

Tobias Neumann

LEAD BIOINFORMATICIAN · DATA ANALYST

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Personal information

Date of Birth December 17, 1986
Nationality Austria
Family status Married, 2 daughters

Experience

Quantro Therapeutics GmbH

LEAD BIOINFORMATICIAN

Vienna, Austria

August 2020 - PRESENT

IMP Research Institute for Molecular Pathology

BIOINFORMATICIAN

Vienna, Austria

May 2014 - July 2020

- Lead bioinformatics method and algorithm development for the **SLAM-seq** sequencing technology
- Design of the genome-wide **Vienna sgRNA libraries** for pooled CRISPR screens
- Co-development of the **VBC score** for selection of sgRNAs that effectively produce loss-of-function alleles
- Data mining of big data such as **The Cancer Genome Atlas** (11k samples, 100 TB data) in the cloud (AWS)
- Database and front-end development for integrating, visualizing and querying screening and NGS data and metadata utilizing the on-campus sequencing facility API
- Establishment of Oxford Nanopore Sequencing (ONT) protocols in the lab (first lab at IMP)

Lexogen GmbH

CONTRACTOR

Vienna, Austria

September 2017 - 2019

- Lead development of the **SLAMdunk** product backend
- Optimizing and porting established variant-callers for nucleotide-conversion detection
- Containerization of software packages using Docker
- Deployment of Docker containers on the **Bluebee** private cloud platform
- License assessment and resource benchmarking

Sophia Genetics SA

BIOINFORMATICIAN

Lausanne, Switzerland

October 2012 - May 2014

- Lead development, maintenance and optimization of a targeted gene sequencing and exome-sequencing pipeline building system forming the bioinformatics backend of the **Sophia DDM®** SaaS platform
- Tailoring pipelines for diagnostic gene panel kits on various sequencing platforms (Roche 454 / IonTorrent PGM / Illumina MiSeq) for major hospitals and labs in Switzerland and across Europe
- Conducting genetic test kit validation studies with key diagnostic kit developers at European level
- Development of genetic tests with Swiss hospitals
- Exploratory data analysis on prospective gene test data
- Product presentations for prospective and established customers and on conferences

Max F. Perutz Laboratories

BIOINFORMATICIAN

Vienna, Austria

April 2012 - September 2012

- De-novo genome assembly of *Clunio marinus*
 - Contig assembly, filtering and completeness assessment
 - Setup of the de-novo gene annotation pipeline and genome browser (MAKER, GMOD)
- Scaffold N50 of 1.9 Mb, 98% completeness
- Better assembly quality than honeybee, *Tribolium* or the monarch butterfly
- Served as basis to study the genomic basis of circadian and circalunar timing adaptations
- Hosted at **ClunioBase** and published in *Nature*

CIBIV Center for Integrative Bioinformatics Vienna

PROJECT STUDENT

Vienna, Austria

June 2010 - February 2012

- Massive parallelization of sequence alignments on the CPU and cluster
- Software development of an evaluation framework for reference-mapping software
- De-novo transcript assembly of RNA-seq data for *Idiosepius pygmaeus*

SBC Stockholm Bioinformatics Center

RESEARCH INTERN

Stockholm, Sweden

March 2009 - June 2009

- Network analysis of the gene interaction database **FunCoup** to in-silico identify and evaluate novel neurodegenerative disease candidate genes

Education

University Vienna

PHD IN LIFE SCIENCES

- Center for Integrative Bioinformatics Vienna (CIBIV)
- Working title: TBA

Vienna, Austria

April 2020 - PRESENT

Medical University Vienna

DIPLOM-INGENIEUR (M.Sc.ENG.)

- Master's program Medical Informatics (major: Bioinformatics)
- Master's thesis: Challenges of de-novo assembling the transcriptome of *Idiosepius pygmaeus* for novel gene identification

Vienna, Austria

October 2009 - April 2012

University for Applied Sciences Hagenberg

BACHELOR OF SCIENCE IN ENGINEERING (HONORS)

- Bachelor's program Bioinformatics

Hagenberg, Austria

October 2006 - July 2009

High school

A-LEVELS (DISTINCTION)

Bad Ischl, Austria

June 2005

Skills

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|---------------------|--|
| NGS data | Amplicon sequencing, genome-seq, RNA-seq, ChIP-seq, SLAM-seq, GRO-seq, PRO-seq |
| Sequencers | Illumina GA / HiSeq / MiSeq, Oxford Nanopore Technologies MinION, Ion Torrent PGM, Roche 454 |
| Programming | C/C++, Python, R / Bioconductor, Java, Perl, Bash, LaTeX |
| Technologies | Nextflow, Shiny, EJB / CDI, Hibernate / JPA, JSF + PrimeFaces, SSE/AVX, OpenCL, OpenMP, MPI |
| Platforms | Linux (Ubuntu, CentOS, SUSE), Docker, AWS, Mac OS X |
| Databases | Oracle 10g, MySQL, SQL, PL/SQL, XML |
| Versioning | Git, Svn |
| Building | CMake, Maven |

