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Visualizing alpha-helical peptides in R with helixvis

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Software

- Review
- Repository
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Summary

Studying the interactions of short peptides is conceptually non-trivial, even when the peptide's primary and secondary structures are known. The difficulty is often a result of the three-dimensional spatial complexity present in protein secondary structure. Here, we focus on α-helical secondary structure. Two-dimensional visualizations, specifically helical wheels (Figure 1, left panel) and wenxiang diagrams (Figure 1, right panel), are used by biochemists to study α-helices. Helical wheels provide a bird's eye view of a helical peptide with the amino acids forming a perfect circle, and allow for rapid identification of the peptide's hydrophobic faces (Schiffer & Edmundson, 1967), helping solve a common challenge in biochemistry research. In contrast, wenxiang diagrams incorporate residue order by making residue distance from the center directly proportional to residue position in the peptide (Chou, Zhang, & Maggiora, 1997). However, this makes the identification of hydrophobic faces less intuitive. Together, these two forms of visualization allow researchers to more clearly understand the underlying structure of α-helical peptides. Given the existence of databases listing thousands of peptides, all of which need to be visualized for manual inspection prior to wet-lab experiments, there is a need for software that allows for rapid programmatic construction of large numbers of publication-quality helical wheels and wenxiang diagrams.

The helixvis R package allows researchers to programmatically create helical wheels and wenxiang diagrams for short, α-helical peptides (Figure 1). Although there exist several web tools that do the same, there is currently no package on the Comprehensive R Archive Network (CRAN) to implement this functionality in R. Additionally, programmatic creation and design of graphics allows for greater customization with fewer restrictions than tools that interact with users via a graphical interface. By allowing programmatic customization and design of helical wheels and wenxiang diagrams, helixvis reduces the number of manual steps required to create these visualizations to essentially zero. Thus, helixvis facilitates reproducibility, a critical component of computational research (Sandve, Nekrutenko, Taylor, & Hovig, 2013).

Researchers can apply helixvis to help answer a multitude of scientific questions. In particular, helical wheels and wenxiang diagrams have been heavily used in the design of antimicrobial peptides. There currently exist carefully curated databases listing sequences for thousands of antimicrobial peptides (Waghu et al., 2014; G. Wang, Li, & Wang, 2016). An important research goal in this area is the design of synthetic antimicrobial peptides, and the presence of strongly hydrophobic faces is known to play a role in the toxicity of α-helical antimicrobial peptides. The helixvis package allows researchers to rapidly and reproducibly produce helical wheels and wenxiang diagrams for known and potential antimicrobial peptide sequences, thus facilitating the design of new antimicrobial peptides. The senior author of this paper (RST) is using helixvis for the aforementioned purpose

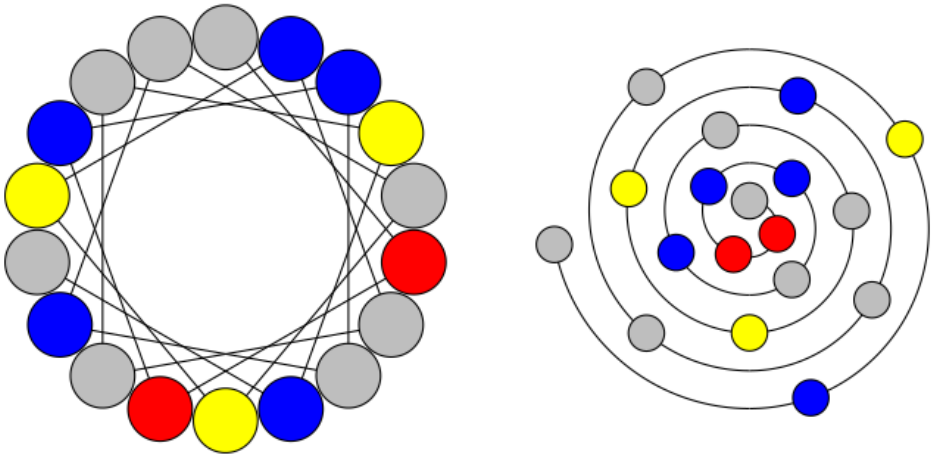

Figure 1: Two-dimensional visualizations of an alpha-helical oligopeptide. Left: helical wheel, particularly useful for identifying hydrophobic faces formed by secondary structure. Right: wenxiang diagram, visually incorporates amino acid order lost in helical wheels at the cost of a less intuitive visualization.

in current research projects (Wadhwa & Stevens-Truss, 2017). The code for helixvis can be found at its GitHub repository (Wadhwa, Subramanian, & Stevens-Truss, 2018); a Python version of helixvis is also currently under production (Subramanian, Wadhwa, & Stevens-Truss, 2018).

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