



Czech Society for Structural Biology

11th Structural Biology Club of the Czech Society for Structural Biology

online on

26 October 2022, 13:00

with the following scientific talks kindly delivered by our guests

Expert modeling of RNA 3D structure - examples from CASP-RNA

Presented by **Marta Szachniuk, Institute of Computing Science, Poznan University of Technology**

Since the beginning of XXI century, interdisciplinary research teams have worked to develop a computational system capable of predicting reliable 3D RNA structure from a sequence. It has already been largely successful for proteins - the AI-based algorithm AlphaFold2 predicts the structures of new proteins with high accuracy. RNA still waits for such a breakthrough. The 3D RNA structure modeling competitions (RNA-Puzzles) held since 2010 have shown the little progress that has been made for 12 years in automated prediction of RNA 3D structures. The 3D models predicted by human participants are usually closer to the native structure than models generated fully automatically. Why is this the case? What knowledge cannot be sewn into 3D RNA prediction software to make it better and more accurate? The presentation will show examples of molecules that have been modeled in recent puzzles, including CASP-RNA, along with the procedure scheme adopted in expert modeling.

Exploring the functional potential of nucleic acids using artificial evolution

Presented by **Edward A. Curtis, Institute of Organic Chemistry and Biochemistry, Czech Academy of Sciences, Prague**

Our group uses artificial evolution to learn more about the functional potential of nucleic acids. This typically involves purifying DNA and RNA sequences molecules with interesting properties (such as the ability to bind a ligand or catalyze a reaction) from large random sequence libraries. In my presentation I will highlight some of our recent progress in this area. This includes the discovery of Supernova, a DNA enzyme that catalyzes a chemiluminescent reaction, and the development of new methods to explore sequence space using secondary structure libraries and one-step selections.

Moderator: Jiří Černý, Institute of Biotechnology, Czech Academy of Sciences, Vestec

Please, join us on this Zoom link (join 5-10 minutes before the beginning)

<https://cesnet.zoom.us/j/98867419047?pwd=WEF6THZuU01YQVpmMmxsV1hFaWZjQT09>

Meeting ID: 988 6741 9047

Passcode: 726237

Jiří Černý and Jan Dohnálek

on behalf of the Czech Society for Structural Biology

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