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| Course name: Heatmaps for analyzing gene expression data | Credits: 3 ECTS |
| Class type: On-line lectures + individual practice | Hours per week: |
| Type of the exam: questionnaire | |
| Prerequisites (if exist): Basics about high throughput gene expression experiments. | |
| Course description: Introduction of the frequently applied approaches to create heatmap plots from gene expression data using online and local software tools <ul style="list-style-type: none"> • Theoretical background of heatmap analysis • Methodological overview including statistics and software aspects • Practice with the heatmap tool at Gene Expression Omnibus • Optional practice: How to create heatmaps with R? | |
| Required reading: | |
| Recommended reading: | |
| Lecturer (<i>name, position, degree</i>): Attila Csikász-Nagy, associate professor, PhD | |
| Additional lecturers , if exist: | |