

Physical and biological structure

Zachary Shifrel

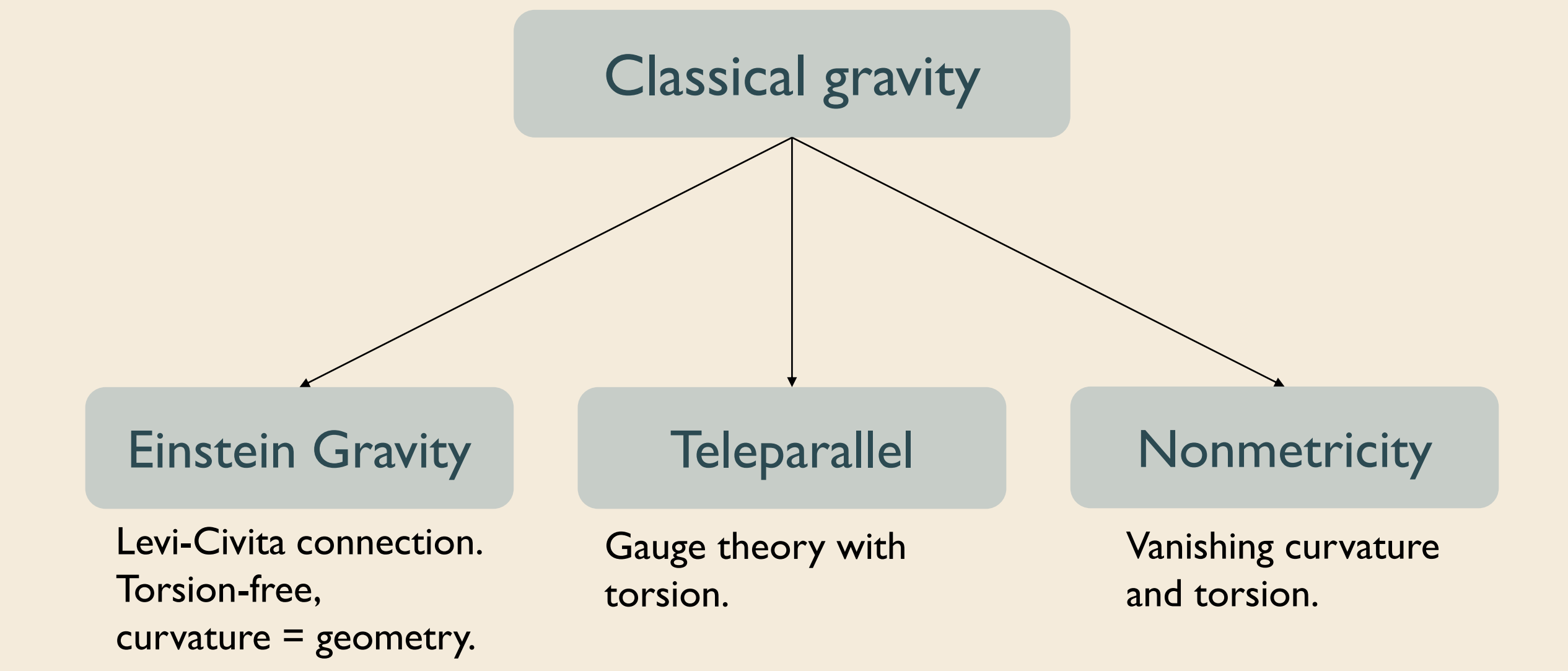
Virginia Tech

Abstract

Historical challenges to realism sourced in the graveyard of discarded scientific theories inspired a retreat from referential continuity to structural continuity. Structural realists take structure to (at least approximately) survive theory change, the invariance of structure over time conferring support on success-to-truth inferences. One argues, for example, that successor theories retrieve the mathematical structure of their predecessors, or degenerate to them in some limit. The realist asserts that the successful recovery of structure should hint at representational success. Yet many worry that structure alone is unable to do the work realists leave to it. In both physical and biological contexts, I make salient how these worries arise and the forms they take.

