

ECCB 2026 Accepted Proceeding papers

Genomics, epigenomics and genome editing

ARGformer: learning on ancestral recombination graphs with transformers.

David Bonet, Cole Shanks, Marçal Comajoan Cara, Jordi Abante and Alexander Ioannidis.

BaGGLS: A Bayesian Shrinkage Framework for Interpretable Modeling of Interactions in High-Dimensional Biological Data.

Marta Lemanczyk, Lucas Kock, Johanna Schlimme, Nadja Klein and Bernhard Renard.

Episode Clustering in Phylogenetic Networks.

Pawel Gorecki, Agnieszka Mykowiecka and Jarosław Paszek

GUANinE v1.1 Reveals Complementarity of Supervised and Genomic Language Models.

Eyes Robson and Nilah Ioannidis.

Knowledge-Guided Learning with Curated Prior Genetic Biomarkers for Robust Model Interpretation

Beomsu Baek, Eunyong Jang, Sai Phani Parsa, Youngsoon Kim and Mingon Kang.

Large-scale simulation of coverage and error rate trade-offs for cancer detection in cell-free DNA whole-genome sequencing.

Li-Ting Chen, Jeroen de Ridder and Myrthe Jager.

Leveraging ONT move table values for signal aware variant calling.

Xian Yu, Zhenxian Zheng, Lei Chen, Zilan Qin, Minggao He and Ruibang Luo.

Liquid biopsies reveal dual compartments of cancer risk from tumor and host-derived mutations.

Federica Malighetti, Ivan Civettini, Andrea Aroldi, Alberto Maria Villa, Matteo Villa, Luca Sala, Nicoletta Cordani, Massimiliano Cadamuro, Diego Cortinovis, Rocco Piazza, Luca Mogni and Daniele Ramazzotti.

Micropeptides encoded by lncRNAs associated with cancer progression reveal novel immunogenic epitopes.

Michal Linial and Stav Zok.

Modeling time-varying genetic effects on binary disease risk via functional Mendelian Randomization

Nicole Fontana, Piercesare Secchi, Emanuele Di Angelantonio and Francesca Ieva.

Nerpa 2: probabilistic linking of biosynthetic gene clusters to nonribosomal peptides.
Ilia Olkhovskii, Aleksandra Kushnareva, Azat Tagirdzhanov and Alexey Gurevich.

PRISM-G: an interpretable privacy scoring framework for assessing risk in synthetic human genome data.

Alejandro Correa Rojo, Yves Moreau and Gökhan Ertaylan.

RSHash: A fast and space-efficient hash table for k-mers.

Jonas Schulte-Mattler and Knut Reinert.

Transcriptomics and gene regulation

An End-to-End Computational Framework for 'Record-seq' Transcriptional Recording Data.

Florian Hugi, Tanmay Tanna and Randall J Platt.

CellTypeAI: cell annotation for scRNA-seq using local generative-AI.

Rufus Daw, Harry Deijnen, Magnus Rattray and John Grainger.

Chiron3D: an interpretable deep learning framework for understanding the DNA code of chromatin looping.

Sebastian Hönig, Aayush Grover, Piero Neri, Didier Surdez and Valentina Boeva.

DESpace2: detection of differential spatial patterns in spatial omics data.

Peiying Cai, Mark Robinson and Simone Tiberi

ExoShorkie: Predicting RNA-seq coverage of exogenous genomes in yeast by transfer learning.

Jonathan Mandl and Yaron Orenstein.

miRBind2 enables sequence-only prediction of miRNA binding and transcript repression.

David Čechák, Dimosthenis Tzimotoudis, Stephanie Sammut, Katarina Gresova, Eva Marsalkova, David Farrugia and Panagiotis Alexiou.

Network-based stratification of allele-specific expression reveals patient subgroups in Huntington's disease.

