<table>
<thead>
<tr>
<th><strong>Course name</strong>: Genomics, Transcriptomics and Proteomics</th>
<th><strong>Credits</strong>: 5 ECTS</th>
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<tbody>
<tr>
<td><strong>Class type</strong>: On-line lectures + individual practice</td>
<td><strong>Hours per week</strong>:</td>
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<tr>
<td><strong>Type of the exam</strong>: Project work</td>
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<td><strong>Prerequisites</strong> (if exist): basic biochemistry and molecular biology.</td>
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<tr>
<td><strong>Course description</strong>: Familiarity with Internet sources for genome-wide data; basic skills in using tools at these web sites; understanding how modern high-throughput methods generate sequence data and gene and protein expression data; practical skill of using genome browsers to access genome data and genome comparison data; understanding gene prediction and genome annotation pipelines; skill of performing individual gene predictions; understanding different levels of variation in human genomes; understanding basic workflows of microarray data analysis and next-generation sequencing data analysis; basic knowledge of experimental methods in proteomics and metabolomics which enables understanding data analysis in these fields; skill of identifying proteins from mass spectroscopic data.</td>
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<td><strong>Required reading</strong>:</td>
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<tr>
<td><strong>Lecturer</strong> <em>(name, position, degree)</em>: Attila Csikász-Nagy, associate professor, PhD</td>
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<td><strong>Additional lecturers</strong>, if exist:</td>
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