Hanze

# Course: Genomics & Transcriptomics — credits: 10

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| **Course code** | BFVH23GENOMICS |
| **Name** | Genomics & Transcriptomics |
| **Study year** | 2025-2026 |
| **ECTS credits** | 10 |
| **Language** | Dutch, with parts in English |
| **Coordinator** | M. Kempenaar |
| **Modes of delivery** | Project-based learning |
| **Assessments** | Genomics - Other assessment<br>Transcriptomics - Other assessment |

**Learning outcomes**

This module has the following learning outcomes:

You design, implement, document and evaluate a genome analysis pipeline for determining variants within a workflow manager, such as Galaxy.

You design, implement, document and evaluate an expression analysis pipeline for determining and interpreting expression patterns.

You can use relevant tools and visualisations to assess whether an NGS data set is of sufficient quality and improve it if necessary.

You can apply statistical analysis to genomics and/or transcriptomics data in relation to phenotypes and external factors, and visually display and interpret the results.

You can use annotation to link biological knowledge to found results. For example, linking structural variants to disorders or using pathway and/or (gene-set) enrichment analysis to interpret the effects of a transcriptomics experiment.

You keep a logbook for all analyses in which the steps taken and results are recorded.

You present your research results in an attractive way and at the appropriate level to your fellow students.

**Content**

During this large 10 EC project, several facets of working on genome research are addressed. You search for a suitable - published, for instance available in the NCBI SRA - data set with which to complete both projects ('genomics' & 'transcriptomics'). During the genomics project, you look for variations between the data set found and a reference genome. An important aspect here is assessing the quality of the data (the 'raw reads') before setting up an analysis pipeline in a workflow manager. Found variants are annotated and interpreted for biological effect.

Furthermore, you need to have mastered some statistical concepts in order to be able to perform the necessary analyses for the transcriptomics project. For instance, we use statistical tests to determine which genes show significantly different patterns and enrichment analysis to link this group of genes to biological function. You will report extensively with visualisations to validate choices made and present the results.

To make your research reproducible, making a logbook is also part of this module. In this logbook, you keep track of the steps taken and the corresponding results.

To be able to perform statistical analyses, among other things, a basic level of programming in R is expected, as explained in module '1.4.1: The scientific cycle'. To work out (steps of) an analysis pipeline, terminal experience is required. Knowledge from module 2.1.1 is required to follow this module.

**Included in programme(s)**

Bio-Informatics

**School(s)**

Institute for Life Science & Technology

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