

# sanderbollen

Molecular biologist/Bioinformatician



## Personal details

**Full name:** Alexander Henriette Bernardus (Sander) Bollen

**Date of birth:** 11 June 1990

**Place of birth:** Heerlen, the Netherlands

**Nationality:** Dutch

**Marital status:** Unmarried. No children

## contact

Erasmusweg 1181P  
2542PW Den Haag  
Netherlands

+31 6 2125 4645

sander@sndrtj.eu  
<http://sndrtj.eu>

## languages

Dutch: mother tongue  
English: Near-native  
German: Good  
French: Basic  
Japanese: Basic  
Hebrew: Basic

## programming

Python, R, Scala,  
Javascript, Java & Perl

## education

Sep 2011 - Apr 2014 **Master** of Science in Biomedical Sciences Utrecht University, Utrecht, NL

Specialization: Cancer Genomics & Developmental Biology

*CAFE: an R package on caffeine*

This thesis describes the CAFE package, an R package I developed to detect gross chromosomal abnormalities from microarray expression data (rather than aCGH data). I received an excellent final mark of 9.3 (on a scale of 1 to 10) for the CAFE project and thesis, and the project resulted in a publication in *Bioinformatics*. I received my graduation certificate in April 2014.

Sep 2007 - Jul 2011 **Bachelor** of Applied Science in Biomedical Sciences Zuyd University, Heerlen, NL

Biomedical Sciences.

Four year programme. First two years mixed with Chemistry and Chemical Technology.

Sep 2002 - Jul 2007 **HAVO** high school certificate Porta Mosana College, Maastricht, NL

HAVO at Porta Mosana College high school in Maastricht, the Netherlands.

Mixed profile NG & EM.

## experience

Jun 2014 - current **Leiden University Medical Center** Leiden, NL

*Bioinformatician*

Bioinformatician at the department of Clinical Genetics at Leiden University Medical Center in Leiden, the Netherlands. I build and maintain Next-Generation Sequencing pipelines and tools for diagnostics, primarily for Whole Exome Sequencing and Non-Invasive Prenatal Testing (NIPT) applications. Technologies used include, but are not limited to:

- GNU Make
- SnakeMake
- GATK Queue
- Python
- Scala
- Javascript
- Bash
- Samtools
- Genome Analysis Toolkit (GATK)
- Variant Effect Predictor (VEP)
- Git
- MongoDB

Dec 2012 - Aug 2013 **Max Delbrück Center for Molecular Medicine**

Berlin, Germany

*Intern*

Master internship at the Computational Biology and Data Mining Group at the Max Delbrück Center for Molecular Biology in Berlin as part of my Master studies. I developed an R package called *CAFE* for the analysis of chromosomal abnormalities using Affymetrix microarray expression data as input. *CAFE* includes a range of plotting tools for easy visualization of detected abnormalities, and runs on Linux, Mac and Windows. Technologies learned during this internship include:

- R, with special priority to the following packages
  - ggplot2
  - affy
  - shiny
- git
- LaTeX
- Python

An article describing *CAFE* is currently in press in *Bioinformatics*. *CAFE* is available from <https://bitbucket.org/cob87icW6z/caffe/wiki/Home>. I received an excellent final mark of 9.3 (on a scale of 1 to 10) for this project and its resulting thesis.

Sep 2011 - Aug 2012 **UMC Utrecht**

Utrecht, the Netherlands

*Intern*

Master internship at the department of Medical Oncology at the lab of Susanne Lens, as part of my Master studies. I investigated the spatial localization of the Chromosomal Passenger Complex onto chromosomal arms during prophase and prometaphase. Techniques learned during this internship include:

- Tissue Culture
- Cloning
- PCR
- Western blots
- Immunoprecipitation
- Immunofluorescence microscopy
- Confocal microscopy

Nov 2010 - Jun 2011 **Leiden University**

Leiden, the Netherlands

*Intern*

Internship as researcher at the department of Molecular Genetics at the lab of Remus Dame, as part of my bachelor studies. I conducted research on chromatin condensation. Techniques learned during this internship include:

- Tethered Particle Motion
- Atomic Force Microscopy
- Cloning
- PCR

Aug 2010 - Feb 2011 **Koninklijke TNT Post**

Maastricht, the Netherlands

*Mail carrier*

Maastricht branch of Dutch postal services. Company now renamed to "PostNL".

