

# Bioinformatics

## Faculty of Science

**Study programme: Bioinformatics**

**Language of instruction: English**

**Structure of study: 3-year cross-border joint Bachelor's study**

**Form of study: Full-time**

### Introduction

University of South Bohemia in Ceske Budejovice (USB) together with Johannes Kepler Universität in Linz (JKU) provide cross-border joint study of Bioinformatics. Cross-border study, full-time education, where half of the time students are based in Budweis, Czech Republic and the second half they spend in Linz, Austria. Bioinformatics represents new interdisciplinary part of applied informatics. It is using advanced IT methods to solve secrets of modern biology.

The study programme itself is conducted by Faculty of Science of the USB in Budweis and Faculty of Technology of the JKU in Linz. This cross-border study is realized as a double-degree study programme, where students obtain appropriate degree from both Universities.

### Bioinformatics as a Scientific Discipline

Bioinformatics is a multidisciplinary field of study which, as is clear from the name, unites the words biology and informatics. Stress is therefore laid on efficient processing of biological data using computer technology and methodology. The basic pillar upon which the study is built in biology centers around genomes, molecular biology and genetics. In the informatics area, it involves studies ranging from parallel computation through to mass data processing and data structures, image processing and data mining methods.

Bioinformatics has seen enormous disciplinary development in recent times. The high-level employment of modern computational technology and a transition away from traditional biological methods is leading to the acceleration and optimization of research in related areas, as well. It may be anticipated that this discipline encapsulates the future of the new era of biology, particularly in the field of genetics.

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## The Study Program and Its Aims

Study for the bachelor degree lasts three years. The program culminates in a double diploma and upon successfully completing their work, graduates are granted the academic title of Bc./BSc. by the universities.

During the first year of their bachelor studies, students receive instruction in the basics of informatics, biology and mathematics at the university in Ceske Budejovice. During the second year, instruction takes place at the university in Linz and focuses on interdisciplinary studies such as bioinformatics, chemistry and applied informatics. The third year is divided proportionately between Ceske Budejovice and Linz and is devoted to elective subjects, work on bachelor projects and seminar participation. During the final semester, instruction will be offered in blocks; thus students defending their thesis in Ceske Budejovice will go to Linz only a few times.

During the second year, the students themselves will choose the focus of their final thesis. Depending upon the character of the thesis, the focus may lie in the discipline of Biology (in which case it is anticipated that the majority of time during the third year will be spent in Ceske Budejovice) or in the area of Bioinformatics (in which case more time will be spent in Linz). If students choose to focus on pure informatics, with minimal crossover into the areas discussed above, they may choose which campus they wish to spend the majority of their time at during the third year.

The emphasis during instruction is laid on modern forms of study focused on practical instruction with the use of modern information technology.

Students will have the chance to obtain a stipend during the course of their studies.

## Employment Areas for Graduates – Graduate profile

Graduates in Bioinformatics may find employment in the following fields:

- Healthcare (for example, issues to do with novel illnesses and uncovering their causes, pathology and diagnosis and processing background data for clinical studies)
- Pharmaceuticals (including the development of novel medicaments and effective substances)
- Ecology (understanding the interaction between organisms and uncovering the causes of genetic mutations)
- Food processing industry
- Biotechnology companies
- Biology (genomics, proteins and new generation sequencing – NGS)
- Genetics and foetal medicine, or assisted reproduction
- Informatics (areas which require knowledge of image processing, parallel computation and databases or data structures) The development of laboratory software and program databases

<http://www.prf.jcu.cz/bioinf>

<http://www.prf.jcu.cz/en/action/cross-border-study-of-bioinformatics.html>

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## Study plan valid in the academic year 2017/2018

Annex 1: Global map of study subjects - Bachelor's Program in Bioinformatics (2017)