Aishwarya Iyer, Daan van Beek, Friederike Ehrhart, Chris Evelo, Theo de Kok, Ilja Arts, Michiel Adriaens and Martina Summer-Kutmon.

scTimeBench: A streamlined benchmarking platform for single-cell time-series analysis.

Adrien Osakwe, Eric Haoran Huang and Yue Li.

Sensitivity Analysis of Cell Fate Trajectories from Single-Cell Transcriptomics.

Abdullah Al Noman and Palash Sashittal.

SlotDeconv: Spatial Transcriptomics Deconvolution via Diversity Constrained Prototype Learning and Spatial Refinement.

Hanzhang Fang, Cong Qi, Yuanjie Zou, Yeqing Chen and Zhi Wei.

SPIDER: Spatially Integrated Denoising via Embedding Regularization with Single Cell Supervision.

Md Istiaq Ansari, Muhtasim Noor Alif and Wei Zhang.

Proteins and structural biology

Attracting Cavities 3.0: Faster and More Versatile Molecular Docking for the SwissDock Webservice.

Ute F. Röhrig, Marine Mathieu-Bugnon and Vincent Zoete.

De Novo Epitope-Specific Antibody Design via Time-Dependent Guidance.

Yunji Kim and Minkyung Baek.

Mitigating Goodhart's Law in Epitope-Conditioned TCR Generation Using Plug-and-Play Reward Designs.

Pengfei Zhang, Xiaoyi He, Fredo Guan, Hao Mei, Gloria Grama, Seojin Bang and Heewook Lee.

Optimizing Protein Design Through Uncertainty-weighted Steering of Protein Language Models.

Alif Bin Abdul Qayyum, Yingdong Zhou, Xiaoning Qian and Byung-Jun Yoon.

PepGen: Conditional generation of peptides for MHC binding.

Dani Korpela, Alexandru Dumitrescu, Martin Stražar, Rui Li, Ramnik Xavier, Daniel Graham and Harri Lähdesmäki.

PI-Mamba: Linear-Time Protein Backbone Generation via Spectrally Initialized Flow Matching.

Tianyu Wu and Lin Zhu.

Pocket-PROTACs: An Interpretable Pocket-Aware Deep Learning Framework for Predicting PROTAC-Induced Protein Degradation.

Kai Chen, Zhijian Huang, Yinbo Wang, Siyuan Shen, Jinmiao Song and Lei Deng.

PreFold-dG: estimating binding affinity of protein–protein interaction from intermediate representations of protein folding model.

Sungjoon Park, Soorin Yim, Dongyun Kim, Kiwoong Yoo, Doyeong Hwang, Kyungwook Lee, Jongseong Jang and Kiyoun Kim.

RIBEX: Predicting and Explaining RNA Binding Across Structured and Intrinsically Disordered Regions (IDR)-rich Proteins

Samuele Firmani, Felix Steinbauer, Gjergji Kasneci, Marc Horlacher and Annalisa Marsico.

Stoic: Fast and accurate protein stoichiometry prediction.

Daniil Litvinov, Lorenzo Pantolini, Peter Škrinjar, Gerardo Tauriello, Caitlyn McCafferty, Benjamin Engel, Torsten Schwede and Janani Durairaj.

Structure-Conditioned Self-Supervised Learning of Residue Interaction Constraints in Protein Kinases for Variant Interpretation

Shakiba Fadaei, Fanny Krebs and Vincent Zoete.

usiGrabber: Automating the curation of proteomics spectra data at scale, making large datasets ready for use in machine learning systems.

Georg Auge, Matthias Clausen, Konstantin Ketterer, Jacob Schaefer, Nils Schmitt, Tom Altenburg, Yannick Hartmaring, Hendrik Raetz, Christoph N. Schlaffner and Bernhard Y. Renard.

Systems biology, multi-omics integration and modelling

A linear interpretable model for Drug Target Prediction.

Santiago Noto, Santiago Ferreyra, Ruben Jimenez, Diego Galeano and Alberto Paccanaro.

