
Kornel Labun

Nationality: Polish

Email: kornel.labun@gmail.com

Phone: +47 405 741 63

[Github](#) | [Website](#) | [Linkedin](#) | [Publications](#)



SUMMARY

Bioinformatician with 10 years of experience in **genome engineering, precision medicine, and omics**. I excel at scalable software development (CHOPCHOP, ampliCan, ORFik) to translate complex biological data into actionable insights for research and development.

SKILLS

Bioinformatics: Broad experience across Omics data types and NGS data analysis (e.g. amplicon-Seq, RNA-Seq, Ribo-Seq, GUIDE-seq, Oxford Nanopore, PacBio). Genome engineering expert (CRISPR design and data analysis), as well as Genomics, Translation and Functional analysis.

Tool Development: Designed and developed impactful bioinformatics tools ([ORFik](#), [ampliCan](#), [RareVariantVis](#), [CHOPCHOP](#), [tailfindR](#), [riboCrypt](#), [CHOPOFF](#)).

Programming: R (Bioconductor, tidyverse), Python (Keras, scikit-learn, SciPy), Julia (Biojulia), Javascript (nodejs, angular), bash & shell scripting

Databases: MySQL, PostgreSQL, Redis, MongoDB, Neo4j

DevOps: Cloud (Microsoft Azure, Google Cloud Platform, OpenStack), High-Performance Computing (HPC), Docker, Kubernetes

Languages: Polish (native), English (fluent), Norwegian (basic)

EXPERIENCE

January 2021 - Present | **Postdoctoral fellow / Researcher** | University of Bergen

- Invented [CHOPOFF](#), a CRISPR off-target detection tool achieving 10x speed improvement and 100% sensitivity. (Julia, 96% code coverage, Preprint: 2025)
- Collaborating with Emma Håpanniemi group by analyzing their datasets for precision pediatrics and gene editing (GUIDE-seq, amplicon-seq, PacBio, Nanopore; Publications: Elife 2021, Mol Therapy 2022).
- Conceived [ORFik](#) to streamline analysis of RCP-seq (RNA/80S/SSU sequencing) datasets to study translation in cancer metastasis and obesity (Publications: NAR G&B 2021, BMC Bioinfo 2021).
- Analyzed Oxford Nanopore sequencing and developed methods for detecting RNA modifications and 5' cap (Publications: NAR 2022).
- Developed [ribocrypt.org](#) interactive visualizations for genomics data (Preprint: 2025).

November 2019 - December 2020 | **Senior Consultant** | Sonat Consulting AS

- Youwell/Helse I Hardanger - Led development of Android application for Bluetooth smartwatch biometrics (RxJava, Dagger2, Retrofit, MVVM). Contributed to backend development (Azure/C#, Redux/React).
- Cutters - Developed backend services and built a marketing analytics platform on Google Cloud Platform (Python, SQL), including Facebook API integration for campaign analysis.
- Absa - Designed and implemented Big Data ETL pipelines and a data warehouse solution using SQL Server Analysis Services (SSAS multidimensional cube), involving schema design and dimensional data modeling.

Sep 2015 - Oct 2019 | **PhD Fellow** | University of Bergen

- Thesis: "In silico design and analysis of gene editing experiments." Supervisor: Prof. Eivind Valen.
- Developed widely used bioinformatics pipelines and tools: [CHOPCHOP](#), [RareVariantVis](#), [ampliCan](#), (Publications: NAR 2016/2019, Bioinformatics 2016, Genome Res 2019)
- Implemented machine learning models for predicting poly(A) tail length from Nanopore data ([tailfindR](#)) and CRISPR repair outcomes (Publications: RNA 2019).
- Taught programming and bioinformatics courses (Computer Programming for Science, R Crash Course, Social Networks Theory).

Jul 2014 - Jul 2015 | **Software Developer** | rspective (now Voucherify)

- Developed full-stack scalable web applications. (Node.js/Angular and Spring/Java)

EDUCATION

September 2015 - October 2019 | **PhD: Computational Biology** | University of Bergen, Norway

- Title: "In silico design and analysis of gene editing experiments."

October 2009 - September 2014 | **MSc Eng** | Silesian University of Technology, Poland

- Title: "Spatial evolutionary games as a tool for modeling inter-population interactions."

SELECTED PUBLICATIONS

Total number of publications: **~20** h-index: **10**

CHOPCHOP v3: expanding the CRISPR web toolbox beyond genome editing.

[Labun K](#), Montague TG, Krause M, Torres Cleuren YN, Tjeldnes H, Valen E

Nucleic acids research, 47(W1):W171–W174. (2019)

Citations: **1690+**

CHOPCHOP v2: a web tool for the next generation of CRISPR genome engineering.

[Labun K](#), Montague TG, Gagnon JA, Thyme SB, Valen E

Nucleic acids research, 44(W1):W272–6 (2016)

Citations: **1059+**

tailfindr: alignment-free poly(A) length measurement for Oxford Nanopore RNA and DNA sequencing.

Krause M, Niazi AM, [Labun K](#), Torres Cleuren YN, Müller FS, Valen E

RNA, 25(10):1229–1241. (2019)

Citations: **93+**

Accurate analysis of genuine CRISPR editing events with ampliCan.
Labun K, Guo X, Chavez A, Church G, Gagnon JA, Valen E
Genome Research , 29 (5) (2019)

Citations: **69+**

ORFik: a comprehensive R toolkit for the analysis of translation.
Tjeldnes H, Labun K, Torres Cleuren YN, Chyżyńska K, Świrski M, Valen E
BMC bioinformatics 22 (1), 336 (2021)

Citations: **33+**

Long-read single-molecule RNA structure sequencing using nanopore.
Bizuayehu TT, Labun K, Jakubec M, Jefimov K, Niazi AM, Valen E
Nucleic acids research 50 (20), e120-e120 (2022)

Citations: **26+**

Rapid genome editing by CRISPR-Cas9-POLD3 fusion.
Reint G, Li Z, Labun K, Keskitalo S, Soppa I, Mamia K, Tolo E, et al.
Elife 10, e75415 (2021)

Citations: **21+**

TEACHING EXPERIENCE

Organizer & Teacher: R Crash Course for NORBIS & MCB research schools (2017, 2019, 2021). Course website: r-crash-course.github.io

Teaching Assistant at University of Bergen: INF109 Computer Programming for Science (Spring 2017, 2018) and INF207 Social Network Theory (Autumn 2016, 2018).