1 <sup>st</sup> Semester (WS)		2 <sup>nd</sup> Semester (SS)		3 <sup>rd</sup> Semester (WS)		4 <sup>th</sup> Semester (SS)		5 <sup>th</sup> Semester (WS)		6 <sup>th</sup> Semester (SS)	
USB Budweis		USB Budweis		JKU Linz		JKU Linz		USB Budweis		JKU Linz	
Subject/Module	ECTS	Subject/Module	ECTS	Subject/Module	ECTS	Subject/Module	ECTS	Subject/Module	ECTS	Subject/Module	ECTS
Procedural Programming	4	Working with Operating Systems	3	Software Engineering and Information Systems	3	Software Engineering and Information Systems	3	Parallel Programming	4	Software Engineering and Information Systems	6
Algorithms and Data Structures	4	Calculus II	6	Genome Analysis & Transcriptomics and Structural Bioinformatics	9	Introduction to R	3	Biostatistics	5	Bachelor's Thesis	6
Calculus I	6	Introduction to Bioinformatics	6	Machine Learning	4.5	Genome Analysis & Transcriptomics and Structural Bioinformatics	6	Bioinformatics Project	8	Area of Specialisation (USB-JKU)	11.1
Linear Algebra	3	Diversity of life	5	Bioanalytics	4.5	Organic Chemistry	2.6	Computational Chemistry and Molecular Modelling of Biomolecules	4	Bachelor's Examination (USB)	4
Biology of Microorganisms	5	Introduction to Genomics	3	Organic Chemistry	3	Gender Studies	3	Molecular Phylogenetics	6	Free Electives	3
Molecular Biology and Genetics	3	General Chemistry	3	English for Scientists	3.2	English for Scientists	1.6	Area of Specialisation	3		
Free Electives	3	Academic Writing for Cross Border Studies	3	Area of Specialisation	3	Area of Specialisation	7.5				
		Ethics	3			Free Electives	3				
28		32		30.2		29.7		30		30.1	
										Total:	180.00

[http://www.studium-bioinformatik.at/curriculum/Overview\\_WS2017.pdf](http://www.studium-bioinformatik.at/curriculum/Overview_WS2017.pdf)

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## Detailed description of courses

### 1st Semester (University of South Bohemia)

#### **Procedural Programming**

*Objectives:* Knowledge of Procedural Programming

*Subject:* Computers, People, and Programming, Types, and Values - Computation, Errors - Writing a Program, Completing a Program - Technicalities: Function, Classes, etc. - Input and Output Streams, Customizing Input and Output - Display model, Graphic: Classes, Class Design, Functions and Data, User Interfaces - Functions and Data, User Interfaces - Vector and Free Store, Vector and Arrays, Templates, and exception - Containers and Integrators, Algorithms and Maps - Text Manipulation, Numeric - GUI Implementation, Use the Fast Light Tool Kit "full tick" - C Programming language - Getting started with Visual Studio - .NET Platform

#### **Algorithms and Data Structures**

*Objectives:* This course is a basic introduction to the data structures and algorithms used in informatics. During the course students gain basic skills in algorithm design and construction and knowledge of basic types of data structures such as arrays, lists, trees, hash tables etc. Furthermore, some sorting and searching algorithms for data structures will be discussed.

*Subject:* The algorithm as a concept - Algorithm design and construction - Basic data structures - Sorting data - Searching data

#### **Calculus I**

*Objectives:* To develop basic concepts of differential calculus.

*Subject:* Review (Functions, Inverse Functions, Trig Functions, Exponential Functions, Logarithm Functions, Common Graphs) - Limits (One-sided limits, Tangent Lines and Rates of Change, Limit Properties, Computing Limits, Limits Involving Infinity) - Continuity (Definition, One-sided limits, Upper and Lower Bound Theorem, Mean Value Theorem) - Derivatives (Definition, Interpretation of the Derivative, Non-differentiable functions) - Differentiation Formulas (Product and Quotient Rule, Derivatives of Trig Functions, Derivatives of Exponential and Logarithm Functions, Derivatives of Inverse Trig Functions, Derivatives of Hyperbolic Trig Functions, Chain Rule, Implicit Differentiation, Higher Order Derivatives) - Applications of Derivatives (Critical Points, Minimum and Maximum Values, Increasing and Decreasing Functions, Inflection points, Concavity, the Second Derivative Test) - Mean Value Theorem, Optimization Problems, L'Hospital's Rule and Indeterminate Forms, Linear Approximations, Differentials, Newton's Method

#### **Linear Algebra**

*Objectives:* Knowledge of Linear Algebra

*Subject:* Matrices and their properties - Systems of linear equations - Vector spaces and subspaces - Linear independence, basis, dimensions - Determinants and their properties - Applications of determinants - Vector spaces with scalar product - Eigenvalues and eigenspaces of matrices

#### **Biology of Microorganisms**

*Objectives:* Introduction to the fundamentals of the biology of microorganisms

*Subject:* Fundamentals of the biology of microorganisms

#### **Molecular Biology and Genetics**

*Objectives:* Understanding the fundamentals of molecular biology and genetics

*Subject:* Fundamentals of molecular biology and genetics

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### Diversity of life

*Objectives:* Introduction to basic up-to-date biology. This course is designed to significantly and sensitively expand biological horizons of overspecialized persons.