Teaching assistance

University of Vienna

DARE WINTERSCHOOL TRAINER

- Lecturing on next-generation sequencing data processing
- Setting up and assisting students in practical exercises

Vienna, Austria

February 2012

University of Vienna

TEACHING ASSISTANT

- Infrastructure setup
- Student program review and testing
- Leading discussions during student presentations

Vienna, Austria

Summer semester 2011

Languages

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|----------------|-------------------------------|
| German | Native |
| English | Full professional proficiency |
| Spanish | Elementary proficiency |
| French | Elementary proficiency |

Leisure activities

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|---------------|---|
| Sports | Beachvolleyball, Cycling, Boulderling, Slacklining, Badminton |
| Music | Piano, Guitar, Drums |
| Others | Reading news, languages, travelling |

Selected publications

SLAMseq technology

- Neumann T, Herzog VA, Muhar M, von Haeseler A, Zuber J, Ameres SL & Rescheneder P: Quantification of experimentally induced nucleotide conversions in high-throughput sequencing datasets. *BMC Bioinformatics*, 2019. 20(1), 258. <http://doi.org/10.1186/s12859-019-2849-7>
- Muhar M, Ebert A, Neumann T, Umkehrer C, Jude J, Wieshofer C, Rescheneder P, Lipp JJ, Herzog VA, Reichholf B, Cisneros DA, Hoffmann T, Schlapansky MF, Bhat P, von Haeseler A, Köcher T, Obenauf AC, Popow J, Ameres SL & Zuber J: SLAM-seq defines direct gene regulatory functions of the BRD4-MYC axis. *Science*, 2018. 360(6390), 800–805. <http://doi.org/10.1126/science.aao2793>
- Herzog VA, Reichholf B, Neumann T, Rescheneder P, Bhat P, Burkard TR, Wlotzka W, von Haeseler A, Zuber J & Ameres SL: Thiol-linked alkylation of RNA to assess expression dynamics. *Nature Methods*, 2017. 14(12), 1198–1204. <http://doi.org/10.1038/nmeth.4435>
- Matsushima W, Herzog VA, Neumann T, Gapp K, Zuber J, Stefan L, Ameres SL & Miska EA: Sequencing cell type-specific transcriptomes with SLAM-ITseq. *Nature Protocols*, 2019. 87(13), 166. <http://doi.org/10.1038/s41596-019-0179-x>

CRISPR technology

- Michlits G*, Jude J*, Hinterndorfer M, de Almeida M, Vainorius G, Hubmann M, Neumann T, Schleiffer A, Burkard T, Fellner M, Gijsbertsen M, Traunbauer A, Zuber J & Elling U: Multilayered VBC-score predicts sgRNAs that efficiently generate loss-of-function alleles. *Nature Methods*, 2020. <https://doi.org/10.1038/s41592-020-0850-8>
- Umkehrer C, Holstein F, Formenti L, Jude J, Froussios K, Neumann T, Cronin SM, Haas L, Lipp JJ, Burkard TR, Fellner M, Wiesner T, Zuber J & Obenauf AC: Isolating live cell clones from barcoded populations using CRISPRa-inducible reporters. *Nature Biotechnology*, 2020. <https://doi.org/10.1038/s41587-020-0614-0>

Genomics

- Kaiser T, Poehn P, Szkiba D, Preussner M, Sedlazeck F, Zrim A, Neumann T, Nguyen LT, Betancourt A, Hummel T, Vogel H, Dorner S, Heyd F, Arndt von Haeseler A & Tessmar-Raible K: The genomic basis of circadian and circalunar timing adaptations in a midge. *Nature*, 2016. 540(7631), 69–73. <http://doi.org/10.1038/nature20151>
- Fitz J, Neumann T, Steininger M, Wiedemann EM, Cantoran Garcia A, Athanasiadis A, Schoeberl UE & Pavri RR: Spt5-mediated enhancer transcription directly couples enhancer activation with physical promoter interaction. *Nature Genetics*, 2020. 52(5), 505–515. <http://doi.org/10.1038/s41588-020-0605-6>

Cancer

- Rathert P*, Roth M*, Neumann T, Muerdter F, Roe J-S, Muhar M, Deswal S, Cerny-Reiterer S, Peter B, Jude J, Hoffmann T, Boryn LM, Axelsson E, Schweifer N, Tontsch-Grunt U, Dow LE, Gianni D, Pearson M, Valent P, Stark A, Kraut N, Vakoc CR & Zuber J: Transcriptional plasticity promotes primary and acquired resistance to BET inhibition. *Nature*, 2015. 525(7570), 543–547. <http://doi.org/10.1038/nature14898>

Invited talks

SLAMdunk – a pipeline for analyzing SLAMseq data in established and emerging applications

ADVANCES IN GENOME BIOLOGY AND TECHNOLOGY (AGBT)

Orlando, FL, USA

February 2018

Conference posters

Quantifying experimentally induced nucleotide-conversions in high-throughput sequencing

ADVANCES IN GENOME BIOLOGY AND TECHNOLOGY (AGBT)

Orlando, FL, USA

February 2018