CB-L2: Comparative genomics, phylogenetics and other sequence-based analyses

<table>
<thead>
<tr>
<th>Person in charge and Representative</th>
<th>Lauber</th>
</tr>
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<tbody>
<tr>
<td>Contact person</td>
<td>BIOMEDAS Office</td>
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<tr>
<td>Semester</td>
<td>3</td>
</tr>
<tr>
<td>Topic cluster</td>
<td>Computational biology</td>
</tr>
<tr>
<td>Duration/Credit</td>
<td>4-7 lectures of 1.5 hours</td>
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<tr>
<td>Time</td>
<td>The exact date incl. time will be announced separately</td>
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<tr>
<td>Place</td>
<td>Online. Dial-in data are sent separately</td>
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<tr>
<td>Prerequisite for the lecture</td>
<td>The students should already have attended the Introduction lectures, in particular the &quot;Introduction to bioinformatics and computational biology&quot; lecture.</td>
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**Aim of the lecture**

The lecture will cover

- the following topics:

1. **Sequence analysis**
   - 1.1 Gene finding
   - 1.2 TF binding motif analysis
   - 1.3 UCSC genome browser

2. **Comparative genomics**
   - 2.1 Ortholog vs. Paralog vs. Analog
   - 2.2 Alignment building and curating
   - 2.3 Interactive alignment viewing
   - 2.4 Homology search (Blast, HMMer)

3. **Molecular phylogenetics**
   - 3.1 Evolutionary model selection
   - 3.2 Tree reconstruction methods
   - 3.3 Time-calibration of phylogenies

4. **Advanced evolutionary analyses**
   - 4.1 Natural selection inference
   - 4.2 Ancestral state reconstruction
   - 4.3 Gene sharing networks
   - 4.4 Phylogenetic networks