*Subject:* Evolution. How to survive survival of the fittest? Short list of evolutionary basics. - Phylogenetics. Short cookbook for beginners. - History of Life. From origin of Earth to recent ice ages. - Archaeal & bacterial view of life. Mamavirus and other viruses also included. - Eukaryota. Their origin and diversity. - Great story of plastid lineages. Primary vs. secondary endosymbiosis. Archaeoplastida. - Land plants. Conquering land with green cells. Embryophyta. - Origin and diversity of flowering plants. - Metazoa. Flourishing world of animals. - Origin and diversity of chordates. - Ecology. Key adaptations and strategies for successful life. - Biogeography. Patterns of life on various scales. - How to protect environment without prejudices.

### Introduction to Genomics

*Objectives:* Knowledge of, understanding in, and approaches to topics in Genomics.

*Subject:* Introduction to the 'Genome' (definition of the genome/genetic material, types and variety of genome in biology, genome-transcriptome-proteome central dogma, genome structure i.e. concept of genes, regulatory elements and repetitive DNA, genome organisation i.e. chromosomes and histones/ chromatin, DNA replication). - Historical overview of first 'Genomic' methods i.e. chromosome mapping, laborious genetic linkage analyses, chromosome walking, QTLs. Introduction to nucleic acid sequencing from a historical perspective; first organisms – bacteriophages (MS2 PhiX174), bacteria (Haemophilus influenza, E. coli). Individual research group led DNA sequencing of specific loci of more complex organisms. Creation of common databases for this information – need to consolidate and coordinate DNA sequencing efforts - Scaled-up DNA sequencing to tackle larger genomes (use of human genome project as a case study). – Historical perspective and public versus private initiatives. Techniques used to perform large scale sequencing, Genome sequencing of model organisms – which, how and why? Creation of synthetic organisms (Craig Venter). - Interpreting the sequenced genome – identifying genes/ transcripts in the sequence and cataloguing them – birth of 'Bioinformatics'. Databases. Development of more sophisticated genome browsers with increasing amounts of annotation. 'Gene cards' and gene specific information features and using BLAST searches to identify experimentally derived sequences against the genome sequence reference datasets (nomenclature definitions). - Using the genomic sequence and bioinformatics to identify functionally important information e.g. Comparative genomics - phylogenetic analyses of bacteria or viruses (e.g. H5N1 influenza), identification of specific transcription factor binding sites and candidate target genes (e.g. REST and neurogenesis) - Applying genomics at the bench (development of numerous experimental strategies e.g. originally microarray based now based on novel large scale sequencing technologies) – inclusion of relevant case study examples e.g. the international ENCODE consortium - Depositing, retrieving and interpreting bench-based genomic experiment data/ results – cross referencing with our experimental databases and web resources

### Academic Writing I

*Objectives:* Preparation for the authoring of scientific reports using the correct technical language

*Subject:* Authoring of scientific reports using the correct technical English language

### Ethics

*Objectives:* To introduce students to law, monitoring, and influence of biotechnologies on the quality of life.

*Subject:* Basic ethical principles. - Ethical dimension, connection and difference between technology category, and people's goals and approach. - Personal and institutional responsibility. - Connection of science with practical applications. - Research ethics. - Social and ecological sustainability of biotechnologies, fundamentalism and ideology. - The progress of international system of monitoring of distribution from OEM to consumer.

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## 2nd Semester (University of South Bohemia)

### **Working with Operating Systems**

*Objectives:* Knowledge of Working with Operating Systems

*Subject:* Variables, expressions and basic commands - Structured commands - Input and output - Functions - Debugging - Regular expressions - Using SED and GAWK - Statistic and graphic scripting for using R and GNUplot - Alternative shells

### **Calculus II**

*Objectives:* Mastering integration of functions of one variable.

