Kornel Labun

Nationality**:** Polish

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Github | Website | Linkedin | Publications

SUMMARY

Computational biologist and bioinformatician with **10 years of experience** developing scalable software and applying AI/ML methods to solve complex problems in genomics and translational medicine. Expert in multi-omics data analysis (**RNA-Seq, Ribo-Seq, Nanopore**) and **genome engineering** (CRISPR). Proven track record of creating impactful open-source tools (CHOPCHOP, ORFik, ampliCan) that translate large-scale biological data into actionable insights for therapeutic target identification, precision medicine, and drug discovery.

SKILLS

Computational Biology & Bioinformatics:

- **Omics Analysis:** RNA-Seq, Ribo-Seq (Translatomics), Single-Cell & Spatial Transcriptomics concepts, Genomics, Proteomics concepts.
- **Sequencing Technologies:** Illumina (NGS), Oxford Nanopore & PacBio (Long-Read).
- **Functional Genomics:** Genome Engineering (CRISPR Design & Off-Target Analysis), Gene Regulation, RNA Biology (Translation, Modifications, Splicing, Polyadenylation), Variant Analysis.
- **Specializations:** Therapeutic Target Identification, Biomarker Discovery, Precision Medicine, Computational Drug Discovery.

Software & AI/ML Development:

- **Programming:** R (Bioconductor, tidyverse, Shiny), Python (Pandas, SciPy, scikit-learn, Keras, TensorFlow/PyTorch), Julia, Javascript (Node.js, React, Angular), Bash.
- **AI / Machine Learning:** Predictive Modeling, Deep Learning, Model Development & Validation for biological applications (e.g., CRISPR outcomes, transcriptomics).
- **Data Visualization:** Interactive Dashboards & Graphics (D3.js, ggplot2, Plotly, Shiny), UI/UX principles.
- **Tool Development:** Creator of widely used bioinformatics tools (crisprtools.org, ORFik, ampliCan, RareVariantVis, CHOPCHOP, tailfindR, riboCrypt, CHOPOFF).

Data Engineering & DevOps:

- **Databases:** SQL (PostgreSQL, MySQL), NoSQL (MongoDB, Redis, Neo4j).
- **Infrastructure:** High-Performance Computing (HPC), Cloud Platforms (Azure, Google Cloud Platform), Docker, Kubernetes.
- **Best Practices:** End-to-end pipeline development, CI/CD, version control (Git), reproducible research.

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

EXPERIENCE

January 2021 - Present | **Postdoctoral fellow / Researcher** | University of Bergen
- Initiated and developed crisprtools.org, an integrated platform for genome engineering with webtools for the design of experiments: CHOPOFF, SNIPSNP, Dual-Cas13a, and a full reddit-like forum to foster scientific collaboration.
- 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).