Christoph Feinauer

ASSISTANT PROFESSOR · COMPUTER SCIENCE

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Birthday: 31/07/1986

Skills

Programming Languages	**C/C++, Julia, Python, Bash**
Libraries	**PyTorch, Tensorflow, Flux, Numpy, Kaldi**
Tools	**Bash, Git, Vim, Awk, Grep, Sed, Tmux, ssh**
Natural Languages	**German, English, Italian**

Research Interests

- Machine Learning Applied to Biological Data
- Generative Protein Sequence Models
- Natural Language Processing and Speech Recognition
- Analysis of Loss Landscapes of Deep Neural Networks
- Interpretable Machine Learning

Professional Experience

Assistant Professor Computer Science   *Milan, Italy*
BOCCONI UNIVERSITY   *2019 - current*
- Research: Deep Learning Applied to Biological Sequence Data, Generative Protein Sequence Models, Interpretable Machine Learning, Loss Landscapes of Neural Networks
- Teaching: Machine Learning I & II, Programming in C, Algorithms, Data Analytics for Risk Assessment
- Supervision: 7 Master Theses, 7 Bachelor Theses

Machine Learning Scientist   *Berlin, Germany*
I2X GMBH   *2017 - 2018*
- R & D: Implementation of Speech Recognition System, Research in related NLP tasks
- Patents: 3 registered
- Other tasks: Candidate Interviews

Postdoctoral Researcher   *Paris, France*
UPMC PARIS, MARTIN WEIGHT'S GROUP   *2016 - 2017*
- Research: Prediction of Pathogenicity of Genomic Mutations

Education

Politecnico di Torino   *Turin, Italy*
PHD PHYSICS AND MARIE-CURIE FELLOW   *2013 - 2016*
- Advisors: Andrea Pagnani & Riccardo Zecchina
- Thesis: The Statistical Mechanics Approach to Protein Sequence Data: Beyond Contact Prediction

Microsoft Research New England   *Boston, USA*
RESEARCH VISIT   *Oct. 2015 - Dec. 2015*
- Host: Jennifer Chayes & Riccardo Zecchina

UPMC Paris   *Paris, France*
RESEARCH VISIT   *Oct. 2014 - Dec. 2014*
- Host: Prof. Martin Weigt

KTH Stockholm   *Stockholm, Sweden*
RESEARCH VISIT   *Oct. 2013 - Dec. 2013*
- Host: Prof. Erik Aurell

Heidelberg University

DIPLOMA IN PHYSICS

Heidelberg, Germany

2008 - 2012

- Advisor: Dieter W. Heermann
- Minor: Biology
- Thesis: The Effect of Flexible Linkers on the Binding Affinity and the Binding Distribution of Zinc Finger Proteins

Publications

Feinauer, C., Meynard, B., Lucibello, C., 2021, Interpretable Pairwise Distillations for Generative Protein Sequence Models
NeurIPS 2021 Workshop on Machine Learning in Structural Biology

Pittorino, F., Lucibello, C., **Feinauer, C.**, Perugini, G., Baldassi, C., Demyanenko, E., Zecchina, R., 2021, Entropic gradient descent algorithms and wide flat minima
International Conference on Learning Representations 2021

Feinauer, C., Carlo L., 2021, Reconstruction of Pairwise Interactions using Energy-Based Models
Mathematical and Scientific Machine Learning 2021 / Proceedings of Machine Learning Research.

Negri, M., Bergamini, D., Baldassi, C., Zecchina, R., **Feinauer, C.**, 2019, Natural representation of composite data with replicated autoencoders.
arXiv preprint arXiv:1909.13327

Schwarz, D., Kollo, M., Bosch, C., **Feinauer, C.**, Whiteley, I., Margrie, T. W., Schaefer, A. T., 2018, Architecture of a mammalian glomerular domain revealed by novel volume electroporation using nanoengineered microelectrodes
Nature communications, 9(1), 1-14.

Cocco, S., **Feinauer, C.**, Figliuzzi, M., Monasson, R., Weigt, M., 2018, Inverse statistical physics of protein sequences: a key issues review
Reports on Progress in Physics, 81(3), 032601.

Feinauer, C., Weigt, M., 2017, Context-aware prediction of pathogenicity of missense mutations involved in human disease
arXiv preprint arXiv:1701.07246.

Couce, A., Caudwell, L. V., **Feinauer, C.**, Hindré, T., Feugeas, J. P., Weigt, M., Tenaillon, O., 2017, Mutator genomes decay, despite sustained fitness gains, in a long-term experiment with bacteria
Proceedings of the National Academy of Sciences, 114(43), E9026-E9035.

Feinauer, C., Szurmant, H., Weigt, M., Pagnani, A., 2016, Inter-protein sequence co-evolution predicts known physical interactions in bacterial ribosomes and the Trp operon
PloS one, 11(2), e0149166.

Feinauer, C., Skwark, M. J., Pagnani, A., Aurell, E., 2014, Improving contact prediction along three dimensions
PLoS Computational Biology, 10(10), e1003847.

Baldassi, C., Zamparo, M., **Feinauer, C.**, Procaccini, A., Zecchina, R., Weigt, M., Pagnani, A., 2014, Fast and accurate multivariate Gaussian modeling of protein families: predicting residue contacts and protein-interaction partners
PloS one, 9(3), e92721.

Feinauer, C., Hofmann, A., Goldt, S., Liu, L., Mate, G., Heermann, D. W., 2013, Zinc finger proteins and the 3D organization of chromosomes
Advances in protein chemistry and structural biology, 90, 67-117.

Patents

Christoph Feinauer, Samuel Brown, Systems and methods for selecting accent and dialect based on context, US10839788B2, Assignee: I2x GmbH

Christoph Feinauer, Samuel Brown, System and methods for accent and dialect modification, US20200193971A1, Assignee: I2x GmbH

Claudio Martay, **Christoph Feinauer**, Michael Brehm, Computing platform and method for modifying voice data, EP3573050B1, Assignee: I2x GmbH

Thesis Supervision

MASTER

2021	**Castellini, D.**, An Analysis of Protein Structure and Mutational Effect Prediction using Self-Attention based Neural Networks
2021	**Hu, J.**, Analysis of COVID-19 spike protein mutations with variational auto-encoders
2021	**Fabbri, C.**, Protein Interaction Partner Prediction as a translation problem using Transformer Neural Networks
2021	**Ferraro, A.**, Empirical analysis of polygonal and quadratic paths between sharp and flat minima of the neural network loss landscape
2020	**Demyanenko, E.**, Continuous distributed representation of biological sequences using covariate information
2020	**Facchetti, M.**, Prediction of the Pathogenicity of Genetic Mutations with Energy-based Models
2020	**Martinelli, D.**, Conditional VAN: modelling families of high-dimensional distributions with autoregressive neural networks

BACHELOR

2021	**Principi, B.**, Mitigation of the impact of label errors in machine learning models for classification tasks through robust ensembling techniques and wide flat minima.
2020	**Ferrari, E.**, Online auctions for consumer goods: a behavioral analysis with machine learning techniques
2020	**Negrisolo, A.**, Protein Fitness Landscape Modelling and the Prediction of Effects of Mutations
2020	**Veludo, M.**, Optimization of an Ensemble of Replicated Deep Neural Networks
2020	**Georgieva, R.**, Bias Discovery and Reduction in Machine Learning for Medical Diagnosis
2019	**Nigro, V.**, Fintech in Financial Inclusion: The Role of Machine Learning in Assessing Credit Risk