

**Institut für Biomedical Informatics**  
**Perl Programming for Bioinformatics**  
**[BioPerl]**  
**VU 720.500, 5 SWS**

The course provides an introduction to the Perl programming language and its application in the fields of Bioinformatics and Genomics. Perl is an open-source programming language often used for preparing input files for more specialized software such as R, and also to post-process the output from R and various other bioinformatics tools. It is a scripting language that is easy to learn and efficient to use, allowing the construction of analysis pipelines of arbitrary complexity. The course uses a problem-based approach to expose the underlying concepts and in-lecture exercises and programming assignments to implement them. Specifically, the course covers the following topics:

- Scalar variables
- Arrays and lists
- Loops and decisions
- Input and output
- Subroutines
- Strings and regular expressions
- Matching with regular expressions
- Processing text with regular expressions
- Hashes
- References
- Sorting
- Modules
- Object-oriented Perl and BioPerl



**Target audience:** M.Sc. students interested in gaining practical programming experience in the context of genomic data

**Lecturer:** Prof. Dr. Leila Taher

**Time:** Mondays, 8:30 – 12:30

**Place:** IT-lecture room I (SZ01070), Inffeldgasse 10, 1<sup>st</sup> floor