Graduate Conference and Academic Travel Fund Report

1. Personal Details
Name: Prarthana Agrawal
Course: DPhil Theoretical Physics
Conference Name: DPG Condensed Matter Section, Dresden, Germany and Foundations of Nanoscience (FNANO), Munich, Germany
Location: Germany
Dates of Travel: 7 March 2026 to 19 March 2026
(DPG, Dresden: 8–13 March 2026; FNANO, Munich: 16–19 March 2026)

2. Purpose of the Trip
The purpose of this trip was to attend and participate in two international conferences relevant to my research on self-assembly.

At the DPG Spring Meeting, I presented a talk titled *"Bias towards symmetry and simplicity in protein self-assembly"*, which examines how genotype–phenotype maps favour simple, symmetric structures.

Across both conferences, I attended talks in biological physics and nanoscale self-assembly, including the focus session on *"Sequence, Spaces, and Evolution"*. I also engaged with researchers during poster sessions and informal discussions, receiving feedback and establishing connections within the field.

3. Activities Undertaken

- Presented a contributed talk at the DPG Spring Meeting
- Attended talks on biological physics, self-assembly, and nanoscience
- Participated in the "Sequence, Spaces, and Evolution" focus session
- Engaged in discussions during poster sessions and networking events

4. Outcomes and Benefits

- Gained insight into current research in biological physics and nanoscience, especially molecular programming
- Received feedback on my work
- Developed connections with researchers in related areas

- Informed future directions of my research

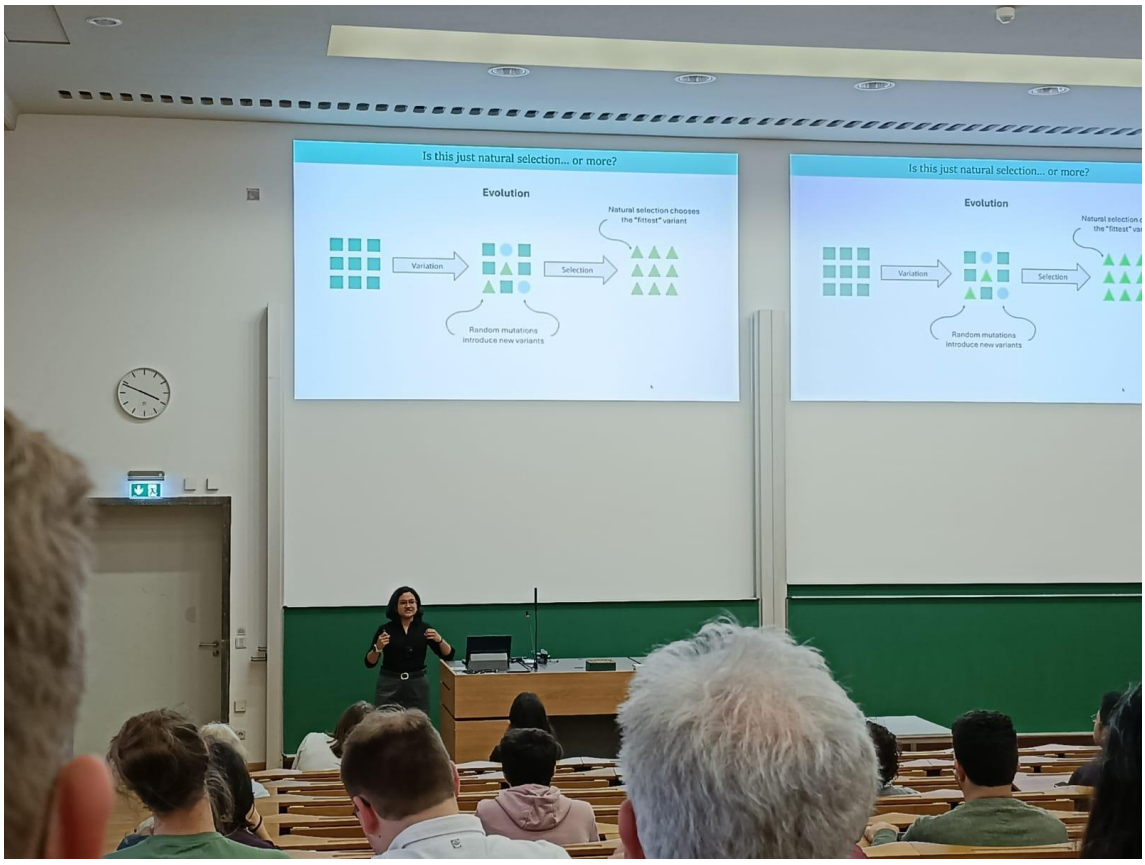
5. Reflection

The trip was productive and well aligned with my research. Both conferences provided useful perspectives and opportunities for discussion. This will help shape my future research endeavours.

6. Acknowledgement

I am grateful to the Graduate Conference and Academic Travel Fund for supporting this trip.

7. Photographs



8. Details about my research

Symmetry is ubiquitous in protein complexes and other biological assemblies and is often attributed to natural selection. Algorithmic information theory offers an alternative explanation: when structures are generated by simple local rules, outcomes that require less information to specify are intrinsically more likely [1]. Because symmetry enables reuse of the same assembly instructions, symmetric structures typically have low algorithmic (Kolmogorov) complexity and are therefore strongly favored. We test this idea using a three-dimensional polycube self-assembly model as an abstract representation of protein quaternary structure. By sampling interaction rule spaces, we find a strong bias toward low-complexity assemblies, with symmetric structures occurring far more frequently than asymmetric ones. We further show that not all symmetries are equally accessible: some symmetry operations reduce assembly complexity more effectively than others and are therefore disproportionately likely. These results indicate that biases toward simple and symmetric structures in self-assembly arise from intrinsic generative constraints rather than natural selection alone, suggesting that evolutionary outcomes are shaped not only by selection but also by how phenotypic variation is generated.

[1] I.G. Johnston, K. Dingle, S.F. Greenbury, C.Q. Camargo, J.P.K. Doye, S.E. Ahnert, & A.A. Louis, Symmetry and simplicity spontaneously emerge from the algorithmic nature of evolution, Proc. Natl. Acad. Sci. U.S.A. 119 (11) e2113883119, https://doi.org/10.1073/pnas.2113883119 (2022).