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| Module Name | Module Code |
| Introduction to Bioinformatics and Computational Genomics | agricAEF022-01a |
| Module Coordinator | |
| Prof. Dr. Remco Stam | |
| Organizer | |
| AgriGenomics | |
| Faculty | |
| Faculty of Agricultural and Nutritional Sciences | |
| Examination Office | |
| Examination Office AEF | |

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| ECTS Credits | 6 |
| Evaluation | Graded |
| Duration | One semester |
| Frequency | once per year, semester winter term |
| Workload per ECTS Credit | 30 hours |
| Total Workload | 180 hours |
| Contact Time | 120 hours |
| Independent Study | 60 hours |
| Teaching Language | English |

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| Recommended Requirements | | | |
| Basic knowledge genes, genome structure and of gene expression, Knowledge of R or Rstudio | | | |
| Module Courses | | | |
| Course Type | Course Name | Compulsory / Optional | SWS |
| Lecture | Introduction to Bioinformatics and Computational genomics | Compulsory | 2 |
| Exercise | Introduction to Bioinformatics and Computational genomics | Compulsory | 6 |
| Assessed assignment (Prüfungsvorleistungen, up to 50% grade, as improvement) | | | |
| Written Exam | | | |

| Examination(s) | | | | |
|--|----------------------------|-------------------|-------------------|------------------|
| Examination Name | Type of Examination | Evaluation | Compulsory | Weighting |
| Written exam | W | graded | compulsory | 100% |
| Further Information on the Examination(s) | | | | |
| 1.+2. Examination Period in the Wintersemester 1. Examination Period of the Summersemester Prüfer: Stam | | | | |
| Course Content | | | | |
| <p>The module is aimed at teaching basic methods for the analysis of genomic data. This includes an overview of the theory and practice of computational methods for the identification and characterization of genetic elements from DNA sequence data and transcriptomics data</p> <p>Topics include Introduction to the linux environments, Genomic data mining, quality control, sequence comparison, genome sequencing and assembly, genome annotation, identification of genomic (structural) variants, Transcriptomics</p> | | | | |
| Learning Outcome | | | | |
| <ul style="list-style-type: none"> - be proficient in command line usage; - run existing genome data analysis tools using the command line; - write small computer scripts for data analysis; describe the analysis process - work with large data volumes from NGS; - describe the biological interpretation and implication of the analysis results. | | | | |
| Reading List | | | | |
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| Further information | | | | |

