Personal Information

Name and initials: Peters, C.C.
First name: Casper
Date of birth: 12 October 1998
Place of birth: Arnhem
Nationality: Dutch
Gender: Male

Profile

I have been studying at the Hanze Hogeschool Institute for Life Science & Technology in the Netherlands since 2015. I have experience dealing with big datasets, statistical analysis, making web applications and constructing software pipelines.

Currently, I am working on my minor "High Throughput/High-Performance Biocomputing" and will specialize myself to deal with big datasets.

When working on our practicals/projects I prefer to dive in right away, do some concise research and divide tasks. I like to get a decent result as soon as possible and try improving on it further down the road if time allows it.

My professional interests lie in programming and doing microbiological research, preferably in the fields of proteomics, metabolomics, epigenetics and gene regulation. For my personal interests, I like to mess around as a programming and electronics hobbyist. I love nature and travelling as well as trying out different sports and such. Also, because I am curious by nature, I like to educate myself about different topics.

Education

September 2015 – July 2019:   HBO Bioinformatics Bachelor (current education, ongoing, 3rd years)
September 2010 - May 2015:   Havo – Christelijk Lyceum Veenendaal
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Work experience

Ijselgrow Greenhouse worker (April 2016 – August 2017)
Iddink Warehouse Employee (3 weeks, July 2015)
Volunteering as an assistant caretaker at: De Oranjeschelp in Veenendaal (2013)

Languages: Dutch (native speaker).

English (full professional proficiency).

Computer skills: Microsoft windows OS

Linux administrator

Python programming language

Java programming language

SQL database management

Bash

HTML

CSS

Javascript

R programming language

Biological knowledge (Books used in studies):

- Biochemistry A Short Course 3e (Tymoczko Berg Stryer)
- Bioinformatics and Functional Genomics (3rd Ed)
- Brock Biology of Microorganisms, 14th Edition- Madigan
- Campbell Biology 10th Edition
- Concept of genetics global 11th ed Klug
- Dale From Genes to Genomes Concepts Applications 3rd
- Dale J.W., et al. From genes to genomes. Concepts and applications of DNA technology (3ed., Wiley, 2012)
- Data Mining 4th ed Practical Machine Learning Tools and Techniques Ian H. Witten, Eibe Frank, Mark A. Hall, Christopher J. Pal
- Data Structures and Algorithms Using Python - Rance D. Necaise
- Kuby Immunology 7th Edition
- Recombinant DNA James D. Watson
- Statistics for the Life Sciences, Fourth Edition - Myra L. Samuels, Jeffrey A. Witmer, Andrew Schaffner

Here I have listed some projects I have worked on in the past or am currently working on:

MetaToKrona:
MetaToKrona is a web-application that combines MetaPhlAn 2 and Kronatools. The reason for this is because Krona plots are interactive and give an easier to understand view of a metagenomic sample than the static plots Metaphlan2 produces. The webtool has a queuing system that allows multiple users to submit their jobs. When a job is done running, you should receive an email with a link to the output.

Evaluating the best combination of aligners for both single-cell and multi-cell data:
This project is a general RNA-seq pipeline made for comparing single-cell RNA and multi-cell RNA expression data as close as possible with a certain combination of commands and a combination of aligners and mappers.

NCBI_SRA_TO_EBI_FASTQ:
This python script will download .fastq/.fq files from the EBI (http://www.ebi.ac.uk/) using any ftp link of the NCBI (https://www.ncbi.nlm.nih.gov/) containing .sra (Sequence Read Archives file) files. This is, to prevent the need of using the poorly documented fastq-dump (https://trace.ncbi.nlm.nih.gov/Traces/sra/sra.cgi?view=toolkit_doc&f=fastq-dump) command line tool and understanding all its parameters. Also to prevent unnecessary conversion and waste CPU cycles.

Re-estimating the reproduction numbers of Ebola virus disease (EVD) during the 2014-2016 outbreak in West Africa using a complete dataset:
This project aimed to get a better guess at the reproduction numbers of Ebola after the 2014-2016 outbreak in Africa. The original study did not provide a complete dataset as the outbreak was ongoing. We repeated the said study and recalculated the reproduction numbers behind the outbreak.

LeapingPymol:
This project aims to combine the Leap sensor with Pymol with help of the Leap SDK and python3.

All these projects can also be found here: http://ccpeters98.com/projects.html

Programming and Electronics
Traveling
Trying out different sports
Nature
Learning new things