

Wifi code: Bioinformatika
Pswd: Bioinfo2017

Protein bioinformatics tools in practice

Zsuzsanna Dosztányi
MTA-ELTE Lendület Bioinformatics Group
dosztanyi@caesar.elte.hu

2016

Approach

Aim: Become familiar with using basic bioinformatic databases and methods

It is a practical course:

Short introduction (theory, basic approaches, pitfalls)

- Tutorial

- The exercises help to understand how to use basic tools and how to interpret the results

- **Interactive**: discussions, questions, challenges

EMBO Practical Courses

- 2011 Heidelberg
- 2012 Berlin
- 2013 Sydney
- 2014 Cape Town
- 2015 Norwich
- 2016 Budapest

- Toby Gibson, Aidan Budd, Holger Dinkel (ELM)
- Lars Juhl Jensen (Switch)
- Marco Punta (PFAM)
- Scooter Morris (Chimera)

- Various online courses
- Tutorials (EBI, NCBI)
- Youtube!!!

Outline

0. Introduction
1. Databases
2. Alignments, sequence searches
3. Evolutionary analyses (Mátyás Pajkos)

4. Structure (Erdős Gábor)
5. Structure analysis with Chimera (Erdős Gábor)
6. Domains
 1. 1D predictions

8. 3D predictions
9. IDPs
10. Linear motifs, PTMs
11. Protein-protein interactions (Hajdu-Soltész Borbála)

12. Working with own data
13. Discussions

Linux/Windows/Mac

- | Web browser
- ▣ Jalview
- ▣ Chimera

Introduction

1994-2014

Institute of Enzymology

2014. September 1st -

Department of Biochemistry ELTE

MTA-ELTE Momentum

Bioinformatics Group

- **Globular proteins**
- **Transmembrane proteins**
- **Intrinsically disordered proteins**

Introduce yourself !

- your name
- research project
- your protein

Training material

http://dosztanyi.web.elte.hu/ELTE_2016_Ph/
<http://dlab.elte.hu/index.php/education/>