KNOTTING PATTERNS IN PROTEINS: INSIGHTS FROM REPOIFFUSION AND EVODIFF

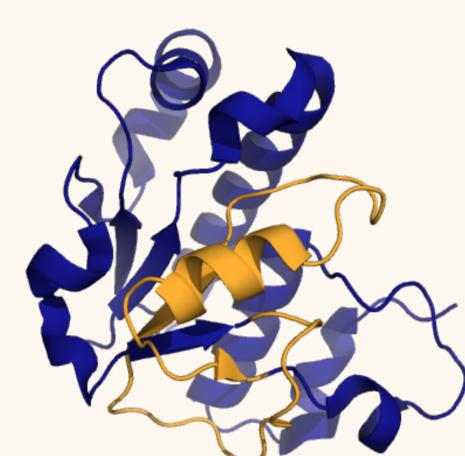
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MHAS

- proteins with a knotted backbone are a very rare phenomenon (0.35% of AFdb) [1]
- amino acid patterns responsible for the entanglement, or the role of the knot is still unknown [2]
- some knotted protein families hold potential for industrial and pharmaceutical applications (eg. the design of new antimicrobial drugs) [3]
- knotted proteins are clustered into only a few protein families [4]

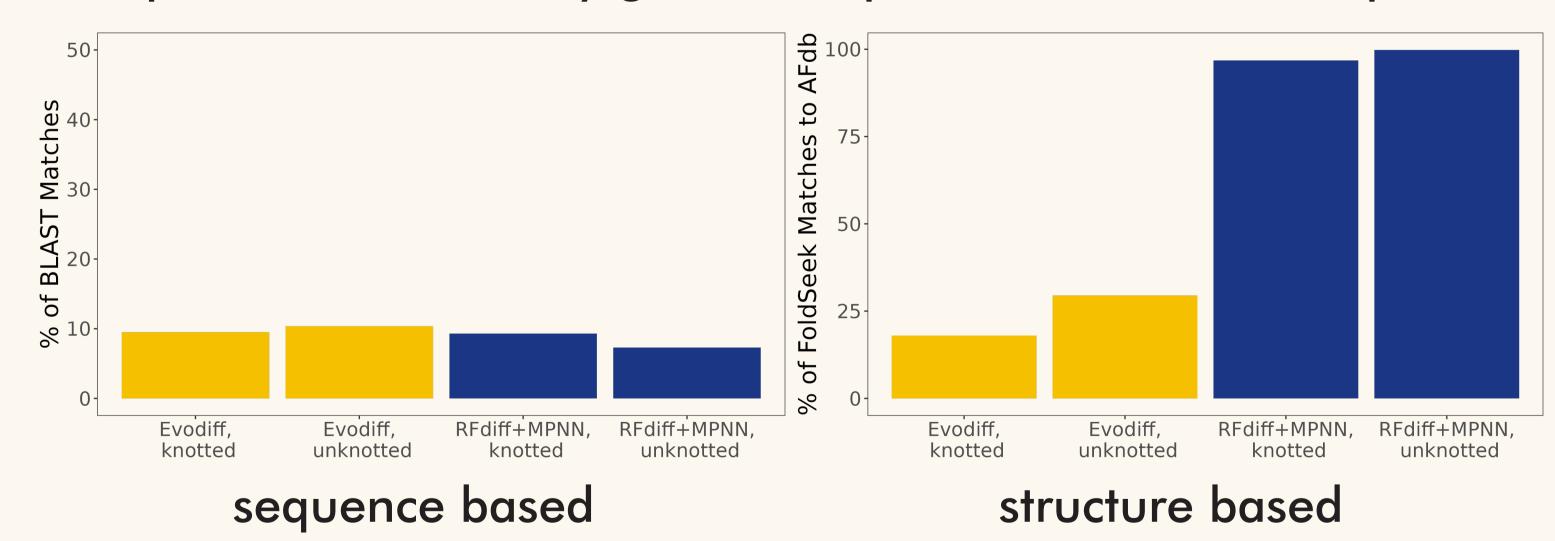


Human protein 5NFJ with a knotted backbone

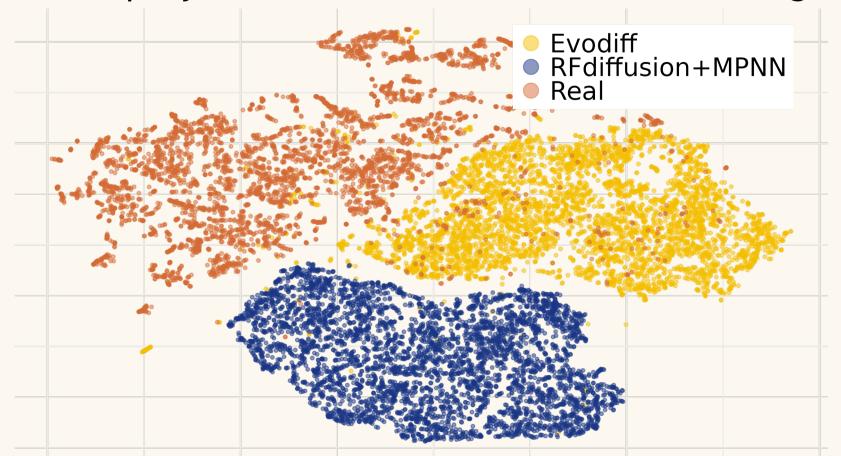
STAHW

- we created a dataset of artificial knotted proteins by unconditionally generating proteins with RFdiffusion [5] + ProteinMPNN [6] and EvoDiff [7] and analyzing their
- knotting status
- approximately 0.5% (2 016) of the freely generated proteins (425 362) are knotted, which corresponds to the ratio in nature [4]
- most of the generated knotted proteins are 3, (the simplest knot), but we also have rare cases: $3_1#3_1$ (composite knot), 5_1 , 7_4 and 8_{19}
- generated proteins are far from the natural sequence space
- structures of proteins from EvoDiff are different from the natural ones, but RFdiffusion+PMPNN generate similar protein structures