The Physical Application

Case One: Classical gravity affords at least three different formulations, all of which reproduce identical physics at low energies. However, they seem to entail possible conceptual and ontological differences. It’s not clear whether their structure captures all the relevant information.



Case Two: It’s informative to ask what the retrieval of classical and semi-classical gravity might look like from the perspective of possible theories of quantum gravity. Because propositions like “GR is the unique low energy theory for interacting massless spin 2 particles” (Arkani-Hamed, 2011) are popular in particle physics pedagogy, this is often thought to be trivial. But, when we include higher derivatives, the uniqueness vanishes: there is a large class of other Lorentz invariant theories of the graviton.

- Q1: can structural realism even be formulated prospectively?
- Q2: does the preservation of structure being non-exact threaten realism in cases where a large space of near equivalents exist (e.g., unimodular gravity in this context)?

Making The Choice

- In general, there is no unique choice for representing structure. “Natural” choices are more rare in biology.
- The choice of morphism between the structure of one theory and another varies with the initial choice of representation.
- Choice of formalism might plague the output of different structural continuity proofs with important disagreements.
- Choosing which theory to start with when facing a space of equivalents is often intractable without empirical models; the ubiquitous practice of theory space constraint is also something we would want to capture.

Some Caveats

- The status of theory change in biology is controversial, as is the question of whether to extend structural realism (however conceived) into it.
- Objections to structural realism in biology tend to take aim at the ontic variant (Lyre, 2013). We can be far more modest, opting for weak epistemic versions.
- The success of *horizontal* (intertheoretic) continuity proofs are to some extent contingent on the details of *vertical* (between theory and data model) continuity proofs.
- Case two is complicated by

The Biological Application

The history of taxonomy is rich and long, its roots stretching from Aristotle to the contemporary construction and analysis of molecular phylogenies. Theory change in biological classification presents a clear opportunity for showing the problems that arise in proofs of continuity. Proving that structure is retained from one theory to the next usually begins with a choice of representation. We express the structure formally with, for example, set theory, Ramsey sentences, category theory, etc.

- Some have taken equations to exhaust the structure of a theory. This would prove problematic in biology, but it also runs into walls in physics.
- We’re forced to choose representations and morphisms more explicitly in some biological cases given the dearth of methods of retrieval, such as limiting cases.
- The paradigms I’ve chosen are Linnaean taxonomy, phylogenetic systematics, and reticulate evolutionary networks.

Theory 1: Linnaean taxonomy imposes a hierarchical structure on organisms, identifying and sorting organisms into taxa based on overall resemblance. Its structure is a partial ordering T of taxa on the set of organisms O , whose minimal element is the set of species S . Species classification defines a function $f: O \rightarrow S$, and we demand that the S be a coverage on T .

Theory 2: Phylogenetic systematics introduces the notion of descent with modification where a division is introduced in homology between similarity sourced in immediate shared ancestry, or synapomorphy, and similarity sourced in more distant ancestry, or symplesiomorphy. We must append models of nucleotide substitution and metrics for genetic distance to the Linnaean consideration of mere morphological resemblance and phenetics

Theory 3: phylogenetics suffers from being unable to capture horizontal evolution; reticulate evolution captures this better than the bifurcating phylogenetic trees, accounting for phenomena like horizontal gene transfer.

Representation options	Morphism options
(1) Leave the trees in their original tree form	(1) Check for an isomorphism or partial iso.
(2) Convert the trees to graphs	(2) Specify a graph homomorphism
(3) Construct operads from the trees	(3) Use the set of operad morphisms

Lessons

- Without empirical frameworks and applications as a guide, structure fares poorly in continuity proofs (e.g., scattering and cosmological experiments coupled with structure of theories of the graviton, but not structure alone, allow us to make and justify choices).
- There’s reason to suspect that apparently clean cases of structural continuity in physics are, like biological cases, messier behind the scenes.
- It’s not clear how much structure examples like limiting cases preserve, nor if that which is preserved is important.

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