*Subject:* Indefinite integral, substitution method, integration by parts - Riemann (definite) integral (Riemann sums, existence of Riemann integral), relationship between indefinite and Riemann integrals - Application of definite integral (area between two curves, volumes of solids of revolution, lengths of curves, centers of mass, mean value, etc.) - Transcendental functions (exponential, logarithmic, general power), inverse functions to trigonometric functions and hyperbolic functions - Methods of integration (integration by parts, substitution method, integration of trigonometric functions, method of partial fractions, integration of rational functions) - Improper integrals - Methods of numerical integration (using programs Mathematica/Maple/Matlab)

### **Introduction to Bioinformatics**

*Objectives:* The subject aims at being an introduction to applied bioinformatics. Techniques and applications of bioinformatics in molecular-biological and biochemical research as well as in biotechnology are given.

*Subject:* Introduction into bioinformatics: history, definition, terminology and methodology of bioinformatics. - Sequence database: sequencing of DNA, DNA databases, searching in DNA databases, BLAST tools, in silico translation of DNA, protein databases, searching in protein databases. - Genomic databases: genome sequencing, strategies of genome sequencing, complete sequences of prokaryotic and eukaryotic genomes related databases, principles of ESTs - Molecular phylogenetics: How to align nucleotide and amino acid sequences, phylogenetic reconstructions, methods for phylogenetic analyses, models for nucleotide and amino acid substitutions, phylogenetic artifact and methods for their elimination, evolution of an organism, evolution of a gene, multiprotein-based-phylogeny, evolution of metabolic pathways. - Introduction into biomolecular stereochemistry and reactivity: terminology, introduction into protein and nucleic reactivity. - Protein structure, function and chemical and physical properties of proteins: classification of protein structures, in silico methods for a prediction of the function, physical and chemical properties of proteins, prediction of the spectral properties of proteins and their use in interpretation of experimental data. - Protein families: structural blocks of protein structure, methods for protein structure prediction and determination, functional vs. structural homology. - Protein localization: protein targeting and in silico prediction of their intracellular localization - Databases and web-tools for structural genomics and proteomics. - Structure-function relationship in nucleic acid. - Structure-function relationship in saccharides and small organic compounds, bioinformatics approaches to drug design development. - Bioinformatics approaches to gene expression, microarray data analysis

### **General Chemistry**

*Objectives:* Knowledge of, understanding in, and approaches to topics in General Chemistry.

*Subject:* Physical properties, atoms and compounds, chemical nomenclature, chemical equations, equilibrium, periodic table, ions, stoichiometry, bonds (ionic, covalent, metallic), molecules and their bonding, gases, liquids, water and solutions, acids and bases, oxidation and reduction.

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### 3rd Semester (Johannes Kepler University Linz)

#### Information systems (2KV)

##### Topics in Genetics & Evolution (2VL)

*Objectives:* To provide an introduction to genetics and evolution to aid in the interpretation of genomic data  
2. Focus on relevant definitions and topics in genetics and evolution  
3. Introduce students to main concepts in evolution

*Subject:* The flow of information - Basic concepts in Population genetics - Processes that change our genome - Mutations - Meiotic recombination - Random neutral evolutionary processes - Selection - The evolution of our genome

##### Sequence Analysis and Phylogenetics (2VL)

*Objectives:* This course focuses on basic methods for comparing biological sequences, such as, DNA, RNA, and amino acid sequences. This is complemented by an introduction to the field of phylogenetics, which is concerned with identifying evolutionary relationships among groups of organisms. No prior knowledge in biology is required for this course. Basics of molecular biology are provided up to the minimum that is necessary to understand the ideas behind the bioinformatics tools and algorithms discussed in this lecture.

*Subject:* Basics of molecular biology, Simple sequence comparisons and scoring schemes, Pairwise sequence alignment, Statistical analysis of sequence alignments, Multiple sequence alignment, Methods for computing evolutionary distance, Methods for computing phylogenetic trees

##### Sequence Analysis and Phylogenetics (2UE)

*Objectives:* This practical course complements the lecture "Sequence Analysis and Phylogenetics" and aims at practicing the concepts and methods acquired in the lecture.

