New insights into computational disorder prediction

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Disorder predictions enjoy a relatively strong interest and find a wide range of applications, from disorder annotations, proteome analysis, to structural and functional studies.[1] In spite of a strong, recent push towards development of (more) accurate predictive models,[2] this field is still characterized by a relatively large room for further improvements.[2,3] We will summarize our current efforts in assessment of modern disorder predictors that are available to end users (which complements and goes beyond the CASP-based evaluations),[3] development of full-chain based predictors,[4] and insights into building (new) consensus-based predictors of disordered residues. We will also demonstrate, both empirically and with case studies, that full-chain predictors are helpful for the residue-level predictions.

References

*1. B. He, K. Wang, Y. Liu, B. Xue, V.N. Uversky, and A.K. Dunker. Predicting intrinsic disorder in proteins: an overview. Cell Res. 2009,**19**(**8**), 929-49.*
*2. O. Noivirt-Brik, J. Prilusky, J.L. Sussman. Assessment of disorder predictions in CASP8. Proteins 2009, **77** Suppl **9**: 210-6.*
3. Z. Peng, Kurgan L. Comprehensive comparative assessment of in-silico predictors of disordered regions. Current Protein and Peptide Science 2011, in print
*4. M.J. Mizianty, T. Zhang, B. Xue, Y. Zhou, A.K. Dunker, V.N. Uversky, and L. Kurgan L. In-silico prediction of disorder content using hybrid sequence representation. BMC Bioinformatics 2011, **12**, 245*