# itmo

## **BIOINFORMATICS ALGORITHMS**

| Course Workload |       | Assessment form |
|-----------------|-------|-----------------|
| ECTS            | Hours | ungraded test)  |
| 3               | 108   | Exam            |

The course deals with the number of bioinformatics problems, both classical and modern, and the algorithms and data structures used to solve them.

## **Course structure:**

#### 1. CLASSIC BIOINFORMATICS PROBLEMS

- 1.1. Sequence alignment.
- 1.2. Genome assembly.
- 1.3. Hidden Markov Models.
- 1.4. Phylogeny reconstruction.
- 1.5. Genome rearrangements.

### 2. CURRENT ALGORITHMIC PROBLEMS

- 2.1. Active module problem.
- 2.2. Algorithms for gene set enrichment analysis.
- 2.3. Privacy-preserving genome-wide association studies.
- 2.4. Reconstruction of evolutionary histories.
- 2.5. Reconstruction of gene regulatory networks.