# AGRIS9Z03: Bioinformatics

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| **Full Title:** | Bioinformatics |
| **Language of Instruction:** | English |

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| **Module Code:** | AGRIS9Z03 |

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| **Credits:** | 7.5 |

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| **Valid From:** | Semester 1 - 2019/20 ( June 2019 ) |

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| **Module Delivered in** | 2 programme(s) |

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| **Module Description:** | This module aims to provide students with knowledge and competence in the use of computational biology in the analysis of molecular data. This course has emphasis on bioinformatics related to High-Throughput Sequencing (HTS) processing, analysis and interpretation of output of genomics data using bioinformatical tools. |

**Learning Outcomes:**

*On successful completion of this module the learner should be able to*

1. Discuss the omics technologies and the impacts of bioinformatics in the agricultural sector
2. Demonstrate a mastery of advanced theoretical knowledge and skills relating to high-throughput sequencing applications
3. Critically assess, interpret and manipulate raw sequencing data
4. Evaluate the impact of high-throughput sequencing in the agricultural sector

## Module Content & Assessment

| Indicative Content |
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| **Bioinformatics and its Applications**<br>High-Throughput Sequencing workflow, denovo genome assembly and annotation, transcriptomics using RNA-seq, 16S metagenomics, epigenomics |
| **Bioinformatics Workstation**<br>Working on a Unix system, filesystem basics, commands for working with directories and files, issuing commands on a Unix system, viewing and editing files |
| **Tools for Bioinformatics**<br>n/a |
| **Sequence analysis, pairwise alignment and database searching**<br>Using search engines, NCBI, BLAST, Ensembl, UniprotKB, Pfam, Global and local pairwise alignment, pairwise sequencing comparison using specialised software (e.g. splign), prediction of protein structure and function, multiple sequence alignment |
| **High-Throughput Sequencing**<br>Genome assembly, interpretation and quality check of raw sequencing data, align HTS data against a reference genome, annotating and analysing whole genome sequencing |
| **Practical Exercises**<br>Practicals will be delivered through computer based sessions. Computer-based practicals will allow the Student to become familiar with different types of genetic data sets and the use of various open source software for sequence/genome analyses. By completing these practicals, students will strengthen their understanding of basic bioinformatics applications in an agricultural context. |
| **Learning and Teaching Resources**<br>n/a |
| **Students will receive feedback in the following ways:**<br>- Discussions with the lecturer will provide feedback throughout the module - Academic feedback will be provided on continuous assessment - Feedback on final examination will be given in line with the Institute's policy |
| **Students will be supported in their learning in the following ways:**<br>- Formal lectures - IT based tutorials - Small group investigation - MOODLE site with tutor directed materials (e.g. links to literature, e-learning materials and contemporary scientific related topics) - Independent study |

| Assessment Breakdown | % |
|---|---|
| Project | 60.00% |
| Practical | 40.00% |

## Full Time

| No Course Work |
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**Project**

| *Assessment Type* | *Assessment Description* | *Outcome addressed* | *% of total* | *Marks Out Of* | *Pass Marks* | *Assessment Date* | *Duration* |
|---|---|---|---|---|---|---|---|
| Project | Students will conduct research in a current omics related project. During this project, students will analyse and evaluate the used of omics technologies relating to the agricultural sector. | 1,2,4 | 60.00 | 0 | 0 | n/a | 0 |

| Practical | | | | | | | |
|---|---|---|---|---|---|---|---|
| *Assessment Type* | *Assessment Description* | *Outcome addressed* | *% of total* | *Marks Out Of* | *Pass Marks* | *Assessment Date* | *Duration* |
| Practical/Skills Evaluation | Students will participate in weekly computer-based practicals. During practical sessions, students will evaluate and appraise different bioinformatical tools pertinent to sequence/genome analysis. The students will use specialised techniques, skills and modern computer-based tools necessary for genome assembly and annotation. | 2,3 | 40.00 | 0 | 0 | n/a | 0 |

No End of Module Formal Examination

**Reassessment Requirement**

**A repeat examination**
*Reassessment of this module will consist of a repeat examination. It is possible that there will also be a requirement to be reassessed in a coursework element.*

**DKIT reserves the right to alter the nature and timings of assessment**

## Module Workload & Resources

**Workload: Full Time**

| Workload Type | Workload Description | Hours | Frequency | Average Weekly Learner Workload |
|---|---|---|---|---|
| Lecture | No Description | 1.00 | Every Week | 1.00 |
| Practical | No Description | 2.00 | Every Week | 2.00 |
| Directed Reading | No Description | 3.00 | Every Week | 3.00 |
| Independent Study | No Description | 5.00 | Every Week | 5.00 |
| Online Learning (non contact) | No Description | 1.00 | Every Week | 1.00 |
| | | | Total Weekly Learner Workload | 12.00 |
| | | | Total Weekly Contact Hours | 3.00 |

**This course has no Part Time workload.**

**Resources**

*Recommended Book Resources*

**Andreas D. Baxevanis, B. F. Francis Ouellette 2004, *Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins*, 3rd Ed., Wiley-Blackwell**

**Shui Qing Ye 2007, *Bioinformatics: A Practical Approach*, Chapman and Hall/CRC**

*Recommended Article/Paper Resources*

***BMC Bioinformatics***
https://bmcbioinformatics.biomedcentral.com/

*Supplementary Article/Paper Resources*

***Bioinformatics***
https://academic.oup.com/bioinformatics

*Other Resources*

**Website: *n/a***
https://www.ncbi.nlm.nih.gov/

**Website: *n/a***
https://www.ensembl.org/index.html

## Module Delivered in

| Programme Code | Programme | Semester | Delivery |
|---|---|---|---|
| DK_SAGBI_9 | Master of Science in Agricultural Biotechnology | 1 | Mandatory |
| DK_SAGPD_9 | Postgraduate Diploma in Agricultural Biotechnology | 1 | Mandatory |