Hauptseminar WS 2014/2015

Edda Kloppmann
General

- Attendance obligatory
- Aim: practice presenting and report writing
- Take part in discussion!
- Grading: 50% talk, 25% report, 25% discussion
Topics

1. Conditional random fields for named entity recognition, Anna-Kathrin Kopetzki
2. Prediction of drug-drug interactions …, Maria Wörheide
3. Predicting the effect of mutations on protein–protein interactions, Joel Daon
4. Nuclear import and sorting of proteins, Meshal Ansari
5. Protein disorder — a breakthrough invention of evolution?, Kerstin Dörner
6. Mass-spectrometry-based draft of the human proteome, Barias Philippe
7. Robustness and evolvability of proteins, Valérie Marot-Lassauzaie
8. Potassium channels, Joseph Schneider
9. Structure comparisons and structure searches…, Simon Weck
10. Three-dimensional reconstruction of protein networks, René Schneider
11. HIV Mutatioal Pathways, Andre Ofner
12. Burhanettin Yerlikaya
Available topics

• Protein localization prediction from evolutionary profiles
• PolyPhobius: Prediction of transmembrane helices in protein sequences
• Predicting functional effects of sequence variants
Dates

1. Oct 13
2. Oct 20
3. Oct 27
4. Nov 3
5. Nov 10
6. Nov 17
7. Nov 24
8. Dec 1
9. Dec 8
10. Dec 15
11. Jan 12
12. Jan 19
13. Jan 26
Preparation

• *Starting* material provided by supervisor
• Research additional material
• In case of questions consult supervisor
• Discuss content / focus and slides with supervisor
  make an appointment 2 weeks before the talk!
Textbook / paper reading

- First get general idea / take-home lesson
- Understand Methods and Validation
- Look for open questions
- Follow references
Talk

- Duration: 30 minutes
- Story-line
- Talk slowly and clearly
- Address the audience
- Rehearse!
Slides

- Avoid too much text; Font size >18 pt
- All key points should appear on the slides
- Do not animate (too much)
- Include slide numbers
- Use examples to illustrate complex matter
- Cite your sources on the slide
- Graphics should have:
  - Title
  - Axis definitions
  - Sources
# Talk feedback

<table>
<thead>
<tr>
<th></th>
<th>Good ratio between main and side topics</th>
<th></th>
<th>Ratio imbalanced</th>
<th></th>
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</thead>
<tbody>
<tr>
<td><strong>Topic weighting</strong></td>
<td>Clear, precise, comprehensible, easy to understand with a clear structure</td>
<td></td>
<td>Incomprehensible, confusing and chaotic</td>
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<tr>
<td><strong>Structure</strong></td>
<td>Clear, good layout and design, no typos</td>
<td></td>
<td>Chaotic, too many animations, typos</td>
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<tr>
<td><strong>Rhetoric</strong></td>
<td>Meaningful figures, clear captions / axis description, clear tables</td>
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<td>Too much information, meaningless figures or/and tables, too few figures/table</td>
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<tr>
<td><strong>Language</strong></td>
<td>Special ideas, creative way of describing content, use of punch line</td>
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<td>Obvious, without fantasy, boring</td>
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<td><strong>Speed</strong></td>
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<td><strong>Slides</strong></td>
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<td><strong>Visualization</strong></td>
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<td><strong>Creativity</strong></td>
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Talk feedback is a process of evaluating a presentation based on various criteria. The table above outlines the feedback on different aspects of a talk, such as topic weighting, structure, rhetoric, language, speed, slides, visualization, and creativity. Each aspect is rated based on specific criteria, and the feedback is provided at the end of the talk for improvement.
Report

- Write in Latex or MS Word
- Use “Bioinformatics” journal format (defines font, citation style, etc.)
- Length: 5 pages
- Write full sentences
- Use spell checking
- Include figure legends
- Give references
- Avoid passive voice
- Avoid complex sentences