A Novel ILP Framework to Identify Compensatory Pathways in Genetic Interaction Networks with GIDEON.

Jocelyn Garcia, Kevin Yu, Catherine Freudenreich and Lenore Cowen.

ARCADIA Reveals Spatially Dependent Transcriptional Programs through Integration of scRNA-seq and Spatial Proteomics

Bar Rozenman, Kevin Hoffer-Hawlik, Elham Azizi and Nicholas Djedjos.

Discovering Reference-missing Cell Types from Bulk Transcriptomics.

Yimin Fan, Yixuan Liu, Yunhua Zhong, Yue Wang, Kin Hei Lee, Yixuan Wang, Xinyuan Liu, Jiayi Li, Xuesong Wang, Ziqian Lin, Lei Li and Yu Li.

Informing agent-based models with spatial data using convolutional autoencoders.

Bi-Rong Wang, Chen-Yi Liao, Erik Danen, Elsa Neubert and Federica Eduati.

MAAMOUL: Metabolic network-based discovery of mi-crobiome-metabolome shifts in disease.

Elhanan Borenstein, Efrat Muller and Shiri Baum.

Multimodal contrastive learning for integrating molecular representations and cellular phenotypes in drug-target interaction prediction.

Ying-Ju Lai, Tianyuzhou Liang, Po-Yuan Chen, Yu-Che Tsai, George C. Tseng, Yufei Huang and Yu-Chiao Chiu.

SELFormerMM: multimodal molecular representation learning via SELFIES, structure, text, and knowledge graph integration.

Erva Ulusoy, Şevval Bostancı, Bora Engin Deniz and Tunca Dogan.

Semi-Supervised Learning for Automated Perineural Invasion Detection in Multi-Organ H&E Whole Slide Images.

Ahmad Alkhan, Michael Lynch, Maire Lavelle and Aedin Culhane.

Tail-Aware Heterogeneous Graph Neural Networks for Multi-Class Drug-Drug Interaction Prediction.

Varshini Venkatesh, Varsha G and Dhannya S M.

Universal differential equations for quantifying NF- κ B - p53 signaling crosstalk.

Umur Kaya, Xhemal Kodragjini, Samuel Zambrano and Katharina Baum.

Biodiversity, sustainability, and environmental bioinformatics

A Spectrum of Gut Microbiota Signatures Predicts Long-Term Health Status.

Himmi Lindgren, Chandler Ross, Matti Ruuskanen, Veikko Salomaa, Rob Knight, Teemu Niiranen, Aki Havulinna and Leo Lahti.

Agent-Based Modelling Identifies many paths for Inflammation Resolution.

Hermès Desgrez Dautet, David Bernard, Cousin Béatrice, Paul Monsarrat and Sylvain Cussat-Blanc.

GiantHost: A Domain-Adaptive and Uncertainty-Aware Framework for Giant Virus Host Prediction.

Fuchuan Qu, Guowei Chen and Yanni Sun.

Relation Extraction for Diet, Non-Communicable Disease and Biomarker Associations (RECoDe): A CoDiet study.

Donghee Choi, Yajie Gu, Kai Qi Zong, Antoine Lain, Dimitrios Zaikis, Thomas Rowlands, Marek Rei, Tim Beck and Joram Posma.

TheBIGbam: compression and interactive exploration of large-scale sequencing alignments with circular mapping support.

Martin Boutroux, Evan Thomas, Wai Hoe Chin and Hannes Peter.

TPMM: Three-component Posterior Mixture Model Enables Robust Inverton Detection in Low-Depth Metagenomes and Suggests Potential Viral Invertons.

Yi Lu, Jiaojiao Guan, Yang Shen, Jiayu Shang and Yanni Sun.

ViralQC: A Tool for Assessing Completeness and Contamination of Predicted Viral Contigs.

Cheng Peng, Jiayu Shang, Jiaojiao Guan and Yanni Sun.