Joint Integrative Computational Biology workshop and CAPRI Meeting

Monday, 12 February 2024

<u>Computational Methods and Deep Learning: Chair: Sergei Grudinin</u> - IBS seminar room (13:40 - 15:20)

| time | [id] title | presenter |
|-------|---|---------------------|
| | [45] Integrative modeling meets deep learning: applications to crosslinking mass spectrometry | Dr SCHNEIDMAN, Dina |
| 14:05 | [28] Analysis of protein-nucleic acid interactions in the PPI3D web server | DAPKUNAS, Justas |
| | [17] Studying specificity in protein–glycosaminoglycan recognition with umbrella sampling | Dr SEBASTIAN, Anila |
| 14:55 | [11] VTX: High-performance molecular structure and dynamics visualization | MONTES, Matthieu |

<u>Computational Methods and Deep Learning: Chair: Dina Schneidman</u> - IBS seminar room (15:50 - 17:55)

| time | [id] title | presenter |
|-------|---|------------------------|
| 15:50 | [46] Generating backbone conformational changes with seven league boots | CAZALS, Frederic |
| | [4] Analysis of interfaces in protein complexes using Voronoi tessellations and graph neural networks | Dr OLECHNOVIC, Kliment |
| 16:40 | [52] Complementarity based peptide docking and design | KHRAMUSHIN, Alisa |
| 17:05 | [54] Protein structure evolution and convergence | CARPENTIER, Mathilde |
| | [3] Hybrid methods for analyzing conformational variability in cryo-EM and cryo-ET data | Dr JONIC, Slavica |

Tuesday, 13 February 2024

Computational Methods and Deep Learning: Chair: Frédéric Cazals - IBS seminar room (08:10 - 09:50)

| time | [id] title | presenter |
|-------|--|------------------------|
| | [40] Generative models and analysis tools for the study of highly-flexible (intrinsically disordered) proteins | CORTÉS, Juan |
| 08:35 | [44] Dissecting peripheral protein-membrane interfaces | Prof. REUTER, Nathalie |
| 09:00 | [27] Spectral partitioning into protein structural domains | SARTI, Edoardo |
| 09:25 | [61] Integrative structure of a histone chaperone-histone complex | VAN INGEN, Hugo |

Computational Methods and Deep Learning: Chair: Juan Cortès - IBS seminar room (10:20 - 12:00)

| time | [id] title | presenter |
|-------|--|--------------------|
| | [42] Exploring the conformational space of proteins by enumeration in the frame of the Distance Geometry Problem | MALLIAVIN, Therese |
| 10:45 | [48] Integrative spatiotemporal map of nucleocytoplasmic transport | RAVEH, Barak |
| 11:10 | [62] Integrative modeling of protein oligomers using Heligeom | PRÉVOST, Chantal |
| 11:35 | [24] Asymmetric hydrophobic mismatch in assembly of ATP synthase rotor ring | GUSHCHIN, Ivan |