Comparison of artificially generated proteins to real-world proteins



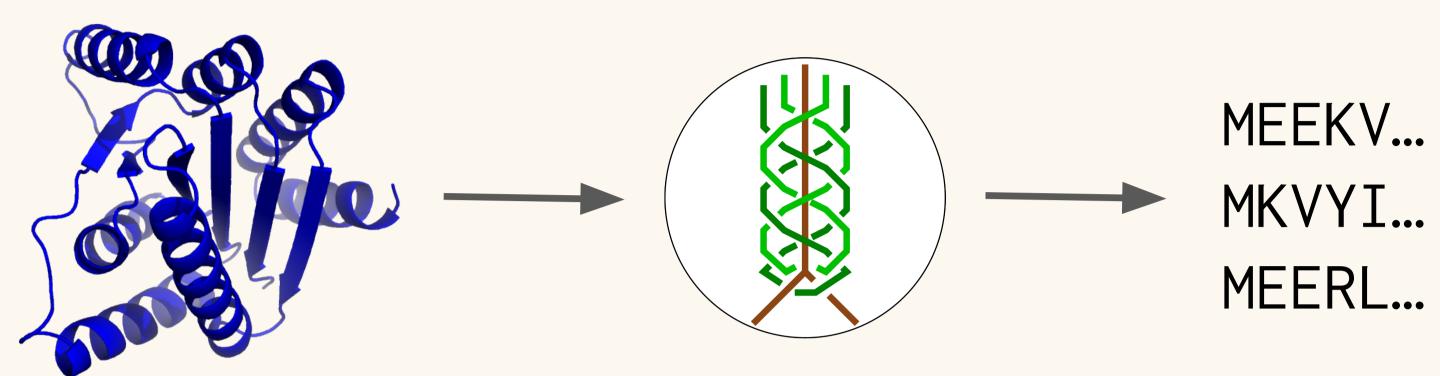
t-SNE projection of ProtBert-BFD embeddings



Mixture of knotted and unknotted proteins from EvoDiff, RFdiffusion+PMPNN and fraction of real proteins from UniProt

Hows

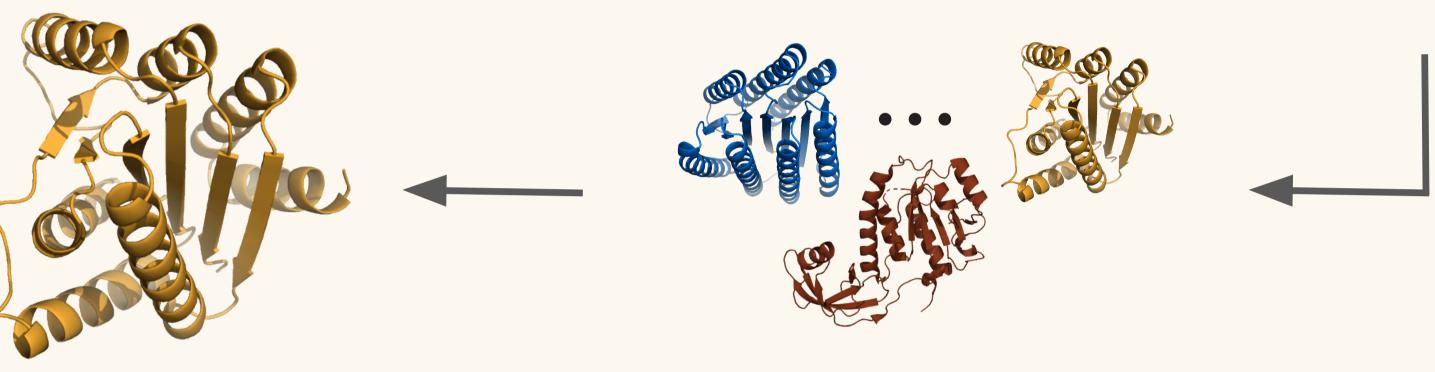
A) RFdiffusion + ProteinMPNN



unconditionally generate structures with RFdiffusion

select knotted structures with Topoly [8]

design 8 sequences per structure with **PMPNN**



if possible, pick one with pLDDT > 70holding the same topology

re-predict 3D structure for each sequence

B) EvoDiff **MEEKVIEIR**

unconditionally generate sequences with EvoDiff

predict 3D structure

select knotted structures with Topoly

MHAT NEXT S

- we will attempt to crystalize one of the artificial knotted proteins
- we plan to enrich the dataset of real knotted proteins with those generated artificially and look for knotting patterns

REFERENCES

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- [4] Šrámková, D. et al. (2023) Knot or not? sequence-based identification of knotted proteins with machine learning. bioRxiv.
- [5] Watson J. L., et al. (2023). De novo design of protein structure and function with RFdiffusion. Nature. [6] Dauparas, J., et al. (2022). Robust deep learning-based protein sequence design using proteinmenn. Science.
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- [8] Dabrowski-Tumanski, P., et al. (2020). Topoly: Python package to analyze topology of polymers. Briefings in Bioinformatics.



