| 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
- 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** *(name, position, degree)*: Attila Csikász-Nagy, associate professor, PhD

**Additional lecturers**, if exist: