# THIJMEN WEIJGERTZE

THIRD YEAR LIFESCIENCES STUDENT

## **TOP 5 SKILLS**

- Reliable
- Driven
- Polite
- Understanding
- Communicative

## **PERSONALIA**

#### **Adress**

Sartrestate 24 6716SE, Ede Netherlands

## **Date of Birth**

- 27-01-2003

#### Contact

- 0630477492
- thijmen.weijgertze@student.hu.nl

## Links

- Data Science portfolio
- GitHub
- LinkedIn

## **WORK EXPERIENCE**

## **Iddink Nederland, Ede:**

Year: Summer 2019 & 2020 Timespan: 5 to 6 week (36 hours per week)

## **DRIVING LICENCE**

Type B

## **HOBBIES**

- Piano
- Spending time with friends in weekends (activities like: swimming, GeoCaching & soccer)
- Photography (on vacation)
- Observing plant and ditch water monsters under a microscope
- Free time code projects

## **ABOUT ME**

Since a young age biology has fascinated me. I continued this passion by studying 'Life Sciences' at the HU. During this study I specialized in Biomolecular Research and followed two data science courses as my minor. In the future I hope to contribute to fundamental laboratory research and possibly combine it with data science.

## **DEGREE**

# **HAVO-degree, Marnix College Ede**

Sep 2015 - Mei 2020

- Curriculum: "Nature & Technology" and "Nature & Health"

# Bachelor Biology and Medical laboratory research (Life Sciences), HU University of Applied Sciences Utrecht

September 2020 - ~Juli 2025

- Specialised in: Biomolecular Research (BMR)

- Minor in: Data Science

- Propaedeutic average: 7.73

## PRACTICAL SKILLS

# Lab

Molecular cloning, calcium phosphate transfection, RNA/DNA isolation, cDNA synthesis, (q)PCR, Sonication, Cell culture, SDS-page, Western blot, ELISA, Agarose gel electrophoresis, Paper electrophoresis, Äktaprime, TLC & SEC chromatography, Differential centrifugation, Spectrophotometry, light dark & fluorescent microscopy, safe microbiological techniques, C. elegans

# **Data Science**

R, Rmarkdown, Rbookdown, Rpackage, Git/github, Bash\*, SQL\*, Machine Learning\*, frequentist statistics, Reproducible research, RNAseq pipeline in R, Antibiotic resistance pipeline in Bash\*\*, Metagenomics pipeline in R, <a href="Data-Science-portfolio">Data-Science-portfolio</a>

\* Basic knowledge

\*\* Minor project

# THEORETICAL KNOWLEDGE

## Theoretical knowledge within the subjects:

- Molecular biology
- Tumor cell biology
- Genetics
- Data science
- Advanced lab tools (incl: FACS, NGS, proteomics, MS)
- Experimental Design & Cell Culture
- Immunology
- Cellular Biochemistry
- Biotechnology
- Pharmacology
- Haematology
- Physiological Regulation systems

## **PROJECT INFO**

## **Data Science**

Result planning: 9.2 Result product: 8.0

Result presentation/GitHub: 7.8

Group: 3 students Study year: 3

## **Biomolecular Research**

Result project proposal: 6.5 Result practical work: 8.0 Result presentation: 6.6 Group: 2 students Study year: 3

## **Pharmaceuticals**

Result: 8.5 Group: 8 students Study year: 2

# **Microbiology**

Result report: 8.0 Result assessment: 8.1 Group: 8 students Study year: 2

## **Genes and Proteins**

Result: 9.0 Group: 8 students Extra: chairperson Study year: 2

## **MAIN PHASE PROJECTS**

# **Project Data Science (minor)**

The Data Science project involved creating a pipeline commissioned by the RIVM. The pipeline consisted of a combination of tools: fastq-dump, fastqc, trimagalore, unicycler, plasmidEC, gplas2 and abricate, Using these tools the pipeline was capable of taking SRA codes with Illumina data (short read) from a bacterial sample as input. After which it outputs the antibiotic resistance genes in plasmids. Throughout this project we also worked on: version control of R packages, creating a vignette and working with a GitHub workflow.

## **Project Biomolecular Research (specialisation)**

During this project, an attempt was made to produce HPO lyase. The HPO lyase gene had been isolated from cucumber in a previous project and inserted into *Escherichia coli* using cloning techniques. The bacterial suspension was scaled up to 80 mL and induced with IPTG. After which the protein was isolated through a combination of sonication, centrifugation and ÄKTAprime. The concentration was measured using spectrophotometry. Lastly a new gene was also isolated from self-planted garden cress through RNA isolation, cDNA synthesis and a two-step PCR process.

## **Project Pharmaceuticals**

The aim of this project was researching the effect of a reduced mucus layer (using N-acetylcysteine) on the susceptibility to an S. typhimurium infection. This involved cultivating *C. elegans* on a N-acetlycysteine-containing medium, infecting the nematodes at the L4 stage and measuring the infection using a combination of qPCR and Kve/CFU determination. Additionally, an attempt was made to stain the mucus layer in *C. elegans*. Using PAS staining. The protocols and observations from the PAS staining were documented for further research. Unfortunately, the conclusion could not be confirmed due to a lack of results.

# **Project Microbiology**

The aim of the microbiology project was determining whether patient X had an influenza A (H1N1) lung infection and possibly a bacterial co-infection. The influenza A (H1N1) infection was examined using a combination of cDNA synthesis and Real-time PCR techniques. The bacterial infection was studied through determination and disk diffusion tests on sputum and urine cultures. The final product included a literature review and resulted in the identification of a group of G streptococcus / staphylococcus epidermidis infections.

# **Project Genes and Proteins**

The aim of this project was to design a functional pAcGFP-IL-8 DNA construct for investigating IL-8 gene expression. IL-8 inserts were isolated from plasmids and inserted into pAcGFP1 vectors. Techniques like molecular cloning SDS-PAGE, western blot, agarose gel electrophoresis and fluorescence microscopy were used to create and test the construct. The final product included a literature review and a functional pAcGFP1-IL8p DNA construct.