

# Master in Life Sciences

A cooperation between  
BFH, FHNW, HES-SO, ZHAW

<b>Module title</b>	<b>Bioinformatics Methods for Genomics and Applications</b>
<b>Code</b>	CO6
<b>Degree Programme</b>	Master of Science in Life Sciences (MSLS)
<b>Group</b>	Computation
<b>Workload</b>	3 ECTS (90 student working hours: 42 lessons contact = 32 h; 58 h self-study)
<b>Module Coordinator</b>	<p><b>Name:</b> Prof. Dr. Enkelejda Miho  <b>Phone:</b> +41 (0) 61 228 58 47  <b>Email:</b> <a href="mailto:enkelejda.miho@fhnw.ch">enkelejda.miho@fhnw.ch</a>  <b>Address:</b> FHNW, HLS, Hofackerstrasse 30, 4132 Muttenz</p>
<b>Lecturers</b>	<ul style="list-style-type: none"> <li>• Prof. Dr. Enkelejda Miho, FHNW</li> <li>• Dr. Manuel Gil, ZHAW</li> <li>• Prof. Dr. Maria Anisimova, ZHAW</li> </ul>
<b>Entry requirements</b>	<ul style="list-style-type: none"> <li>• Background in coding in R and/or python</li> <li>• Basic knowledge in life sciences (cell biology, immunology, genomics)</li> <li>• Self-study material</li> </ul>
<b>Learning outcomes and competences</b>	<p>After completing the module, students will be able to:</p> <ul style="list-style-type: none"> <li>• Understand sequencing workflows</li> <li>• Know immunology concepts and adaptive immunity cells</li> <li>• Basic understanding for phylogenetics methods for pathogen monitoring and tracing, 16S rRNA</li> <li>• Know how to access and process real-world high-throughput sequencing datasets</li> <li>• Know how to perform basic sequence analysis (alignment, trees, graphs)</li> <li>• Apply machine learning models to sequencing data</li> <li>• Insights on industry-relevant topics</li> </ul>
<b>Module contents</b>	<p>Preliminaries (Self-study prior to the summer school)</p> <ul style="list-style-type: none"> <li>• Basic introduction to cell biology</li> <li>• Basic introduction to genomics</li> <li>• Basic introduction to immunology</li> <li>• Installation of software</li> </ul> <p><i>Sequencing technology (Enkelejda Miho, Day 1)</i></p> <ul style="list-style-type: none"> <li>• Introduction: single-cell sequencing technology (transcripts, barcoding cell-types)</li> <li>• Applications sequencing antibody genes</li> <li>• Sequencing data workflow</li> <li>• From raw high-throughput sequencing data to annotated data</li> </ul> <p><i>Phylogenetics (Maria Anisimova, Gil Manuel, Day 2–3)</i></p> <ul style="list-style-type: none"> <li>• Fundamentals: genomic sequence formats, homology, alignment, phylogeny</li> <li>• Viral genomics and biomarkers</li> <li>• Phylogenetics for pathogen tracing and epidemic monitoring</li> </ul>

	<p><i>Machine Learning (Enkelejda Miho, Day 4–5)</i></p> <ul style="list-style-type: none"> <li>• Large-scale sequencing data analyses: graph and clustering analysis of complementarity-determining regions (CDR) and frameworks (FWR)</li> <li>• Applying machine learning for diagnostic biomarker and antibody therapeutics discovery (encoding sequence to vector and models e.g., random forest, support vector machines, neural networks, large language models)</li> <li>• Seminal case studies from industry</li> </ul>
<b>Teaching / learning methods</b>	self-study, lecture and practical exercise
<b>Assessment of learning outcome</b>	<ul style="list-style-type: none"> <li>• Entry exam on preparatory self-study materials (20%)</li> <li>• Active participation in at least 80% of the sessions (10%)</li> <li>• The final assessment will be a project work and report (70%)</li> </ul>
<b>Format</b>	5 days of lectures (summer school) with self-study preparation phase
<b>Timing of the module</b>	Spring semester, CW 23
<b>Venue</b>	Olten
<b>Bibliography</b>	Enkelejda Miho et al. "Computational Strategies for Dissecting the High-Dimensional Complexity of Adaptive Immune Repertoires." <i>Frontiers in Immunology</i> 9 (2018): 224. <a href="https://www.frontiersin.org/articles/10.3389/fimmu.2018.00224/full">https://www.frontiersin.org/articles/10.3389/fimmu.2018.00224/full</a> .
<b>Language</b>	English
<b>Links to other modules</b>	-
<b>Comments</b>	-
<b>Last Update</b>	18.03.2025