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Peer Review

Review of: "Over Half a Century of Burial of ρ, θ and ϕ in PDB"

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The manuscript proposes an “Atomic Bonding Network-based Spherical Coordinate System (ABN-SCS)” as an alternative to the conventional Cartesian representation of atomic coordinates in the Protein Data Bank. The author suggests that describing atomic positions using spherical parameters (ρ, θ, ϕ) could better reflect chemical connectivity and improve geometric feature extraction in modern structure-prediction tools such as AlphaFold2.

The topic—reconsidering the geometric representation of biomolecular structures—is conceptually interesting. However, the work remains entirely theoretical and speculative. It lacks mathematical formulation, computational implementation, and any quantitative validation demonstrating practical benefit.

Major comments

1. The premise that Cartesian coordinates “bury” chemical connectivity is incorrect. Bonding information is encoded explicitly in topology definitions and CONECT/mmCIF records; the coordinate system itself is not responsible for chemical connectivity.
2. The transformation between Cartesian and spherical coordinates is mathematically trivial and has been used for decades in quantum chemistry, internal-coordinate, and Z-matrix formalisms. The manuscript does not introduce a new representational method beyond this standard relationship.
3. Defining ρ as an “equilibrium covalent bond length” is physically inconsistent. In spherical geometry, ρ is simply the distance from a chosen origin, not a fixed bond parameter. This definition breaks down for branched or cyclic macromolecules.
4. The ABN-SCS framework is described only verbally. No algorithm, equation set, or implementation is provided. The supplementary files list AlphaFold2 feature arrays and bond pairs for each amino acid but contain no computed data or coordinate transformations.

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5. The examples (pentapeptide, Caenopore-5) are illustrative only and lack numerical results or comparisons to existing coordinate descriptions. Claims of improved feature extraction or AlphaFold2 performance are speculative and unsupported.
6. The assertion that spherical coordinates would enhance AlphaFold2 feature learning is unfounded. AlphaFold2 already uses complete geometric descriptors (distances, torsions, orientations). No gap or deficiency justifying ABN-SCS is demonstrated.
7. The “flipping coins” figure and similar metaphors are conceptually creative but add no scientific evidence. A reproducible coordinate-conversion example would be far more convincing.
8. The manuscript does not engage with extensive prior work on internal-coordinate or graph-based molecular representations, which already address similar aims with established mathematical rigor.
9. The writing style is heavily rhetorical. A clearer, data-driven presentation would strengthen the message and make the intent more accessible to computational structural biologists.
10. Overall, the paper reads as a conceptual reflection rather than a research contribution. As such, it may serve as a discussion piece but not as a validated methodological study.
11. If the author intends to develop this idea further, it would help to:
    1. Provide a formal mathematical definition of the ABN-SCS framework—perhaps a transformation matrix or algorithmic pseudocode that converts a PDB structure into spherical coordinates and back, with numerical validation on at least one real protein.
    2. Engage with prior work on internal-coordinate and graph-based molecular representations, such as the Z-matrix formalism (used in quantum chemistry), torsion-angle systems in macromolecular modeling, and graph neural-network embeddings for molecular structures. Situating ABN-SCS relative to these would clarify novelty and potential utility.
12. To validate the ABN-SCS framework, the author could:
    1. Apply the coordinate transformation explicitly to one or two representative proteins (for example, lysozyme or ubiquitin) and compare spherical and Cartesian-derived metrics such as interatomic distance distributions or RMSD under rotation/translation.
    2. Quantify whether spherical features offer any numerical stability or compression advantages in feature extraction pipelines.
    3. Cite prior work on coordinate and internal representations in structural biology, such as:
        1. The Z-matrix and internal coordinate systems used in Gaussian and CHARMM.
        2. Abagyan & Totrov’s ICM internal-coordinate molecular mechanics (*Proteins* 1994).

3. Graph neural network representations of molecular geometry (Gilmer et al., *ICML* 2017; Schütt et al., *Nat. Commun.* 2017).
4. Torsion- and rotation-invariant representations used in AlphaFold2 (Jumper et al., *Nature* 2021).

Summary

The idea of revisiting coordinate systems is not without merit, but the current work does not demonstrate theoretical novelty or computational value. A future version would need a formal mathematical framework, a reproducible transformation pipeline, and quantitative benchmarking to substantiate its claims.

Declarations

Potential competing interests: No potential competing interests to declare.