*Subject:* Simple sequence comparisons and scoring schemes, Pairwise sequence alignment, Statistical analysis of sequence alignments, Multiple sequence alignment, Methods for computing evolutionary distance, Methods for computing phylogenetic trees

##### Artificial Intelligence (2VL)

*Objectives:* Introduction to the field of Artificial Intelligence (AI), its basic assumptions, models, and algorithms.

*Subject:* Definitions of AI. Problem solving as a search process: search algorithms (uninformed and heuristic), heuristic search in games. Knowledge representation and logical reasoning: inference in propositional logic and predicate logic. Reasoning with uncertain knowledge: knowledge representation and inference in Bayesian nets. Machine learning: inductive concept learning, reinforcement learning. Basics of computer perception.

##### Artificial Intelligence (1UE)

*Objectives:* Introduction to Artificial Intelligence (AI), its basic assumptions, models, and algorithms.

*Subject:* This exercise course helps students deepen their understanding of some of the technical contents taught in the AI lectures. Students solve regularly assigned exercises, in preparation for the lecture examination.

##### Bioanalytics I (2VL)

*Objectives:* Sound understanding of the principles and methods of Bioanalytics

*Subject:* Bioanalytics of proteins - Bioanalysis of nucleic acids

##### Bioanalytics I (1UE)

*Objectives:* Detailed insight into the rationales and strategies of DNA sequencing

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*Subject:* Optimized versions of automated Sanger sequencing Second generation sequencing Third generation sequencing

#### **Chemistry for Physicist II (2VL)**

*Objectives:* Successful students of this course will be able to:  
define and employ the vocabulary of organic chemistry.  
draw structural representations of organic molecules.  
write transformations and mechanisms for alkanes, alkenes, alkynes, alkyl halides and alcohols.  
Employ stereochemical considerations when analyzing mechanisms and transformations

*Subject:* Introduction to organic chemistry

#### **English for Chemistry 1 (understanding) (2KV)**

### **4th Semester (Johannes Kepler University Linz)**

#### **Software engineering (2KV)**

##### **Introduction to R (2KV)**

*Objectives:* The scientific computing platform (and programming language) R was originally designed for statistical analyses but has quickly emerged as a de facto standard in bioinformatics and is also rapidly becoming important in machine learning. In this regard, R is a platform of the future. Knowing R well is a great plus in statistics and machine learning, and a must in bioinformatics. The goal of this course is to provide an in-depth view of the R platform and programming language. Students should be enabled to implement and document their own R programs and packages making use of advanced concepts, such as, S4 classes and foreign language interfaces. Students should further be made able to identify and avoid performance bottlenecks. This course is complemented by a practical introduction to applications of R in bioinformatics, mainly focussing on packages that are part of the Bioconductor project.

*Subject:* The R platform and programming language - Applications in bioinformatics

##### **Genome Analysis & Transcriptomics (2KV)**

*Objectives:* The goal of this course is to provide an overview of foundational and computational aspects of genetic variation and gene expression. The first part is mainly concerned with genetic commonalities and differences between individuals, how these commonalities and differences emerge, and how they can be associated to diseases and other traits. The second part is concerned with the dynamics of genes, how they are organized, how they can be detected, how the activation of genes is controlled, and how gene expression can be measured and analyzed computationally.

*Subject:* Genome Analysis - Transcriptomics

##### **Structural Bioinformatics (2KV)**

*Objectives:* The goal of this course is to provide an overview of foundational and computational aspects of 3D structures of biological macromolecules, such as, DNA, RNA, and proteins. The main goal of structural bioinformatics is to provide computational approaches for predicting and analyzing 3D structures. Understanding the 3D structures of biological macromolecules is crucial for understanding their function. Applications of structural bioinformatics are oriented towards medical fields and pharmacological research, especially, drug design.

*Subject:* Databases for 3D structures and molecular viewers - Structure prediction (threading, ab initio prediction, molecular dynamics) - Structural alignments - Protein classification - Motif search - Functional and structural annotation

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### Computational Chemistry and Molecular Modelling of Biomolecules

*Objectives:* The lectures are concerned with the subject of theoretical research of the structure, function and dynamics of molecules. Students will become familiar with the following topics: various computer representations of molecular structures, searching in structural databases, the acquisition of protein structural parameters, a brief overview of structure-based methods of energy computation, homology modelling and energy minimisation-based modelling, molecular dynamics, protein-ligand interactions, prediction of protein structure and docking of ligands. The course also includes practical exercises concerning visualisation, modification and structure-based computations on real molecular systems. Recommended literature, demonstration and application software will be available during the course.

