should weaken or disappear in low-EPS systems or under persistent high-shear fragmentation. This hypothesis directly defines the hydraulic boundary of the proposed feedback. (H3) Bio-physical models that include measured biological state and architecture will outperform matched physical-only baselines for independent predictions of floc-size distribution, settling, or contaminant incorporation. Improvement should be evaluated with predefined out-of-sample metrics and uncertainty intervals, rather than a universal percentage reduction in error. (H4) Three-dimensional architecture metrics such as porosity, permeability, and internal heterogeneity will explain transport or reaction outcomes beyond equivalent diameter and a single apparent fractal dimension under otherwise comparable conditions.

Testing H1–H4 requires standardized, non-destructive imaging with paired physical and biological measurements, plus targeted tomography (Figure 1E).

By narrowing the framework to a comparison of measurable biological and architectural state variables against physical-only baselines, the living-microecosystem concept becomes falsifiable rather than merely descriptive. Fractal models retain value where they are sufficient; the proposed framework is warranted only where biological state produces reproducible gains in explanation or prediction. The practical objective is therefore not to rename flocs, but to identify the environmental regimes in which biology changes aggregate structure enough to matter for water-quality and contaminant-transport models.

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DECLARATION OF INTERESTS

The authors declare no competing interests.