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

Vienna, Austria

LEAD BIOINFORMATICIAN

August 2020 - PRESENT

- Planning and setup of the cloud-based production-grade computational environment for concurrent processing of >100k targeted SLAM-seq libraries
- Leading the computational development of the innovative time-resolved high-throughput transcriptomics QUANTROseq drug discovery platform
- Machine-learning driven identification of highly-selective transcriptional fingerprints of disease causing transcription factors in our reference compound datasets
- Building and leading QUANTRO's computational team
- Planning and overseeing QUANTRO's IT and computational infrastructure and processes

Research Institute for Molecular Pathology

Vienna, Austria

SENIOR BIOINFORMATICIAN

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
- Development a cloud-computing virus screening pipeline on **Amazon Web Services (AWS)** that scales to the entire 11,000 patient samples (100 TB raw data) of **The Cancer Genome Atlas**
- Application of Machine learning approaches to derive biomarkers that accurately classify HPV-positive and HPV-negative tumors.
- Technology development on the **Oxford Nanopore Sequencing** platform to detect translocations at single-base pair resolution genome-wide
- Member of the **Vienna Covid-19 Detection Initiative** performing comparative genomics of > 5M sequenced SARS-CoV-2 genomes worldwide to identify conserved domains for sensitive primer design to detect COVID-19 infections, de-novo assembly and quantification of viral RNAs for primer target selection for sensitive SARS-CoV-2 detection.
- Leading projects as corresponding author and mentoring of undergraduate students to successful publications

Vienna, Austria

CONTRACTOR

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™

Lausanne, Switzerland

BIOINFORMATICIAN

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 PERUTZ LABS VIENNA

BIOINFORMATICIAN

- 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

Vienna, Austria

PROJECT STUDENT

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

Stockholm, Sweden

RESEARCH INTERN

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

Vienna, Austria

PHD IN MOLECULAR BIOSCIENCES

April 2020 - September 2023

- Center for Integrative Bioinformatics Vienna (CIBIV)
- PhD thesis: Recovery, quantification and error correction of nucleotide conversions in epitranscriptomics sequencing datasets

Medical University Vienna

Vienna, Austria

DIPLOM-INGENIEUR (M.SC.ENG.)

October 2009 - April 2012

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

University for Applied Sciences Hagenberg

Hagenberg, Austria

BACHELOR OF SCIENCE IN ENGINEERING (HONORS)

October 2006 - July 2009

- Bachelor's program Bioinformatics

High school

Bad Ischl, Austria

A-LEVELS (DISTINCTION)

June 2005

Skills

Data exposure	Amplicon sequencing, WGS, WES, RNA-seq, ChIP-seq, SLAM-seq, HiC, CRISPR/Cas9 screens, RNAi screens
Sequencers	Illumina NovaSeq / HiSeq / MiSeq, Oxford Nanopore Technologies MinION, Ion Torrent PGM, Roche 454
Programming	C/C++, Python, R / Bioconductor, Java, Perl, Bash, LaTeX
Technologies	Nextflow, Tidyverse, AWS Batch, Shiny, Plotly, 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
DevOps	Git, Gitlab, CI/CD
Building	CMake, Maven

Teaching assistance

University of Vienna

Vienna, Austria

DARE WINTERSCHOOL TRAINER

February 2012

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

University of Vienna

Vienna, Austria

Teaching assistant

Summer semester 2011

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

Languages

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

Selected publications

Transcriptomics

- Popitsch N*, Neumann T*, von Haeseler A & Ameres SL. *Splice_sim*: a nucleotide-conversion enabled RNA-seq simulation and evaluation framework. Submitted to *Genome Biology* March 2023.