*Subject:* MK1. Computer representations of molecular structure, techniques of visualization and modification of molecular structures, structural formats - MK2. Structural databases of inorganic and organic molecules and biomolecules (proteins, nucleic acids and their complexes), overview of experimental methods for acquisition of molecular structure, complex search in structural databases - RE3. Protein structure: dominant effects during the process of protein folding, geometrical parameters of polypeptide chain - RE4. Sequential analysis: sequence alignment, dynamic programming by use of Needleman-Wunsch and Smith-Waterman algorithms, substitution matrix. - RE5. Prediction of protein structure and function - RE6. Verification of structural parameters, stereochemistry of bio(macro)molecules, verification of folding. - MK7. Energy modelling: Empirical models (force field method). Functional of potential energy, parameters, application, advantages and limitations. - MK8. Energy modelling: Quantum chemical (QCH) models, approximation levels, numerical computations applied in solution of Schroedinger equation for multielectron system like nonhydrogen atoms and molecules, limits of a QCH method. - MK9: Application of quantum-chemical methods for a computation of molecular and atomic features (atomic and molecular orbitals, electron density, charges, dipol and transition moments), optical and NMR spectra. Matrix method for the computation of multimer excitation states. Computations for systems in solvent environment. Statistical thermodynamics (enthalpy of formation, entropy, Gibbs energy, etc.), computation of energy released in chemical reactions. Transition state searching, chemical kinetics. - MK10. Potential energy as a hypersurface, its features, fysical-chemical interpretation of stationary points of hypersurface - local minimas and maximas, first and higher order saddle points. Energy minimisation: non-derivative methods, derivative methods - steepest descent method, conjugate gradient, Monte Carlo, etc. - RE11. Comparable modelling: methods of space restriction, probability density function (PDF), space limitations. Fragment methods, root mean square deviation, structural frame, library of rotamers. - RE12. Molecular dynamics: numerical integration, Verlet algorithm, force fields, water models, periodicity in water box, particle Mesh-Ewalds, restriction of rotational and vibrational modes. - RE13. Docking of ligands: Autodock, flexible-rigid, genetic algorithms, Monte-Carlo simulated annealing

### Molecular Phylogenetics

*Objectives:* To introduce the molecular biology techniques of modern phylogenetics and taxonomy to undergraduate and graduated students of biology.

*Subject:* Annotation - Application of molecular biology techniques in taxonomy, epidemiology, forensic medicine, evolutionary biology, sociobiology. Basic laboratory techniques, sequencing, molecular fingerprinting, DNA hybridization, allozyme analysis, immunological techniques. Genetic distances, construction of phylogenetic trees, analysis of statistical support for the trees.

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### **Biochemistry (2VL)**

*Objectives:* The course provides a broad array of fundamental knowledge in general biochemistry with respect to structural and functional relationships living organisms. It is based on principal chemistry of organic and inorganic biologically active compounds and on fundamental non-covalent interactions which take place in biological systems on the level of molecules and cells. Structural and functional properties of components which play a role in signaling and energy transmission are emphasized.

*Subject:* Introduction to Biochemistry, The origin of life, Mechanisms of molecular interactions, Covalent and non-covalent bonds in biochemistry. - Chemistry of principal biomolecules: Amino acids, Peptides, Proteins, Carbohydrates, Lipids, Nucleic acids. - Enzymology and enzyme catalysis: Principles of catalysts and enzyme activity, Enzyme kinetics, Enzyme properties, Examples of enzymes. - Gene expression and proteosynthesis. - Biological membranes and membrane transport. - Introduction to metabolism and bioenergetics. - Carbohydrate metabolism, Glycolysis and Gluconeogenesis. - Lipid metabolism. - Citric acid cycle, Electron transport, Oxidative phosphorylation. - Metabolism of amino acids. - Photosynthesis and photosynthetic machinery. - Integration and regulation of energetic metabolism.