Sep 2009 - Feb 2010 **Erasmus Medical Center**

Rotterdam, the Netherlands

*Intern*

Internship as researcher at the department of *Pediatrics Oncology* at the lab of Ronald Stam, as part of bachelor studies. Conducted research on apoptosis inhibition in MLL-rearranged infant acute lymphoblastic leukemia. Techniques learned during this internship include:

- RT-PCR
- Western blot
- Tissue Culture
- RNA interference

Finalized internship with an *excellent* rating (final mark: 9.0).

Oct 2008 - Aug 2009 **Vroom & Dreesmann**

Maastricht, the Netherlands

Cashier

Maastricht branch of Vroom & Dreesmann department stores

May 2006 - May 2007 **Albert Heijn**

Maastricht, the Netherlands

Cashier

Most successful branch of Albert Heijn supermarkets in the Netherlands

## computer skills

### Programming Languages

I have command of the following programming and scripting languages:

- R: I have excellent command of the R language. I usually make heavy use of bioconductor packages and the ggplot2 plotting package.
- Python: I have excellent command of Python including both versions 2.7 and 3 and over, which I used to develop tools for use in Next-Generation Sequencing pipelines. I have good command of the numpy, scipy, scikit-learn, biopython, pyvcf and pysam scientific packages as well as the matplotlib plotting engine and the Flask micro web framework. I am familiar with PySide for Qt integration
- Scala & Java: I have good command of Scala, and by extension, Java, which I use to develop Next-Generation Sequencing pipelines using the GATK Queue framework
- GNU Make: I have excellent command of GNU Make, which I use to develop Next-Generation Sequencing pipelines.
- SnakeMake: I have good command of the SnakeMake workflow system, which I use to develop Next-Generation Sequencing pipelines.
- Javascript: I use Javascript for front-end development.
- Perl: BioPerl and the Ensembl Perl API. Have been trained in BioPerl during my master's degree.

### Tools

I have command of the following tools facilitating software development

- Shiny for R. This allows one to construct interactive GUI interfaces to R applications on a webserver.
- The git source code management system. I use git for all my projects, as well as documents.
- The (Bio)Conda packaging system.
- $\LaTeX$ : I have used LaTeX to write internship reports, my thesis and this resume.

### Operating Systems

I have good knowledge of Linux operating systems, in particular Debian-derived systems

## other activities

2010 - 2012 **Apollo Rotterdam**

Rotterdam, the Netherlands

Volunteer at Apollo Rotterdam, a social organization focused on providing a comfortable area for young LGBT people (up to 27 years old) in the Rotterdam metropolitan area. My activities included organizing *theme evenings* and bar tending.

2009 - 2011 **Zuyd University**

Heerlen, the Netherlands

Member of the student education committee (*opleidingscommissie* in Dutch) of the Life Sciences faculty at Zuyd University. This committee is tasked with improving the level of education, in close cooperation with faculty staff.

2006 - 2008 **COC Maastricht**

Maastricht, the Netherlands

Volunteer at the Maastricht branch of COC, a nation-wide LGBT rights organization in the Netherlands. I helped set up the *Jong & Out* youth group (until 18 years old), the first in the country. This concept later went nation-wide, with *Jong & Out* groups now available in most major cities in the Netherlands.

## communication skills

2010 **Poster**

14th Molecular Medicine Day, Rotterdam

As part of my internship at the Erasmus MC, I presented my work on the inhibition of apoptosis in MLL-rearranged infant acute lymphoblastic leukemia.

## interests

**professional:** Next Generation Sequencing, data analysis, stem cells, iPSCs, developmental biology, oncology, apoptosis, software development

**personal:** guitar, reading (science fiction)

## publications

### article in peer-reviewed journal

CAFE: an R package for the detection of gross chromosomal abnormalities from gene expression microarray data

Bollen, S., Leddin, M., Andrade-Navarro, M. A., and Mah, N.

*Bioinformatics* (2014). 2014

CRISPR immunity relies on the consecutive binding and degradation of negatively supercoiled invader DNA by Cascade and Cas3

Westra, E. R., Erp, P. B. van, Künne, T., Wong, S. P., Staals, R. H., Seegers, C. L., Bollen, S., Jore, M. M., Semenova, E., Severinov, K.

*Molecular cell* 46.5 (2012) pp. 595–605. Elsevier, 2012