- 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

Genomics

- Peycheva M, Neumann T, Malzl D, Nazarova M, Schoeberl UE & Pavri R: DNA replication timing directly regulates the frequency of oncogenic chromosomal translocations. *Science*, 2022. 377(6612), 1277. http://doi.org/10.1126/science.abj5502

- Malzl D*, Peycheva M*, Rahjouei A, Gnan S, Klein K, Nazarova M, Schoeberl UE, Gilbert DM, Buonomo S, Di Virgilio M, Neumann T[†] & Pavri R[†]: RIF1 regulates replication origin activity and early replication timing in B cells. *bioRxiv*, 2023. https://doi.org/10.1101/2023.03.31.535086

- 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

CRISPR tech development

- 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. 17, 708–716. https://doi.org/10.1038/s41592-020-0850-8

- de Almeida M*, Hinterndorfer M*, Brunner H, Grishkovskaya I, Singh K, Schleiffer A, Jude J, Deswal S, Kalis R, Vunjak M, Lendl T, Imre R, Roitinger E, Neumann T, Kandolf S, Schutzbier M, Mechtler K, Versteeg G, Haselbach D[†] & Zuber J[†]: AKIRIN2 controls the nuclear import of proteasomes in vertebrates. *Nature*, 2021. 599, 491–496. https://doi.org/10.1038/s41586-021-04035-8

- 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. 39, 174–178. https://doi.org/10.1038/s41587-020-0614-0

Cancer

- Leiendecker L, <u>Neumann T</u>, Jung PS, Cronin SM, Steinacker TL, Schleiffer A, Schutzbier M, Mechtler K, Kervarrec T, Laurent E, Bachiri K, Coyaud E, Murali R, Busam KJ, Itzinger-Monshi B, Kirnbauer R, Cerroni L, Calonje E, Rutten A, Stubenrauch F, Griewank KG, Wiesner T[†] & Obenauf AC[†]: Human papillomavirus 42 drives digital papillary adenocarcinoma and elicits a germ-cell like program conserved in HPV-positive cancers. *Cancer Discovery*, 2023. 13(1):70-84. https://doi.org/10.1158/2159-8290.CD-22-0489

- Rathert P*, Roth M*, <u>Neumann T</u>, 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

- Haas L, Elewaut A, Gerard CL, Umkehrer C, Leiendecker L, Pedersen M, Krecioch I, Hoffmann D, Novatchkova M, Kuttke M, <u>Neumann T</u>, de Silva IP, Witthock H, Cuendet MA, Carotta S, Harrington KJ, Zuber J, Scolyer RA, Long GV, Wilmott JS, Michielin O, Vanharanta S, Wiesner T & Obenauf AC: Acquired resistance to anti-MAPK targeted therapy confers an immune-evasive tumor microenvironment and cross-resistance to immunotherapy in melanoma. *Nature Cancer*, 2021. 2, 693–708. https://doi.org/10.1038/s43018-021-00221-9

SARS-CoV-2 (part of the VCDI team)

- Yelagandula R, Bykov A, Vogt A, Heinen R, Özkan E, Strobl MM, Baar JC, Uzunova K, Hajdusits B, Kordic D, Suljic E, Kurtovic-Kozaric A, Izetbegovic S, Schaeffer J, Hufnagl P, Zoufaly A, Seitz T, <u>VCDI</u>, Födinger M, Allerberger F, Stark A, Cochella L[†] & Elling U[†]: Multiplexed detection of SARS-CoV-2 and other respiratory infections in high throughput by SARSeq. *Nature Communications*, 2021. 12, 3132. https://doi.org/10.1038/s41467-021-22664-5

- Kellner MJ*[†], Ross JJ*, Schnabl J*, Dekens MPS, Matl M, Heinen R, Grishkovskaya I, Bauer B, Stadlmann J, Menéndez-Arias L, Straw AD, Fritsche-Polanz R, Traugott M, Seitz T, Zoufaly A, Födinger M, Wenisch C, Zuber J, <u>VCDI</u>, Pauli A[†], & Brennecke J[†]: A Rapid, Highly Sensitive and Open-Access SARS-CoV-2 Detection Assay for Laboratory and Home Testing. *Frontiers in Molecular Biosciences*, 2022. 9. https://doi.org/10.3389/fmolb.2022.801309

Invited talks

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

Orlando, FL, USA

Advances in Genome Biology and Technology (AGBT)

February 2018

Conference posters

Quantifying experimentally induced nucleotide-conversions in high-throughput sequencing

Orlando, FL, USA

Advances in Genome Biology and Technology (AGBT)

February 2018

Networking

Biotech computational leader network

Vienna, Austria

Founder and organizer

2023

Leisure activities

Sports	Beachvolleyball, Cycling, Bouldering, Slacklining, Badminton
Music	Piano, Guitar, Drums
Others	Reading news, languages, travelling