### **Gender Studies**

*Objectives:* Courses of social and legal context, which are important for the professional and social environment.

*Subject:* Definition/Construction of Gender/Sex - social-cultural (gender) versus anatomic/physical/biological (sex), Gender in science and technology in methodology and epistemology, biological/medical definition of gender and social influences and impacts, situations of women/man in science and technology (diverse historical/cultural mechanism of including and excluding).

### **English for Chemistry 2 (writing & presenting) (1KV)**

## **5th Semester (University of South Bohemia)**

### **Parallel Programming**

*Objectives:* Knowledge of, understanding in, and approaches to topics in Parallel Programming.

*Subject:* Introduction to parallel programming; Problems connected to parallel programming: - Parallel programming computer architecture demands; - Parallel strategy; - Parallel tasks division, shared vs. distributed memory; - MPS vs. OpenMP environments; - What is MPI, Parallel environment prerequisites and creation; - Simple parallel program observation; - Parallel programming in OpenMP, basic commands; - Parallel programming in MPI, basic commands (MPI SEND, MPI REDUCE, MPI ALLREDUCE etc.); - Input and output in parallel programming, methods comparison; - Command for parallel environment control and administration; - Communication vs. computational time, compromise finding; - Application: Parallel calculations in mathematics, Monte Carlo method; - Parallel molecular dynamics.

### **Biostatistics**

*Objectives:* Understanding and application of statistical methods for evaluating experimental results in biology

*Subject:* Statistical methods for evaluating experimental results in biology

### **Bioinformatics Project**

*Objectives:* The aim is to provide students with valid biological data sources, which they have to evaluate and transform them into useful structures, which can be used for scientific purposes later on.

*Subject:* Independent semester project done in cooperation with biologists in their labs.

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## 6th Semester (Johannes Kepler University Linz)

### **Information Systems for Bioinformatics (4KV)**

*Objectives:* Information Systems (IFS) play a central role in bioinformatics, not least due to the massive and constantly growing amount of data. The spatio-thematic fragmentation of the world-wide bioinformatic research community, however, led to a strong specialisation of existing information systems. Resolving current bioinformatic research questions currently requires access of 5 to 10 different information systems. With this lecture, graduates gain knowledge about existing information systems in bioinformatics as well as about current concepts and technologies for their integration. Students are especially capable of employing diverse XML technologies for representing and integrating existing bioinformatic data. Exercise: Deeper study of the topics of the lecture on basis of exercises

*Subject:* Lecture:

- \* Overview about existing information systems in bioinformatics (requirements and categories)
- \* Dimensions of information integration and integration architectures (Distribution, Autonomy and Heterogeneity; Federated DB, Data Warehouses, Mediator-based DB, Peer DB)
- \* XML-technologies for bioinformatics (XML Schema, XSLT, XQuery, XML and DB)
- \* Schema- und Metadatamanagement in integrated information systems (Matching- and Mapping-techniques)

Exercise:

- \* Search in existing bioinformatic information systems
- \* Conceptual modeling of a bioinformatics DB in UML and generation of logical schemata - relational DB schema and XML Schema
- \* Integration of data into the DB schema based on heterogeneous data sources and XML-based queries
- \* Integration of further data sources (e.g., SwissProt) using mediators
- \* Data exchange using XML, especially resolving heterogeneities using matching and mapping approaches

### **Bachelor's Seminar (ISE)**

*Objectives:* The goal of this seminar is that students report on the progress of their bachelor theses and practice the presentation of scientific results.

Every student is required to give a 20 min presentation summarizing and evaluating the progress of his/her bachelor thesis (which must be at least 30 pages long). Pro's and con's of the approach pursued in the bachelor thesis must be discussed in context with other published approaches.

The final grade is determined by an assessment of the oral presentation and the quality of the presented evaluation.

<http://www.studium-bioinformatik.at/curriculum/description.html>

## **Curriculum**

If any further information needed, please use the link below and you will be redirected to CURRICULUM FOR THE BACHELOR'S PROGRAM IN BIOINFORMATICS.

[http://www.studium-bioinformatik.at/curriculum/4\\_BS\\_Bioinformatics\\_MTB28\\_270616.pdf](http://www.studium-bioinformatik.at/curriculum/4_BS_Bioinformatics_MTB28_270616.pdf)

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