DESIGN OF PATCHY POLYMERS INTERPLAY BETWEEN GEOMETRICAL CONSTRAINS

AND ALPHABET SIZE

Cardelli C., Coluzza I., Bianco V., Computational Physics Group, Physics Department, University of Vienna





Der Wissenschaftsfonds.





What allows different heteropolymers to fold?





Protein

universität wien

What allows different heteropolymers to fold?

- Specific sequences fold into stable structures
- Made by 20 different types of amminoacids



Protein

universität Wien

What allows different heteropolymers to fold?

Valence is the key to understand protein folding

The system is designable if a minimum number of valence limiting interactions is included \rightarrow reduce the configurational space of compact structures



Protein

Coluzza, I., & Dellago, C. (2012).. Journal of Physics: Condensed Matter, 24(28), 284111 Coluzza, I., Van Oostrum, P. D. J., Capone, B., Reimhult, E., & Dellago, C. (2013). Physical Review Letters, 110(7), 075501. Coluzza, I., Van Oostrum, P. D. J., Capone, B., Reimhult, E., & Dellago, C. (2012). Soft Matter, DOI, 10.1039/2sm26967h.

universität ∧/ier

What allows different heteropolymers to fold?

Valence is the key to understand protein folding

• The system is designable if a minimum number of valence limiting interactions is included \rightarrow reduce the configurational space of compact structures





Patchy Polymers as bionic proteins

 Following this principle we can copy protein design and folding into an artificial system



universität wien

Patchy Polymers as bionic proteins

- Following this principle we can copy protein design and folding into an artificial system
- Valence = directional interactions between the patches



universität wien

Patchy Polymers as bionic proteins

- Following this principle we can copy protein design and folding into an artificial system
- Valence = directional interactions between the patches
- Specific sequence = alphabet of different isotropic interactions





Patchy Polymers as bionic proteins





Patchy Polymers as bionic proteins

Production of novel materials with specific self-assembly properties





Peter van Oostrum et al. BOKU, Vienna Austria



universität wien

Design and Folding of Patchy Polymers



universität wien

Design and Folding of Patchy Polymers



Design and Folding of Patchy Polymers

universität Wien



Design and Folding of Patchy Polymers

universität Wien







Free energy landscape vs Distance Root Mean Square Displacement (DRMSD) for **one free patch** with alphabet size of 3.





Free energy landscape vs DRMSD for **3 free** patches with alphabet size of 3.





Free energy landscape vs DRMSD for **one patch constrained to the backbone** with alphabet size of 3.





Free energy landscape vs DRMSD for **2 patches constrained to the backbone** with alphabet size of 3.













Free energy landscape vs Distance Root Mean Square Displacement (DRMSD) for three free patches with alphabet size of 3.





Free energy landscape vs Distance Root Mean Square Displacement (DRMSD) for three free patches with alphabet size of 10.





Free energy landscape vs Distance Root Mean Square Displacement (DRMSD) for three free patches with alphabet size of 20.





Free energy landscape vs DRMSD for **three free patches** with **different alphabet sizes**.



Free energy landscape vs DRMSD for **one** and **two patches constrained to the backbone** with **different alphabet sizes**. All systems fold into the target structures.



Conclusions

- Polymers with free patches fold only with large enough alphabets
- Polymers with patches constrained to the backbone fold also with small alphabets

The system is designable if:

The **alphabet** is increased **OR**

The **valence** reduces the space of compact structures (directional interactions: patches)



- Acknowledgements
- Prof. Christoph Dellago and Dr. Ivan Coluzza
- Theory and simulations of designable modular bionic proteins
- Dr. Valentino Bianco





Der Wissenschaftsfonds.

- Star polymers with a temperature-dependent valence: empty liquids from soft building blocks
- Dr. Lorenzo Rovigatti



• Dr. Luca Tubiana





- Computational protein design of highly selective tumour targeting drugs with the Vienna Protein Simulator
- Msc. Francesca Nerattini



Der Wissenschaftsfonds.











Free energy landscape vs DRMSD for three systems with **different valence**. The alphabet size is fixed to 3. Only the structure with one constrained patch folds into the target structure.